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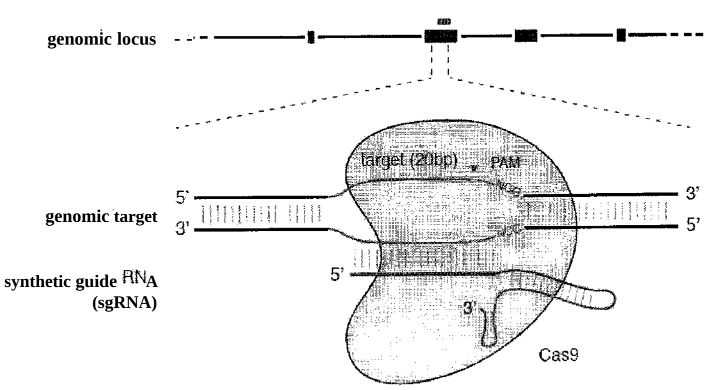

FIG. 1

(57) Abstract: The invention provides for systems, methods, and compositions for altering expression of target gene sequences and related gene products. Provided are structural information on the Cas protein of the CRISPR-Cas system, use of this information in generating modified components of the CRISPR complex, vectors and vector systems which encode one or more components or modified components of a CRISPR complex, as well as methods for the design and use of such vectors and components. Also provided are methods of directing CRISPR complex formation in eukaryotic cells and methods for utilizing the CRISPR-Cas system. In particular the present invention comprehends optimized functional CRISPR-Cas enzyme systems.

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SYSTEMS, METHODS AND COMPOSITIONS FOR SEQUENCE MANIPULATION WITH **OPTIMIZED** FUNCTIONAL **CRISPR-CAS SYSTEMS**

RELATED APPLICATIONS AND INCORPORATION BY REFERENCE

[0001] This application claims priority from: LIS provisional patent applications 61/915,251, filed December 12, 2013; 61/930,214 filed January 22, 2014; 61/939,242 filed February 12, 2014; 61/980,012 filed April 15, 2014; 62/055,484 filed September 25, 2014; 62/087,537, filed December 4, 2014; 61/915,267, filed December 12, 2013; and 61/939,256, filed Feburary 12, 2014.

[0002] The foregoing applications, and all documents cited therein or during their prosecution ("appln cited documents") and all documents cited or referenced in the appln cited documents, and all documents cited or referenced herein ("herein cited documents"), and all documents cited or referenced in herein cited documents, together with any manufacturer's instructions, descriptions, product specifications, and product sheets for any products mentioned herein or in any document incorporated by reference herein, are hereby incorporated herein by reference, and may be employed in the practice of the invention. More specifically, all referenced documents are incorporated by reference to the same extent as if each individual document was specifically and individually indicated to be incorporated by reference.

FIELD OF THE INVENTION

[0003] The present invention generally relates to systems, methods and compositions used for the control of gene expression involving sequence targeting, such as genome perturbation or gene-editing, that may use vector systems related to Clustered Regularly Interspaced Short Palindromic Repeats (CRJSPR) and components thereof. In particular the present invention comprehends optimized functional CRJSPR-Cas enzyme systems.

STATEMENT AS TO FEDERALLY SPONSORED RESEARCH

[0004] This invention was made with government support under NIH Pioneer Award DP1MH100706, awarded by the National Institutes of Health. The government has certain rights in the invention.

[0005] This invention was made with government support under PRESTO (Precursory Research for Embryonic Science and Technology, Sakigake) in the field of "Structural life science and advanced core technologies for innovative life science research", awarded by JST (japan Science and Technology Agency) in 2012. JST has certain rights in the invention.

[0006] This invention was made with government support under the field of "Development of New CRISPR Cas9 System Set and Its Medical Application", awarded by Ministry of Education, Culture, Sports, Science and Technology (MEXT) in 2014. MEXT has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0007] Recent advances in genome sequencing techniques and analysis methods have significantly accelerated the ability to catalog and map genetic factors associated with a diverse range of biological functions and diseases. Precise genome targeting technologies are needed to enable systematic reverse engineering of causal genetic variations by allowing selective perturbation of individual genetic elements, as well as to advance synthetic biology, biotechnological, and medical applications. Although genome-editing techniques such as designer zinc fingers, transcription activator-like effectors (TALEs), or homing meganucleases are available for producing targeted genome perturbations, there remains a need for new genome engineering technologies that are affordable, easy to set up, scalable, and amenable to targeting multiple positions within the eukaryotic genome.

SUMMARY OF THE INVENTION

[0008] There exists a pressing need for alternative and robust systems and techniques for sequence targeting with a wide array of applications. This invention addresses this need and provides related advantages. The CRISPR/Cas or the CRISPR-Cas system (both terms are used interchangeably throughout this application) does not require the generation of customized proteins to target specific sequences but rather a single Cas enzyme can be programmed by a short RNA molecule to recognize a specific DNA target, in other words the Cas enzyme can be recruited to a specific DNA target using said short RNA molecule. Adding the CRISPR-Cas system to the repertoire of genome sequencing techniques and analysis methods may significantly simplify the methodology and accelerate the ability to catalog and map genetic factors associated with a diverse range of biological functions and diseases. To utilize the CRISPR-Cas system effectively for genome editing without deleterious effects, it is critical to understand aspects of engineering and optimization of these genome engineering tools, which are aspects of the claimed invention.

[0009] In an aspect the invention provides a non-naturally occurring or engineered composition comprising a guide RNA (sgRNA) comprising a guide sequence capable of hybridizing to a target sequence in a genomic locus of interest in a cell, wherein at least one loop of the sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins, and wherein the adaptor protein is associated with one or more functional domains. And when there is more than one functional domain, the functional domains can be same or different, e.g., two of the same or two different activators or repressors. in an aspect the invention provides a non-naturally occurring or engineered CRISPR-Cas complex composition comprising the herein-mentioned sgRNA and a CRISPR enzyme. In an aspect the invention provides a herein-mentioned non-naturally occurring or engineered CRISPR-Cas complex composition wherein: the CRISPR enzyme comprises at least one mutation, such that the CRISPR enzyme has no more than 5% of the nuclease activity of the CRISPR enzyme not having the at least one mutation; and/or at least one or more nuclear localization sequences.

[0010] In an aspect the invention provides the herein-mentioned sgRNA or the CRISPR-Cas complex wherein one or more adaptor proteins associated with one or more functional domains is present and bound to the distinct RNA sequence(s) inserted into the at least one loop of the sgRNA.

[0011] In an aspect the invention provides a non-naturally occurring or engineered composition comprising: one or more guide RNA (sgRNA) comprising a guide sequence capable of hybridizing to a target sequence in a genomic locus of interest in a cell, a CRISPR enzyme comprising at least one or more nuclear localization sequences, wherein the CRISPR enzyme comprises at least one mutation, such that the CRISPR enzyme has no more than 5% of the nuclease activity of the CRISPR enzyme not having the at least one mutation, wherein at least one loop of at least one sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins, and wherein the adaptor protein is associated with one or more functional domains.

[0012] In an aspect the invention provides any herein-mentioned composition wherein the CRISPR enzyme has a diminished nuclease activity of at least 97%, or 100% as compared with the CRISPR enzyme not having the at least one mutation. In an aspect the invention provides any aforementioned composition wherein the CRISPR enzyme comprises two or more mutations wherein two or more of D10, E762, H840, N854, N863, or D986 according to SpCas9 protein or any corresponding ortholog or N580 according to SaCas9 protein are mutated, or the CRISPR enzyme comprises at least one mutation wherein at least H840 is mutated. In an aspect the invention provides a herein-mentioned composition wherein the CRISPR enzyme comprises two or more mutations comprising D10A, E762A, H840A, N854A, N863A or D986A according to SpCas9 protein or any corresponding ortholog, or N580A according to SaCas9 protein, or at least one mutation comprising H840A. In an aspect the invention provides any herein-mentioned composition wherein the CRISPR enzyme comprises H840A, or D10A and H840A, or D10A and N863A, according to SpCas9 protein or any corresponding ortholog. In an aspect the invention provides any herein-mentioned composition wherein the CRISPR enzyme comprises: N580A according to SaCas9 protein or any corresponding ortholog; or D10A according to SpCas9 protein, or any corresponding ortholog, and N580A according to SaCas9 protein.

[0013] In an aspect the invention provides any herein-mentioned composition wherein the CRISPR enzyme is associated with one or more functional domains. In an aspect the invention provides any herein-mentioned composition wherein the one or more functional domains associated with the adaptor protein is a heterologous functional domain. In an aspect the invention provides any herein-mentioned composition wherein the one or more functional domains associated with the CRISPR enzyme is a heterologous functional domain.

[0014] In an aspect the invention provides a composition as herein discussed, wherein the adaptor protein is a fusion protein comprising the functional domain, the fusion protein optionally comprising a linker between the adaptor protein and the functional domain, the linker optionally including a GiySer linker.

[0015] In an aspect the invention provides a composition as herein discussed composition of any one of the preceding claims, wherein the at least one loop of the sgRNA is not modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins and wherein, optionally one of the unmodified sgRNA loops is either one of the tetraloop or the stem-loop 2.

[0016] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains associated with the adaptor protein is a transcriptional activation domain.

[0017] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains associated with the CRISPR enzyme is a transcriptional activation domain.

[0018] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains associated with the adaptor protein is a transcriptional activation domain comprising VP64, p65, MyoDl, HSFl, RTA or SET7/9. Other refererences herein to activation (or activator) domains in respect of those associated with the adaptor protein(s) include any known transcriptional activation domain and specifically VP64, p65, MyoDl, HSFl, RTA or SET7/9.

[0019] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains associated with the CRISPR enzyme is a transcriptional activation domain comprises VP64, p65, MyoDl, HSFL, RTA and SET7/9. Other refererences herein to activation (or activator) domains in respect of those associated with the CRISPR enzyme include any known transcriptional activation domain and specifically VP64, p65, MyoD1, HSFl, RTA or SET7/9.

[0020] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains associated with the adaptor protein is a transcriptional repressor domain.

[0021] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains associated with the CRISPR enzyme is a transcriptional repressor domain.

[0022] In an aspect the invention provides a composition as herein discussed wherein the transcriptional repressor domain is a KRAB domain.

[0023] In an aspect the invention provides a composition as herein discussed wherein the transcriptional repressor domain is a NuE domain, NcoR domain, SID domain or a SID4X domain.

[0024] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains associated with the adaptor protein have one or more activities comprising **methylase** activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histoiie modification activity, RNA cleavage activity, DNA cleavage activity, DNA integration activity or nucleic acid binding activity.

[0025] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains associated with the CRISPR enzyme have one or more activities comprising methylase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity, DNA cleavage activity, DNA integration activity, nucleic acid binding activity, or molecular switch activity or chemical inducibility or light inducibility.

[0026] Histone modifying domains are also preferred in some embodiments. Exemplary histone modifying domains are discussed below. Transposase domains, HR (Homologous Recombination) machinery domains, recombinase domains, and/or integrase domains are also preferred as the present functional domains. In some embodiments, DNA integration activity includes HR machinery domains, integrase domains, recombinase domains and/or transposase domains.

[0027] In an aspect the invention provides a composition as herein discussed wherein the DNA cleavage activity is due to a nuclease

[0028] In an aspect the invention provides a composition as herein discussed wherein the nuclease comprises a Fokl nuclease.

[0029] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains is attached to the CRISPR enzyme so that upon binding to the sgRNA and target the functional domain is in a spatial orientation allowing for the functional domain to function in its attributed function.

[0030] In an aspect the invention provides a composition as herein discussed wherein the one or more functional domains is attached to the CRISPR enzyme via a linker, optionally a GlySer linker. In an aspect the invention provides a composition as herein discussed, wherein the sgRNA is modified so that, after sgRNA binds the adaptor protein and further binds to the CRISPR enzyme and target, the functional domain is in a spatial orientation allowing for the functional domain to function in its attributed function.

[0031] In an aspect the invention provides a composition as herein discussed wherein the at least one loop of the sgRNA is tetraloop and/or loop2.

[0032] In an aspect the invention provides a composition as herein discussed wherein the tetraloop and loop 2 of the sgRNA are modified by the insertion of the distinct RNA sequencers).

[0033] In an aspect the invention provides a composition as herein discussed wherein the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins is an aptamer sequence.

[0034] In an aspect the invention provides a composition as herein discussed wherein the aptamer sequence is two or more aptamer sequences specific to the same adaptor protein.

[0035] In an aspect the invention provides a composition as herein discussed wherein the aptamer sequence is two or more aptamer sequences specific to different adaptor proteins.

[0036] In an aspect the invention provides a composition as herein discussed wherein the adaptor protein comprises MS2, PP7, Qβ, F2, GA, fr, JP501, M12, R17, BZ13, JP34, JP500, KU1, M11, MX1, TW18, VK, SP, FI, ID2, NL95, TW19, AP205, φCb5, φCb8r, φCb12r, φCb23r, 7s, PRR1.

[0037] In an aspect the invention provides a composition as herein discussed wherein the cell is a eukaryotic cell, optionally a mammalian cell.

[0038] In an aspect the invention provides a composition as herein discussed wherein the cell is a human cell or a mouse cell.

[0039] In an aspect the invention provides a mammalian cell as herein discussed, e.g., wherein the cell comprises a cell line and is, optionally, a human cell line or a mouse cell line.

[0040] In an aspect the invention provides a transgenic mammalian model, optionally a mouse, e.g., wherein the model has been transformed with a composition as herein discussed or is progeny of said transformant.

[0041] In an aspect the invention provides a method for introducing a genomic locus event comprising the administration of to a host or expression in a host one or more of the compositions as herein discussed.

[0042] In an aspect the invention provides a method as herein discussed, wherein the genomic locus event comprises affecting gene activation, gene inhibition, or cleavage in the locus, or insertion of DNA.

[0043] In an aspect the invention provides a method as herein discussed, comprising the delivery of the composition or nucleic acid molecule(s) coding therefor, wherein said nucleic acid molecule(s) are operatively linked to regulatory sequence(s) and expressed in vivo. Expression in vivo can be via a lentivirus, an adenovirus, or an AAV.

[0044] In an aspect the invention provides a vector comprising: a nucleic acid molecule encoding a guide RNA (sgRNA), comprising a regulatory element operable in a eukaryotic cell including a guide sequence (sgRNA) operably linked to a promoter, the sgRNA being capable of hybridizing to a target sequence in a genomic locus of interest in a cell, wherein at least one loop of the sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins.

[0045] In an aspect the invention provides a vector comprising a regulatory element operable in a eukaryotic cell including a a nucleic acid molecule encoding a CRISPR enzyme operably linked to a promoter, the enzyme comprising at least one or more nuclear localization sequences, wherein the CRISPR enzyme comprises at least one mutation, such that the CRISPR enzyme has no more than 5% of the nuclease activity of the CRISPR enzyme not having the at least one mutation, and wherein the CRISPR enzyme is associated with one or more functional domains.

[0046] In an aspect the invention provides nucleic acid molecule(s) encoding sgRNA or the CRISPR-Cas complex or a composition as herein discussed.

[0047] In an aspect the invention provides a method of screening for gain of function (GOF) or loss of function (LOF) comprising the cell line or cells of the model herein-discussed containing or expressing Cas9 and introducing a composition of claim 1 into cells of the cell line or model, whereby the sgRNA includes either an activator or a repressor, and monitoring for GOF or LOF respectively as to those cells as to which the introduced sgRNA includes an activator or as to those cells as to which the introduced sgRNA includes a repressor.

[0048] In an aspect there is provided a CRISPR Cas complex comprising a CRISPR enzyme and a guide RNA (sgRNA), wherein the CRISPR enzyme comprises at least one mutation, such that the CRISPR enzyme has no more than 5% of the nuclease activity of the CRISPR enzyme not having the at least one mutation and, optional, at least one or more nuclear localization sequences; the guide RNA (sgRNA) comprises a guide sequence capable of hybridizing to a target sequence in a genomic locus of interest in a cell; and wherein: the CRISPR enzyme is associated with two or more functional domains, which may be the same or different, and are preferably different functional domains; or at least one loop of the sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins, and wherein the adaptor protein is associated with two or more functional domains; or the CRISPR enzyme is associated with one or more functional domains and at least one loop of the sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins, and wherein the adaptor protein is associated with one or more functional domains.

[0049] In an aspect the invention provides a herein-discussed composition wherein the CRISPR enzyme includes one or more functional domains. In such a composition there can be more than one sgRNA, and the sgRNAs target different sequences whereby when the composition is employed, there is multiplexing. The composition can include more than one sgRNA modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins. The composition can involve wherein one or more adaptor proteins associated with one or more functional domains is present and bound to the distinct RNA sequencers) inserted into the at least one loop of the sgRNA.

[0050] In one aspect, the invention provides a method for altering or modifying expression of a gene product. The said method may comprise introducing into a cell containing and expressing a DNA molecule encoding the gene product an engineered, non-naturally occurring CRISPR-Cas system comprising a Cas protein and guide RNA that targets the DNA molecule, whereby the guide RNA targets the DNA molecule encoding the gene product and the Cas protein cleaves the DNA molecule encoding the gene product, whereby expression of the gene product is altered; and, wherein the Cas protein and the guide RNA do not naturally occur together. The invention comprehends the guide RNA comprising a guide sequence fused to a tracr sequence. The invention further comprehends the Cas protein being codon optimized for expression in a Eukaryotic cell. In a preferred embodiment the Eukaryotic cell is a mammalian cell and in a more preferred embodiment the mammalian cell is a human cell. In a further embodiment of the invention, the expression of the gene product is decreased.

[0051] In an aspect, in herein-discussed compositions, the target sequencers) can be non-coding or regulator}' (including promoter, especially the proximal promoter) or enhancer or silencer sequence(s).

[0052] In one aspect, the invention provides an engineered, non-naturally occurring CRISPR-Cas system comprising a Cas protein and a guide RNA that targets a DNA molecule encoding a gene product in a cell, whereby the guide RNA targets the DNA molecule encoding the gene product and the Cas protein cleaves the DNA molecule encoding the gene product, whereby expression of the gene product is altered; and, wherein the Cas protein and the guide RNA do not naturally occur together. The invention comprehends the guide RNA comprising a guide sequence fused to a tracr sequence. In an embodiment of the invention the Cas protein is a type II CRISPR-Cas protein and in a preferred embodiment the Cas protein is a Cas9 protein. The invention further comprehends the Cas protein being codon optimized for expression in a Eukaryotic cell. In a preferred embodiment the Eukaryotic cell is a mammalian cell and in a more preferred embodiment the mammalian cell is a human cell. In a further embodiment of the invention, the expression of the gene product is decreased.

[0053] In another aspect, the invention provides an engineered, non-naturally occurring vector system comprising one or more vectors comprising a first regulatory element operably linked to a CRISPR-Cas system guide RNA that targets a DNA molecule encoding a gene product and a second regulatory element operably linked to a Cas protein. Components (a) and (b) may be located on same or different vectors of the system. The guide RNA targets the DNA molecule encoding the gene product in a cell and the Cas protein cleaves the DNA molecule encoding the gene product, whereby expression of the gene product is altered; and, wherein the Cas protein and the guide RNA do not naturally occur together. The invention comprehends the guide RNA comprising a guide sequence fused to a tracr sequence. In an embodiment of the invention the Cas protein is a type II CRISPR-Cas protein and in a preferred embodiment the Cas protein is a Cas9 protein. The invention further comprehends the Cas protein being codon optimized for expression in a Eukaryotic cell. In a preferred embodiment the Eukaryotic cell is a mammalian cell and in a more preferred embodiment the mammalian cell is a human cell. In a further embodiment of the invention, the expression of the gene product is decreased.

[0054] In one aspect, the invention provides a vector system comprising one or more vectors. In some embodiments, the system comprises: (a) a first regulatory element operably linked to a tracr mate sequence and one or more insertion sites for inserting one or more guide sequences upstream of the tracr mate sequence, wherein when expressed, the guide sequence directs sequence-specific binding of a CRISPR complex to a target sequence in a eukaryotic cell, wherein the CRISPR complex comprises a CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence; and (b) a second regulatory element operably linked to an enzyme-coding sequence encoding said CRISPR enzyme comprising a nuclear localization sequence; wherein components (a) and (b) are located on the same or different vectors of the system. In some embodiments, component (a) further comprises the tracr sequence downstream of the tracr mate sequence under the control of the first regulatory element. In some embodiments, component (a) further comprises two or more guide sequences operably linked to the first regulatory element, wherein when expressed, each of the two or more guide sequences direct sequence specific binding of a CRISPR complex to a different target sequence in a eukaryotic cell. in some embodiments, the system comprises the tracr sequence under the control of a third regulatory element, such as a polymerase III promoter. In some embodiments, the tracr sequence exhibits at least 50%, 60%, 70%, 80%, 90%, 95%, or 99% of sequence complementarity along the length of the tracr mate sequence when optimally aligned. Determining optimal alignment is within the purview of one of skill in the art. For example, there are publically and commercially available alignment algorithms and programs such as, but not limited to, ClustalW, Smith-Waterman in matlab, Bowtie, Geneious, Biopython and SeqMan. In some embodiments, the CRISPR complex comprises one or more nuclear localization sequences of sufficient strength to drive accumulation of said CRISPR complex in a detectable amount in the nucleus of a eukaryotic cell. Without wishing to be bound by theory, it is believed that a nuclear localization sequence is not necessary for CRISPR complex activity in eukaryotes, but that including such sequences enhances activity of the system, especially as to targeting nucleic acid molecules in the nucleus. In some embodiments, the CRISPR enzyme is a type II CRISPR system enzyme. In some embodiments, the CRISPR enzyme is a Cas9 enzyme. In some embodiments, the Cas9 enzyme is S. pneumoniae, S. pyogenes, or S. thermophilus Cas9, and may include mutated Cas9 derived from these organisms. The enzyme may be a Cas9 homolog or orthoiog. In some embodiments, the CRISPR enzyme is codon-optimized for expression in a eukaryotic cell. In some embodiments, the CRISPR enzyme directs cleavage of one or two strands at the location of the target sequence. In some embodiments, the first regulatory element is a polymerase III promoter. In some embodiments, the second regulatory element is a polymerase II promoter. In some embodiments, the guide sequence is at least 15, 16, 17, 18, 19, 20, 25 nucleotides, or between 10-30, or between 15-25, or between 15-20 nucleotides in length. In general, and throughout this specification, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. Vectors include, but are not limited to, nucleic acid molecules that are single-stranded, double-stranded, or partially double-stranded; nucleic acid molecules that comprise one or more free ends, no free ends (e.g. circular); nucleic acid molecules that comprise DNA, RNA, or both; and other varieties of polynucleotides known in the art. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments can be inserted, such as by standard molecular cloning techniques. Another type of vector is a viral vector, wherein virally-derived DNA or RNA sequences are present in the vector for packaging into a virus (e.g. retroviruses, replication defective retroviruses, adenoviruses, replication defective adenoviruses, and adeno-associated viruses). Viral vectors also include polynucleotides carried by a virus for transfection into a host cell. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g. bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host ceil upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors." Common expression vectors of utility in recombinant DNA techniques are often in the form of plasmids.

[0055] Recombinant expression vectors can comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory elements, which may be selected on the basis of the host cells to be used for expression, that is operativery-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory element(s) in a manner that allows for expression of the nucleotide sequence (e.g. in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell).

[0056] The term "regulatory element" is intended to include promoters, enhancers, internal ribosomal entry sites (IRES), and other expression control elements (e.g. transcription termination signals, such as polyadenylation signals and poly-U sequences). Such regulatory elements are described, for example, in Goeddei, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). **Regulatory** elements include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulator}' sequences). A tissue-specific promoter may direct expression primarily in a desired tissue of interest, such as muscle, neuron, bone, skin, blood, specific organs (e.g. liver, pancreas), or particular cell types (e.g. lymphocytes). Regulatory elements may also direct expression in a temporal-dependent manner, such as in a cell-cycle dependent or developmental stage-dependent manner, which may or may not also be tissue or cell-type specific. In some embodiments, a vector comprises one or more pol III promoter (e.g. 1, 2, 3, 4, 5, or more pol I promoters), one or more pol II promoters (e.g. 1, 2, 3, 4, 5, or more pol II promoters), one or more pol I promoters (e.g. 1, 2, 3, 4, 5, or more pol I promoters), or combinations thereof. Examples of pol III promoters include, but are not limited to, U6 and H1 promoters. Examples of pol II promoters include, but are not limited to, the retroviral Rous sarcoma vims (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) [see, e.g., Boshart et al, Cell, 41:521-530 (1985)], the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglyceroi kinase (PGK) promoter, and the EFla promoter. Also encompassed by the term "regulatory element" are enhancer elements, such as WPRE; CMV enhancers; the R-U5' segment in LTR of HTLV-I (Mol. Cell. Biol., Vol. 8(1), p. 466-472, 1988); SV40 enhancer; and the intron sequence between exons 2 and 3 of rabbit β-globin (Proc. Natl. Acad. Sci. USA., Vol. 78(3), p. 1527-31, 1981). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression desired, etc. A vector can be introduced into host cells to thereby produce transcripts, proteins, or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., clustered regularly interspersed short palindromic repeats (CRISPR) transcripts, proteins, enzymes, mutant forms thereof, fusion proteins thereof, etc.).

[0057] Advantageous vectors include lentiviruses and adeno-associated viruses, and types of such vectors can also be selected for targeting particular types of cells.

[0058] In one aspect, the invention provides a eukaryotic host cell comprising (a) a first regulatory element operably linked to a tracr mate sequence and one or more insertion sites for inserting one or more guide sequences upstream of the tracr mate sequence, wherein when expressed, the guide sequence directs sequence-specific binding of a CRISPR complex to a target sequence in a eukaryotic cell, wherein the CRISPR complex comprises a CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence; and/or (b) a second regulatory element operably linked to an enzyme-coding sequence encoding said CRISPR enzyme comprising a nuclear localization sequence. In some embodiments, the host cell comprises components (a) and (b). In some embodiments, component (a), component (b), or components (a) and (b) are stably integrated into a genome of the host eukaryotic cell. In some embodiments, component (a) further comprises the tracr sequence downstream of the tracr mate sequence under the control of the first regulatory element. In some embodiments, component (a) further comprises two or more guide sequences operably linked to the first regulatory element, wherein when expressed, each of the two or more guide sequences direct sequence specific binding of a CRISPR complex to a different target sequence in a eukaryotic cell. In some embodiments, the eukaryotic host cell further comprises a third regulatory element, such as a polymerase III promoter, operably linked to said tracr sequence. In some embodiments, the tracr sequence exhibits at least 50%, 60%, 70%>, 80%, 90%, 95%, or 99% of sequence complementarity along the length of the tracr mate sequence when optimally aligned. The enzyme may be a Cas9 homolog or ortholog. In some embodiments, the CRISPR enzyme is codon-optimized for expression in a eukaryotic cell. In some embodiments, the CRISPR enzyme directs cleavage of one or two strands at the location of the target sequence. In some embodiments, the CRISPR enzyme lacks DNA strand cleavage activity. In some embodiments, the first regulatory element is a polymerase III promoter. In some embodiments, the second regulatory element is a polymerase II promoter. In some embodiments, the guide sequence is at least 15, 16, 17, 18, 19, 20, 25 nucleotides, or between 10-30, or between 15-25, or between 15-20 nucleotides in length. In an aspect, the invention provides a non-human eukaryotic organism; preferably a multicellular eukaryotic organism, comprising a eukaryotic host cell according to any of the described embodiments. In other aspects, the invention provides a eukaryotic organism; preferably a multicellular eukaryotic organism, comprising a eukaryotic host cell according to any of the described embodiments. The organism in some embodiments of these aspects may be an animal; for example a mammal. Also, the organism may be an arthropod such as an insect. The organism also may be a plant. Further, the organism may be a fungus.

[0059] In one aspect, the invention provides a kit comprising one or more of the components described herein. In some embodiments, the kit comprises a vector system and instructions for using the kit. In some embodiments, the vector system comprises (a) a first regulatory element operably linked to a tracr mate sequence and one or more insertion sites for inserting one or more guide sequences upstream of the tracr mate sequence, wherein when expressed, the guide sequence directs sequence-specific binding of a CRISPR complex to a target sequence in a eukaryotic cell, wherein the CRISPR complex comprises a CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence; and/or (b) a second regulatory element operably linked to an enzyme-coding sequence encoding said CRISPR enzyme comprising a nuclear localization sequence. In some embodiments, the kit comprises components (a) and (b) located on the same or different vectors of the system. In some embodiments, component (a) further comprises the tracr sequence downstream of the tracr mate sequence under the control of the first regulatory element. In some embodiments, component (a) further comprises two or more guide sequences operably linked to the first regulatory element, wherein when expressed, each of the two or more guide sequences direct sequence specific binding of a CRISPR complex to a different target sequence in a eukaryotic cell. In some embodiments, the system further comprises a third regulatory element, such as a polymerase III promoter, operably linked to said tracr sequence. In some embodiments, the tracr sequence exhibits at least 50%, 60%, 70%, 80%, 90%, 95%, or 99% of sequence complementarity along the length of the tracr mate sequence when optimally aligned. In some embodiments, the CRISPR enzyme comprises one or more nuclear localization sequences of sufficient strength to drive accumulation of said CRISPR enzyme in a detectable amount in the nucleus of a eukaryotic cell. In some embodiments, the CRISPR enzyme is a type II CRISPR system enzyme. In some embodiments, the CRISPR enzyme is a Cas9 enzyme. In some embodiments, the Cas9 enzyme is *S. pneumoniae, S. pyogenes* or *S. thermophilics* Cas9, and may include mutated Cas9 derived from these organisms. The enzyme may be a Cas9 homolog or ortholog. In some embodiments, the CRISPR enzyme is codon-optimized for expression in a eukaryotic cell. In some embodiments, the CRISPR enzyme directs cleavage of one or two strands at the location of the target sequence. In some embodiments, the CRISPR enzyme lacks DNA strand cleavage activity. In some embodiments, the first regulatory element is a polymerase III promoter. In some embodiments, the second regulatory element is a polymerase II promoter. In some embodiments, the guide sequence is at least 15, 16, 17, 18, 19, 20, 25 nucleotides, or between 10-30, or between 15-25, or between 15-20 nucleotides in length.

[0060] In one aspect, the invention provides a method of modifying a target polynucleotide in a eukaryotic cell. In some embodiments, the method comprises allowing a CRISPR complex to bind to the target polynucleotide to effect cleavage of said target polynucleotide thereby modifying the target polynucleotide, wherein the CRISPR complex comprises a CRISPR enzyme compiexed with a guide sequence hybridized to a target sequence within said target polynucleotide, wherein said guide sequence is linked to a tracr mate sequence which in turn hybridizes to a tracr sequence. In some embodiments, said cleavage comprises cleaving one or two strands at the location of the target sequence by said CRISPR enzyme. In some embodiments, said cleavage results in decreased transcription of a target gene. In some embodiments, the method turther comprises repairing said cleaved target polynucleotide by homologous recombination with an exogenous template polynucleotide, wherein said repair results in a mutation comprising an insertion, deletion, or substitution of one or more nucleotides of said target polynucleotide. In some embodiments, said mutation results in one or more amino acid changes in a protein expressed from a gene comprising the target sequence. In some embodiments, the method further comprises delivering one or more vectors to said eukaryotic cell, wherein the one or more vectors drive expression of one or more of: the CRISPR enzyme, the guide sequence linked to the tracr mate sequence, and the tracr sequence. In some embodiments, said vectors are delivered to the eukaryotic cell in a subject. In some embodiments, said modifying takes place in said eukaryotic cell in a cell culture. In some embodiments, the method further comprises isolating said eukaryotic cell from a subject prior to said modifying. In some embodiments, the method further comprises retaining said eukaryotic cell and/or cells derived therefrom to said subject.

[0061] In one aspect, the invention provides a method of modifying expression of a polynucleotide in a eukaryotic cell. In some embodiments, the method comprises allowing a CRISPR complex to bind to the polynucleotide such that said binding results in increased or decreased expression of said polynucleotide; wherein the CRISPR complex comprises a CRISPR enzyme compiexed with a guide sequence hybridized to a target sequence within said polynucleotide, wherein said guide sequence is linked to a tracr mate sequence which in turn hybridizes to a tracr sequence. In some embodiments, the method further comprises delivering one or more vectors to said eukaryotic cells, wherein the one or more vectors drive expression of one or more of: the CRISPR enzyme, the guide sequence linked to the tracr mate sequence, and the tracr sequence.

[0062] In one aspect, the invention provides a method of generating a model eukaryotic cell comprising a mutated disease gene. In some embodiments, a disease gene is any gene associated an increase in the risk of having or developing a disease. In some embodiments, the method comprises (a) introducing one or more vectors into a eukaryotic ceil, wherein the one or more vectors drive expression of one or more of: a CRISPR enzyme, a guide sequence linked to a tracr mate sequence, and a tracr sequence; and (b) allowing a CRISPR complex to bind to a target polynucleotide to effect cleavage of the target polynucleotide within said disease gene, wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence within the target polynucleotide, and (2) the tracr mate sequence that is hybridized to the tracr sequence, thereby generating a model eukaryotic cell comprising a mutated disease gene. In some embodiments, said cleavage comprises cleaving one or two strands at the location of the target sequence by said CRISPR enzyme. In some embodiments, said cleavage results in decreased transcription of a target gene. In some embodiments, the method further comprises repairing said cleaved target polynucleotide by homologous recombination with an exogenous template polynucleotide, wherein said repair results in a mutation comprising an insertion, deletion, or substitution of one or more nucleotides of said target polynucleotide. In some embodiments, said mutation results in one or more amino acid changes in a protein expression from a gene comprising the target sequence.

[0063] In one aspect, the invention provides a method for developing a biologically active agent that modulates a cell signaling event associated with a disease gene. In some embodiments, a disease gene is any gene associated with an increase in the risk of having or developing a disease. In some embodiments, the method comprises (a) contacting a test compound with a model ceil of any one of the described embodiments; and (b) detecting a change in a readout that is indicative of a reduction or an augmentation of a cell signaling event associated with said mutation in said disease gene, thereby developing said biologically active agent that modulates said cell signaling event associated with said disease gene.

[0064] In one aspect, the invention provides a recombinant polynucleotide comprising a guide sequence upstream of a tracr mate sequence, wherein the guide sequence when expressed directs sequence-specific binding of a CRISPR complex to a corresponding target sequence present in a eukaryotic cell. In some embodiments, the target sequence is a viral sequence present in a eukaryotic cell. In some embodiments, the target sequence is a proto-oncogene or an oncogene.

[0065] In one aspect the invention provides for a method of selecting one or more cell(s) by introducing one or more mutations in a gene in the one or more cell (s), the method comprising: introducing one or more vectors into the cell is), wherein the one or more vectors drive expression of one or more of: a CRISPR enzyme, a guide sequence linked to a tracr mate sequence, a tracr sequence, and an editing template; wherein the editing template comprises the one or more mutations that abolish CRISPR enzyme cleavage; allowing homologous recombination of the editing template with the target polynucleotide in the cell(s) to be selected; allowing a CRISPR complex to bind to a target polynucleotide to effect cleavage of the target polynucleotide within said gene, wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence within the target polynucleotide, and (2) the tracr mate sequence that is hybridized to the tracr sequence, wherein binding of the CRISPR complex to the target polynucleotide induces cell death, thereby allowing one or more cell(s) in which one or more mutations have been introduced to be selected. In a preferred embodiment, the CRISPR enzyme is Cas9. In another preferred embodiment of the invention the cell to be selected may be a eukaryotic cell. Aspects of the invention allow for selection of specific cells without requiring a selection marker or a two-step process that may include a counter-selection system.

[0066] In another aspect the invention comprehends a CRISPR-Cas9 (S. pyogenes) system having an X-ray diffraction pattern corresponding to or resulting from any or all of the foregoing and/or a crystal having the structure defined by the co-ordinates of the Crystral Structure Table in Example 8 (the CRISPR~eas9 crystal structure) or as further described in Example 12.

[0067] In a further aspect, the invention involves a computer-assisted method for identifying or designing potential compounds to fit within or bind to CRISPR-Cas9 system or a functional portion thereof or vice versa (a computer-assisted method for identifying or designing potential CRISPR-Cas9 systems or a functional portion thereof for binding to desired compounds) or a computer-assisted method for identifying or designing potential CRISPR-Cas9 systems (e.g., with regard to predicting areas of the CRISPR-Cas9 system to be able to be manipulated—for instance, based on crystral structure data or based on data of Cas9 orthologs, or with respect to where a functional group such as an activator or repressor can be attached to the CRISPR-Cas9 system, or as to Cas9 truncations or as to designing nickases), said method comprising:

using a computer system, e.g., a programmed computer comprising a processor, a data storage system, an input device, and an output device, the steps of:

(a) inputting into the programmed computer through said input device data comprising the three-dimensional co-ordinates of a subset of the atoms from or pertaining to the CRiSPR-Cas9 crystal structure, e.g., in the CRISPR-Cas9 system binding domain or alternatively or additionally in domains that vary based on variance among Cas9 orthologs or as to Cas9s or as to nickases or as to functional groups, optionally with structural information from CRISPR-Cas9 system complexes), thereby generating a data set;

(b) comparing, using said processor, said data set to a computer database of structures stored in said computer data storage system, e.g., structures of compounds that bind or putatively bind or that are desired to bind to a CRISPR-Cas9 system or as to Cas9 orthologs (e.g., as Cas9s or as to domains or regions that vary amongst Cas9 orthologs) or as to the CRISPR-Cas9 crystal structure or as to nickases or as to functional groups;

(c) selecting from said database, using computer methods, structure(s)—e.g., CRISPR-Cas9 structures that may bind to desired structures, desired structures that may bind to certain CRISPR-Cas9 structures, portions of the CRISPR-Cas9 system that may be manipulated, e.g., based on data from other portions of the CRISPR-Cas9 crystral structure and/or from Cas9 orthologs, truncated Cas9s, novel nickases or particular functional groups, or positions for attaching functional groups or fimctionai-group-CRISPR-Cas9 systems;

(d) constructing, using computer methods, a model of the selected structure(s); and

(e) outputting to said output device the selected structure's);

and optionally synthesizing one or more of the selected structure(s);

and further optionally testing said synthesized selected structure(s) as or in a CRISPR-Cas9 system;

or, said method comprising: providing the co-ordinates of at least two atoms of the CRISPR-Cas9 crystal structure, e.g., at least two atoms of the herein Crystral Structure Table of the CRISPR-Cas9 crystal structure or co-ordinates of at least a sub-domain of the CRiSPR~Cas9 crystral structure ("selected co-ordinates"), providing the structure of a candidate comprising a binding molecule or of portions of the CRI8PR-Cas9 system that may be manipulated, e.g..

based on data from other portions of the CRISPR-Cas9 crystal structure and/or from Cas9 orthologs, or the structure of functional groups, and fitting the structure of the candidate to the selected co-ordinates, to thereby obtain product data comprising CRISPR-Cas9 structures that may bind to desired structures, desired structures that may bind to certain CRISPR-Cas9 structures, portions of the CRISPR-Cas9 system that may be manipulated, truncated Cas9s, novel nickases, or particular functional groups, or positions for attaching functional groups or functional-group-CRISPR-Cas9 systems, with output thereof; and optionally synthesizing compound(s) from said product data and further optionally comprising testing said synthesized compound(s) as or in a CRISPR-Cas9 system.

[0068] The testing can comprise analyzing the CRISPR~Cas9 system resulting from said synthesized selected structure(s), e.g., with respect to binding, or performing a desired function.

[0069] The output in the foregoing methods can comprise data transmission, e.g., transmission of information via telecommunication, telephone, video conference, mass communication, e.g., presentation such as a computer presentation (eg POWERPOINT), internet, email, documentary communication such as a computer program (eg WORD) document and the like. Accordingly, the invention also comprehends computer readable media containing: atomic co-ordinate data according to the herein Crystal Structure Table and/or the Figures, said data defining the three dimensional structure of CRISPR-Cas9 or at least one sub-domain thereof, or structure factor data for CRISPR-Cas9, said structure factor data being derivable from the atomic co-ordinate data of herein Crystal Structure Table and/or the Figures. The computer readable media can also contain any data of the foregoing methods. The invention further comprehends methods a computer system for generating or performing rational design as in the foregoing methods containing either: atomic co-ordinate data according to herein Crystal Structure Table and/or the Figures, said data defining the three dimensional structure of CRISPR-Cas9 or at least one sub-domain thereof, or structure factor data for CRISPR-Cas9, said structure factor data being derivable from the atomic co-ordinate data of herein Crystal Structure Table and/or the Figures. The invention further comprehends a method of doing business comprising providing to a user the computer system or the media or the three dimensional structure of CRISPR-Cas9 or at least one sub-domain thereof, or structure factor data for CRISPR-Cas9, said structure set forth in and said structure factor data being derivable from the atomic co-ordinate data of herein

Crystal Structure Table and/or the Figures, or the herein computer media or a herein data transmission.

[0070] A "binding site" or an "active site" comprises or consists essentially of a site (such as an atom, a functional group of an amino acid residue or a plurality of such atoms and'or groups) in a binding cavity or region, which may bind to a compound such as a nucleic acid molecule, which is/are involved in binding.

[0071] By "fitting", is meant determining by automatic, or semi-automatic means, interactions between one or more atoms of a candidate molecule and at least one atom of a structure of the invention, and calculating the extent to which such interactions are stable. Interactions include attraction and repulsion, brought about by charge, steric considerations and the like. Various computer-based methods for fitting are described further

[0072] By "root mean square (or rms) deviation", we mean the square root of the arithmetic mean of the squares of the deviations from the mean.

[0073] By a "computer system", is meant the hardware means, software means and data storage means used to analyze atomic coordinate data. The minimum hardware means of the computer-based systems of the present invention typically comprises a central processing unit (CPU), input means, output means and data storage means. Desirably a display or monitor is provided to visualize structure data. The data storage means may be RAM or means for accessing computer readable media of the invention. Examples of such systems are computer and tablet devices running Unix, Windows or Apple operating systems.

[0074] By "computer readable media", is meant any medium or media, which can be read and accessed directly or indirect!)' by a computer e.g. so that the media is suitable for use in the above-mentioned computer system. Such media include, but are not limited to: magnetic storage media such as floppy discs, hard disc storage medium and magnetic tape; optical storage media such as optical discs or CD-ROM; electrical storage media such as RAM and ROM; thumb drive devices; cloud storage devices and hybrids of these categories such as magnetic/optical storage media.

[0075] In particular embodiments of the invention, the conformational variations in the crystal structures of the CRISPR-Cas9 system or of components of the CRISPR-Cas9 provide important and critical information about the flexibility or movement of protein stracture regions relative to nucleotide (RNA or DNA) structure regions that may be important for CRISPR-Cas system function. The structural information provided for Cas9 (e.g. S. pyogenes Cas9) as the CRISPR enzyme in the present application may be used to further engineer and optimize the CRISPR-Cas system and this may be extrapolated to interrogate structure-function relationships in other CRISPR enzyme systems as well, e.g. other Type II CRISPR enzyme systems.

[0076] The invention comprehends optimized functional CRISPR-Cas enzyme systems, especially in combination with the present modified guides and also where the CRISPR enzyme is also associated with a functional domain. In particular, the CRISPR enzyme comprises one or more mutations that converts it to a DNA binding protein to which functional domains exhibiting a function of interest may be recruited or appended or inserted or attached. In certain embodiments, the CRISPR enzyme comprises one or more mutations which include but are not limited to D10A, E762A, H840A, N854A, N863A or D986A (based on the amino acid position numbering of a S. pyogenes Cas9) and/or the one or more mutations is in a RuvCl or HNH domain of the CRISPR enzyme or is a mutation as otherwise as discussed herein. In some embodiments, the CRISPR enzyme has one or more mutations in a catalytic domain, wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the enzyme further comprises a functional domain. In some embodiments, a mutation at N580 according to SaCas9 protein is preferred. In particular, it is preferred in place of the mutation, in Sa Cas9, corresponding to H840 in Sp Cas9. In some embodiments, in Sa Cas9, mutation at D10 and N580 are preferred. In some embodiments, the N580 mutation may be N580A according to SaCas9 protein. It is believed, without being bound by theory, that this is a more predictable mutation for protein function than the H840A equivalent, which may change binding behaviour.

[0077] The structural information provided herein allows for interrogation of sgRNA (or chimeric RNA) interaction with the target DNA and the CRISPR enzyme (e.g. Cas9) permitting engineering or alteration of sgRNA structure to optimize functionality of the entire CRISPR-Cas system. For example, loops of the sgRNA may be extended, without colliding with the Cas9 protein by the insertion of adaptor proteins that can bind to RNA. These adaptor proteins can further recruit effector proteins or fusions which comprise one or more functional domains.

[0078] In some preferred embodiments, the functional domain is a transcriptional activation domain, preferably VP64. In some embodiments, the functional domain is a transcription repression domain, preferably KRAB. In some embodiments, the transcription repression domain is SID, or concatemers of SID (e.g. SID4X). In some embodiments, the functional domain is an epigenetic modifying domain, such that an epigenetic modifying enzyme is provided. In some embodiments, the functional domain is an activation domain, which may be the P65 activation domain.

[0079] Aspects of the invention encompass a non-naturally occurring or engineered composition that may comprise a guide RNA (sgRNA) comprising a guide sequence capable of hybridizing to a target sequence in a genomic locus of interest in a cell and a CR1SPR enzyme that may comprise at least one or more nuclear localization sequences, wherein the CRISPR enzyme comprises two or more mutations, such that the enzyme has altered or diminished nuclease activity compared with the wild type enzyme, wherein at least one loop of the sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins, and wherein the adaptor protein further recruits one or more heterologous functional domains. In an embodiment of the invention the CRISPR enzyme comprises two or more mutations in a residue selected from the group consisting of D10, E762, H840, N854, N863, or D986. In a further embodiment the CRISPR enzyme comprises two or more mutations selected from the group comprising D1GA, E762A, H840A, N854A, N863A or D986A. As mentioned above, N580, especially N580A, according to SaCas9 protein is used, especially in Sa Cas9. In another embodiment, the functional domain is a transcriptional activation domain, e.g. VP64. In another embodiment, the functional domain is a transcriptional repressor domain, e.g. KRAB domain, SID domain or a SID4X domain. In embodiments of the invention, the one or more heterologous functional domains have one or more activities selected from the group consisting of methylase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity and nucleic acid binding activity. In further embodiments of the invention the cell is a eukaryotic cell or a mammalian cell or a human cell. In further embodiments, the adaptor protein is selected from the group consisting of MS2, PP7, Qp, F2, GA, fr, JP501, M12, R17, BZ13, JP34, JP500, KU1, M1L, MX1, TW18, VK, SP, FI, ID2, NL95, TW19, AP205, ϕCb5, <|>Cb8r, <|>Cbl2r, ϕCb23r, 7s, PRR1. In another embodiment, the at least one loop of the sgRNA is tetraloop and/or loop2. An aspect of the invention encompasses methods of modifying a genomic locus of interest to change gene expression in a cell by introducing into the cell any of the compositions described herein.

[0080] An aspect of the invention is that the above elements are comprised in a single composition or comprised in individual compositions. These compositions may advantageously be applied to a host to elicit a functional effect on the genomic level.

[0081] In general, the sgRNA are modified in a manner that provides specific binding sites (e.g. aptamers) for adapter proteins comprising one or more functional domains (e.g. via fusion protein) to bind to. The modified sgRNA are modified such that once the sgRNA forms a CRISPR complex (i.e. CRISPR enzyme binding to sgRNA and target) the adapter proteins bind and, the functional domain on the adapter protein is positioned in a spatial orientation which is advantageous for the attributed function to be effective. For example, if the functional domain is a transcription activator (e.g. VP64 or p65), the transcription activator is placed in a spatial orientation which allows it to affect the transcription of the target. Likewise, a transcription repressor will be advantageously positioned to affect the transcription of the target and a nuclease (e.g. Fokl) will be advantageously positioned to cleave or partially cleave the target.

[0082] The skilled person will understand that modifications to the sgRNA which allow for binding of the adapter + functional domain but not proper positioning of the adapter + functional domain (e.g. due to steric hindrance within the three dimensial structure of the CRISPR complex) are modifications which are not intended. The one or more modified sgRNA may be modified at the tetra loop, the stem loop 1, stem loop 2, or stem loop 3, as described herein, preferably at either the tetra loop or stem loop 2, and most preferably at both the tetra loop and stem loop 2.

[0083] As explained herein the functional domains may be, for example, one or more domains from the group consisting of methyiase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity, DNA cleavage activity, nucleic acid binding activity, and molecular switches (e.g. light inducible). In some cases it is advantageous that additionally at least one NLS is provided. In some instances, it is advantageous to position the NLS at the N terminus. When more than one functional domain is included, the functional domains may be the same or different.

[0084] The sgRNA may be designed to include multiple binding recognition sites (e.g. aptamers) specific to the same or different adapter protein. The sgRNA may be designed to bind to the promoter region -1000 - + 1 nucleic acids upstream of the transcription start site (i.e. TSS), preferably -200 nucleic acids. This positioning improves functional domains which affect gene activation (e.g. transcription activators) or gene inhibition (e.g. transcription repressors). The modified sgRNA may be one or more modified sgRNAs targeted to one or more target loci (e.g. at least 1 sgRNA, at least 2 sgRNA, at least 5 sgRNA, at least 10 sgRNA, at least 20 sgRNA, at least 30 sg RNA, at least 50 sgRNA) comprised in a composition.

[0085] Further, the CRISPR enzyme with diminished nuclease activity is most effective when the nuclease activity is inactivated (e.g. nuclease maetivation of at least 70%, at least 80%, at least 90%, at least 95%, at least 97%, or 100% as compared with the wild *type* enzyme; or to put in another way, a Cas9 enzyme or CRISPR enzyme having advantageously about 0% of the nuclease activity of the non-mutated or wild type Cas9 enzyme or CRISPR enzyme, or no more than about 3% or about 5% or about 10% of the nuclease activity of the non-mutated or wild type Cas9 enzyme or CRISPR enzyme). This is possible by introducing mutations into the RuvC and HNH nuclease domains of the SpCas9 and orthologs thereof. For example utilizing mutations in a residue selected from the group consisting of D10, E762, H840, N854, N863, or D986 and more preferably introducing one or more of the mutations selected from the group consisting of D10A, E762A, H840A, N854A, N863A or D986A. A preferable pair of mutations is D10A with H840A, more preferable is D10A with N863A of SpCas9 and orthologs thereof. In some embodiments, N580A according to SaCas9 protein, may be used, as discussed herein.

[0086] The inactivated CRISPR enzyme may have associated (e.g. via fusion protein) one or more functional domains, like for example as described herein for the modified sgRNA adaptor proteins, including for example, one or more domains from the group consisting of methylase activity, demethyiase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity, DNA cleavage activity, nucleic acid binding activity, and molecular switches (e.g. light inducible). Preferred domains are Fokl, VP64, P65, HSF1, MyoDL In the event that Fokl is provided, it is advantageous that multiple Fokl functional domains are provided to allow for a functional dimer and that sgRNAs are designed to provide proper spacing for functional use (Fokl) as specifically described in Tsai et al. Nature Biotechnology, Vol. 32, Number 6, June 2014). The adaptor protein may utilize known linkers to attach such functional domains. In some cases it is advantageous that additionally at least one NLS is provided. In some instances, it is advantageous to position the NLS at the N terminus. When more than one functional domain is included, the functional domains may be the same or different.

[0087] In general, the positioning of the one or more functional domain on the inactivated CRISPR enzyme is one which allows for correct spatial orientation for the functional domain to affect the target with the attributed functional effect. For example, if the functional domain is a transcription activator (e.g. VP64 or p65), the transcription activator is placed in a spatial orientation which allows it to affect the transcription of the target. Likewise, a transcription repressor will be advantageously positioned to affect the transcription of the target, and a nuclease (e.g. Fold) will be advantageously positioned to cleave or partially cleave the target. This may include positions other than the N- / C- terminus of the CRISPR enzyme.

[0088] Due to crystal structure experiments, the Applicant has identified that positioning the functional domain in the Reel domain, the Rec2 domain, the HNH domain, or the PI domain of the SpCas9 protein or any ortholog corresponding to these domains is advantageous. Positioning of the functional domains to the Reel domain or the Rec2 domain, of the SpCas9 protein or any ortholog corresponding to these domains, in some instances may be preferred. Positioning of the functional domains to the Reel domain at position 553, Reel domain at 575, the Rec2 domain at any position of 175-306 or replacement thereof, the HNH domain at any position of 715-901 or replacement thereof, or the PI domain at position 1153 of the SpCas9 protein or any ortholog corresponding to these domains, in some instances may be preferred. Fokl functional domain may be attached at the N terminus. When more than one functional domain is included, the functional domains may be the same or different.

[0089] The adaptor protein may be any number of proteins that binds to an aptamer or recognition site introduced into the modified sgRNA and which allows proper positioning of one or more functional domains, once the sgRNA has been incorporated into the CRISPR complex, to affect the target with the attributed function. As explained in detail in this application such may be coat proteins, preferably bacteriophage coat proteins. The functional domains associated with such adaptor proteins (e.g. in the form of fusion protein) may include, for example, one or more domains from the group consisting of methylase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity, DNA cleavage activity, nucleic acid binding activity, and molecular switches (e.g. light inducible). Preferred domains are Fokl, VP64, P65, HSFl, MyoDL In the event that the functional domain is a transcription activator or transcription repressor it is advantageous that additionally at least an NLS is provided and preferably at the N terminus. When more than one functional domain is included, the functional domains may be the same or different. The adaptor protein may utilize known linkers to attach such functional domains.

[0090] Thus, the modified sgRNA, the inactivated CRISPR enzyme (with or without functional domains), and the binding protein with one or more functional domains, may each individually be comprised in a composition and administered to a host individually or collectively. Alternatively, these components may be provided in a single composition for administration to a host. Administration to a host may be performed via viral vectors known to the skilled person or described herein for delivery to a host (e.g. lentivirai vector, adenoviral vector, AAV vector). As explained herein, use of different selection markers (e.g. for lentivirai sgRNA selection) and concentration of sgRNA (e.g. dependent on whether multiple sgRNAs are used) may be advantageous for eliciting an improved effect.

[0091] On the basis of this concept, several variations are appropriate to elicit a genomic locus event, including DNA cleavage, gene activation, or gene deactivation. Using the provided compositions, the person skilled in the art can advantageously and specifically target single or multiple loci with the same or different functional domains to elicit one or more genomic locus events. The compositions may be applied in a wide variety of methods for screening in libraries in cells and functional modeling in vivo (e.g. gene activation of lineRNA and identification of function; gain-of-function modeling; loss-of-function modeling; the use the compositions of the invention to establish cell lines and transgenic animals for optimization and screening purposes).

[0092] The current invention comprehends the use of the compositions of the current invention to establish and utilize conditional or inducible CRISPR transgenic cell /animals. *(See, e.g.,* Piatt et al, Cell (2014), http://dx.doi.Org/10.1016/j.cell.2014.09.014, or PCT patent publications cited herein, such as WO 2014/093622 (PCT/US2013/074667), which are not believed prior to the present invention or application). For example, the target cell comprises CRISPR enzyme (e.g. Cas9) conditionally or inducibly (e.g. in the form of Cre dependent constructs) and/or the adapter protein conditionally or inducibly and, on expression of a vector introduced into the target cell, the vector expresses that which induces or gives rise to the condition of CRISPR enzyme (e.g. Cas9) expression and/or adaptor expression in the target cell. By applying the teaching and compositions of the current invention with the known method of creating a CRISPR complex, inducible genomic events affected by functional domains are also an aspect of the current invention. One more example of this is the creation of a CRISPR knock-in / conditional transgenic animal (e.g. mouse comprising e.g. a Lox-Stop-polyA-Lox(LSL) cassette) and subsequent delivery of one or more compositions providing one or more modified sgRNA (e.g. -200 nucleotides to TSS of a target gene of interest for gene activation purposes) as described herein (e.g. modified sgRNA with one or more aptamers recognized by coat proteins, e.g. MS2), one or more adapter proteins as described herein (MS2 binding protein linked to one or more VP64) and means for inducing the conditional animal (e.g. Cre recombinase for rendering Cas9 expression inducible). Alternatively, the adaptor protein may be provided as a conditional or inducible element with a conditional or inducible CRISPR enzyme to provide an effective model for screening purposes, which advantageously only requires minimal design and administration of specific sgRNAs for a broad number of applications.

[0093] In some embodiments, the CRISPR enzyme is a Cas9 ortholog of a genus belonging to the group consisting of *Corynebacter, Sutterella, Legionella, Treponema, FUifactor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides, Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillum, Gluconacetobacter, Neisseria, Roseburia, Parvibaculum, Staphylococcus, Nitratifractor, Mycoplasma* and *Campylobacter,* wherein the Cas comprises a helical domain 2 truncation.

[0094] In an aspect the invention provides a composition, method or use as herein discussed wherein the helical domain 2 truncation is substituted with one or more sets of flexible glycine-serine (GlyGIyGlySer) or rigid alpha-helical linkers (Ala(GluAlaAlaAlaLys)Ala) in groups of 3, 6, 9, or 12 repeats to replace helical domain 2 for potential structural stabilization and/or aiding of retaining Cas9:sgRNA specificity.

[0095] In an aspect the invention provides a composition, method or use as herein discussed wherein the CRISPR enzyme is a Cas such as an SpCas9 or SaCas9.

[0096] In an aspect the invention provides a non-naturally occurring CRISPR enzyme wherein the HD2 domain has been truncated. The CRISPR enzyme can be a Cas9, e.g., an Sp Cas9 or an Sa Cas9.

[0097] In an aspect the invention provides a CRISPR enzyme wherein the truncation is replacement of the HD2 domain, e.g., wherein the truncation is replacement of the HD2 domain with a linker, such as a flexible linker; for instance, a GlySer linker.

[0098] In an aspect the invention provides a chimeric 3-component CRISPR enzyme comprising N' and C terminal components from a first CRISPR enzyme, and an internal component from a second CRISPR enzyme, the second CRISPR enzyme being an ortholog of the first CRISPR enzyme; for instance, wherein the first and second CRISPR enzymes each comprise a Cas9, such as an Sp Cas9 or an Sa Cas9 or an St Cas9, e.g., St3 Cas9. In some aspects the CRISPR enzyme as discussed herein can comprise an internal component from the first CRISPR enzyme replaced by an internal component from the second CRISPR enzyme, said internal components being the same or different. In an aspect of the invention the second CRISPR enzyme is an Sa CRISPR enzyme or an St CRISPR enzyme or an St3 CRISPR enzyme. The invention envisions a composition, method, system, or use of as herein discussed wherein the CRISPR enzyme is chimeric or truncated as herein discussed.

[0099] Accordingly, it is an object of the invention not to encompass within the invention any previously known product, process of making the product, or method of using the product such that Applicants reserve the right and hereby disclose a disclaimer of any previously known product, process, or method. It is further noted that the invention does not intend to encompass within the scope of the invention any product, process, or making of the product or method of using the product, which does not meet the written description and enablement requirements of the USPTO (35 U.S.C. §112, first paragraph) or the EPO (Article 83 of the EPC), such that Applicants reserve the right and hereby disclose a disclaimer of any previously described product, process of making the product, or method of using the product.

[00100] It is noted that in this disclosure and particularly in the claims and/or paragraphs, terms such as "comprises", "comprised", "comprising" and the like can have the meaning attributed to it in U.S. Patent law; e.g., they can mean "includes", "included", "including", and the like; and that terms such as "consisting essentially of and "consists essentially of have the meaning ascribed to them in U.S. Patent law, e.g., they allow for elements not explicitly recited, but exclude elements that are found in the prior art or that affect a basic or novel characteristic of the invention. Nothing herein is to be construed as a promise.

[OOlOi] These and other embodiments are disclosed or are obvious from and encompassed by, the following Detailed Description.

BRIEF DESCRIPTION OF THE DRAWINGS

[00102] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[00103] Figure 1 shows a schematic model of the CRISPR system. The Cas9 nuclease from Streptococcus pyogenes (yellow) is targeted to genomic DNA by a synthetic guide RNA (sgRNA) consisting of a 20-nt guide sequence (blue) and a scaffold (red). The guide sequence base-pairs with the DNA target (blue), directly upstream of a requisite 5'-NGG protospacer adjacent motif (PAM; magenta), and Cas9 mediates a double-stranded break (DSB) ~3 bp upstream of the PAM (red triangle).

[00104] Figure **2A-F** shows an exemplary CRISPR system, a possible mechanism of action, an example adaptation for expression in eukaryotic cells, and results of tests assessing nuclear localization and CRISPR activity.

[00105] Figure 3A-D shows results of an evaluation of SpCas9 specificity for an example target.

[0Θ106] Figure **4A-G** show an exemplary vector system and results for its use in directing homologous recombination in eukaryotic cells.

[00107] Figure 5 provides a table of protospacer sequences and summarizes modification efficiency results for protospacer targets designed based on exemplar}' *S. pyogenes* and *S. thermophilus* CRISPR systems with corresponding PAMs against loci in human and mouse genomes. Cells were transfected with Cas9 and either pre-crRNA/tracrRNA or chimeric RNA, and analyzed 72 hours after transfection. Percent indeis are calculated based on Surveyor assay results from indicated cell lines (N=3 for all protospacer targets, errors are S.E.M., N.D. indicates not detectable using the Surveyor assay, and N.T. indicates not tested in this study).

[0Θ108] Figure **6A-C** shows a comparison of different tracrRNA transcripts for Cas9-mediated gene targeting.

[00109] Figure 7 shows a schematic of a surveyor nuclease assay for detection of double strand break-induced micro-insertions and -deletions.

[00110] **Figure 8A-B** shows exemplary bicistronic expression vectors for expression of CRISPR system elements in eukaryotic cells.

[00111] Figure 9A-C shows histograms of distances between adjacent *S. pyogenes* SF370 locus 1 PAM (NGG) (Figure 9A) and *S. thermophilics* LMD9 locus 2 PAM (NNAGAAW) (Figure 9B) in the human genome; and distances for each PAM by chromosome (Chr) (Figure 9C).

[00112] Figure **10A-D** shows an exemplary CRISPR system, an example adaptation for expression in eukaryotic cells, and results of tests assessing CRISPR activity.

[00113] Figure **11A-C** shows exemplary manipulations of a CRISPR system for targeting of genomic loci in mammalian cells.

[00114] Figure **12A-B** shows the results of a Northern blot analysis of crRNA processing in mammalian cells.

[00115] Figure **13A-B** shows an exemplary selection of protospacers in the human *PVALB* and mouse *Th* loci.

[00116] Figure 14 shows example protospacer and corresponding PAM sequence targets of the *S. thermophilus* CRISPR system in the human *EMX1* locus.

[00117] Figure 15 provides a table of sequences for primers and probes used for Surveyor, RFLP, genomic sequencing, and Northern blot assays.

[00118] **Figure 16A-C** shows exemplary manipulation of a CRISPR system with chimeric RNAs and results of SURVEYOR assays for system activity in eukaryotic cells.

[00119] Figure **17A-B** shows a graphical representation of the results of SURVEYOR assays for CRISPR system activity in eukaryotic cells.

[00120] Figure 18 shows an exemplary visualization of some *S. pyogenes* Cas9 target sites in the human genome using the UCSC genome browser.

[00121] Figure **19A-D** shows a circular depiction of the phylogenetic analysis revealing five families of Cas9s, including three groups of large Cas9s (-1400 amino acids) and two of small Cas9s (~1100 amino acids).

[00122] Figure 20A-F shows the linear depiction of the phylogenetic analysis revealing five families of Cas9s, including three groups of large Cas9s (-1400 amino acids) and two of small Cas9s (~1 100 amino acids).

[00123] Figure 21A-D shows genome editing via homologous recombination. (a) Schematic of SpCas9 nickase, with D10A mutation in the RuvC I catalytic domain. (b) Schematic representing homologous recombination (HR) at the human ***EMXl*** locus using either sense or antisense single stranded oligonucleotides as repair templates. Red arrow above indicates sgRNA cleavage site; PGR primers for genotyping (Tables J and K) are indicated as arrows in right panel. (c) Sequence of region modified by HR. d, SURVEYOR assay for wildtype (wt) and nickase (D10A) SpCas9-mediated indels at the ***EMXl*** target 1 locus ***(n=3).*** Arrows indicate positions of expected fragment sizes.

[0Θ124] Figure 22A-B shows single vector designs for SpCas9.

[00125] Figures 23A-M provide: a diagram showing the topology of the Cas9 protein. Provided is a ribbon representation and various views of the CRJSPR-cas complex crystal structure (A-I), chimeric RNA architecture from the crystal structure (J-K), an interaction schematic from the crystal structure (L) and a topology schematic from the crystal structure (M).

[00126] Figures 24A-C show, from the crystal structure, a schematic of showing catalytic domains of SpCas9, sites of mutagenesis for new nickases (A), a schematic showing locations of sgRNAs for testing double nicking (B), and results of a Surveyor gel test results showing 1 HNH mutant N854A that retains nickase activity, and 1 HNH mutant that shows nickase activity (N863A), and 2 RuvCIII mutants that show nickase activity (H983A, D986A) (C).

[00127] Figures 25A-B show Surveyor gel test results of SpCas9 truncation mutants from the crystal structure that retain cleavage activity (A) and a table showing the amino acid truncations and flexible (GGGS) or rigid (A(EAAAK)) linker substitutions of the lanes of the gels of Figure 25A (B).

[00128] Figures 26A-B show SpCas9 sgRNAs from the crystal structure including those mutated to investigate contribution to activity of specific bases or groups to basses.

[00129] Figures 27A-C show truncation and creation of chimeric *(S. pyogenes)* Cas9s based on the herein crystal structure, including mutants for mapping essential functional domains (A), chimeras that contain regions from *S. thermophilics* Cas9 (B), and designs for chemically inducible dimerization of SpCas9 (C).

[00130] Figure 28 shows a picture of Cas9 crystals (0.2 mm).

[00131] Figure 29 shows a structural figure of showing Cas9 in a surface representation; red, sgRNA; cyan, the guide region of sgRNA; gold, target DNA.

[00132] **Figure 30A-D** shows the overall structure. (A) Domain organization of *S. pyogenes* Cas9, and schematic of the sgRNA:target DNA complex. (B) Ribbon representation of the Cas9–sgRNA-DNA complex. Disordered linkers are shown as red dotted lines. (C) Surface representation of the Cas9-sgRNA-DNA complex. The active sites of the RuvC **(DiOA)** and HNH (H840A) domains are indicated by dashed yellow circles. (D) Electrostatic surface potential of the Cas9-sgRNA-DNA complex. The HNH domain is omitted for clarity. Molecular graphic images were prepared using CueMol (see website at cuernol.org). Also refer to Figs. 37 and 38.

[00133] Figure 31A-E shows the REC lobe and PI domain. (A) Structure of the REC lobe. The REC2 domain and Bridge helix are colored dark gray and green, respective!)'. The REC! domain is colored gray, with the repeat-interacting and anti-repeat-interacting regions colored pale blue and pink, respectively. The bound sgRNA:DNA is shown as semi-transparent ribbon representation. (B) Schematics indicating positions of SpCas9 truncations in the REC1 and REC2 domains. Bars on the right show indel mutations generated by the truncation mutants, measured by SURVEYOR assay (n = 3, error bars show mean ± S.E.M., N.D., not detectable). (C) Western blot showing expression of tiamcation mutants in HEK 293FT cells. (D) Stnicture of the PI domain. The bound sgRNA is shown as semi-transparent ribbon representation. (E) Schematics showing wild-type SpCas9 and St3Cas9, chimeric Cas9, as well as SpCas9 PI domain truncation constructs. Cas9s are assayed for indel generation at target sites upstream of either NGG (left bar graph) or NGGNG (right bar graph) PAMs (n = 3, error bars show mean ± S.E.M., V P ., not detectable). See also Figs. 39-41.

[00134] Figure 32A-F shows the NUC lobe. Helices are shown as tubes and beta sheets are shown as arrows. (A) Structure of the RuvC domain. The core structure of the RNase H fold core is highlighted in cyan. The active-site residues are shown as stick models. (B) Structure of the *T. thermophilics* RuvC dimer in complex with a Holliday junction (PDB ID 4LD0). The two protomers are colored cyan and gray, respectively. (C) Sequence (top) illustrates Cas9 nicking targets on opposite strands of DNA. Targets 1 and 2 are offset by a distance of 4-bp in between. Heatmap (bottom) shows the ability of each catalytic mutant to induce double- (with either

sgRNA 1 or 2) or single-stranded breaks (only with both sgRNA together). Gray boxes: not assayed. (D) indel formation by Cas9 nickases depends on off-set distance between sgRNA pairs (right panel). Off-set distance is defined as the number of base pairs between the PAM-distal (5′) ends of the guide sequence of a given sgRNA pair (n = 3, error bars show mean ± S.E.M., N.D., not detectable). (E) Structure of the HNH domain. The core structure of the ββα-metal fold is highlighted in magenta. The active-site residues are shown as stick models. (F) Structure of the T4 Endo VII dimer in complex with a Holliday junction (PDB ID 2QNC). The two protomers are colored pink and gray, respectively, with the ββα-metal fold core highlighted in magenta. The bound Mg^{2+} ion is shown as an orange sphere.

[00135] Figure 33A-D shows sgRNA and its target DNA. (A) Schematic of the sgRNA:DNA complex. The guide and repeat regions of the crRNA sequence are colored skyblue and blue, respectively. The tracrRNA sequence is colored red, with the linker region colored violet. The target DNA and tetraloop are colored yellow and black, respectively. The numbering of the 3' tails of tracrRNA is shown on red background. Watson-Crick and non-Watson-Crick base pairs are indicated by black and gray lines, respectively. Disordered nucleotides are boxed by dashed lines. (B) Structure of the sgRNA:DNA complex. (C) Structure of the repeatanti-repeat duplex and three-way junction. Key interactions are shown as gray dashed lines. (D) Effect of sgRNA mutations on ability to induce indels. Base changes from the +83 sgRNA scaffold are shown at respective positions, with dashes indicating unaltered bases (n = 3, error bars show mean ± S.E.M.,/; values based on unpaired Student's t-test, N.D., not detectable). See also Fig. 42.

[00136] **Figure 34A-K** shows Recognition of the sgRNA:DNA. (A) Schematic of sgRNA:DNA recognition by Cas9. Residues that interact with the sgRNA:DNA via their main chain are shown in parentheses. (B and C---K) Recognition of the guide (B), guide:DNA duplex (D), repeat (E), anti-repeat (F), three-way junction (G), stem loop 1 (H) , linker (I) , stem loop 2 (j) and stem loop 3 (K). Hydrogen bonds and salt bridges are shown as dashed lines. (C) Effect of Cas9 (top) and sgRNA (bottom) mutations on ability to induce indels (n = 3, error bars show mean ± S.E.M., *p* values based on unpaired Student's t-test. N.D., not detectable).

[00137] Figure 35A-D shows Structural flexibility of the complex. (A) Structural comparison of Mol A and Mol B. In Mol A (left), disordered linker between the RuvC and HNH domain is indicated by a dotted line. In Mol B (right), the disordered HNH domain is shown as a dashed circle. The flexible connecting segment (a40 and α41) in the RuvC domain is highlighted in

orange. (B) Superimposition of the Cas9 proteins in Mol A and Mol B. The two complexes are superimposed based on the core β-sheet of their RuvC domains. The **HNH** domain and bound sgRNA:DNA are omitted for clarity. (C) Superimposition of the bound sgRNA:DNA in Mol A and Mol B. After superimposition of the two complexes as in (B), the Cas9 proteins are omitted to show the sgRNA:DNA. (D) Molecular surface of Cas9. The HNH domain and bound sgRNArDNA complex are omitted for clarity. Note that there is no direct contact between the REC and NUC lobes, expect for the interactions between the a2-α3 loop and β17-β18 loop.

[00138] Figure 36 shows a Model of RNA-guided *UNA* cleavage by Cas9.

[00139] **Figure** 37 shows Electron density map. The $2mF_O - DF_C$ electron density map around the three-way junction is shown as a gray mesh (contoured at 2.5σ).

[00140] **Figure 38A-C** shows Di-cysteine mutant (C80L/C574E) is functional in HEK 293FT cells. (A) Schematic illustrating positions of cysteine mutations (C80L and C574E) in Cas9. (B) Sequence of the target site used to test the function of the C80L/C574E mutant of Cas9. (C) SURVEYOR nuclease assay showing indeis generated by either the wild-type or C80L/C574E mutant (n = 3).

[00141] Figure 39 shows a schematic drawing of the secondary structural elements of Cas9.

[00142] Figure 40A-B shows the sequence alignment of Cas9 orthologs in families II-A and II-C. The catalytic residues are shown in red triangles. Critical arginine residues on Bridge helix are shown in green triangles. The secondary structure of *S. pyogenes* Cas9 is shown above the sequences. The figure was prepared using TCoffee (Notredame et al., 2000) and ESPript (Gouet et al, 1999). Sp, *S. pyogenes;* Sm, Streptococcus mutatis; St3, *Streptococcus thermophilus* CRISPR-3; St1, *Streptococcus thermophilus* CRISPR-1; Cj, *Campylobacter jejuni;* Mm; *Neisseria meningiditis.*

[00143] Figure 41 shows the sequence alignment of Cas9 orthologs in families II-A, II-B and II-C. 35 Cas9 orthologs from families IIA, IIB and IIC are aligned (BLOSUM62) and clustered (Jukes-Cantor model Neighbor- Joining method, with *S. pyogenes* Cas9 as outgroup). Bars on top show conservation by amino acid. In each line, black bars show residues with at least 75% consensus, and gray bars non-conserved residues.

[00144] Figure 42 shows the comparison of the sgRNA:DNA heteroduplex with a canonical A-form RNA duplex. The sgRNA:DNA heteroduplex are superimposed on an A-form RNA

duplex based on their phosphorus atoms. The A-form RNA duplex is colored dark gray. Nucleotides 51-97 of the sgRNA are omitted for clarity.

[00145] **Figure** 43 shows DNA construct design of the previously studied dCas9 activator design. An activation domain is fused to the C-term of a catalytically inactive dCas via a linker. An NLS is incorporated between Cas9 and VP64.

[00146] Figure 44 shows illustration of insertions of MS2 loops in at the end of the Tetraloop and loop 2 of the sgRNA. An MS2-VP64 fusion protein is recruited to these two loops. Together with dCas9 this leads to a recruitment of the VP64 activation domain to the target DNA of the target locus. Inserted MS2 RNA stem loops are colored dark green.

[00147] Figure 45 shows a graphical representation of the upregulation of Neurog2 expression in Neuro2A cells. 4 different guide RNAs including an Ms2 loop inserted in either the tetraloop or loop 2, both loops or none were tested in combination with dCas9 and MS2-vp64, dCas9-vp64 and MS2-vp64 or dCas9-vp64 alone. TL:MS2, MS2 loop insertion into the sgRNA tetraloop; L2: MS2, MS2 loop insertion into loop 2 of the sgRNA. Colors indicate which protein-coding constructs were co-transfected with the corresponding guide.

[00148] Figure 46 shows Human ASCL1 upregulation with Cas9 - MS2 activators.

[00149] Figure 47 shows Human MYODl upregulation with Cas9 - MS2 activators.

[00150] **Figure** 48 shows an illustration of orthogonal PP7/MS2 gene targeting. In the schematic, sgRNA targeting different loci are modified with distinct RNA loops in order to recruit MS2-VP64 or PP7-SID4X, which activate and repress their target loci, respectively.

[00151] Figure 49 shows the positions of transcriptional domain replacements and insertions in Cas9.The HNH domain is colored pink. The curved arrow indicates the movement of the HNH domain relative to the DNA (yellow) RNA (blue) duplex due to a conformational change. The A in a red circle indicates the first loop (AA G533) used for insertion of a transcriptional effector domain and its position relative to the target DNA. The third loop (K1153) for insertion of a transcriptional effector domain is indicated by a C on a red circle.

[00152] **Figure** 50 shows effects of sgRNA modifications on ASCLI activation. 3' MS2 and modified MS2 1.0 sgRNA architectures were tested for their ability to activate ASCLI.

[00153] Figure 51 shows effects of sgRNA modifications MYODl activation. 3' MS2 and modified MS2 1.0 sgRNA architectures were tested for their ability to activate ASCLI .

[00154] Figure 52 shows effects of dCas9 NLS and N863A modifications on ASCL1 activation.

[00155] **Figure** 53 shows effects of dCas9 NLS and N863A modifications on MYOD1 activation.

[00156] Figure 54 shows a comparison of different NLS and point mutation dCas-VP64 architectures in combination with MS2 fused to individual or combined activation domains. SV40: SV40 NLS; a-imp: a-importin NLS; DV: dCas-SV40 NLS-VP64; Mm: MS2-ASCL1TAD; MP: MS2-p65; MPH; MS2-p65-HSFi; MPm: MS2-p65-ASCLlTAD. All dCas9 proteins contain D10A mutation and H840A (unless indicated otherwise).

[00157] Figure 55 shows a comparison of different NLS and point mutation dCas-VP64 architectures in combination with MS2 fused to individual or combined activation domains. SV40: SV40 NLS; a-imp: a-importin NLS; DV: dCas-SV40 NLS-VP64; Mm: MS2-MyodTAD; MP: MS2-p65; MPH: MS2-p65-HSFl; MPm: MS2-p65-MyodTAD. All dCas9 proteins contain D10A mutation and H840A (unless indicated otherwise).

[00158] Figure 56 shows MS2 double activator fusion proteins for ASCL1 activation. Comparisons of MS2-VP64 and MS2-p65 with and without an additional HSF1 activation domain fusion. The greatest relative improvement occurred for dCas9 without its own activation domain. This improvement is particularly important for the future use of the system in multimodal transcriptional modulation, wherein transcriptional modulation occurs only by way of the sgRNA and its aptamerized proteins, not the dCas9, allowing distinct guide sequences to target distinct functionalities.

[00159] **Figure** 57 shows MS2 double activator fusion proteins for MYOD1 activation.

[00160] Figure 58 shows fold expression levels activated by single sgRNA guide sequences for 12 difficult to modulate genes. All activation shown with MS2-p65~H8Fl / SV40-dCas9-VP64 system. Guide locations are plotted relative to the TSS of each target.

[00161] Figure 59 shows a plot of the fold expression of the best guide sequence against the deltaCt value from qPCR for that gene in control samples for the difficult targets listed above.

[00162] Figure 60 shows multiplexed activation of ten genes.

[00163] Figure 61 shows multiplexed activation of target genes.

[00164] Figure 62 shows targeting of combinations of 2, 4, 6, 8 or 10 genes simultaneously using the optimal single guide as previously determined. All experiments use NLS-dCAS(D10,H840A)-NLS-VP64 in combination with MS2-NLS-P65-HSF1.

[00165] Figure 63 shows multiplexed activation groups of target genes.

[00166] Figure 64A-F shows structure-guided design and optimization of an RNA-guided transcription activation complex. a, The crystal structure of the Cas9-sgRNA-target DNA tertiary complex (PDB ID: 4008) reveals the occlusion of N- and C- terminal fusion sites from the target DNA. The sgRNA tetraloop and stem loop 2 largely do not contact Cas9 amino acid residues in this conformation and can be modified without altering existing Cas9-sgRNA interactions. b, Diagram of three-component transcriptional activation system (SAM): sgRNA2.0, the MS2-p65-HSFl transcription transactivator, and the dCas9-VP64 fusion protein. MS2 stem-loop additions on the sgRNA are highlighted in red. c, Design and optimization of sgRNA scaffolds for optimal recruitment of MS2-VP64 transactivators. d, MS2 stem-loop placement within the sgRNA significantly affects transcription activation efficiency. e, Combinations of different activation domains act in synergy to further enhance the level of transcription activation. f, Addition of the HSF1 transactivation domain to MS2-p65 further increases the efficiency of transcription activation. All values are mean +- SEM with n = 3. * indicate p <0.05 based on Student's t-test.

[00167] Figure 65A-D shows characterization of SAM-mediated gene activation and selection rules for efficient sgRNAs. a, Fold activation of 12 different genes plotted against the location of the sgRNA. Distances are measured in bp relative to the TSS at +1. sgRNALO with dCas9-VP64 (grey), sgRNA2.0 with dCas9-VP64 and MS2-p65-HSFl (blue). Arrows indicate sgRNA target sites with poor transcription activation. All values are mean ± SEM with *n* = 3. b, Comparison of activation efficiency achieved using dCas9-VP64 and a single sgRNA] .0 for the target gene; dCas9-VP64, a single sgRNA2.0 for the same target site as the single sgRNALO, and MS2-p65-HSFl; and dCas9-VP64 and a mixture of 8 sgRNAs targeting the same gene. c, Efficiency of target gene transcription activation as a function of their baseline expression levels. Genes with a higher basal level of transcription exhibit a lower fold up-regulation. For each target gene, the baseline expression level is measured using qPCR in the GFP-transfeeted control cells and expressed as level relative to GAPDH (fold lower expression compared to GAPDH on x-axis). d, Correlation of gene activation efficiency with sgRNA targeting position in the

proximal promoter region expressed as distance to the TSS. Activation efficiencies of each sgRNA for the same target gene is normalized against the highest-activating sgRNA. Proximity to the TSS is positively correlated with target up-regulation. Blue lines indicate median values, boxes indicate 25th and 75th percentiles.

[00168] Figure 66A-B shows SAM activates characterized and uncharacterized lincRNA transcripts. a, Fold activation of 6 lincRNAs plotted against the location of the sgRNA2.0 relative to the TSS. All values are mean +- SEM with n = 3. b, Correlation of sgRNA lincRNA-activation efficiency with sgRNA target distance to the TSS. Activation efficiencies of each sgRNA for the same target lincRNA is normalized against the highest-activating sgRNA. In contrast to coding genes, no significant correlation is observed. Blue lines indicate median values, boxes indicate 25th and 75th percentiles.

[00169] Figure 67A-E shows simultaneous activation of endogenous genes using multiplexed sgRNA2.0 expression. a, Activation of individual genes by single sgRNA2.0s with dCas9-VP64 and MS2-p65-HSFl. b, Simultaneous activation often genes using a mixture of ten sgRNA2.0s each targeting a different gene. c. The relative efficiency of activation of individual sgRNA2.0 varies depending on the target gene and the number of different-gene targeting sgRNA2.0s. d, Effect of sgRNA dilution on gene activation efficiency. Results are plotted as percentage of activation relative to the fold activation of a single undiluted sgRNA2.0 against the target gene. e, Correlation plot between the activation efficiency of a single 10-fold diluted sgRNA2.0 and the activation efficiency of the same sgRNA2.0 delivered within a mixture of ten different-gene targeting sgRNA2.0s. Performance during sgRNA dilution is significantly predictive of performance in multiplexing, suggesting a guide-autonomous component of multiplexing behaviour. All values are mean +- SEM with n = 3.

[00170] Figure 68A-E shows genome-scale lentiviral screen in mammalian cells using SAM. a, Design of three lentiviral vectors for expressing sgRNA2.0, dCas9-VP64, and MS2-p65-HSF1. Each vector contains a distinct selection marker to enable co-selection of cells expressing all three vectors. b, Lentiviral delivery of SAM components was tested by first generating 293FT cell lines stably integrated with dCas9-VP64 and MS2-p65-HSFl, and subsequently transducing these cells with single-gene targeting lentiviral sgRNA2.0s at MOI <0.2. Transcription activation efficiency is measured 4 days post sgRNA2.0s lentivirus transduction and selection with Zeocin or Puromycin. All values are mean +- SEM with n = 3. c, Flow chart of transcription activation

screening using SAM. d. Cumulative frequency of sgRNA2.0s 3 and 21 days after transduction in A375 cells. Shift in the 21-day curve represents the depletion in a subset of sgRNA2.0s. Less than 0.1% of all guides are not detected at day 3 (detected by less than 10 reads). e, Gene categories showing significant depletion based on Ingenuity Pathway Analysis ($p<0.01$ after B-H FDR correction). Categories on the left are based on the 1000 most depleted guides and categories on the right are based on the 1000 genes with the highest depletion based on the average of all 3 guides/gene.

[00171] Figure 69A-F shows genome-scale gene activation screening identifies mediators of BRAF inhibitor resistance. a, Box plot showing the distribution of sgRNA2.0 frequencies at different time points post lentiviral transduction, with and without treatment with PLX-4720. Vehicle is DMSO. Two infection replicates are shown. b, Scatterpiot showing enrichment of specific sgRNA2.0s after PLX-4720 treatment. c, Identification of top candidate genes using the RIGER *P* value analysis (KS method) based on the average of both infection replicates. Genes are organized by positions within chromosomes. d, RIGER *P* values for the top 100 hits from SAM and GeCKO screens, for gene perturbations resulting in BRAF inhibitor resistance. e, The top 10 shared candidates from Puromycin and Zeocin screens, identified using RIGER are shown. For both screens, the percent of unique sgRNA2.0s targeting each gene that are in the top 5% of all enriched sgRNA2.0s is plotted. f. Heat map of z-scores with each column representing a different $\mathrm{BRAF}^{\mathrm{V60o}}$ melanoma short-term culture and rows representing expression of BIMF-inhibitor marker genes and signatures (upper panel), expression of SAM top screen hits (middle panel) and screen signature scores (see methods for signature generation using single-sample Gene Set Enrichment Analysis) (bottom panel). A distinct transcriptional state of genes and signatures represents BRAF-inhibition resistance as previously defined (Konieczkowski, D. J. *et al. Cancer discovery* 4, 816-827, doklQ.l 158/2159-8290.CD-13-0424 (2014)). Columns are sorted by MITF expression with high expression indicating BRAF inhibitor sensitivity. Top hits from the SAM screen are significantly associated with the resistant state (MITF low expression and high levels of resistance markers). A subset of samples were previously tested for PLX sensitivity (blue text/arrows) and resistance (red text/arrows). IC: Information Coefficient (see methods for details). P-vaiues are generated using a permutation test ($n = 10{,}000$).

[00172] Figure 70A-E shows structure-guided engineering of Cas9 sgRNA. a. Schematic of the sgRNA stem-loops showing contacts between each stem-loop and Cas9. Contacting amino acid residues are highlighted in yellow. Tetraloop and stem-loop 2 do not have any contacts with Cas9 whereas stem-loops 1 and 3 share extensive contacts with Cas9. b, sgRNA2.0 with MS2 stem-loops inserted into the tetraloop and stem-loop 2. c, Addition of a second NLS or an alternative HNH domain inactivating point mutation in Cas9 improve efficiency of transcription activation for *MYODl.* d, dCas9-VP64 activators exhibit improved performance by recruitment of MS2-P65 to the tetraloop and stem-loop 2. Addition of an AU flip or extension in the tetraloop does not increased effectiveness of dCas9-mediated transcription activation. e, Tetraloop and stem-loop 2 are amenable to replacement with MS2 stem-loops. Base changes from the sgRNA2.0 scaffold are shown at the respective positions, with dashes indicating unaltered bases and bases below dashes indicating insertions. Deletions are indicated by absence of dashes at respective positions. All figures are $n = 3$ and mean ± SEM.

[00173] Figure 71A-C shows SAM mediates efficient activation of a panel of 12 genes with low levels of non-specific activation. a, Comparison of the activation levels of 12 genes with dCas9-VP64 in combination with MS2-P65, MS2-P65-HSF1, or MS2-P65-MYOD1. MS2-P65-HSF1 mediated significantly higher activation than MS2-P65 alone for 9 out of 12 genes. The best guide out of 8 tested for each gene (see Fig. 2a) was used is used in this experiment. Activation levels for each type of MS2-fusion is presented as a percentage relative to the activation achieved using MS2-P65. b, Non-specific background activation by dCas9~VP64 and MS2-p65-HSFl activator components was determined for all 12 genes. dCas9-VP64 and MS2-p65-HSFl were co-transfected with non-targeting (scrambled) guides. Cells transfected with GFP were used to measure the baseline expression level for each gene. Only activation of IL1R2 by scrambled guides is significantly different from GFP samples. $p < 0.05$ by Student's t-test. c, The average activation for both scrambled guides shown as % of the on-target activation as shown in a. Activation by scrambled guides measures below 1% of on-target activation for ail 12 genes. Error bars indicate SEM. $n = 3$.

[00174] Figure 72 shows activation of characterized and imcharacterized lincRNAs by SAM. Six lincRNAs were targeted using SAM. For each !incRNA, 8 sgRNAs were designed to target the proximal promoter region (+1 to -800bp from the TSS) with 4 different MS2 activators (MS2-P65-HSF1, MS2-P65-MyoDi, MS2-P65, and MS2-VP64) in combination with dCas9-

VP64. MS2 activators with a combination of 2 different domains (M82-p65~HSFl or MS2-p65-MyoDl) consistently provided the highest activation for each lincRNA, $p < 0.01$ for MS2-p65-HSF1 or MS2-p65-MyoDl vs. MS2-p65.

[00175] Figure 73 shows multiplexed activation using SAM. Activation of a panel of 10 genes by combinations of 2, 4, 6, or 8 sgRNAs simultaneously. The mean fold up-regulation is shown on a $\log_{10}$ scale. Error bars indicate S.E.M. and $n = 3$.

[00176] Figure 74A-B shows activation of a panel of 12 genes as a function of the dosage of SAM components. a, Effect of MS2-P65-HSF1 and dCas9-VP64 dilution, at 1:1, 1:4, 1:10, and 1:50 of the original dosage for each component, on the effectiveness of transcription up-regulatkm. The amount of sgRNA expression plasmid is kept constant. b, Effect of diluting all three SAM components (dCas9-VP64, MS2-p65-HSFl, and sgRNA2.0) at 1:4, 1:10, and 1:50 of the original dosage for each component. Fold up-regulation is calculated using GFP-transfected cells as the baseline. Error bars indicate S.E.M. and $n = 3$.

[00177] Figure 75A-B shows components of Cancer survival and proliferation pathways are depleted in a genome-wide SAM screen. IPA analysis on the top 300 depleted genes based on average depletion of all 3 guides/gene resulted in 2 networks with scores >30. Depleted genes are indicated in red. a, network score = 39 with 26 depleted genes in the network. b, network score = 37 with 25 depleted genes in the network. Components on all layers of both networks exhibit depletion.

[00178] Figure 76A-D shows genome-scale lentiviral screen using Puromycin-resistant SAM sgRNA2.0 library. a, Cumulative frequency of sgRNA2.0s 3 and 21 days after transduction of A375 cells with Puromycin-resistant sgRNA2.0 lentivirus. Shift in the 21-day curve represents the depletion of a subset of sgRNA2.0s. b, Box plot showing the distribution of sgRNA2.0 frequencies at different time points post lentiviral transduction with the Puromycin library, after treatment with DMSO vehicle or PLX-4720. Two infection replicates are shown. c, Identification of top candidate genes using the RJGER P value analysis (KS method) based on the average of both infection replicates. Genes are organized by positions within chromosomes. d, Overlap between the top 20 hits from the Zeo and Puro screens. Genes belonging to the same family are indicated by the same color. There is a 50% overlap between the top hits of each screen as shown at the intersection of the Venn diagram.

[00179] Figure 77 shows validation of top screen hits using Cancer Cell Line Encyclopedia expression and pharmacological data from additional melanoma cell lines. Heat map of z-scores, with each column representing a different BRAF^{V600E} melanoma cell lines and rows representing sensitivity to different drugs (upper panel), expression of SAM top screen hits (middle panel), and SAM screen signature scores (bottom panel, see methods for signature generation). Drug sensitivity is measured as 8-Activity Area (AA) (Barretina, J. *et al. Nature* 483, 603-607, doi:10.1038/naturel 1003 (2012)). The melanoma cell lines are sorted by PLX drug sensitivity where a lower value (blue) corresponds to increased sensitivity. Also displayed are the sensitivities to related MAPK inhibitors. There is a fraction of cell lines that demonstrate resistance to MAPK inhibitors and in these cell lines, many of the SAM top hits are highly expressed. The signatures comprised of these top hits also are highly scored within the resistant cell lines. Associations are measured using the information coefficient (IC) between PLX-4720 sensitivity (index) and each of the features and p-values are determined using a permutation test. RAF inhibitors: PLX4720 and RAF265; MEK inhibitors: AZD6244 and PD-0325901.

[00180] Figure 78 shows validation of top screen hits in primary and metastatic melanoma patient samples from The Cancer Genome Atlas. Heat map of z-scores with each column representing a different BRAF$^{\wedge 600}$ patient melanoma (primary or metastatic) and rows representing expression of gene/signature markers for BRAF-inhibitor sensitivity (top panel), expression of SAM top screen hits (middle panel) and screen signature scores (see methods for signature generation) (bottom panel). Because no pharmacological data is available for these TCGA melanoma samples, TCGA gene expression data is first mapped onto a previously defined transcriptional state for BRAF-inhibitor sensitivity/resistance based on a panel of gene markers and signatures (Konieczkowski, D. J. *et al. Cancer discovery* 4, 816-827, doi:10.1158/2159-8290.CD-13-0424 (2014)). The expression of top SAM screen individual hits is increased and significantly associated with tumors displaying a resistant state (defined as low MITF expression and high expression of resistant markers/signatures). Signatures comprised of the top genes from the SAM screens also are significantly associated with the resistant tumors. The panel of melanoma samples is sorted by decreasing MITF expression where a higher value (red) corresponds to samples that are more sensitive to BRAF inhibition. Associations are measured using the information coefficient (IC) between MITF expression (index) and each of the features and p-values are determined using a permutation test.

[00181] Figure 79A-D shows correlation between sgRNA sequence content and level of depletion in significantly depleted genes. Heat maps of sgRNA nucleotide content versus depletion after 2d days. sgRNA targeting significantly depleted genes (from RIGER analysis) in sgRNA-zeo (a, b) or sgRNA-puro (c, d) screens were analyzed for trends with G content (a, c) or T content (b, d) in the sgRNA sequence. sgRNA depletion is positively correlated with G content and negatively correlated with T content. Other bases analyzed (A and C) had significant ($p < 0.0007$) but weak ($r < 0.2$) negative correlation.

[00182] Figure 80A-EE shows exemplary supplementary sequences of Example 20.

[00183] **Figure** 81A-E shows exemplary target guide sequences used in Example 20.

[00184] Figure 82A-I shows top 300 depleted genes for A375 in Example 20. Mean depletion for each gene is given as the log2 ratio of Day 21 vs. Day 3 averaged over all sg RNAs for the gene.

[00185] Figure 83A-C shows top 100 genes from the output of the RIGER algorithm for the sgRNA-Zeo PLX screen comparing PLX (mean of the two replicates at Day 21) to DMSO control (mean of the two replicates at Day 21) in Example 20. The Kolmogorov-Smirnov method was used to score genes.

[00186] Figure 84A-C shows top 100 genes from the output of the RIGER algorithm for the sgRNA-Puro PLX screen comparing PLX (mean of the two replicates at Day 21) to DMSO control (mean of the two replicates at Day 21) in Example 20. The Kolmogorov-Smirnov method was used to score genes.

[00187] **Figure** 85 shows TaqMan qPCR probe ID's used to quantify relative RNA expression levels for each gene (Life Technologies).

[00188] Figure 86: shows testing of chimera between Sp, Sa and St3 Cas9 based on crystal structure. A) domain organization and amino acid (AA) positions of Sp Cas9. The REC lobe is a newly identified structural component of Cas9. B) Chimera maps of partial or complete swaps of the Nuc lobe, with AA positions of chimera boundaries indicated C) indel % achieved with each corresponding chimera on the left. Labels indicate the sgRNA used. TGS = targeting sequences (20bp spacer portion of the sgRNA), BB = sgRNA backbone.

[00189] The figures herein are for illustrative purposes only and are not necessarily drawn to scale.

DETAILED DESCRIPTION OF THE INVENTION

[00190] In particular, Applicants have found that the MS2~binding loop ggccAACATGAGGATCACCCATGTCTGCAGggcc may replace nucleotides +13 to +16 and nucleotides +53 to +56 of the standard sgRNA backbone. The resulting structure is an sgRNA scaffold in which the tetraloop and stemloop 2 sequences have been replaced by an MS2 binding loop. Without being bound by theory, the tetraloop and stemloop 2 were selected for replacement based on information obtained from the Cas9/RNA/DNA crystal structure. Specifically, the tetraloop and stemloop 2 were found to protrude from the Cas9 protein in such a way which suggested that adding an MS2 binding loop would not interfere with any Cas9 residues. Additionally, the proximity of the tetraloop and stemloop 2 sites to the DNA suggested that localization to these locations would result in a high degree of interaction between the DNA and any recruited protein, such as a transcriptional activator.

[00191] In some embodiments, the guide is modified such that nucleotides corresponding to +13 to +16 and/or nucleotides corresponding to +53 to +56 of the standard sgRNA backbone are replaced by the distinct RNA.

[00192] In some embodiments, the adaptor protein is an RNA-binding protein. The RNA-binding protein recognises corresponding distinct RNA sequences, which may be aptamers. For example, the MS2 RNA-binding protein recognises and binds specifically to the MS2 aptamer (or *visa versa).*

[00193] In some embodiments, the repression domain(s) for the guide and/or the CRISPR enzyme may be those show in Example 15 to act as follows:

- SID4X domain, which represses transcriptional activity;
- KRAB domain, which represses transcriptional activity;
- the NUE domain, which increases repressive histone methylation; and
- the NcoR domain, which recruits histone deacetylases leading to repressive histone modifications.

[00194] Exemplary sequences for repressor domains are to be found in Example 15.

[00195] Example 15 also shows an orthogonal approach, see particularly Figure 48. One guide with a first aptamer/RNA-binding protein pair can be linked or fused to an activator, whilst a second guide with a second aptamer/RNA-binding protein pair can be linked or fused to a

repressor. The guides are for different targets (loci), so this allows one gene to be activated and one repressed. For example, the following schematic shows such an approach:

[00196] Guide 1- MS2 aptamer--------MS2 RNA-binding protein--------VP64 activator; and

[00197] Guide 2 - PP7 aptamer--------PP7 RNA-binding protein--------SID4x repressor.

[00198] Figure 48 is an illustration of orthogonal PP7/MS2 gene targeting. In this example, sgRNA targeting different loci are modified with distinct RNA loops in order to recruit MS2-VP64 or PP7-SID4X, which activate and repress their target loci, respectively. PP7 is the RNA-binding coat protein of the bacteriophage Pseudomonas. Like MS2, it binds a specific RNA sequence and secondary structure. The PP7 RNA-recognition motif is distinct from that of MS2. Consequently, PP7 and MS2 can be multiplexed to mediate distinct effects at different genomic loci simultaneously. For example, an sgRNA targeting locus A can be modified with MS2 loops, recruiting MS2-VP64 activators, while another sgRNA targeting locus B can be modified with PP7 loops, recruiting PP7-SID4X repressor domains. In the same cell, dCas9 can thus mediate orthogonal, locus-specific modifications. This principle can be extended to incorporate other orthogonal RNA-binding proteins such as Q-beta.

[00199] The use of two different aptamers (distinct RNA) allows an activator-adaptor protein fusion and a repressor-adaptor protein fusion to be used, with different guides, to activate expression of one gene, whilst repressing another. They, along with their different guides can be administered together, or substantially together, in a multiplexed approach. A large number of such modified guides can be used all at the same time, for example 10 or 20 or 30 and so forth, whilst only one (or at least a minimal number) of Cas9s to be delivered, as a comparatively small number of Cas9s can be used with a large number modified guides. The adaptor protein may be associated (preferably linked or fused to) one or more activators or one or more repressors. For example, the adaptor protein may be associated with a first activator and a second activator. The first and second activators may be the same, but they are preferably different activators. For example, one might be VP64, whilst the other might be p65, although these are just examples and other transcriptional activators are envisaged. Three or more or even four or more activators (or repressors) may be used, but package size may limit the number being higher than 5 different functional domains. Linkers are preferably used, over a direct fusion to the adaptor protein, where two or more functional domains are associated with the adaptor protein. Suitable linkers might include the GlySer linker.

[00200] It is also envisaged that the enzyme-guide complex as a whole may be associated with two or more functional domains. For example, there may be two or more functional domains associated with the enzyme, or there may be two or more functional domains associated with the guide (via one or more adaptor proteins), or there may be one or more functional domains associated with the enzyme and one or more functional domains associated with the guide (via one or more adaptor proteins).

[00201] The fusion between the adaptor protein and the activator or repressor may include a linker. For example, GlySer linkers GGGS can be used. They can be used in repeats of 3 ((GGGGS)$_3$) or 6, 9 or even 12 or more, to provide suitable lengths, as required. Linkers can be used between the RNA-binding protein and the functional domain (activator or repressor), or between the CRISPR Enzyme (Cas9) and the functional domain (activator or repressor). The linkers the user to engineer appropriate amounts of "mechanical flexibility";

[00202] In some embodiments, use of an NLS is envisaged. Applicants found that the NLS from SV40 was helpful in this regard, especially when using lentiviral delivery methods.

[00203] A PP7 variant may be used in some embodiments. For example, Applicants found that the PP7 Pseudomonas bacteriophage coat protein (with amino acids 68-69 mutated to SG and amino acids 70-75 deleted from the wild type protein as described in Wu, Bin, Jeffrey A. Chao, and Robert H. Singer. "Fluorescence fluctuation spectroscopy enables quantitative imaging of single mRNAs in living cells. "*Biophysical journal* 102.12 (2012): 2936-2944. and Chao, Jeffrey A., et al. "Structural basis for the convolution of a viral RNA-protein complex." *Nature structural & molecular biology* 15.1 (2007): 103-105.), worked well. As such, in some embodiments, where the adaptor protein is an RNA-binding protein and that RNA-binding protein is PP7, the PP7 may be the variant described above, i.e. with amino acids 68-69 mutated to SG and/or amino acids 70-75 deleted from the wild type protein.

[00204] Similarly, an MS2 variant may also be used, such as the N55 mutant, especially the N55K mutant. This is the N55K mutant of the MS2 bacteriophage coat protein (shown to have higher binding affinity than wild type MS2 in Lim, F., M. Spingola, and D. S. Peabody. "Altering the RNA binding specificity of a translational repressor." Journal of Biological Chemistry 269.12 (1994): 9006-9010.), and was shown to work in Example 14

[00205] Applicants have shown in Example 13 that both insertions in the tetraloop and loop 2 are effective. In this particular example, the most efficient combination uses an insertion of

aptamers (in this case MS2 loops, but we later show that other aptamers may be used as well) in *both* in the tetraloop and in loop 2 of the sgRNA. We also show that this may be used in combination with a dCas9-vp64 and MS2-vp64 construct, in other words where the CRISPR enzyme is also modified. This new activator design (illustrated in Fig. 44 and shown as red bar for the TL + L2: Ms2 guide in Fig. 45) was found to mediate much higher target gene upregulation compared to the previous design (illustrated in Fig. 43 and shown as the green bar for the regular guide in Fig. 45).

[00206] It is also envisaged that other activators may be used. For instance, Example 14, showed that an improved Cas9 activator architecture consists of a sgRNA with MS2 loop insertions in the tetraloop and loop 2 in combination with either MS2-VP64 and dCas9-P65 or M82-P65 and dCas9-VP64. In other words, 2 different activators can be used, one associated with the CRISPR enzyme (Cas9) and one with the guide via the aptamer. Applicants showed increased effectiveness of this design compared to the standard C-terminai fusion of VP64 to Cas9. Applicants further confirmed the hypothesis that a combination of two different activation domains could improve target gene activation (via synergy, e.g. by recruiting different epigenetic modulators, general transcription factors and co-activators). Applicants also determined that the alternative guide architecture optimized for CRISPR/Cas9 imaging in: Chen, Baohui, et al. "Dynamic imaging of Genomic Loci in Living Human Cells by an Optimized CRISPR/Cas System." Cell 155.7 (2013): 1479-1491 did not exhibit any improvement over the standard architecture.

[00207] Of course, it is envisaged that the activators in these instances may be replaced with repressors.

[00208] Applicants also looked at the arrangement of the distinct RNA sequences (preferably aptamers) within the stem loop 2 and tetraloop of the modified guides of the present invention. Example 14 further looks at the use of GC tracts. These are preferred in some embodiments. The GC tract may be GC or GGGGC or CCCCG or CGCC or compliments thereof or a mixture of C and G from 2 nucleotides up to, for example 10, 15 or 20 nucleotides. In the particular instance, the MS2-binding loop sequence:

ggccAACATGAGGATCACCCATGTCTGCAGggcc

replaced nucleotides +13 to +16 of the standard sgRNA backbone, as above. Of interest here, the sequence CGCC replaced nucleotides +49 to +52 of the standard sgRNA backbone. The sequence GGCG also replaced nucleotides +57 to +60 of the standard sgRNA backbone. The tetraloop MS2-binding loop insertion was designed with the same rationale as described herein. Essentially, CGCC and GGCG sequences replace the stem portion of stemloop 2. The increased base-pairing strength of the CGCC-GGCG stem compared to the original ACTT-AAGT stem was hypothesized to provide additional stability to the stemloop 2 structure, thereby increasing sgRNA performance or longevity.

[00209] Accordingly, in some embodiments, one or more GC tracts may replace stem portion of stemloop 2. In some embodiments, one or more GC tracts may replace stern portion of the tetraloop.

[00210] When reference is made to the stemloop 2 or tetraloop being modified (including replaced) by distinct RNA sequence(s) then this preferably encompasses modification (or replacement) of the 3 or 4 nucleotides of the guide that were found to protrude beyond the enzyme-sgRNA-DNA complex. Suitable numbering will be apparent based on the secondary structure of the guide on its own, i.e. by looking for the loops corresponding to the stem loop 2 and the tetraloop (or by engineering them in), but exemplary number is around +13-36 and/or either side of +49-52 (with one or two nucleotides leeway either side possible, such as +48-52, or +49 to 53 for example).

[00211] A particularly preferred arrangement is to have the aptamer followed by a GGGS linker, preferably (GGGS)3, together with an NLS, preferably that from SV40.

[00212] Applicants, in Example 16, generated a dCas9-based light-inducible MS2-effector, characterized by an MS2-CIB1 recruitment component bound to dCas9-sgRNA, and a CRY2-VP64 transcriptional activator domain. Upon activation with blue light, CRY2-VP64 associate with MS2-CIB1, enabling the recruitment of the transcriptional machinery to the target locus.

[00213] Thus, in some embodiments, the adaptor protein may be fused to (or otherwise associated with) a first inducible element, whilst the functional domain may be fused (or otherwise associated) to a second and complimentary inducible element. The complementarity may be provided by heterodimeric binding partners. A preferred example of first and second complementary inducible elements is the CIB1 and CRY2 system. The CIB1 domain is a heterodimeric binding partner of the light-sensitive Cryptochrome 2 (CRY2).

[00214] In Example 17 Applicants replaced dCas9 Rec2 domain with a transcriptional effector domain; replace dCas9 HNH domain with a transcriptional effector domain; inserted a

transcriptional effector domain at sites of flexible linkers within dCas9 (amino acid 553, 575, or 1153); and created catalytically inactive dCas9 by combination of DIOA and N863A mutations, rather than DIOA and H840A mutations. Any of these are preferred in certain distinct embodiments.

[00215] In some embodiments, Rec2 may be modified, preferably where amino acids 175-306 of dCas9 were replaced with one of the following inserts, with subdomains listed from N- to C-terminus:

- VP64 activation domain
- 3X GGGGS linker, VP64 activation domain, 3X GGGGS linker
- p65 activation domain
- 3X GGGGS linker, p65 activation domain, 3X GGGGS linker

[00216] In some embodiments, HNH may be modified. For example, in Applicants replaced AA775-9Q1 (of the HNH domain). This may be with either an activator, such as vp64 or P65, or a repressor. The activator or repressor may be flanked by a (GGGGS)3 or a (GGGGS)6 linker on both sides of the inserted transcriptional effector domain.

[00217] Insertions of transcriptional domains into 3 loops of dCas9 are also envisaged. In addition to replacing an existing domain (e.g. HNH, Rec2) with a transcriptional effector domain, it may be useful, in some embodiments, to insert a transcriptional effector domain at different positions in the Cas9 protein. Applicants identified three favorable positions: G533, F575 and K1153. The locations of G533 and K1153 in the Cas9 protein is indicated in the corresponding Fig. 49. Applicants insert either vp64 or P65 flanked by a (GGGGS) 1 or a (GGGGS)3 linker on both sides of the inserted transcriptional effector domain at these three locations. As such, in some embodiments, the Cas9 may be modified by insertion of one or more functional domains at any one or more of position corresponding to G533, F575 and Kl 153 according to SpCas9.

[00218] In some embodiments, novel dCas9 mutants are provoided. Catalytically inactive dCas9 may be generated by combination of D10A and N863A mutations, rather than D1OA and H840A mutations, as shown in Example 18. This numbering refers to Sp Cas9, so corresponding positions in orthologs are envisaged. We also provide N580A as a preferred alternative in Sa Cas9, especially in combination with D10.

[00219] As shown in Example 19, N863, especially N863A, referring to Sp Cas9, is also useful in a dead Cas9 and is preferred in some embodiments.

[00220] This Example also showed that a combination of different activator domains had an improved effect. For example the construct with a p65-HSF1 fusion was found to be a more potent activator than the construct with p65 alone (Figs. 56 and 57). Thus, fusions of two or more activators are preferred in some embodiments. Fusions of two or more repressors are also preferred in some embodiments. The activators or repressors may be in any combination of those known in the art and in particular those especially reference herein.

[00221] Of particular note was the use in this Example of an orthogonal system, a combined approach using one activator and one repressor. Different guides and different RNA/adaptor protein pairs allowed for activation at one locus and repression at another locus.

[00222] Applicants observed significant activation for each of a number purportedly difficult gene targets. Additionally, Applicants observed that the success rate of guide sequences typically increased with closer proximity to the transcriptional start site (TSS) of the target gene. In a preferred embodiment of the invention, for particular targets, within 200bp of the TSS is deemed to be an advantageous window to select guide RNAs. This information may also be useful for selection of sgRNA guide sequences.

[00223] Multiplexed activation has also been shown in Example 19. One important possible advantage of the ability of Applicants' system to provide robust activation with a single guide would be the capacity to easily activate a panel of genes simultaneously (by co-delivery to multiple guides for these genes), which would be intractable if a large number of guides would be required for activation of each gene alone. In order to test the ability of Applicants' system (NLS-dCAS(D10,H840A)-NLS-VP64 in combination with MS2-NLS-P65-HSF1) to activate multiple genes simultaneously, Applicants co-transfected guides targeting 2, 4, 6, 8 or 10 genes at once. Activation of multiple genes was highly successful, as even for a combination of 10 genes each gene was activated significantly. (see Figs. 60-63). In some embodiments, therefore, an adaptor protein may advantageously be linked or fused to fused or linked activators, as also discussed above, or repressors. This may then be delivered with multiple guides to different targets. This is therefore especially useful in a screening method where the activation or repression of one or more genes is to be interrogated.

[00224] Example 20 is particularly interesting. This focuses on the identification of two 4nt stretches in the guides that are exposed "outside" of Cas9-guide-target DNA complex. One 4nt stretch falls in the tetraloop, the other 4nt stretch falls in the stem loop 2. These 4nt stretches can be replaced by aptamer sequence. The one or more aptamer(s) is a polynucleotide and may be DNA or RNA, but RNA is preferred. The aptamer has a corresponding RNA-binding protein that recognises a specific RNA sequence.

[00225] Thus, the MS2 system used here comprises an RNA sequence inserted into the guide (at one or both of the above locations) and a corresponding MS2 (RNA-binding) protein. The RNA-binding protein may then be fused to a functional domain such as an activator or a repressor. instead of being fused directly to a functional domain, the RNA-binding protein could be fused to a further element such as an antibody that can then bind to and recognise a functional domain or a molecule fused to a functional domain, similar to the heterduplex CIBl - Cry2 system described above. This may allow for greater temporal or spatial control.

[00226] In short, a specific RNA sequence may be inserted into the exposed guide loop(s) and a corresponding RNA-binding protein may be used, whether that is fused to a functional domain, or a further element which in turn recognises or binds specifically to a functional domain. The functional domain maybe a transacting activator or a repressor.

[00227] This can be used in Screening Methods to assess G.O.F (Gain Of Function) and/or L.O.F. (Loss of Function).

[00228] identification of the stemloop 2 and the tetraloop has been discussed above, but the skilled person may also want to refer to Figures 44, 48, 64 (especially a and b) and 70 for guidance. Figure 70 shows nucleotide numbering corresponding to the stem loop 2 and the tetraloop. For example, in some embodiments, the tetraloop is or includes nucleotides G29 to A41 of the guide tested and comprises 5'-GCUAGAAUAGCA-3 ' (positions 29-41). Guide nucleotides, such as C40, may preferably interact with Cas9 amino acid Arg340. In some embodiments, stem loop 2 may be or include nucleotides A68 to G81 of the guide used (5'-AACUUGAAAAAGUG-3 '). Enzyme amino acids His1349 and Serl351 may, in some embodiments, interact with guide nucleotides, such as A68. In some embodiments, Lys33 and Tyr1356 may interact with nucleotide G81.

[00229] In some embodiments, it is preferable to use complimentary GGCC inserts (GC tracts) flanking the MS insert (the 5'-GGCC-3' being complimentary to the same sequence at the 3' end (and in the opposite orientation i.e. 3'CCGG-5', as shown Fig 70).

[00230] Although single MS2 addition (i.e. to one or other of the tetraloop or stem loop 2) shows an improvement in terms of Gain of Function (gene upregulation) compared to a standard guide, the double addition (MS2 on both loops) shows even stronger upregulation. The use of two or more functional domains with the guide is therefore preferred.

[00231] As mentioned herein, having one activator, such as VP64, bound to Cas9 and a separate similar activator, again VP64 in this example, bound to the guide via MS2 shows the greatest improvement in terms of Gain of Function (gene upregulation). Other activators or repressors may be exchanged here for the activator mentioned.

[00232] We also show in this Example an improvement in terms of Gain of Function (gene upregulation) compared to a prior art MS-guide RNA arrangement where the MS2 is attached at the 3' end of the guide. This art approach is as opposed to the present loops which are both internal and certainly not 3' terminal or are at least followed (in the 3' direction) by an additional loop (stem loop 3).

[00233] LincRNAs (a non-coding RNA produced from bi-directional promoters - the other direction being RNA corresponding to the gene of interest) may also be targeted via the guides and/or interrogated.

[00234] This Example also shows that lentivirus based delivery is useful. Overall, the system showed enhanced transcriptional activation. It is thus useful in a genome-wide transcriptional activation or overexpression screening methods. For example, the invention may be used to identify genes whose upregulation causes a certain phenotypic result - in this example, it was resistance to BRAF kinase inhibitor in cancer cells.

[00235] Applicants, without being bound by theory, believe that guide direction does not significantly affect activation activity, instead the primary factor influencing activation potency is that the sgRNA site is located within the -200 to +1 bp proximal promoter region. This region is therefore a preferred target for the guide(s).

[00236] The adaptor protein (and hence its corresponding distinct RNA (preferably an aptamer) is preferably chosen from within bacteriophage coat proteins. Preferred examples include those already listed elsewhere herein.

[00237] Example 21 shows that an inducible structural design activation mediator transgenic model, in this case a mouse, may be established. A repression model may be similarity generated. Preferably, a mouse engineered with the Lox-Stop-poiyA-Lox(LSL) cassette upstream to the coding region of the SpCas9 - VP64 fusion protein is established. A second mouse may be engineered with the Lox-Stop-polyA-Lox(LSL) cassette upstream to the coding region of the SpCas9 - VP64 fusion protein and upstream to the coding region of the M82-P65-HSF1 fusion protein.

[00238] Example 22 investigates targeted lincRNAs of unknown function to determine aberrant phenotypes. It includes an investigation of Gain of Function and Loss of function in human cell lines (using Cre mducibiiity) and mice through use of guides that target the regulatory regions of these genes, with guides including an activator or a repressor.

[00239] When looking at lincRNAs, guides may be designed to target the promoter region. Ideally, this should be within 1000 nucleotides upstream of the TTS of the target, in this case, lincRNAs of unknown function. Animals, such as mice, may then be screened for aberrant phenotypes.

[00240] Cells for which the sgRNA has an activator may be monitored for Gain of Function, whilst cells for which the sgRNA has a repressor may be monitored for Loss of Function. In this fashion, mammalian, including mouse and human cells, can be screened.

[00241] In an aspect, the vector systems used in the methods of the invention comprise one or more lentiviral vector(s). In a preferred embodiment, the one or more lentiviral vectors may comprise a codon optimized nuclear localization signal (NLS), a codon optimized P2A bicistronic linker sequence and an optimally placed U6 driven guide RNA cassette. In another aspect the vector system comprises two lentiviral vectors, wherein one lentiviral vector comprises the Cas9 enzyme and the other lentiviral vector comprises the guide RNA selected from the libraries of the invention. In an embodiment of the invention, each vector has a different selection marker, e.g. a different antibiotic resistance marker. The invention also comprehends kits comprising the libraries of the invention. In certain aspects, the kit comprises a single container comprising vectors comprising the library of the invention. In other aspects, the kit comprises a single container comprising plasmids comprising the library of the invention. The invention also comprehends kits comprising a panel comprising a selection of unique CRISPR-Cas system guide sequences from the library of the invention, wherein the selection is indicative

of a particular physiological condition. In preferred embodiments, the targeting is of about 100 or more sequences, about 1000 or more sequences or about 20,000 or more sequences or the entire genome. In other embodiments a panel of target sequences is focused on a relevant or desirable pathway, such as an immune pathway or cell division.

[00242] Accordingly, Examples 21 and 22 show that creation of a non-human animal or cell may be realistically provided. It has preferably been altered, or is a progeny of said altered animal or cell, to constitutively or conditionally express a Cas9 with one or more mutations to modify catalytic activity, as discussed herein. The model may be used for screening with appropriate guides and with different adaptors and activators or repressors as discussed herein for multiplexing to show up and/or down-regulation of target gene function. Thus, corresponding cell lines and transgenic mammalian models are provided. Further guidance on models and cell lines is provided herein.

[00243] The exposed or extraneous portion of the guide (when the guide-Cas9-DNA complex is formed) is preferably a 4 (four) nucleotide stretch. In some embodiments, the stretch may be in the tetraloop. In some embodiments, the stretch may be in the stem loop 2. In some embodiments, stretches in both the tetraloop and the stem loop 2 are envisaged.

[00244] This stretch may be modified, altered or entirely replaced. It is not generally preferred to reduce the number of nucleotides in the exposed stretch to less than 4 for stearic reasons as this could affect the secondary structure of the rest of the guide and thus affect formation of the Cas9-guide-DNA complex or the exposure of the stretch.

[00245] It may be modified or altered in that all four of the original 4 nucleotides in the stretch are retained and additions (or further nucleotides) are made between 1 and 2, 2 and 3, or 3 and 4. It is also envisaged that additions may be made immediately 5' to 1 or 3' immediately to 4. The stern may be flexible, but it is preferred that it is largely self-complementary throughout.

[00246] Unafold is a software tool that can be used to help predict RNA secondary structure in the guide and so assist the skilled person in determine what changes to the guide RNA may be acceptable within the framework discussed herein.

[00247] Ideally, the loop feature should be retained but protein binding section of the distinct RNA added to the guide will determine this. The non-loop ends abutting the edge of the enzyme should ideally be retained in the sense that they need to be present, but the primary sequence of the original guide can be changed, for example by insertion of one or more GC tract(s). Ideally,

this should be done at the non-loop (non-protein-binding end) of the distinct RNA added, which may be extended. The secondary structure of the non-protein-binding region of the distinct RNA should preferably form a stem, as mentioned.

[00248] It is preferred to avoid bulges or loops in the exposed section (non-protein-binding section of the distinct RNA, i.e. that between the edge of the enzyme complex and the protein binding domain of the distinct RNAAptamer). Rather, it is preferred to retain a stem as secondary structure in the exposed section.

[00249] A stem may be formed in the RNA through use of complimentary sections of roughly the same length, with mismatches minimized. The maximum length of the stem (or number of nucleotides forming the stem in both the 5' to 3' and 3'to 5' strands) is preferably 100 nucleotides or so in total (i.e. 2 sections of approx. 50 nucleotides) to reduce stearic effects and reduce possible formation of additional secondary or tertiary structure in the nucleotides. However, 50-60 nucleotides may be a more preferable maximum, but given the general need to keep package size down, 10 to 20 or 30 is most preferable, whilst, 8, 10 or 12 is most preferred.

[00250] A preferred minimum length is 4 nucleotides either side of the protein-binding loop.

[00251] Also provided are methods of upregulation of gene expression in a target locus comprising administration of the present modified guides directed to the target, where the adaptor protein is associated with an activator. The CRiSPR enzyme may also be modified with a functional domain.

[00252] Also provided are methods of downregulation of gene expression in a target locus comprising administration of the present modified guides directed to the target, where the adaptor protein is associated with a repressor. The CRISPR enzyme may also be modified with a functional domain.

[00253] Such methods may be used in a method of treating a subject in need thereof, for example a subject requiring gene upregulation or gene downregulation, as appropriate. A multiplex method may also be used where one gene is upreguiated and another is down regulated for instance by following the orthogonal approach discussed herein.

[00254] Also provided is the present compositions and systems for use in such methods of treatment. Use of the present compositions and systems in the manufacture of a medicament for such treatment is also provided.

[00255] In relation to the guides in general, but specifically in respect of the present modified sgRNA and the complex formed therewith, it is preferable that the guide has one or more of the following features. In some embodiments, the tracr sequence has one or more hairpins and is 30 or more nucleotides in length, more preferably 40 or more nucleotides in length, or more preferably 50 or more nucleotides in length. In some embodiments, the guide sequence is between 10 to 30 nucleotides in length. In some embodiments, the CRISPR/Cas enzyme is a Type II Cas9 enzyme. In some embodiments, the tracr sequence has one or more hairpins and is 30 or more nucleotides in length, more preferably 40 or more nucleotides in length, or more preferably 50 or more nucleotides in length, the guide sequence is between 10 to 30 nucleotides in length and the CRISPR/Cas *enzyme* is a Type II Cas9 enzyme.

[00256] Endogenous transcriptional repression is often mediated by chromatin modifying enzymes such as histone methyltransferases (HMTs) and deacetylases (HDACs). Repressive histone effector domains are known and an exemplary list is provided below. In the exemplary table, preference was given to proteins and functional truncations of small size to facilitate efficient viral packaging (for instance via AAV). In general, however, the domains may include HDACs, histone methyltransferases (HMTs), and histone acetyltransferase (HAT) inhibitors, as well as HDAC and HMT recruiting proteins. The functional domain may be or include, in some embodiments, HDAC Effector Domains, HDAC Recruiter Effector Domains, Histone Methyltransferase (HMT) Effector Domains, Histone Methyltransferase (HMT) Recruiter Effector Domains, or Histone Acetyltransferase Inhibitor Effector Domains.

[00257] HDAC Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
HDAC I	**HDAC8**	-	-	*X. laevis*	325	1-325	325	1-272: HDAC
HDAC I	**RPD3**	-	-	*S. cerevisiae*	433	19-340	322 (Vannier)	19-331: HDAC
HDAC IV	**MesoLo4**	-	-	*M. loti*	300	1-300 (Gregoretti)	300	-
HDAC IV	**HDAC11**	-	-	*H. sapiens*	347	1-347 (Gao)	347	14-326: HDAC
HD2	**HDT1**	-	-	*A. thaliana*	245	1-211 (Wu)	211	-
SIRT I	**SIRT3**	H3K9Ac H4K16Ac H3K56Ac	-	*H. sapiens*	399	143-399 (Scher)	257	126-382: SIRT
SIRT I	**HST2**	-	-	*C. albicans*	331	1-331 (Hnisz)	331	-

SIRT T	CobB	-	-	*E. coii (K12)*	242	1-242 (Landry)	242	-
SIRT I	HST2	-	-	*$. cerevisiae*	357	8-298 (Wilson)	291	-
SIRT III	SIRT5	H4K8Ac H4K16AC	-	*H. sapiens*	310	37-310 (Gertz)	274	41-309: SIRT
SIRT III	Sir2A	-	-	*P. falciparum*	273	1-273 (Zhu)	273	19-273: SIRT
SIRT IV	**SIRT6**	H3K9Ac H3K56Ac	-	*H. sapiens*	355	3-289 (Tennen)	289	35-274: SIRT

[00258] Accordingly, the repressor domains of the present invention may be selected from histone methyltransferases (HMTs), histone deacetylases (HDACs), histone acetyltransferase (HAT) inhibitors, as well as HDAC and HMT recruiting proteins.

[00259] The HDAC domain may be any of those in the table above, namely: HDAC8, RPD3, MesoLo4, HDACl l, HDTl, SIRT3, HST2, CobB, HST2, SIRT5, Sir2A, or SIRT6.

[00260] In some embodiment, the functional domain may be a HDAC Recniiter Effector Domain. Preferred examples include those in the Table below, namely MeCP2, MBD2b, Sin3a, NcoR, SALLl , RCOR1. NcoR is exemplified in the present Examples and, although preferred, it is envisaged that others in the class will also be useful.

[00261] Table of HDAC Recruiter Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
Sin3a	**MeCP2**	-	-	*R. norvegicus*	492	207-492 (Nan)	286	-
Sin3a	**MBD2b**	-	-	*H. sapiens*	262	45-262 (Boeke)	218	-
Sin3a	**Sin3a**	-	-	*H. sapiens*	1273	524-851 (Laherty)	328	627-829: HDAC1 interaction
NcoR	**NcoR**	-	-	*H. sapiens*	2440	420-488 (Zhang)	69	-
NuRD	**SALL1**	-	-	*M. musculus*	1322	1-93 (Lauberth)	93	-
CoREST	**RCOR1**	-	-	*H. sapiens*	482	81-300 (Gu, Ouyang)	220	-

[00262] In some embodiment, the functional domain may be a Methy!transferase (HMT) Effector Domain. Preferred examples include those in the Table below, namely NUE, vSET, EHMT2/G9A, SUV39H1, dim-5, KYP, SUVR4, SET4, SET1, SETD8, and TgSETS. NUE is

exemplified in the present Examples and, although preferred, it is envisaged that others in the class will also he useful.

[00263] Table of Histone Methyltransferase (HMT) Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
SET	**NUE**	H2B, H3, H4	-	*C. trachomatis*	219	1-219 (Pennini)	219	-
SET	**vSET**	-	H3K27me3	*P. bursaria chlorella virus*	119	1-119 (Mujtaba)	119	4-112: SET2
SUV39 family	**EHMT2/G9A**	H1.4K2, H3K9, H3K27	H3K9me1/2, H1K25me1	*M. musculus*	1263	969-1263 (Tachibana)	295	1025-1233: preSET, SET, postSET
SUV39	**SUV39H1**	-	H3K9me2/3	*H. sapiens*	412	79-412 (Snowden)	334	172-412: preSET, SET, postSET
Suvar3-9	**dim-5**	-	H3K9me3	*N. crassa*	331	1-331 (Rathert)	331	77-331: preSET, SET, postSET
Suvar3-9 (SUVH subfamily)	**KYP**	-	H3K9me1/2	*A. thaliana*	624	335-601	267 (Jackson)	-
Suvar3-9 (SUVR subfamily)	**SUVR4**	H3K9me1	H3K9me2/3	*A. thaliana*	492	180-492	313 (Thorstensen)	192-462: preSET, SET, postSET
Suvar4-20	**SET4**	-	H4K20me3	*C. elegans*	288	1-288 (Vielle)	288	-
SET8	**SET1**	-	H4K20me1	*C. elegans*	242	1-242 (Vielle)	242	-
SET8	**SETD8**	-	H4K20me1	*H. sapiens*	393	185-393	209 (Couture)	256-382: SET
SET8	**TgSET8**	-	H4K20me1/2/3	*T. gondii*	1893	1590-1893 (Sautel)	304	1749-1884: SET

[00264] In some embodiment, the functional domain may be a Histone Methyitransferase (HMT) Recruiter Effector Domain. Preferred examples include those in the Table below, namely Hp la, PHF19, and NIPPl.

[00265] Table of Histone Methyitransferase (HMT) Recruiter Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
-	**Hp1a**	-	H3K9me3	*M. musculus*	191	73-191	119 (Hathaway)	121-179: chromoshadow
-	**PHF19**	-	H3K27me3	*H. sapiens*	580	(1-250) + GGSG linker + (500-580)	335 (Ballaré)	163-250: PHD2
-	**NIPP1**	-	H3K27me3	*H. sapiens*	351	1-329 (Jin)	329	310-329: EED

[00266] In some embodiment, the functional domain may be Histone Acety!transferase Inhibitor Effector Domain. Preferred examples include SET/TAP- 1β listed in the Table below.

[00267] Table of Histone Acetyltransferase Inhibitor Effector Domains

Subtype/ Complex	Name	Substrate (if known)	Modification (if known)	Organism	Full size (aa)	Selected truncation (aa)	Final size (aa)	Catalytic domain
-	**SET/TAF-1β**	-	-	*M. musculus*	289	1-289 (Cervoni)	289	-

[00268] It is also preferred to target endogenous (regulatory) control elements (such as enhancers and silencers) in addition to a promoter or promoter-proximal elements. Thus, the invention can also be used to target endogenous control elements (including enhancers and silencers) in addition to targeting of the promoter. These control elements can be located upstream and downstream of the transcriptional start site (TSS), starting from 200bp from the TSS to 100kb away. Targeting of known control elements can be used to activate or repress the gene of interest. In some cases, a single control element can influence the transcription of multiple target genes. Targeting of a single control element could therefore be used to control the transcription of multiple genes simultaneously.

[00269] Targeting of putative control elements on the other hand (e.g. by tiling the region of the putative control element as well as 200bp up to 1OOkB around the element) can be used as a means to verify such elements (by measuring the transcription of the gene of interest) or to detect novel control elements (e.g. by tiling lOOkb upstream and downstream of the TSS of the gene of interest). In addition, targeting of putative control elements can be useful in the context of

understanding genetic causes of disease. Many mutations and common SNP variants associated with disease phenotypes are located outside coding regions. Targeting of such regions with either the activation or repression systems described herein can be followed by readout of transcription of either a) a set of putative targets (e.g. a set of genes located in closest proximity to the control element) or b) whole-transcriptome readout by e.g. RNAseq or microarray. This would allow for the identification of likely candidate genes involved in the disease phenotype. Such candidate genes could be useful as novel drug targets.

[00270] The term "associated with" is used here in respect of how one molecule 'associates' with respect to another, for example between an adaptor protein and a functional domain, or between the CRISPR enzyme and a functional domain. In the case of such protein-protein interactions, this association may be viewed in terms of recognition in the way an antibody recognises an epitope. Alternatively, one protein may be associated with another protein via a fusion of the two, for instance one subunit being fused to another subunit. Fusion typically occurs by addition of the amino acid sequence of one to that of the other, for instance via splicing together of the nucleotide sequences that encode each protein or subunit. Alternatively, this may essentially be viewed as binding between two molecules or direct linkage, such as a fusion protein. In any event, the fusion protein may include a linker between the two subunits of interest (i.e. between the enzyme and the functional domain or between the adaptor protein and the functional domain). Thus, in some embodiments, the CRISPR enzyme or adaptor protein is associated with a functional domain by binding thereto. In other embodiments, the CRISPR enzyme or adaptor protein is associated with a flmctional domain because the two are fused together, optionally via an intermediate linker.

[00271] RNA sequences that bind to protein sequences are known, in particular aptamers, but the way in which they bind to, for example, an adaptor protein is that the RNA sequence recognises and forms a complex with a corresponding RNA-binding domain or portion on the protein. This is an analogous situation to the manner in which an antibody recognises an epitope. Thus, in some embodiments, the distinct RNA sequence recognises and binds to a complementary RNA-binding domain or portion on the adaptor protein. In some embodiments, the distinct RNA sequence is an aptamer. The functioning of an aptamer is well-known in the way that is associates with its corresponding protein.

[00272] The distinct RNA sequence is a sequence that is different in origin and/or sequence from the guide into which it is inserted. The insertion may include the replacement (deletion) of one or more of the original guide nucleotides at the insertion site. Alternatively, the original guide nucleotides may be retained with the insertion site between them such that the inserted nucleotides separate the previously neighbouring (in terms of primary structure) original nucleotides. The distinct RNA sequence thus may differs in the sense that it has a different primary stmcture (nucleotide sequence) from the nucleotides that it is replacing. Either way. if replacing or if merely inserting without deletion, the overall primary sequence of the resulting modified guide will change. Thus, in one embodiment. a distinct RNA sequence is one that results in a different sequence (primary structure) in the resulting modified guide.

[00273] In some embodiments, the methods provided herein may occur *ex vivo* unless otherwise apparent.

[00274] Applicants have found, both in Example 9 and in Example 24, is that the Helical Domain 2 (HD2) of Sp Cas9 may be deleted. While some activity may be lost, this may only be around 50%; and this truncation may be advantageous. Although relatively small, a modest reduction in the total number of amino acids for Sp Cas9 is seen. This can only help with packaging Cas9 or the coding for Cas9 and guides into a single vector for delivery. In some circumstances a functional but less active Cas9, or relatively active Cas9 is advantageous; for instance if off-target effects are a concern, or when a functional domain is associated with the CRISPR Cas9 complex (e.g., with the Cas9 protein). In place of the portion of Cas9 truncated, Applicants added a linker in Example 9.

[00275] Applicants also found, in Example 24, that chimeric three-component enzymes can be created, focusing on the HD2 and surrounding regions of Sp Cas9. To date, work has focused on creating chimeras where the N' or C' terminal domains are swapped out of Sp and replaced with corresponding domains from St Cas9, for example providing [N' terminal Sp Cas9 - C terminal St Cas9] chimeras. These two-component chimeras are useful but Applicants have now found that chimeric 3-component enzymes are possible and functional.

[00276] Accordingly, in an aspect, the present invention provides a CRISPR enzyme or Cas enzyme, preferably Cas9, wherein the HD2 domain has been truncated. In some embodiments, the truncation is replacement of the HD2 domain (i.e. in its entirety). In some embodiments, the truncation is replacement of the HD2 domain or truncated portion thereof with a linker,

preferably a GlySer or other flexible linker, or a rigid linker such as alpha-helical linkers (Ala(GluAlaAlaAlaLys)Ala). A suitable example of an HD2 domain (in this instance from Sp Cas9) is provided in Example 9 and examples of truncated sequences lacking said HD2 domain are also provided for guidance.

[00277] In some embodiments, the CRISPR enzyme is a Cas9 ortholog of a genus belonging to the group consisting of *Corynebacter, Sutterella, Legionella, Treponema, Filifactor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides, Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillum, Gluconacetobacter, Neisseria, Roseburia, Parvibaculum, Staphylococcus, Nitratifractor, Mycoplasma* and *Campylobacter*, wherein the Cas comprises a helical domain 2 truncation.

[00278] In some embodiments, the helical domain 2 truncation is substituted with one or more sets of flexible glycine-serine (GlyGlyGlySer) or rigid alpha-helical linkers (Ala(GluAlaAlaAlaLys)Ala) in groups of 1, 3, 6, 9, or 12 repeats to replace helical domain 2. This may provide potential structural stabilization and/or aiding of retaining Cas9:sgRNA specificity.

[00279] Accordingly, in another aspect, the present invention provides a chimeric 3-component CRISPR enzyme or Cas enzyme, preferably Cas9. The chimeric 3-component enzyme preferably comprises N' and C terminal components from a first CRISPR enzyme or Cas enzyme, for example Sp Cas9, and an internal component from a different enzyme, i.e. a second CRISPR enzyme or Cas enzyme. The second CRISPR enzyme or Cas enzyme is typically an ortholog of the first CRISPR enzyme or Cas enzyme. In some embodiments, the second CRISPR enzyme or Cas enzyme may be any of the orthologs described herein. In some embodiments, the second CRISPR enzyme or Cas enzyme is Sa. In some embodiments, the second CRISPR enzyme or Cas enzyme is an St enzyme. In some embodiments, the second CRISPR enzyme or Cas enzyme is an St3 enzyme.

[00280] The internal component of the second CRISPR enzyme or Cas enzyme does not comprise any amino acids that would be at, or within, 2 or 3 amino acids from the N' or C terminal ends of the functional wild type second CRISPR enzyme or Cas enzyme (including any post-transcriptional processing). A minimal distance from the N' or C terminal ends of functional wild type second CRISPR enzyme or Cas enzyme would ideally be 5 to 10 amino acids, in some embodiments.

[00281] The components of the first CRISPR enzyme or Cas enzyme or the second CRISPR enzyme or Cas enzyme may, in some embodiments, comprise at least one domain or may span the boundaries between two or more domains. Examples of this can be seen in Example 24 and Fig 86B where the components swapped in an out of the Sp Cas9 (being the first CRISPR enzyme or Cas enzyme) span the boundaries of the various domains identified in Fig 86A. In some embodiments, one or more full domains are preferred. In some embodiments, one or more partial domains are preferred. In some embodiments, the Rec lobe is fully or partially swapped out, so that the internal component from a second CRISPR enzyme or Cas enzyme comprises a full or partial Rec lobe. As such, the N' and C terminal components from a first CRISPR enzyme or Cas enzyme would lack the Rec lobe.

[00282] In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme is the HD2 domain.

[00283] In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme replaces one or more corresponding components in the first CRISPR enzyme or Cas enzyme. In some embodiments, HD2 domain of the first CRISPR enzyme or Cas enzyme is truncated or replaced entirely. The truncation may be by at least 20%, more preferably by at least 30%, more preferably by at least 40%, more preferably by at least 50%, more preferably by at least 60%, more preferably by at least 70%, more preferably by at least 70%, more preferably by at least 80%, more preferably by at least 90%, more preferably by at least 95%, more preferably by at least 98%, and more preferably by at least 99%. As mentioned above, a suitable example of an HD2 domain (in this instance from Sp Cas9) is provided in Example 9 and examples of truncated sequences lacking said HD2 domain are also provided for guidance. In some embodiments, the components may be only portions of domains, for example a preferred N' terminal component is amino acids 1-10 of Sp which is only part of the RuvCI domain in Sp.

[00284] In some embodiments, the internal component from the first CRISPR enzyme or Cas enzyme is replaced by an internal component from the second CRISPR enzyme or Cas enzyme. The two said internal components may be the same (i.e. correspond to one another between orthologs, comparable by sequence alignment for instance) or different.

[00285] In some embodiments, the chimeric 3-component enzyme comprises N' and C terminal components from Sp Cas9, and internal domains from Sa or St3. This provides Sp-St3-Sp or Sp-Sa~Sp chimeric 3 component enzymes (in the N' to C direction).

[00286] In some embodiments, the N' terminal component of the first CRISPR enzyme or Cas enzyme is Sp 1-10 (amino acids 1-10 of Sp Cas 9). In some embodiments, the N' terminal component of the first CRISPR enzyme or Cas enzyme is Sp 1-189. In some embodiments, the N' terminal component of the first CRISPR enzyme or Cas enzyme is Sp 1-299.

[00287] In some embodiments, the C' terminal component of the first CRISPR enzyme or Cas enzyme is Sp 729-1404. In some embodiments, the C terminal component of the first CRISPR enzyme or Cas enzyme is Sp 190-1404. In some embodiments, the C terminal component of the first CRISPR enzyme or Cas enzyme is Sp 328-1404.

[00288] In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme is SO 87-712. In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme is SO 174-712. In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme is SO 87-173. In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme is SO 174-311. In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme is SO 312-712. Thus, in some embodiments, suitable lower range points for the the internal component of the second CRISPR enzyme or Cas enzyme is SO 87, or 174, or 312. Also, in some embodiments, suitable upper range points for the the internal component of the second CRISPR enzyme or Cas enzyme is SO 712, or 172/173, or 311. Any of these combinations are preferred, except where the upper and lower end points are adjacent each other or at least within 10 amino acids.

[00289] In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme is Sa 125-200. In some embodiments, the internal component of the second CRISPR enzyme or Cas enzyme is Sa 125-200 and the the N' terminal component of the first CRISPR enzyme or Cas enzyme is Sp 1-189 and the C terminal component of the first CRISPR enzyme or Cas enzyme is Sp 328-1404.

[00290] Some variation on these boundaries (except where the amino acid is the very first or very last of the wildtype) is envisaged, bearing in mind the requirement above regarding distances from the ends. Suitable ranges of these boundaries would be in the region of 1, 2, 3, 4, 5, 8, 10 15 or 20 amino acids.

[00291] It will be appreciated that the chimeric 3-component CRISPR enzyme or Cas9 enzyme is functional and preferably has at least at least 20%, more preferably at least 30%, more

preferably at least 40%, more preferably at least 50%, more preferably at least 60%, more preferably at least 70%, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably at least 95%, more preferably at least 98%, and more preferably at least 99% or more preferably 100% or more of the activity of the wildtype enzyme (an enzyme not modified as herein discussed).

[00292] Hybrid guides are preferred for use with the chimeric 3-component CRISPR enzyme or Cas9 enzyme, in some embodiments. A hybrid guides comprises a backbone and a targeting sequence. The backbone comprises the tracr RNA scaffold (tracr mate and tracr sequence) and the targeting sequence comprises the guide (spacer) sequence, of approx. 20 nts for DNA targeting. The backbone may correspond to that from an endogenous a guide from the same species as the first CRISPR enzyme or Cas enzyme or the backbone may correspond to that from an endogenous a guide from the same species as the second CRISPR enzyme or Cas enzyme. The targeting sequence may correspond to that from an endogenous a guide from the same species as the first CRISPR enzyme or Cas enzyme or the targeting sequence may correspond to that from an endogenous a guide from the same species as the second CRISPR enzyme or Cas enzyme.

[00293] Exemplary arrangement for truncations and chimeric 3-component CRISPR enzyme or Cas9 enzymes are shown in Fig 27 A and B, with reference to wt Sp Cas9, except for the last chimera in Fig 27B which is a two-component chimera. The truncation shown in the third arrangement in Fig 27A is preferred as this is an HD2 truncation and wherein the HDS region has been replaced by a linker. Suitable linkers are Gly Ser linkers as discussed herein or alpha-helical linkers (Ala(GluAlaAlaAlaLys)Ala).

[00294] The CRISPR-Cas enzymes described herein are preferably type II CRISPR-Cas enzymes. In some embodiments it may be preferred in a CRISPR complex that the tracr sequence has one or more hairpins and is 30 or more nucleotides in length, 40 or more nucleotides in length, or 50 or more nucleotides in length; the guide sequence is between 10 to 30 nucleotides in length, the CRISPR/Cas enzyme is a Type II Cas9 enzyme.

[00295] With respect to general information on CRISPR-Cas Systems, components thereof, and delivery of such components, including methods, materials, delivery vehicles, vectors, particles, AAV, and making and using thereof, including as to amounts and formulations, all useful in the practice of the instant invention, reference is made to: US Patents Nos. 8,697,359,

8,771,945, 8,795,965, 8,865,406, 8,871,445, 8,889,356, 8,889,418 and 8,895,308; US Patent Publications US 2014-0310830 (US APP. Ser. No. 14/105,031), US 2014-0287938 Al (U.S. App. Ser. No. 14/213,991), US 2014-0273234 Al (U.S. App. Ser. No. 14/293,674), US2014-0273232 Al (U.S. App. Ser. No. 14/290,575), US 2014-0273231 (U.S. App. Ser. No. 14/259,420), US 2014-0256046 Al (U.S. App. Ser. No. 14/226,274), US 2014-0248702 Al (U.S. App. Ser. No. 14/258,458), US 2014-0242700 Al (U.S. App. Ser. No. 14/222,930), US 2014-0242699 Al (U.S. App. Ser. No. 14/183,512), US 2014-0242664 Al (U.S. App. Ser. No. 14/104,990), US 2014-0234972 Al (U.S. App. Ser. No. 14/183,471), US 2014-0227787 Al (U.S. App. Ser. No. 14/256,912), US 2014-0189896 Al (U.S. App. Ser. No. 14/105,035), US 2014-0186958 (U.S. App. Ser. No. 14/105,017), US 2014-0186919 Al (U.S. App. Ser. No. 14/104,977), US 2014-01 86843 Al (U.S. App. Ser. No. 14/104,900), US 2014-0179770 Al (U.S. App. Ser. No. 14/104,837) and US 2014-0179006 Al (U.S. App. Ser. No. 14/183,486), US 2014-01 70753 (US App Ser No 14/183,429); European Patent Applications EP 2 771 468 (EP13818570.7), EP 2 764 103 (EP13824232.6), and EP 2 784 162 (EP14170383.5); and PCX Patent Publications WO 2014/093661 (PCT/US20 13/074743), WO 2014/093694 (PCT/US20 13/074790), WO 2014/093595 (PCT/US20 13/0746 11), WO 2014/093718 (PCT/US20 13/074825), WO 2014/093709 (PCT/US20 13/0748 12), WO 2014/093622 (PCT/US20 13/074667), WO 2014/093635 (PCT7US20 13/074691), WO 2014/093655 (PCT/US20 13/074736), WO 2014/093712 (PCT/US20 13/0748 19), WO2014/093701 (PCT/US2G 13/074800), and WO20 14/01 8423 (PCT/1JS2013/051418). Reference is also made to US provisional patent applications 61/758,468; 61/802,174; 61/806,375; 61/814,263; 61/819,803 and 61/828,130, filed on January 30, 2013; March 15, 2013; March 28, 2013; April 20, 2013; May 6, 2013 and May 28, 2013 respectively. Reference is also made to US provisional patent application 61/836,123, filed on June 17, 2013. Reference is additionally made to US provisional patent applications 61/835,931, 61/835,936, 61/836,127, 61/836, 101, 61/836,080 and 61/835,973, each filed June 17, 2013. Further reference is made to US provisional patent applications 61/862,468 and 61/862,355 filed on August 5, 2013; 61/871,301 filed on August 28, 2013; 61/960,777 filed on September 25, 2013 and 61/961,980 filed on October 28, 2013. Reference is yet further made to: PCX Patent applications Nos: PCT/US20 14/04 1803, PCT/US20 14/04 1800, PCX/US20 14/04 1809, PCT/US20 14/04 1804 and PCT/US20 14/04 1806, each filed June 10, 2014 6/10/14; PCT/US20 14/04 1808 filed June 11, 2014; and

PCT/US2014/62558 filed October 28, 2014, and US Provisional Patent Applications Serial Nos.: 61/915,150, 61/915,301, 61/915,267 and 61/915,260, each filed December 12, 2013; 61/757,972 and 61/768,959, filed on January 29, 2013 and **February** 25, 2013; 61/835,936, 61/836,127, **61/836,101, 61/836,080,** 61/835,973, and 61/835,931, filed June 17, 2013; **62/010,888** and 62/010,879, both filed June 11, 2014; 62/010,329 and 62/010,441, each filed June 10, 2014; 61/939,228 and 61/939,242, each filed February 12, 2014; 61/980,012, filed April 15,2014; 62/038,358, filed August 17, 2014; 62/054,490, 62/055,484, 62/055,460 and 62/055,487, each filed September 25, 2014; and 62/069,243, filed October 27, 2014. Reference is also made to US provisional patent applications Nos. 62/055,484, 62/055,460, and 62/055,487, filed September 25, 2014; US provisional patent application 61/980,012, filed April 15, 2014; and US provisional patent application 61/939,242 filed February 12, 2014. Reference is made to PCX application designating, inter alia, the United States, application No. PCT/US 14/41806, filed June 10, 2014. Reference is made to US provisional patent application 61/930,214 filed on January 22, 2014. Reference is made to US provisional patent applications 61/915,251; 61/915,260 and 61/915,267, each filed on December 12, 2013. Reference is made to US provisional patent application USSN 61/980,012 filed April 15, 2014. Reference is made to PCX application designating, inter alia, the United States, application No. PCX/US 14/41806, filed June 10, 2014. Reference is made to US provisional patent application 61/930,214 filed on January 22, 2014. Reference is made to US provisional patent applications 61/915,251; 61/915,260 and 61/915,267, each filed on December 12, 2013. Each of these patents, patent publications, and applications, and all documents cited therein or during their prosecution ("appln cited documents") and all documents cited or referenced in the appln cited documents, together with any instructions, descriptions, product specifications, and product sheets for any products mentioned therein or in any document therein and incorporated by reference herein, are hereby-incorporated herein by reference, and may be employed in the practice of the invention. All documents (e.g., these patents, patent publications and applications and the appln cited documents) are incorporated herein by reference to the same extent as if each individual document was specifically and individually indicated to be incorporated by reference.

[00296] Also with respect to general information on CRISPR-Cas Systems, mention is made of the following (also hereby incorporated herein by reference):

- *Multiplex genome engineering using CRISPR/Cas systems.* Cong, L., Ran, F.A., Cox, D., Lin, S., Barretto, R., Habih, N., Hsu, P.D., Wu, X., Jiang, W., Marraffini, LA., & Zhang, F. *Science* Feb 15;339(6121):819-23 (2013);
- *RNA-guided editing of bacterial genomes using CRISPR-Cas systems.* Jiang W., Bikard D., Cox D., Zhang F, Marraffini LA. Nat Biotechnol Mar;31(3):233-9 (2013);
- *One-Step Generation of Mice Carrying Mutations in Multiple Genes by CRISPR/Cas-Mediated Genome Engineering.* Wang H., Yang H., Shivalila CS., Dawlaty MM., Cheng AW, Zhang F., Jaemsch R. Cell May 9;153(4):910-8 (2013);
- *Optical control of mammalian endogenous transcription and epigenetic states.* Konermann S, Brighara MD, Trevmo AE, Bsu PD, Heidenreich M, Cong L, Plait RJ, Scott DA, Church GM, Zhang F. Nature. 2013 Aug 22;500(7463):472-6. doi: 10.1038/Naturel2466. Epub 2013 Aug 23;
- *Double Nicking by RNA-Guided CRISPR Cas9for Enhanced Genome Editing Specificity.* Ran, FA., Hsu, PD., Lin, CY., Gootenberg, JS., Konemiami, S., Trevino, AE., Scott, DA., Inoue, A., Matoba, S., Zhang, Y., & Zhang, F. *Cell Aug* 28. pii: 80092-8674(13)01015-5. (2013);
- *DNA targeting specificity of RNA-guided Cas9 nucleases.* Hsu, P., Scott, D., Weinstem, J., Ran, FA., Konermann, S., Agarwala, V., Li, Y., Fine, E., Wu, X., Shalem, O., Cradick, TJ., Man-affmi, LA., Bao, G., & Zhang, F. *Nat Biotechnol* doi:10.1038/nbt.2647 (2013);
- *Genome engineering using the CRISPR-Cas9 system.* Ran, FA., Hsu, PD., Wright, J., Agarwala, V., Scott, DA., Zhang, F. Nature Protocols Nov;8(i 1):2281-308. (2013);
- *Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells.* Shalem, O., Sanjana, NE., Hartenian, E., Shi, X., Scott, DA., Mikkelson, T., Heckl, D., Ebert, BL., Root, DE., Doench, JG., Zhang, F. *Science* Dec 12. (2013). [Epub ahead of print];
- *Crystal structure of cas9 in complex with guide RNA and target DNA.* Nishimasu, H., Ran, FA., Hsu, PD., Konermann, S., Shehata, SI., Dohmae, N., Ishitani, R., Zhang, F., Nureki, O. *Cell* Feb 27. (2014). 156(5):935-49;
- *Genome-wide binding of the CRISPR endonuclease Cas9 in mammalian cells.* Wu X., Scott DA., Kriz A.)., Chiu AC, Hsu PD., Dadon DB., Cheng AW., Trevino AE., Konermann S., Chen S., Jaenisch R., Zhang F., Sharp PA. *Nat Biotechnol.* (2014) Apr 20. doi: 10.1038/nbt.2889,

- *CRISPR-Cas9 Knockin Mice for Genome Editing and Cancer Modeling,* Piatt et al., Cell 159(2): 440-455 (2014) DOI: 10.1016/j.cell.2014.09.014,
- *Development and Applications of CRISPR-Cas9 for Genome Engineering*, Hsu et al, Cell 157, 1262-1278 (June 5, 2014) (Hsu 2014),
- *Genetic screens in human cells using the CRISPR/Cas9 system,* Wang et al., Science. 2014 January 3; 343(6166): 80-84. doi:10.1 126/science. 1246981,
- *Rational design of highly active sgRNAs for CRISPR-Cas9-mediated gene inaciivation,* Doench et al., Nature Biotechnology published online 3 September 2014; doi:10.1038/nbt.3026, and
- *In vivo interrogation of gene junction in the mammalian brain using CRISPR-Cas9,* Swiech et al, Nature Biotechnology ; published online 19 October 2014; doi:10.1038/nbt.3055.

each of which is incorporated herein by reference, and discussed briefly below:

[00297] Cong *et al.* engineered type II CRISPR/Cas systems for use in eukaryotic cells based on both *Streptococcus thermophilus* Cas9 and also *Sirepioccocus pyogenes* Cas9 and demonstrated that Cas9 nucleases can be directed by short RNAs to induce precise cleavage of DNA in human and mouse cells. Their study further showed that Cas9 as converted into a nicking enzyme can be used to facilitate homology-directed repair in eukaryotic cells with minimal mutagenic activity. Additionally, their study demonstrated that multiple guide sequences can be encoded into a single CRISPR array to enable simultaneous editing of several at endogenous genomic loci sites within the mammalian genome, demonstrating easy programmability and wide applicability of the RNA-guided nuclease technology. This ability to use **RNA** to program sequence specific DNA cleavage in cells defined a new class of genome engineering tools. These studies further showed that other CRISPR loci are likely to be transplantable into mammalian cells and can also mediate mammalian genome cleavage. Importantly, it can be envisaged that several aspects of the CRISPR/Cas system can be further improved to increase its efficiency and versatility.

[00298] Jiang *et al.* used the clustered, regularly interspaced, short palindromic repeats (CRISPR)-associated Cas9 endonuclease complexed with dual-RNAs to introduce precise mutations in the genomes of *Streptococcus pneumoniae* and *Escherichia coli.* The approach relied on dual-RNA:Cas9~directed cleavage at the targeted genomic site to kill unmutated cells and circumvents the need for selectable markers or counter-selection systems. The study reported reprogramming dual-RNA:Cas9 specificity by changing the sequence of short CRISPR RNA (crRNA) to make single- and multinucieotide changes carried on editing templates. The study showed that simultaneous use of two crRNAs enabled multiplex mutagenesis. Furthermore, when the approach was used in combination with recombineering, in *S. pneumoniae*, nearly 100% of cells that were recovered using the described approach contained the desired mutation, and in *E. coli*, 65% that were recovered contained the mutation.

[00299] Konermann *et al.* addressed the need in the art for versatile and robust technologies that enable optical and chemical modulation of DNA-binding domains based CRISPR Cas9 enzyme and also Transcriptional Activator Like Effectors

[00300] Cas9 nuclease from the microbial CRISPR-Cas system is targeted to specific genomic loci by a 20 nt guide sequence, which can tolerate certain mismatches to the DNA target and thereby promote undesired off-target mutagenesis. To address this, Ran *et al.* described an approach that combined a Cas9 nickase mutant with paired guide RNAs to introduce targeted double-strand breaks. Because individual nicks in the genome are repaired with high fidelity, simultaneous nicking *via* appropriately offset guide RNAs is required for double-stranded breaks and extends the number of specifically recognized bases for target cleavage. The authors demonstrated that using paired nicking can reduce off-target activity by 50- to 1,500-fold in cell lines and to facilitate gene knockout in mouse zygotes without sacrificing on-target cleavage efficiency. This versatile strategy enables a wide variety of genome editing applications that require high specificity.

[00301] Hsu *et al.* characterized SpCas9 targeting specificity in human cells to inform the selection of target sites and avoid off-target effects. The study evaluated >700 guide RNA variants and SpCas9-induced indel mutation levels at >100 predicted genomic off-target loci in 293T and 293FT cells. The authors reported that SpCas9 tolerates mismatches between guide RNA and target DNA at different positions in a sequence-dependent manner, sensitive to the number, position and distribution of mismatches. The authors further showed that SpCas9-mediated cleavage is unaffected by DNA metliylation and that the dosage of SpCas9 and sgRNA can be titrated to minimize off-target modification. Additionally, to facilitate mammalian genome engineering applications, the authors reported providing a web-based software tool to guide the selection and validation of target sequences as well as off-target analyses.

[00302] Ran *et al.* described a set of tools for Cas9-mediated genome editing *via* non-homologous end joining (NHEJ) or homology-directed repair (HDR) in mammalian cells, as well as generation of modified cell lines for downstream functional studies. To minimize off-target cleavage, the authors further described a double-nicking strategy using the Cas9 nickase mutant with paired guide RNAs. The protocol provided by the authors experimentally derived guidelines for the selection of target sites, evaluation of cleavage efficiency and analysis of off-target activity. The studies showed that beginning with target design, gene modifications can be achieved within as little as 1-2 weeks, and modified clonal cell lines can be derived within 2-3 weeks.

[00303] Sbalem *et al.* described a new way to interrogate gene function on a genome-wide scale. Their studies showed that delivery of a genome-scale CRISPR-Cas9 knockout (GeCKO) library targeted 18,080 genes with 64,751 unique guide sequences enabled both negative and positive selection screening in human cells. First, the authors showed use of the GeCKO library to identify genes essential for cell viability in cancer and pluripotent stem cells. Next, in a melanoma model, the authors screened for genes whose loss is involved in resistance to vemurafenib, a therapeutic that inhibits mutant protein kinase BRAF. Their studies showed that the highest-ranking candidates included previously validated genes NF1 and MED12 as well as novel hits NF2, CUL3, TADA2B, and TADAl. The authors observed a high level of consistency between independent guide RNAs targeting the same gene and a high rate of hit confirmation, and thus demonstrated the promise of genome-scale screening with Cas9.

[00304] Nishimasu *et al.* reported the crystal structure of *Streptococcus pyogenes* Cas9 in complex with sgRNA and its target DNA at 2.5 A° resolution. The structure revealed a bilobed architecture composed of target recognition and nuclease lobes, accommodating the sgRNA:DNA heteroduplex in a positively charged groove at their interface. Whereas the recognition lobe is essential for binding sgRNA and DNA, the nuclease lobe contains the HNH and RuvC nuclease domains, which are properly positioned for cleavage of the complementary and non-complementary strands of the target DNA, respectively. The nuclease lobe also contains a carboxyl-terminal domain responsible for the interaction with the protospacer adjacent motif (PAM). This high-resolution structure and accompanying functional analyses have revealed the molecular mechanism of RNA-guided DNA targeting by Cas9, thus paving the way for the rational design of new, versatile genome-editing technologies.

[00305] Wis *et at.* mapped genome-wide binding sites of a catalytically inactive Cas9 (dCas9) from *Streptococcus pyogenes* loaded with single guide RNAs (sgRNAs) in mouse embryonic stem cells (mESCs). The authors showed that each of the four sgRNAs tested targets dCas9 to between tens and thousands of genomic sites, frequently characterized by a 5-nucleotide seed region in the sgRNA and an NGG protospacer adjacent motif (PAM). Chromatin inaccessibility decreases dCas9 binding to other sites with matching seed sequences; thus 70% of off-target sites are associated with genes. The authors showed that targeted sequencing of 295 dCas9 binding sites in mESCs transfected with catalytically active Cas9 identified only one site mutated above background levels. The authors proposed a two-state model for Cas9 binding and cleavage, in which a seed match triggers binding but extensive pairing with target DNA is required for cleavage.

[00306] Hsu 2014 is a review article that discusses generally CRISPR-Cas9 history from yogurt to genome editing, including genetic screening of cells, that is in the information, data and findings of the applications in the lineage of this specification filed prior to June 5, 2014. The general teachings of Hsu 2014 do not involve the specific models, animals of the instant specification.

[00307] Mention is also made of Tsai et al, "Dimeric CRISPR RNA-guided Fold nucleases for highly specific genome editing," Nature Biotechnology 32(6): 569-77 (2014) which is not believed to be prior art to the instant invention or application, but which may be considered in the practice of the instant invention.

[00308] In general, the CRISPR-Cas or CRISPR system is as used in the foregoing documents, such as WO 2014/093622 (PCT/US2013/074667) and refers collectively to transcripts and other elements involved in the expression of or directing the activity of CRISPR-associated ("Cas") genes, including sequences encoding a Cas gene, a tracr (trans-activating CRISPR) sequence (e.g. tracrRNA or an active partial tracrRNA), a tracr-mate sequence (encompassing a "direct repeat" and a tracrRNA-processed partial direct repeat in the context of an endogenous CRISPR system), a guide sequence (also referred to as a "spacer" in the context of an endogenous CRISPR system), or "RNA(s)" as that term is herein used (e.g., RNA(s) to guide Cas9, e.g. CRISPR RNA and transactivating (tracr) RNA or a single guide RNA (sgRNA) (chimeric RNA)) or other sequences and transcripts from a CRISPR locus. In general, a CRISPR system is characterized by elements that promote the formation of a CRISPR complex

at the site of a target sequence (also referred to as a protospacer in the context of an endogenous CRISPR system). In the context of formation of a CRISPR complex, "target sequence" refers to a sequence to which a guide sequence is designed to have complementarity, where hybridization between a target sequence and a guide sequence promotes the formation of a CRISPR complex. A target sequence may comprise any polynucleotide, such as DNA or RNA polynucleotides. In some embodiments, a target sequence is located in the nucleus or cytoplasm of a cell. In some embodiments, direct repeats may be identified *in silico* by searching for repetitive motifs that fulfill any or all of the following criteria; 1. found in a 2Kb window of genomic sequence flanking the type II CRISPR locus; 2. span from 20 to 50 bp; and 3. interspaced by 20 to 50 bp. In some embodiments, 2 of these criteria may be used, for instance 1 and 2, 2 and 3, or 1 and 3. In some embodiments, all 3 criteria may be used.

[00309] The terms "polynucleotide", "nucleotide", "nucleotide sequence", "nucleic acid" and "oligonucleotide" are used interchangeably. They refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three dimensional stmcture, and may perform any function, known or unknown. The following are non limiting examples of polynucleotides: coding or non-coding regions of a gene or gene fragment, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, short interfering RNA (siRNA), short-hairpin RNA (shRNA), micro-RNA (miRNA), ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may comprise one or more modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component.

[00310] In aspects of the invention the terms "chimeric RNA", "chimeric guide RNA", "guide RNA", "single guide RNA" and "synthetic guide RNA" are used interchangeably and refer to the polynucleotide sequence comprising the guide sequence, the tracr sequence and the tracr mate sequence. The term "guide sequence" refers to the about 20bp sequence within the guide RNA that specifies the target site and may be used interchangeably with the terms "guide" or "spacer".

The term "tracr mate sequence" may also be used interchangeably with the term "direct repeat(s)". An exemplary CRISPR-Cas system is illustrated in Figure 1.

[00311] As used herein the term "wild type" is a term of the art understood by skilled persons and means the typical form of an organism, strain, gene or characteristic as it occurs in nature as distinguished from mutant or variant forms.

[00312] As used herein the term "variant" should be taken to mean the exhibition of qualities that have a pattern that deviates from what occurs in nature.

[00313] The terms "non-naturally occurring" or "engineered" are used interchangeably and indicate the involvement of the hand of man. The terms, when referring to nucleic acid molecules or polypeptides mean that the nucleic acid molecule or the polypeptide is at least substantially free from at least one other component with which they are naturally associated in nature and as found in nature.

[00314] "Complementarity" refers to the ability of a nucleic acid to form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. A percent complementarity indicates the percentage of residues in a nucleic acid molecule which can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence. "Substantially complementary" as used herein refers to a degree of complementarity that is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%», 97%, 98%, 99%, or 100% over a region of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, or more nucleotides, or refers to two nucleic acids that hybridize under stringent conditions.

[00315] As used herein, "stringent conditions" for hybridization refer to conditions under which a nucleic acid having complementarity to a target sequence predominantly hybridizes with the target sequence, and substantially does not hybridize to non-target sequences. Stringent conditions are generally sequence-dependent, and vary depending on a number of factors. In general, the longer the sequence, the higher the temperature at which the sequence specifically hybridizes to its target sequence. Non-limiting examples of stringent conditions are described in detail in Tijssen (1993), Laboratory Techniques In Biochemistry And Molecular Biology-

Hybridization With Nucleic Acid Probes Part I, Second Chapter "Overview of principles of hybridization and the strategy of nucleic acid probe assay", Elsevier, N.Y.

[00316] "Hybridization" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson Crick base pairing, Hoogstein binding, or in any other sequence specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi stranded complex, a single self hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of PGR, or the cleavage of a polynucleotide by an enzyme. A sequence capable of hybridizing with a given sequence is referred to as the "complement" of the given sequence.

[00317] As used herein, "expression" refers to the process by which a polynucleotide is transcribed from a DNA template (such as into and mRNA or other RNA transcript) and/or the process by which a transcribed mRNA is subsequently translated into peptides, polypeptides, or proteins. Transcripts and encoded polypeptides may be collectively referred to as "gene product." If the polynucleotide is derived from genomic DNA, expression may include splicing of the mRNA in a eukaryotic cell.

[00318] The terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non amino acids. The terms also encompass an amino acid polymer that has been modified; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation, such as conjugation with a labeling component. As used herein the term "amino acid" includes natural and/or unnatural or synthetic amino acids, including glycine and both the D or L optical isomers, and amino acid analogs and peptidomimetics.

[00319] The terms "subject," "individual," and "patient" are used interchangeably herein to refer to a vertebrate, preferably a mammal, more preferably a human. Mammals include, but are not limited to, murines, simians, humans, farm animals, sport animals, and pets. Tissues, cells and their progeny of a biological entity obtained in vivo or cultured in vitro are also encompassed.

[00320] The terms "therapeutic agent", "therapeutic capable agent" or "treatment agent" are used interchangeably and refer to a molecule or compound that confers some beneficial effect upon administration to a subject. The beneficial effect includes enablement of diagnostic determinations; amelioration of a disease, symptom, disorder, or pathological condition; reducing or preventing the onset of a disease, symptom, disorder or condition; and generally counteracting a disease, symptom, disorder or pathological condition.

[00321] As used herein, "treatment" or "treating," or "palliating" or "ameliorating" are used interchangeably. These terms refer to an approach for obtaining beneficial or desired results including but not limited to a therapeutic benefit and/or a prophylactic benefit. By therapeutic benefit is meant any therapeutically relevant improvement in or effect on one or more diseases, conditions, or symptoms under treatment. For prophylactic benefit, the compositions may be administered to a subject at risk of developing a particular disease, condition, or symptom, or to a subject reporting one or more of the physiological symptoms of a disease, even though the disease, condition, or symptom may not have yet been manifested.

[00322] The term "effective amount" or "therapeutically effective amount" refers to the amount of an agent that is sufficient to effect beneficial or desired results. The therapeutically effective amount may vary depending upon one or more of: the subject and disease condition being treated, the weight and age of the subject, the severity of the disease condition, the manner of administration and the like, which can readily be determined by one of ordinary skill in the art. The term also applies to a dose that will provide an image for detection by any one of the imaging methods described herein. The specific dose may vary depending on one or more of: the particular agent chosen, the dosing regimen to be followed, whether it is administered in combination with other compounds, timing of administration, the tissue to be imaged, and the physical delivery system in which it is carried.

[00323] The practice of the present invention employs, unless otherwise indicated, conventional techniques of immunology, biochemistry, chemistry, molecular biology, microbiology, cell biology, genomics and recombinant DNA, which are within the skill of the art. See Sambrook, Fritsch and Maniatis, MOLECULAR CLONING: A LABORATORY MANUAL, 2nd edition (1989); CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (F. M. Ausubel, et al. eds., (1987)); the series METHODS IN ENZYMOLOGY (Academic Press, Inc.): PGR 2: A PRACTICAL APPROACH (M.J. MacPherson, B.D. Hames and G.R. Taylor eds.

(1995)), Harlow and Lane, eds. (1988) ANTIBODIES, A LABORATORY MANUAL, and ANIMAL CELL CULTURE (R.I. Freshney, ed. (1987)).

[00324] Several aspects of the invention relate to vector systems comprising one or more vectors, or vectors as such. Vectors can be designed for expression of CRISPR transcripts (e.g. nucleic acid transcripts, proteins, or enzymes) in prokaryotic or eukaryotic cells. For example, CRISPR transcripts can be expressed in bacterial cells such as *Escherichia coli,* insect cells (using baculovirus expression vectors), yeast cells, or mammalian cells. Suitable host cells are discussed further in Goeddei, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences and T7 polymerase.

[00325] Vectors may be introduced and propagated in a prokaryote. In some embodiments, a prokaryote is used to amplify copies of a vector to be introduced into a eukaryotic cell or as an intermediate vector in the production of a vector to be introduced into a eukaryotic cell (e.g. amplifying a plasmid as part of a viral vector packaging system). In some embodiments, a prokaryote is used to amplify copies of a vector and express one or more nucleic acids, such as to provide a source of one or more proteins for delivery to a host cell or host organism. Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, such as to the amino terminus of the recombinant protein. Such fusion vectors may serve one or more purposes, such as: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombmant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Example fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

[00326] Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann et al., (1988) ***Gene* 69:301-315)** and pET **11d** (Studier et al, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

[00327] In some embodiments, a vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerivisae* include **pYepSecl (Baldari,** et al., 1987. *EMBO J.* **6:** 229-234), **pMFa** (Kuijan and Herskowitz, 1982, *Cell* 30: 933-943), **pJRY88 (Schultz** et al., 1987. *Gene* 54: 113-123), **pYES2** (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

[00328] In some embodiments, a vector drives protein expression in insect cells using **baculovirus** expression vectors. **Baculo**virus vectors available for expression of proteins in cultured insect cells (e.g., SF9 cells) include the **pAc** series (Smith, et al., 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the **pVL** series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

[00329] In some embodiments, a vector is capable of driving expression of one or more sequences in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include **pCDM8** (Seed, 1987. *Nature* 329: 840) and **pMT2PC** (Kaufman, et al., 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are typically provided by one or more **regulatory** elements. For example, commonly used promoters are derived **from** polyoma, adenovirus 2, **cytomegalovirus,** simian virus 40, and others disclosed herein and known in the art. For other suitable expression systems for both **prokaryotic** and eukaryotic cells see, e.g., Chapters 16 and 17 of **Sambrook,** et **al.,** MOLECULAR CLONING: A LABORATORY MANUAL. 2nd **ed.,** Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

[00330] In some embodiments, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Plnkert, et **al,** 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Baneiji, et ah, 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33:

741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477), pancreas-specific promoters (Edlund, et al., 1985. *Science* 230: 912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmental!)' ~ reguiated promoters are also encompassed, e.g., the murine hox promoters (Kessel and Grass, 1990. *Science* 249: 374-379) and the a-fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546).

[00331] In some embodiments, a regulatory element is operably linked to one or more elements of a CRISPR system so as to drive expression of the one or more elements of the CRISPR system. In general, CRISPRs (Clustered Regularly Interspaced Short Palindromic Repeats), also known as SPlDRs (SPacer Interspersed Direct Repeats), constitute a family of DNA loci that are usually specific to a particular bacterial species. The CRISPR locus comprises a distinct class of interspersed short sequence repeats (SSRs) that were recognized in *E. coli* (Ishiiio et al, J. BacterioL, 169:5429-5433 [1987]; and Nakata et ai, J. BacterioL, 171:3553-3556 [1989]), and associated genes. Similar interspersed SSRs have been identified in *Haioferax mediterranei, Streptococcus pyogenes, Anabaena,* and *Mycobacterium tuberculosis* (See, Groenen et al, Mol. Microbiol., 10:1057-1065 [1993]; Hoe et al., Emerg. Infect. Dis., 5:254-263 [1999]; Masepohi et al., Biochim. Biophys. Acta 1307:26-30 [1996]; and Mojica et al., Mol. Microbiol., 17:85-93 [1995]). The CRISPR loci typically differ from other SSRs by the structure of the repeats, which have been termed short regularly spaced repeats (SRSRs) (Janssen et ai., OMICS J. Integ. Biol., 6:23-33 [2002]; and Mojica et al., Mol. Microbiol., 36:244-246 [2000]). In general, the repeats are short elements that occur in clusters that are regularly spaced by unique intervening sequences with a substantially constant length (Mojica et al., [2000], supra). Although the repeat sequences are highly conserved between strains, the number of interspersed repeats and the sequences of the spacer regions typically differ from strain to strain (van Embden et al., J. BacterioL, 182:2393-2401 [2000]). CRISPR loci have been identified in more than 40 prokaryot.es (See e.g., Jansen et ai., Mol. Microbiol., 43:1565-1575 [2002]; and Mojica et al, [2005]) including, but not limited to *Aeropyrum, Pyrobaculum, Sulfolobus, Archaeoglobus, Halocarcula, Methanobacterium, Meihanococcus, Methanosarcina, Methanopyrus, Pyrococcus, Picrophilus, Thermoplasma, Corynebacterium, Mycobacterium, Streptomyc.es, Aquifex, Porphyromonas, Chlorobium, The.rm.us, Bacillus, Listeria, Staphylococcus, Clostridium,*

Thermoanaerobacter, Mycoplasma, Fusobacterium, Azarcus, Chromobacterium, Neisseria, Nitrosomonas, Desulfovibrio, Geobacter, Myxococcus, Campylobacter, Wolinella, Acinetobacter, Erwinia, Escherichia, Legionella, Methylococcus, Pasteurella, Photobacterium, Salmonella, Xanthomonas, Yersinia, Treponema, and *Thermotoga.*

[00332] In general, "CRISPR system" refers collectively to transcripts and other elements involved in the expression of or directing the activity of CRISPR-associated ("Cas") genes, including sequences encoding a Cas gene, a tracr (trans-activating CRISPR) sequence (e.g. tracrRNA or an active partial tracrRNA), a tracr-mate sequence (encompassing a "direct repeat" and a tracrRNA-processed partial direct repeat in the context of an endogenous CRISPR system), a guide sequence (also referred to as a "spacer" in the context of an endogenous CRISPR system), or other sequences and transcripts from a CRISPR locus. In some embodiments, one or more elements of a CRISPR system is derived from a type I, type II, or type III CRISPR system. In some embodiments, one or more elements of a CRISPR system is derived from a particular organism comprising an endogenous CRISPR system, such as *Streptococcus pyogenes.* In general, a CRISPR system is characterized by elements that promote the formation of a CRISPR complex at the site of a target sequence (also referred to as a protospacer in the context of an endogenous CRISPR system). In the context of formation of a CRISPR complex, "target sequence" refers to a sequence to which a guide sequence is designed to have complementarity, where hybridization between a target sequence and a guide sequence promotes the formation of a CRISPR complex. Full complementarity is not necessarily required, provided there is sufficient complementarity to cause hybridization and promote formation of a CRISPR complex. A target sequence may comprise any polynucleotide, such as DNA or RNA polynucleotides. In some embodiments, a target sequence is located in the nucleus or cytoplasm of a cell. In some embodiments, the target sequence may be within an organelle of a eukaryotic cell, for example, mitochondrion or chloroplast. A sequence or template that may be used for recombination into the targeted locus comprising the target sequences is referred to as an "editing template" or "editing polynucleotide" or "editing sequence". In aspects of the invention, an exogenous template polynucleotide may be referred to as an editing template. In an aspect of the invention the recombination is homologous recombination.

[00333] Typically, in the context of an endogenous CRISPR system, formation of a CRISPR complex (comprising a guide sequence hybridized to a target sequence and complexed with one

or more Cas proteins) results in cleavage of one or both strands in or near (e.g. within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 50, or more base pairs from) the target sequence. Without wishing to be bound by theory, the tracr sequence, which may comprise or consist of all or a portion of a wild-type tracr sequence (e.g. about or more than about 20, 26, 32, 45, 48, 54, 63, 67, 85, or more nucleotides of a wild-type tracr sequence), may also form part of a CRISPR complex, such as by hybridization along at least a portion of the tracr sequence to all or a portion of a tracr mate sequence that is operabiy linked to the guide sequence. in some embodiments, the tracr sequence has sufficient complementarity to a tracr mate sequence to hybridize and participate in formation of a CRISPR complex. As with the target sequence, it is believed that complete complementarity is not needed, provided there is sufficient to be functional. In some embodiments, the tracr sequence has at least 50%, 60%, 70%, 80%, 90%, 95% or 99% of sequence complementarity along the length of the tracr mate sequence when optimally aligned. In some embodiments, one or more vectors driving expression of one or more elements of a CRISPR system are introduced into a host cell such that expression of the elements of the CRISPR system direct formation of a CRISPR complex at one or more target sites. For example, a Cas enzyme, a guide sequence linked to a tracr-mate sequence, and a tracr sequence could each be operabiy linked to separate regulatory elements on separate vectors. Alternatively, two or more of the elements expressed from the same or different regulatory elements, may be combined in a single vector, with one or more additional vectors providing any components of the CRISPR system not inciuded in the first vector. CRISPR system elements that are combined in a single vector may be arranged in any suitable orientation, such as one element located 5' with respect to ("upstream" of) or 3' with respect to ("downstream" of) a second element. The coding sequence of one element may be located on the same or opposite strand of the coding sequence of a second element, and oriented in the same or opposite direction. In some embodiments, a single promoter drives expression of a transcript encoding a CRISPR enzyme and one or more of the guide sequence, tracr mate sequence (optionally operabiy linked to the guide sequence), and a tracr sequence embedded within one or more intron sequences (e.g. each in a different intron, two or more in at least one intron, or ail in a single intron). In some embodiments, the CRISPR enzyme, guide sequence, tracr mate sequence, and tracr sequence are operabiy linked to and expressed from the same promoter. Single vector constructs for SpCas9 are illustrated in Figure 22.

[00334] In some embodiments, a vector comprises one or more insertion sites, such as a restriction endonuclease recognition sequence (also referred to as a "cloning site"). In some embodiments, one or more insertion sites (e.g. about or more than about I, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more insertion sites) are located upstream and/or downstream of one or more sequence elements of one or more vectors. In some embodiments, a vector comprises an insertion site upstream of a tracr mate sequence, and optionally downstream of a regulatory element operably linked to the tracr mate sequence, such that following insertion of a guide sequence into the insertion site and upon expression the guide sequence directs sequence-specific binding of a CRISPR complex to a target sequence in a eukaryotic cell. In some embodiments, a vector comprises two or more insertion sites, each insertion site being located between two tracr mate sequences so as to allow insertion of a guide sequence at each site. In such an arrangement, the two or more guide sequences may comprise two or more copies of a single guide sequence, two or more different guide sequences, or combinations of these. When multiple different guide sequences are used, a single expression construct may be used to target CRISPR activity to multiple different, corresponding target sequences within a cell. For example, a single vector may comprise about or more than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or more guide sequences. In some embodiments, about or more than about I, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more such guide-sequence-containing vectors may be provided, and optionally delivered to a cell.

[00335] In some embodiments, a vector comprises a regulatory element operably linked to an enzyme-coding sequence encoding a CRISPR enzyme, such as a Cas protein. Non-limiting examples of Cas proteins include Casl, CaslB, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csxl2), CaslO, Csyl, Csy2, Csy3, Csel, Cse2, Cscl, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmrl, Cmr3, Cmr4, Cmr5, Cmr6, Csbl, Csb2, Csb3, Csxl7, Csx!4, CsxlO, Csxl6, CsaX, Csx3, Csxl, Csx15, Csfl, Csf2, Csf3, Csf4, homologs thereof, or modified versions thereof. These enzymes are known; for example, the amino acid sequence of *S. pyogenes* Cas9 protein may be found in the SwissProt database under accession number Q99ZW2. In some embodiments, the unmodified CRISPR enzyme has DNA cleavage activity, such as Cas9. In some embodiments the CRISPR enzyme is Cas9, and may be Cas9 from *S. pyogenes* or *S. pneumoniae.* In some embodiments, the CRISPR enzyme directs cleavage of one or both strands at the location of a target sequence, such as within the target sequence and/or within the complement of the target sequence. In some embodiments, the

CRISPR enzyme directs cleavage of one or both strands within about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 50, 100, 200, 500, or more base pairs from the first or last nucleotide of a target sequence. In some embodiments, a vector encodes a CRISPR enzyme that is mutated to with respect to a corresponding wild-type enzyme such that the mutated CRISPR enzyme lacks the ability to cleave one or both strands of a target polynucleotide containing a target sequence. For example, an aspartate-to-alanine substitution (D10A) in the RuvC I catalytic domain of Cas9 from *S. pyogenes* converts Cas9 from a nuclease that cleaves both strands to a nickase (cleaves a single strand). Other examples of mutations that render Cas9 a nickase include, without limitation, H840A, N854A, and N863A. In aspects of the invention, nickases may be used for genome editing via homologous recombination, For example, Figure 21 shows genome editing via homologous recombination. Figure 21 (a) shows the schematic of SpCas9 nickase, with D10A mutation in the RuvC I catalytic domain. (b) Schematic representing homologous recombination (HR) at the human EMXl locus using either sense or antisense single stranded oligonucleotides as repair templates. (c) Sequence of region modified by HR. d, SURVEYOR assay for wildtype (wt) and nickase (D10A) SpCas9-mediated indels at the EMX1 target 1 locus (n=3). Arrows indicate positions of expected fragment sizes.

[00336] In some embodiments, a Cas9 nickase may be used in combination with guide sequencers), e.g., two guide sequences, which target respectively sense and antisense strands of the DNA target. This combination allows both strands to be nicked and used to induce NHEJ. Applicants have demonstrated (data not shown) the efficacy of two nickase targets (i.e., sgRNAs targeted at the same location but to different strands of DNA) in inducing mutagenic NHEJ. A single nickase (Cas9-D10A with a single sgRNA) is unable to induce NHEJ and create indels but Applicants have shown that double nickase (Cas9-D10A and two sgRNAs targeted to different strands at the same location) can do so in human embryonic stem cells (hESCs). The efficiency is about 50% of nuclease (i.e., regular Cas9 without D10 mutation) in hESCs.

[00337] As a further example, two or more catalytic domains of Cas9 (RuvC I, RuvC II, and RuvC III) may be mutated to produce a mutated Cas9 substantially lacking all DNA cleavage activity. In some embodiments, a D10A mutation is combined with one or more of H840A, N854A, or N863A mutations to produce a Cas9 enzyme substantially lacking all DNA cleavage activity. In some embodiments, a CRISPR enzyme is considered to substantially lack ail DNA cleavage activity when the DNA cleavage activity of the mutated enzyme is less than about 25%,

10%, 5%, 1%, 0.1%, 0.01%, or lower with respect to its non-mutated form. Other mutations may be useful; where the Cas9 or other CRISPR enzyme is from a species other than *S. pyogenes*, mutations in corresponding amino acids may be made to achieve similar effects.

[00338] In some embodiments, an enzyme coding sequence encoding a CRISPR enzyme is codon optimized for expression in particular cells, such as eukaryotic cells. The eukaryotic cells may be those of or derived from a particular organism, such as a mammal, including but not limited to human, mouse, rat, rabbit, dog, or non-human primate. In general, codon optimization refers to a process of modifying a nucleic acid sequence for enhanced expression in the host cells of interest by replacing at least one codon (e.g. about or more than about 1, 2, 3, 4, 5, 10, 15, 20, 25, 50, or more a nions) of the native sequence with codons that are more frequently or most frequently used in the genes of that host cell while maintaining the native amino acid sequence. Various species exhibit particular bias for certain codons of a particular amino acid. Codon bias (differences in codon usage between organisms) often correlates with the efficiency of translation of messenger RNA (mRNA), which is in turn believed to be dependent on, among other things, the properties of the codons being translated and the availability of particular transfer RNA (tRNA) molecules. The predominance of selected tRNAs in a cell is generally a reflection of the codons used most frequently in peptide synthesis. Accordingly, genes can be tailored for optimal gene expression in a given organism based on codon optimization. Codon usage tables are readily available, for example, at the "Codon Usage Database", and these tables can be adapted in a number of ways. See Nakamura, Y., et al. "Codon usage tabulated from the international DNA sequence databases: status for the year 2000'Nucl. Acids Res. 28:292 (2000). Computer algorithms for codon optimizing a particular sequence for expression in a particular host cell are also available, such as Gene Forge (Aptagen; Jacobus, PA), are also available. in some embodiments, one or more codons (e.g. 1, 2, 3, 4, 5, 10, 15, 20, 25, 50, or more, or all codons) in a sequence encoding a CRISPR enzyme correspond to the most frequently used codon for a particular amino acid.

[00339] In general, a guide sequence is any polynucleotide sequence having sufficient complementarity with a target polynucleotide sequence to hybridize with the target sequence and direct sequence-specific binding of a CRISPR complex to the target sequence. In some embodiments, the degree of complementarity between a guide sequence and its corresponding target sequence, when optimally aligned using a suitable alignment algorithm, is about or more

than about 50%, 60%, 75%, 80%, 85%, 90%, 95%, 97.5%, 99%, or more. Optimal alignment may be determined with the use of any suitable algorithm for aligning sequences, non-limiting example of which include the Smith-Waterman algorithm, the Needleman-Wunsch algorithm, algorithms based on the Burrows-Wheeler Transform (e.g. the Burrows Wheeler Aligner), ClustalW, Clustal X, BLAT, Novoalign (Novocraft Technologies, ELAND (Illumina, San Diego, CA), SOAP (available at soap.genomics.org.cn), and Maq (available at maq.sourceforge.net). In some embodiments, a guide sequence is about or more than about 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 75, or more nucleotides in length. In some embodiments, a guide sequence is less than about 75, 50, 45, 40, 35, 30, 25, 20, 15, 12, or fewer nucleotides in length. The ability of a guide sequence to direct sequence-specific binding of a CRJSPR complex to a target sequence may be assessed by any suitable assay. For example, the components of a CRISPR system sufficient to form a CRISPR complex, including the guide sequence to be tested, may be provided to a host cell having the corresponding target sequence, such as by transfection with vectors encoding the components of the CRJSPR sequence, followed by an assessment of preferential cleavage within the target sequence, such as by Surveyor assay as described herein. Similarly, cleavage of a target polynucleotide sequence may be evaluated in a test tube by providing the target sequence, components of a CRISPR complex, including the guide sequence to be tested and a control guide sequence different from the test guide sequence, and comparing binding or rate of cleavage at the target sequence between the test and control guide sequence reactions. Other assays are possible, and will occur to those skilled in the art.

[00340] A guide sequence may be selected to target any target sequence. In some embodiments, the target sequence is a sequence within a genome of a cell. Exemplary target sequences include those that are unique in the target genome. For example, for the *S. pyogenes* Cas9, a unique target sequence in a genome may include a Cas9 target site of the form MMMMMMMMNNNNNNNNNNNNXGG where NNNNNNNNNNNNXGG (N is A, G, T, or C; and X can be anything) has a single occurrence in the genome. A unique target sequence in a genome may include an *S. pyogenes* Cas9 target site of the form MMMMMMMMMNNNNNNNNNNNXGG where NNNNNNNNNNNXGG (N is A, G, T, or C; and X can be anything) has a single occurrence in the genome. For the *S. thermophilus* CRISPRl Cas9, a unique target sequence in a genome may include a Cas9 target site of the form

MMMMMMMMNNNNNNNNNNNNXXAGAAW where NNNNNNNNNNNNXXAGAAW (N is A, G, T, or C; X can be anything; and W is A or T) has a single occurrence in the genome. A unique target sequence in a genome may include an *S. thermophilus* CRISPR1 Cas9 target site of the form MMMMMMMMMNNNNNNNNNNNXXAGAAW where N^TONNNNNNNXXAGAAW (N is A, G, T, or C; X can be anything; and W is A or T) has a single occurrence in the genome. For the *S. pyogenes* Cas9, a unique target sequence in a genome may include a Cas9 target site of the form MMMMMMMMNNNNNNNNNNNNXGGXG where NNNNNNNNNNNNXGGXG (N is A, G, T, or C; and X can be anything) has a single occurrence in the genome. A unique target sequence in a genome may include an *S. pyogenes* Cas9 target site of the form MMMMMMMMMNNNNNNNNNNNXGGXG where NNNNNNNNNNNXGGXG (N is A, G, T, or C; and X can be anything) has a single occurrence in the genome. In each of these sequences "M" may be A, G, T, or C, and need not be considered in identifying a sequence as unique.

[00341] In some embodiments, a guide sequence is selected to reduce the degree of secondary structure within the guide sequence. Secondary structure may be determined by any suitable polynucleotide folding algorithm. Some programs are based on calculating the minimal Gibbs free energy. An example of one such algorithm is mFold, as described by Zuker and Stiegler (Nucleic Acids Res. 9 (1981), 133-148). Another example folding algorithm is the online webserver RNAfold, developed at Institute for Theoretical Chemistry at the University of Vienna, using the centroid structure prediction algorithm (see e.g. A.R. Gruber *et al.*, 2008, *Cell* 106(1): 23-24; and PA Carr and GM Church, 2009, *Nature Biotechnology* 27(12): 1151-62). Further algorithms may be found in U.S. application Serial No. 61/836,080 (attorney docket 44790.1 1.2022; Broad Reference B1-2013/G04A); incorporated herein by reference.

[00342] In general, a tracr mate sequence includes any sequence that has sufficient complementarity with a tracr sequence to promote one or more of: (1) excision of a guide sequence flanked by tracr mate sequences in a cell containing the corresponding tracr sequence; and (2) formation of a CRISPR complex at a target sequence, wherein the CRISPR complex comprises the tracr mate sequence hybridized to the tracr sequence. In general, degree of complementarity is with reference to the optimal alignment of the tracr mate sequence and tracr sequence, along the length of the shorter of the two sequences. Optimal alignment may be

determined by any suitable alignment algorithm, and may further account for secondary structures, such as self-complementarity within either the tracr sequence or tracr mate sequence. In some embodiments, the degree of complementarity between the tracr sequence and tracr mate sequence along the length of the shorter of the two when optimally aligned is about or more than about 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97.5%, 99%, or higher. Example illustrations of optimal alignment between a tracr sequence and a tracr mate sequence are provided in Figures 10B and 11B. In some embodiments, the tracr sequence is about or more than about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 40, 50, or more nucleotides in length. In some embodiments, the tracr sequence and tracr mate sequence are contained within a single transcript, such that hybridization between the two produces a transcript having a secondary structure, such as a hairpin. Preferred loop forming sequences for use in hairpin structures are four nucleotides in length, and most preferably have the sequence GAAA. However, longer or shorter loop sequences may be used, as may alternative sequences. The sequences preferably include a nucleotide triplet (for example, AAA), and an additional nucleotide (for example C or G). Examples of loop forming sequences include CAAA and AAAG. In an embodiment of the invention, the transcript or transcribed polynucleotide sequence has at least two or more hairpins. In preferred embodiments, the transcript has two, three, four or five hairpins. In a further embodiment of the invention, the transcript has at most five hairpins. In some embodiments, the single transcript further includes a transcription termination sequence; preferably this is a polyT sequence, for example six T nucleotides. An example illustration of such a hairpin structure is provided in the lower portion of Figure 1IB, where the portion of the sequence 5' of the final "N" and upstream of the loop corresponds to the tracr mate sequence, and the portion of the sequence 3' of the loop corresponds to the tracr sequence. Further non-limiting examples of single polynucleotides comprising a guide sequence, a tracr mate sequence, and a tracr sequence are as follows (listed 5' to 3'), where "N" represents a base of a guide sequence, the first block of lower case letters represent the tracr mate sequence, and the second block of lower case letters represent the tracr sequence, and the final poly-T sequence represents the transcription terminator: (!) NNNNNNNNNN NNNNNNNNNN gtttttgtact ctcaagattt aGAAAtaaat cttgcagaag ctacaaagat aa.ggct.tcat gccgaaatca acaccctgtc attttatggc agggtgtttt cgttatttaa TTTTTT (SEQ ID NO:x); (2) NNNNNNNNNN NNNNNNNNNN gtttttgtac t.ctcaGAAAt gcagaagcta caaagataag gcttcatgcc gaaatcaaca ccctgtcatt ttatggcagg gtgttttcgt tatttaaTTT TTT (SEQ ID NO:x); (3) NNNNNNNNNN NNNNNNNNNN gtttttgtac tctcaGAAAt gcagaagcta caaagataag gcttcatgcc gaaatcaaca ccctgtcatt ttatggcagg gtgtTTTTTT (SEQ ID NO:x); (4) NNNNNNNNNN NNNNNNNNNN gttttagagc taGAAAtagc aagttaaaat aaggctagtc cgttatcaac ttgaaaaagt ggcaccgagt cggtgcTTTT TT (SEQ ID NO:x); (5) NNNNNNNNNN NNNNNNNNNN gttttagagc taGAAATAGc aagttaaaat aaggctagtc cgttatcaac ttgaaaaagt gTTTTTTT (SEQ ID NO:x); and (6) NNNNNNNNNN NNNNNNNNNN gttttagagc tagAAATAGc aagttaaaat aaggctagtc cgttatcaTT TTTTTT (SEQ ID NO:x)In some embodiments, sequences (1) to (3) are used in combination with Cas9 from *S. thermophilus* CRJ8PR1. In some embodiments, sequences (4) to (6) are used in combination with Cas9 from *S. pyogenes*. In some embodiments, the tracr sequence is a separate transcript from a transcript comprising the tracr mate sequence (such as illustrated in the top portion of Figure 1IB).

[00343] In some embodiments, the CRISPR enzyme is part of a fusion protein comprising one or more heterologous protein domains (e.g. about or more than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more domains in addition to the CRISPR enzyme). A CRISPR enzyme fusion protein may comprise any additional protein sequence, and optionally a linker sequence between any two domains. Examples of protein domains that may be fused to a CRISPR enzyme include, without limitation, epitope tags, reporter gene sequences, and protein domains having one or more of the following activities: methylase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity and nucleic acid binding activity. Non-limiting examples of epitope tags include histidine (His) tags, V5 tags, FLAG tags, influenza hemagglutinin (HA) tags, Myc tags, VSV-G tags, and thioredoxin (Trx) tags. Examples of reporter genes include, but are not limited to, glutathione-S-transferase (GST), horseradish peroxidase (HRP), chloramphenicol acetyltransferase (CAT) beta-galactosidase, beta-glucuronidase, luciferase, green fluorescent protein (GFP), HcRed, DsRed, cyan fluorescent protein (CFP), yellow fluorescent protein (YFP), and autofluorescent proteins including blue fluorescent protein (BFP). A CRISPR enzyme may be fused to a gene sequence encoding a protein or a fragment of a protein that bind DNA molecules or bind other cellular molecules, including but not limited to maltose binding protein (MBP), S-tag, Lex A DNA binding domain (DBD) fusions, GAL4 DNA

binding domain fusions, and herpes simplex virus (HSV) BP16 protein fusions. Additional domains that may form part of a fusion protein comprising a CRISPR enzyme are described in US20110059502, incorporated herein by reference. In some embodiments, a tagged CRISPR enzyme is used to identify the location of a target sequence.

[00344] In an aspect of the invention, a reporter gene which includes but is not limited to glutathione-S-transferase (GST), horseradish peroxidase (HRP), chloramphenicol acetyltransferase (CAT) beta-galactosidase, heta-glueuronidase, luciferase, green fluorescent protein (GFP), HcRed, DsRed, cyan fluorescent protein (CFP), yellow fluorescent protein (YFP), and autofluorescent proteins including blue fluorescent protein (BFP), may be introduced into a cell to encode a gene product which serves as a marker by which to measure the alteration or modification of expression of the gene product. In a further embodiment of the invention, the DNA molecule encoding the gene product may be introduced into the cell via a vector. In a preferred embodiment of the invention the gene product is luciferase. In a further embodiment of the invention the expression of the gene product is decreased.

[00345] In some aspects, the invention provides methods comprising delivering one or more polynucleotides, such as or one or more vectors as described herein, one or more transcripts thereof, and/or one or proteins transcribed therefrom, to a host cell. In some aspects, the invention further provides cells produced by such methods, and organisms (such as animals, plants, or fungi) comprising or produced from such cells. In some embodiments, a CRISPR enzyme in combination with (and optionally complexed with) a guide sequence is delivered to a cell. Conventional viral and non-viral based gene transfer methods can be used to introduce nucleic acids in mammalian cells or target tissues. Such methods can be used to administer nucleic acids encoding components of a CRISPR system to cells in culture, or in a host organism. Non-viral vector delivery systems include DNA plasmids, RNA (e.g. a transcript of a vector described herein), naked nucleic acid, and nucleic acid complexed with a delivery vehicle, such as a liposome. Viral vector delivery systems include DNA and RNA viruses, which have either episomal or integrated genomes after delivery to the cell. For a review of gene therapy procedures, see Anderson, Science 256:808-813 (1992); Nabel & Feigner, TIBTECH 11:211-217 (1993); Mitani & Caskey, TIBTECH 11:162-166 (1993); Dillon, TIBTECH 11:167-175 (1993); Miller, Nature 357:455-460 (1992); Van Brunt, Biotechnology 6(10):1149-1154 (1988); Vigne, Restorative Neurology and Neuroscience 8:35-36 (1995); Kremer & Perricaudet, British

Medical Bulletin 51(1):31-44 (1995); Haddada et al., in Current Topics in Microbiology and immunology Doerfler and Bohm (eds) (1995); and Yu et al., Gene Therapy 1:13-26 (1994).

[00346] Methods of non-viral delivery of nucleic acids include lipofection, nucleofection, microinjection, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipid:nucleic acid conjugates, naked DNA, artificial virions, and agent-enhanced uptake of DNA. lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam™ and Lipofectin™). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Feigner, WO 91/17424; WO 91/16024. Delivery can be to cells (e.g. in vitro or ex vivo administration) or target tissues (e.g. in vivo administration).

[00347] The preparation of lipid:nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, Science 270:404-410 (1995); Blaese et al., Cancer Gene Ther. 2:291-297 (1995); Behr et al, Bioconjugate Chem. 5:382-389 (1994); Remy et al., Bioconjugate Chem. 5:647-654 (1994); Gao et al, Gene Therapy 2:710-722 (1995); Ahmad et al., Cancer Res. 52:4817-4820 (1992); U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, and 4,946,787).

[00348] The use of RNA or DNA viral based systems for the delivery of nucleic acids take advantage of highly evolved processes for targeting a virus to specific cells in the body and trafficking the viral payload to the nucleus. Viral vectors can be administered directly to patients (in vivo) or they can be used to treat cells in vitro, and the modified cells may optionally be administered to patients (ex vivo). Conventional viral based systems could include retroviral, lentivirus, adenoviral, adeno-associated and herpes simplex virus vectors for gene transfer. Integration in the host genome is possible with the retrovirus, lentivirus, and adeno-associated virus gene transfer methods, often resulting in long term expression of the inserted transgene. Additionally, high transduction efficiencies have been observed in many different cell types and target tissues.

[00349] The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors that are able to transduce or infect non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system would therefore depend on the target tissue.

Retroviral vectors are comprised of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SIV), human immuno deficiency virus (HIV), and combinations thereof (see, e.g., Buchscher et al., J. Virol. 66:2731-2739 (1992); Johann et al, J. Virol. 66:1635-1640 (1992); Sommnerfelt et al., Virol. 176:58-59 (1990); Wilson et al, J. Virol. 63:2374-2378 (1989); Miller et al, J. Virol. 65:2220-2224 (1991); PCT/US94/05700).In applications where transient expression is preferred, adenoviral based systems may be used. Adenoviral based vectors are capable of very high transduction efficiency in many cell types and do not require cell division. With such vectors, high titer and levels of expression have been obtained. This vector can be produced in large quantities in a relatively simple system. Adeno-associated virus ("AAV") vectors may also be used to transduce cells with target nucleic acids, e.g., in the in vitro production of nucleic acids and peptides, and for in vivo and ex vivo gene therapy procedures (see, e.g., West et al., Virology 160:38-47 (1987); U.S. Pat. No. 4,797,368; WO 93/24641; Kotin, Human Gene Therapy 5:793-801 (1994); Muzyczka, J. Clin. Invest. 94:1351 (1994). Construction of recombinant AAV vectors are described in a number of publications, including U.S. Pat. No. 5,173,414; Tratschin et al., Mol. Cell. Biol. 5:3251-3260 (1985); Tratschin, et al, Mol. Cell. Biol. 4:2072-2081 (1984); Hermonat & Muzyczka, PNAS 81:6466-6470 (1984); and Samulski et al, J. Virol. 63:03822-3828 (1989).

[00350] Packaging cells are typically used to form virus particles that are capable of infecting a host cell. Such cells include 293 cells, which package adenovirus, and ψ2 cells or PA317 cells, which package retrovirus. Viral vectors used in gene therapy are usually generated by producing a cell line that packages a nucleic acid vector into a viral particle. The vectors typically contain the minimal viral sequences required for packaging and subsequent integration into a host, other viral sequences being replaced by an expression cassette for the polynucleotide(s) to be expressed. The missing viral functions are typically supplied in trans by the packaging cell line. For example, AAV vectors used in gene therapy typically only possess ITR sequences from the AAV genome which are required for packaging and integration into the host genome. Viral DNA is packaged in a cell line, which contains a helper plasmid encoding the other AAV genes,

namely rep and cap, but lacking ITR sequences. The cell line may also be infected with adenovirus as a helper. The helper vims promotes replication of the AAV vector and expression of AAV genes from the helper piasmid. The helper plasmid is not packaged in significant amounts due to a lack of ITR sequences. Contamination with adenovirus can be reduced by, e.g., heat treatment to which adenovirus is more sensitive than AAV. Additional methods for the delivery of nucleic acids to cells are known to those skilled in the art. See, for example, US20030087817, incorporated herein by reference.

[00351] In some embodiments, a host cell is transiently or non-transiently transfected with one or more vectors described herein. In some embodiments, a cell is transfected as it naturally occurs in a subject. In some embodiments, a cell that is transfected is taken from a subject. In some embodiments, the cell is derived from cells taken from a subject, such as a cell line. A wide variety of cell lines for tissue culture are known in the art. Examples of cell lines include, but are not limited to, C8161, CCRF-CEM, MOLT, mIMCD-3, NHDF, HeL,a-S3, Huhl, Huh4, Huh7, HUVEC, HASMC, HEKn, HEKa, MiaPaCeli, Panel, PC-3, TF1, CTLL-2, C1R, Rat6, CV1, RPTE, A10, T24, J82, A375, ARH-77, Calu1, SW480, SW620, SKOV3, SK-UT, CaCo2, P388D1, SEM-K2, WEHI-231, HB56, TIB55, Jurkat, J45.01, LRMB, Bcl-1, BC-3, IC21, DLD2, Raw264.7, NRK, NRK-52E, MRC5, MEF, Hep G2, HeLa B, HeLa T4, COS, COS-1, COS-6, COS-M6A, BS-C-1 monkey kidney epithelial, BALB/ 3T3 mouse embryo fibroblast, 3T3 Swiss, 3T3-L1, 132-d5 human fetal fibroblasts; 10.1 mouse fibroblasts, 293-T, 3T3, 721, 9L, A2780, A2780ADR, A2780cis, A172, A20, A253, A431, A-549, ALC, B16, B35, BCP-1 cells, BEAS-2B, bEnd.3, BHK-21, BR 293, BxPC3, C3H-10T1/2, C6/36, Cal-27, CHO, CHO-7, CHO-IR, CHO-K1, CHO-K2, CeO-T, CHO Dhfr -/-, COR-L23, COR-L23/CPR, COR-L23/5010, COR-L23/R23, COS-7, COV-434, CML Tl, CMT, CT26, D17, DH82, DU145, DuCaP, EL4, EM2, EM3, EMT6/AR1, EMT6/AR10.0, FM3, H1299, H69, HB54, HB55, HCA2, HEK-293, HeLa, Hepalclc7, HL-60, HMEC, HT-29, Jurkat, JY cells, K562 cells, Ku812, KCL22, KG1, KYOl, LNCap, Ma-Mel 1-48, MC-38, MCF-7, MCF-IOA, MDA-MB-231, MDA-MB-468, MDA-MB-435, MDCK II, MDCK II, MOR/0.2R, MONO-MAC 6, MTD-1A, MyEnd, NCI-H69/CPR, NCI-H69/LX10, NCI-H69/LX20, NCI-H69/LX4, NIH-3T3, NALM-1, NW-145, OPCN / OPCT cell lines, Peer, PNT-1A / PNT 2, RenCa, RIN-5F, RMA/RMAS, Saos-2 cells, Sf-9, SkBr3, T2, T-47D, T84, THPl cell line, U373, U87, U937, VCaP, Vero cells, WM39, WT-49, X63, YAC-1, YAR, and transgenic varieties thereof. Cell lines are available from a variety of sources known

to those with skill in the art (see, e.g., the American Type Culture Collection (ATCC) (Manassus, Va.)). In some embodiments, a cell transfected with one or more vectors described herein is used to establish a new cell line comprising one or more vector-derived sequences. In some embodiments, a cell transiently transfected with the components of a CRISPR system as described herein (such as by transient transfection of one or more vectors, or transfection with RNA), and modified through the activity of a CRISPR complex, is used to establish a new cell line comprising cells containing the modification but lacking any other exogenous sequence. In some embodiments, cells transiently or non-transiently transfected with one or more vectors described herein, or cell lines derived from such cells are used in assessing one or more test compounds.

[00352] In some embodiments, one or more vectors described herein are used to produce a non-human transgenic animal or transgenic plant. In some embodiments, the transgenic animal is a mammal, such as a mouse, rat, or rabbit. In certain embodiments, the organism or subject is a plant. In certain embodiments, the organism or subject or plant is algae. Methods for producing transgenic plants and animals are known in the art, and generally begin with a method of cell transfection, such as described herein. Transgenic animals are also provided, as are transgenic plants, especially crops and algae. The transgenic animal or plant may be useful in applications outside of providing a disease model. These may include food or feed production through expression of, for instance, higher protein, carbohydrate, nutrient or vitamins levels than would normally be seen in the wildtype. In this regard, transgenic plants, especially pulses and tubers, and animals, especially mammals such as livestock (cows, sheep, goats and pigs), but also poultry and edible insects, are preferred.

[00353] Transgenic algae or other plants such as rape may be particularly useful in the production of vegetable oils or biofuels such as alcohols (especially methanol and ethanol), for instance. These may be engineered to express or overexpress high levels of oil or alcohols for use in the oil or biofuel industries.

[00354] In one aspect, the invention provides for methods of modifying a target polynucleotide in a eukaryotic cell, which may be in vivo, ex vivo or in vitro. In some embodiments, the method comprises sampling a cell or population of cells from a human or non-human animal or plant (including micro-algae), and modifying the cell or cells. Culturing may

occur at any stage ex vivo. The cell or cells may even be re-introduced into the non-human animal or plant (including micro-algae).

[00355] In one aspect, the invention provides for methods of modifying a target polynucleotide in a eukaryotic cell. In some embodiments, the method comprises allowing a CRISPR complex to bind to the target polynucleotide to effect cleavage of said target polynucleotide thereby modifying the target polynucleotide, wherein the CRISPR complex comprises a CRISPR enzyme complexed with a guide sequence hybridized to a target sequence within said target polynucleotide, wherein said guide sequence is linked to a tracr mate sequence which in turn hybridizes to a tracr sequence.

[00356] In one aspect, the invention provides a method of modifying expression of a polynucleotide in a eukaryotic cell. In some embodiments, the method comprises allowing a CRISPR complex to bind to the polynucleotide such that said binding results in increased or decreased expression of said polynucleotide; wherein the CRISPR complex comprises a CRISPR enzyme complexed with a guide sequence hybridized to a target sequence within said polynucleotide, wherein said guide sequence is linked to a tracr mate sequence which in turn hybridizes to a tracr sequence.

[00357] With recent advances in crop genomics, the ability to use CRISPR-Cas systems to perform efficient and cost effective gene editing and manipulation will allow the rapid selection and comparison of single and and multiplexed genetic manipulations to transform such genomes for improved production and enhanced traits. In this regard reference is made to US patents and publications: US Patent No. 6,603,061 - Agrobacterium-Mediated Plant Transformation Method; US Patent No. 7,868,149 - Plant Genome Sequences and Uses Thereof and US 2009/0100536 - Transgenic Plants with Enhanced Agronomic Traits, all the contents and disclosure of each of which are herein incorporated by reference in their entirety. In the practice of the invention, the contents and disclosure of Morrell et al "Crop genomics: advances and applications" Nat Rev Genet. 2011 Dec 29;13(2):85-96 are also herein incorporated by reference in their entirety. In an advantageous embodiment of the invention, the CRISPR/Cas9 system is used to engineer microalgae. That the CRISPR-Cas system is able to be employed in plant systems is also provided in the manuscript "Efficient Genome Editing in Plants using a CRISPR/Cas System", by Feng et al. Cell Res. 2013 Aug 20. doi: 10.1038/cr.2013.114. [Epub ahead of print], incorporated by reference in its entirety, wherein it is demonstrated that

engineered CRISPR/Cas complexes may be used to create double strand breaks at specific sites of the plant genome to achieve targeted genome modifications in both dicot and monocot plants. Accordingly, reference herein to animal cells may also apply, mutatis mutandis, to plant cells unless otherwise apparent.

[00358] In plants, pathogens are often host-specific. For example, *Fusarium oxysporum* f. sp. *lycopersici* causes tomato wilt but attacks only tomato, and *F. oxysporum f. dianthii Puccinia graminis* f. sp. *tritici* attacks only wheat. Plants have existing and induced defenses to resist most pathogens. Mutations and recombination events across plant generations lead to genetic variability that gives rise to susceptibility, especially as pathogens reproduce with more frequency than plants. In plants there can be non-host resistance, e.g., the host and pathogen are incompatible. There can also be Horizontal Resistance, e.g., partial resistance against all races of a pathogen, typically controlled by many genes and Vertical Resistance, e.g., complete resistance to some races of a pathogen but not to other races, typically controlled by a few genes. In a Gene-for-Gene level, plants and pathogens evolve together, and the genetic changes in one balance changes in other. Accordingly, using Natural Variability, breeders combine most useful genes for Yield, Quality, Uniformity, Hardiness, Resistance. The sources of resistance genes include native or foreign Varieties, Heirloom Varieties, Wild Plant Relatives, and Induced Mutations, e.g., treating plant material with mutagenic agents. Using the present invention, plant breeders are provided with a new tool to induce mutations. Accordingly, one skilled in the art can analyze the genome of sources of resistance genes, and in Varieties having desired characteristics or traits employ the present invention to induce the rise of resistance genes, with more precision than previous mutagenic agents and hence accelerate and improve plant breeding programs.

[00359] In one aspect, the invention provides kits containing any one or more of the elements disclosed in the above methods and compositions. In some embodiments, the kit comprises a vector system and instructions for using the kit. In some embodiments, the vector system comprises (a) a first regulatory element operably linked to a tracr mate sequence and one or more insertion sites for inserting a guide sequence upstream of the tracr mate sequence, wherein when expressed, the guide sequence directs sequence-specific binding of a CRISPR complex to a target sequence in a eukaryotic cell, wherein the CRISPR complex comprises a CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr

mate sequence that is hybridized to the tracr sequence; and/or (b) a second regulatory element operably linked to an enzyme-coding sequence encoding said CRISPR enzyme comprising a nuclear localization sequence. Elements may be provided individually or in combinations, and may be provided in any suitable container, such as a vial, a bottle, or a tube. In some embodiments, the kit includes instructions in one or more languages, for example in more than one language.

[00360] In some embodiments, a kit comprises one or more reagents for use in a process utilizing one or more of the elements described herein. Reagents may be provided in any suitable container. For example, a kit may provide one or more reaction or storage buffers. Reagents may be provided in a form that is usable in a particular assay, or in a form that requires addition of one or more other components before use (e.g. in concentrate or lyophilized form). A buffer can be any buffer, including but not limited to a sodium carbonate buffer, a sodium bicarbonate buffer, a borate buffer, a Tris buffer, a MOPS buffer, a HEPES buffer, and combinations thereof. In some embodiments, the buffer is alkaline. In some embodiments, the buffer has a pH from about 7 to about 10. In some embodiments, the kit comprises one or more oligonucleotides corresponding to a guide sequence for insertion into a vector so as to operably link the guide sequence and a regulatory element. In some embodiments, the kit comprises a homologous recombination template polynucleotide.

[00361] In one aspect, the invention provides methods for using one or more elements of a CRISPR system. The CRISPR complex of the invention provides an effective means for modifying a target polynucleotide. The CRISPR complex of the invention has a wide variety of utility including modifying (e.g., deleting, inserting, translocating, inactivating, activating) a target polynucleotide in a multiplicity of cell types. As such the CRISPR complex of the invention has a broad spectrum of applications in, e.g., gene therapy, drug screening, disease diagnosis, and prognosis. An exemplary CRISPR complex comprises a CRISPR enzyme complexed with a guide sequence hybridized to a target sequence within the target polynucleotide. The guide sequence is linked to a tracr mate sequence, which in turn hybridizes to a tracr sequence.

[00362] The target polynucleotide of a CRISPR complex can be any polynucleotide endogenous or exogenous to the eukaryotic cell. For example, the target polynucleotide can be a polynucleotide residing in the nucleus of the eukaryotic cell. The target polynucleotide can be a

sequence coding a gene product (e.g., a protein) or a non-coding sequence (e.g., a regulatory polynucleotide or a junk DNA). The tareget can be a control element or a regulatory element or a promoter or an enhancer or a silencer. The promoter may, in some embodiments, be in the region of +200bp or even +1000 bp from the TTS. In some embodiments, the regulatory region may be an enhancer. The enhancer is typically more than +1000 bp from the TTS. More in particular, expression of eukaryotic protein-coding genes generally is regulated through multiple cis-acting transcription-control regions. Some control elements are located close to the start site (promoter-proximal elements), whereas others lie more distant (enhancers and silencers) Promoters determine the site of transcription initiation and direct binding of RNA polymerase II. Three types of promoter sequences have been identified in eukaryotic DNA. The TATA box, the most common, is prevalent in rapidly transcribed genes. Initiator promoters infrequently are found in some genes, and CpG islands are characteristic of transcribed genes. Promoter-proximal elements occur within about 200 base pairs of the start site. Several such elements, containing up to about 20 base pairs, may help regulate a particular gene. Enhancers, which are usually about 100-200 base pairs in length, contain multiple 8- to 20-bp control elements. They may be located from 200 base pairs to tens of kilobases upstream or downstream from a promoter, within an intron, or downstream from the final exon of a gene. · Promoter-proximal elements and enhancers may be cell-type specific, functioning only in specific differentiated cell types. However, any of these regions can be the target sequence and are encompassed by the concept that the tareget can be a control element or a regulatory element or a promoter or an enhancer or a silencer.

[0363] Without wishing to be bound by theory, it is believed that the target sequence should be associated with a PAM (protospacer adjacent motif); that is, a short sequence recognized by the CRISPR complex. The precise sequence and length requirements for the PAM differ depending on the CRISPR enzyme used, but PAMs are typically 2-5 base pair sequences adjacent the protospacer (that is, the target sequence) Examples of PAM sequences are given in the examples section below, and the skilled person will be able to identify further PAM sequences for use with a given CRISPR enzyme.

[0364] The target polynucleotide of a CRISPR complex may include a number of disease-associated genes and polynucleotides as well as signaling biochemical pathway-associated genes and polynucleotides as listed in US provisional patent applications 61/736,527 and 61/748,427 having **Broad** reference **BI-2011/008/WSGR** Docket No. 44063-701.101 and BI-

2011/008/WSGR Docket No. 44063-701 .102 respectively, both entitled SYSTEMS METHODS AND COMPOSITIONS FOR SEQUENCE MANIPULATION filed on December 12, 2012 and January 2, 2013, respectively, the contents of all of which are herein incorporated by reference in their entirety.

[00365] Examples of target polynucleotides include a sequence associated with a signaling biochemical pathway, e.g., a signaling biochemical pathway-associated gene or polynucleotide. Examples of target polynucleotides include a disease associated gene or polynucleotide. A "disease-associated" gene or polynucleotide refers to any gene or polynucleotide which is yielding transcription or translation products at an abnormal level or in an abnormal form in cells derived from a disease-affected tissues compared with tissues or cells of a non disease control. It may be a gene that becomes expressed at an abnormally high level; it may be a gene that becomes expressed at an abnormally low level, where the altered expression correlates with the occurrence and/or progression of the disease. A disease-associated gene also refers to a gene possessing mutation(s) or genetic variation that is directly responsible or is in linkage disequilibrium with a gene(s) that is responsible for the etiology of a disease. The transcribed or translated products may be known or unknown, and may be at a normal or abnormal level.

[00366] Examples of disease-associated genes and polynucleotides are available from McKusick-Nathans institute of Genetic Medicine, Johns Hopkins University (Baltimore, Md.) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, Md.), available on the World Wide Web.

[00367] Examples of disease-associated genes and polynucleotides are listed in Tables A and B. Disease specific information is available from McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University (Baltimore, Md.) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, Md.), available on the World Wide Web. Examples of signaling biochemical pathway-associated genes and polynucleotides are listed in Table C.

[00368] Mutations in these genes and pathways can result in production of improper proteins or proteins in improper amounts which affect function. Further examples of genes, diseases and proteins are hereby incorporated by reference from US Provisional application. Such genes, proteins and pathways may be the target polynucleotide of a CRISPR complex.

Table A

DISEASE/DISORDERS	GENE(S)
Neoplasia	PTEN; ATM; ATR; EGFR; ERBB2; ERBB3; ERBB4;
	Notch1; Notch2; Notch3; Notch4; AKT; AKT2; AKT3; HIF;
	HIF1a; HIF3a; Met; HRG; Bcl2; PPAR alpha; PPAR
	gamma; WT1 (Wilms Tumor); FGF Receptor Family
	members (5 members: 1, 2, 3, 4, 5); CDKN2a; APC; RB
	(retinoblastoma); MEN1; VHL; BRCA1; BRCA2; AR
	(Androgen Receptor); TSG101; IGF; IGF Receptor; Igf1 (4
	variants); Igf2 (3 variants); Igf 1 Receptor; Igf 2 Receptor;
	Bax; Bcl2; caspases family (9 members:
	1, 2, 3, 4, 6, 7, 8, 9, 12); Kras; Apc
Age-related Macular	Abcr; Ccl2; Cc2; cp (ceruloplasmin); Timp3; cathepsinD;
Degeneration	Vldlr; Ccr2
Schizophrenia	Neuregulin1 (Nrg1); Erb4 (receptor for Neuregulin);
	Complexin1 (Cplx1); Tph1 Tryptophan hydroxylase; Tph2
	Tryptophan hydroxylase 2; Neurexin 1; GSK3; GSK3a;
	GSK3b
Disorders	5-HTT (Slc6a4); COMT; DRD (Drd1a); SLC6A3; DAOA;
	DTNBP1; Dao (Dao1)
Trinucleotide Repeat	HTT (Huntington's Dx); SBMA/SMAX1/AR (Kennedy's
Disorders	Dx); FXN/X25 (Friedrich's Ataxia); ATX3 (Machado-
	Joseph's Dx); ATXN1 and ATXN2 (spinocerebellar
	ataxias); DMPK (myotonic dystrophy); Atrophin-1 and Atn1
	(DRPLA Dx); CBP (Creb-BP - global instability); VLDLR
	(Alzheimer's); Atxn7; Atxn10
Fragile X Syndrome	FMR2; FXR1; FXR2; mGLUR5
Secretase Related	APH-1 (alpha and beta); Presenilin (Psen1); nicastrin
Disorders	(Ncstn); PEN-2
Others	Nos1; Parp1; Nat1; Nat2
Prion - related disorders	Prp
ALS	SOD1; ALS2; STEX; FUS; TARDBP; VEGF (VEGF-a;
	VEGF-b; VEGF-c)
Drug addiction	Prkce (alcohol); Drd2; Drd4; ABAT (alcohol); GRIA2;
	Grm5; Grin1; Htr1b; Grin2a; Drd3; Pdyn; Gria1 (alcohol)
Autism	Mecp2; BZRAP1; MDGA2; Sema5A; Neurexin 1; Fragile X
	(FMR2 (AFF2); FXR1; FXR2; Mglur5)
Alzheimer's Disease	E1; CHIP; UCH; UBB; Tau; LRP; PICALM; Clusterin; PS1;
	SORL1; CR1; Vldlr; Uba1; Uba3; CHIP28 (Aqp1,
	Aquaporin 1); Uchl1; Uchl3; APP
Inflammation	IL-10; IL-1 (IL-1a; IL-1b); IL-13; IL-17 (IL-17a (CTLA8); IL-
	17b; IL-17c; IL-17d; IL-17f); Il-23; Cx3cr1; ptpn22; TNFa;
	NOD2/CARD15 for IBD; IL-6; IL-12 (IL-12a; IL-12b);

	CTLA4; Cx3cll
jParkinson's Disease	α-Synuclein; DJ-1; LRRK2; Parkin; PINK1

Table B:

Blood and coagulation diseases and disorders	Anemia (CDAN1, CDA1, RPS19, DBA, PKLR, PK1, NT5C3, UMPei, PSN1, RHAG, RH50A, NRAMP2, Sf*TB, ALAS2, ANH1, ASB, ABCB7, ABC7, ASAT); Bare lymphocyte syndrome (TAPBP, TPSN, TAP2, ABCB3, PSF2, RING11, MHC2TA, C2TA, RFX5, RFXAP, RFX5), Bleeding disorders (TBXA2R, P2RX1, P2X1); Factor H and factor H-like 1 (HF1, CFH, HUS); Factor V and factor VIII (MCFD2); Factor VII deficiency (F7); Factor X deficiency (F10); Factor XI deficiency (F11); Factor XII deficiency (F12, HAF); Factor XIIIA deficiency (F13A1, FDA); Factor XIIIB deficiency (F13B); Fanconi anemia (FANCA, FACA, FAl, FA, FAA, FAAP95, FAAP90, FLJ34064, FANCB, FANCC, FACC, BRCA2, FANCD1, FANCD2, FANCD, FACD, FAD, FANCE, FACE, FANCF, XRCC9, FANCG, BRIP1, BACH1, FANCJ, PHF9, FANCL, FANCM, KIAA1596); Hemophagocytic lymphohistiocytosis disorders (PRF1, HPLH2, UNCI 3D, MUNCI3-4, HPLH3, HLH3, FHL3); Hemophilia A (F8, F8C, HEMA); Hemophilia B (F9, HEMB), Hemorrhagic disorders (PI, ATT, F5); Leukocyde deficiencies and disorders (ITGB2, CD18, LCAMB, LAD, EIF2B1, EIF2BA, EIF2B2, EIF2B3, EIF2B5, LVWM, CACH, CLE, EIF2B4); Sickle cell anemia (HBB); Thalassemia (HBA2, HBB, HBD, LCRB, HBA1).
Cell dysregulation and oncology diseases and disorders	B-cell non-Hodgkin lymphoma (BCL7A, BCL7); Leukemia (TALI, TCL5, SCL, TAL2, FLT3, NBS1, NBS, ZNFN1AL IK1, LYF1, HOXD4, HOX4B, BCR, CMl., PHL, ALL, ARNT, KRAS2, RASK2, GMPS, AF10, ARHGEF12, LARG, KIAA0382, CALM, CLTFJ, CEBPA, CEBP, CHIC2, BTL, FLT3, KIT, PBT, LPP, NPM1, NUP214, D9S46E, CAN, CAIN, RUNX1, CBFA2, AML1, WHSC1L1, NSD3, FLT3, AF1Q, NPM1, NUMAL ZNFI45, PLZF, PML, MYL, STAT5B, AFIO, CALM, CLTH, ARLl 1, ARLTSl, P2RX7, P2X7, BCR, CML, PHL, ALL, GRAF, NF1, VRNF, WSS, NFNS, PTPN11, PTP2C, SHP2, NS1, BCL2, CCND1, PRAD1, BCL1, TCRA, GATA1, GF1, ERYF1, NFEl, ABL1, NQOl, DIA4, NMOR1, NUP214, D9S46E, CAN, CAIN).
inflammation and immune related diseases and disorders	AIDS (KIR3DL1, NKAT3, NKB1, AMBl 1, KIR3DS1, IFNG, CXCL12, SDF1); Autoimmune lymphoproliferative syndrome (TNFRSF6, APT1, FAS, CD95, ALPS1A); Combined immunodeficiency, (IL2RG, SCIDXl, SCIDX, IMD4); HIV-1 (CCL5, SCYA5, D17S136E, TCP228), HIV susceptibility or infection (IL10, CSIF, CMKBR2, CCR2, CMKBR5, CCCKR5 (CCR5)); Immunodeficiencies (CD3E, CD3G, AICDA, AID, HIGM2, TNFRSF5, CD40, UNG, DGU, HIGM4, TNFSF5, CD40LG, HIGM1, !G\1. FOXP3, IPEX, AIID, XPID, PIDX,

	TNFRSF14B, TACI); Inflammation (IL-!O, IL-1 (IL-1a, IL-!b), IL-13, IL-17 (IL-17a (CTLA8), IL-17b, IL-17c, IL-17d, IL~17f), 11-23, Cx3crl, ptpn22, TNFa, NOD2/CARD15 for IBD, IL-6, IL-12 (IL-12a, IL-12b), CTLA4, Cx3cil); Severe combined immunodeficiencies (SCIDs)(JAK3, JAKL, DCLRE1C, ARTEMIS, SCIDA, RAG1, RAG2, ADA, PTPRC, CD45, LCA, IL7R, CD3D, T3D, IL2RG, SCIDX1, SCIDX, IMD4).
Metabolic, liver, kidney and protein diseases and disorders	Amyloid neuropathy (TTR, PALB); Amyloidosis (APOAl, APP, AAA, CVAP, ADl, GSN, FGA, LYZ, TTR, PALB); Cirrhosis (KRT18, KRT8, CIRHl A, NAIC, TEX292, KIAA1988); Cystic fibrosis (CFTR, ABCC7, CF, MRP7); Glycogen storage diseases (SLC2A2, GLUT2, G6PC, G6PT, G6PT1, GAA, LAMP2, LAMPB, AGL, GDE, GBE1, GYS2, PYGL, PFKM); Hepatic adenoma, 142330 (TCF1, HNF1A, MODY3), Hepatic failure, early onset, and neurologic disorder (SCOD1, SCO I), Hepatic lipase deficiency (L1PC), Hepatoblastoma, cancer and carcinomas (CTNNB1, PDGFRL, PDGRL, PRLTS, AXIN1, AXIN, CTNNB1, TP53, P53, LFS1, IGF2R, MPRL, MET, CASP8, MCH5; Medullary cystic kidney disease (UMOD, HNFJ, FJHN, MCKD2, ADMCKD2); Phenylketonuria (PAH, PKUL, QDPR, DHPR, PTS); Polycystic kidney and hepatic disease (FCYT, PKHD1, ARPKD, PKD1, PKD2, PKD4, PKDTS, PRKCSH, G19P1, PCLD, SEC63).
Muscular / Skeletal diseases and disorders	Becker muscular dystrophy (DMD, BMD, MYF6), Duchenne Muscular Dystrophy (DMD, BMD); Emery-Dreifoss muscular dystrophy (LMNA, LMN 1, EMD2, FPLD, CMD1A, HGPS, LGMD1B, LMNA, LMN1, EMD2, FPLD, CMD1A); Facioscapulohumeral muscular dystrophy (FSHMD1A, FSHDIA); Muscular dystrophy (FKRP, MDC1C, LGMD2I, LAMA2, LAMM, LARGE, KIAA0609, MDC1D, FCMD, TTID, MYOT, CAPN3, CANP3, DYSF, LGMD2B, SGCG, LGMD2C, DMDA1, SCG3, SGCA, ADL, DAG2, LGMD2D, DMDA2, SGCB, LGMD2E, SGCD, SGD, LGMD2F, CMD1L, TCAP, LGMD2G, CMD1N, TRIM32, HT2A, LGMD2H, FKRP, MDC1C, LGMD2I, TTN, CMD1G, TMD, LGMD2J, POMT1, CAV3, LGMD1C, SEPN1, SELN, RSMD1, PLEC1, PLTN, EBS1); Osteopetrosis (LRP5, BMND1, LRP7, LR3, OPPG, VBCH2, CLCN7, CLC7, OPTA2, OSTM1, GL, TCIRGL, TIRC7, OC116, OPTB1); Muscular atrophy (VAPB, VAPC, ALS8, SMN1, SMAl, SMA2, SMA3, SMA4, BSCL2, SPG17, GARS, SMAD1, CMT2D, HEXB, IGHMBP2, SMUBP2, CATF1, SMARDl).
Neurological and neuronal diseases and disorders	ALS (SOD1, ALS2, STEX, FUS, TARDBP, VEGF (VEGF-a, VEGF-b, VEGF-c); Alzheimer disease (APP, AAA, CVAP, ADl, APOE, AD2, PSEN2, AD4, STM2, APBB2, FE65L1, NOS3, PLAU, URK, ACE, DCP1, ACE1, MPO, PACIPL, PAXIP1L, PTIP, A2M, BLMH, BMH, PSEN1, AD3); Autism (Mecp2, BZRAP1, MDGA2, SemaSA, Neurexin 1, GLOl, MECP2, RTT, PPMX, MRX16, MRX79, NLGN3, NLGN4, KIAA1260, AUTSX2); Fragile X Syndrome (FMR2, FXR1, FXR2,

	mGLURS); Huntington's disease and disease like disorders (HD, IT15, PRNP, PRIP, JPH3, JP3, HDL2, TBP, SCA17); Parkinson disease (NR4A2, NURR1, NOT, TINUR, SNCAIP, TBP, SCA17, SNCA, NACP, PARK1, PARK4, DJ1, PARK7, LRRK2, PARKS, PINK1, PARK6, UCHL1, PARKS, SNCA, NACP, PARK1, PARK4, PRKN, PARK2, PDJ, DBH, NDUFV2); Rett syndrome (MECP2, RTT, PPMX, MRX16, MRX79, CDKL5, STK9, MECP2, RTT, PPMX, MRX16, MRX79, x-Synuclein, DJ-l); Schizophrenia (Neuregulinl (Nrgl), Erb4 (receptor for Neuregulm), Complexinl (Cplxl), Tphl Tryptophan hydroxylase, Tph2, Tryptophan hydroxylase 2, Neurexin 1, G8K3, GSK3a, GSK3b, 5-HTT (Slc6a4), COMT, DRD (Drdla), SLC6A3, DAOA, DTNBP1, Dao (Daol)); Secretase Related Disorders (APH-1 (alpha and beta), Preseniiin (Psenl), nicastrin, (Ncstn), PEN-2, Nosl, Parpl, Natl, Nat2); Trinucleotide Repeat Disorders (HTT (Huntington's Dx), SBMA/SMAXl/AR (Kennedy's Dx), FXN/X25 (Friedrich's Ataxia), ATX3 (Machado- Joseph's Dx), ATXN1 and ATXN2 (spinocerebellar ataxias), DMPK (myotonic dystrophy), Atrophin-1 and Atnl (DRPLA Dx), CBP (Creb-BP - global instability), VLDLR (Alzheimer's), Atxn7, AtxnlO).
Occular diseases and disorders	Age-related macular degeneration (Abcr, Ccl2, Cc2, cp (ceruiopiasmin), Timp3, cathepsinD, Vldlr, Ccr2); Cataract (CRYAA, CRYAl, CRYBB2, CRYB2, PITX3, BFSP2, CP49, CP47, CRYAA, CRYAl , PAX6, AN2, MGDA, CRYBAl, CRYB1, CRYGC, CRYG3, CCL, LIM2, MP19, CRYGD, CRYG4, BFSP2, CP49, CP47, HSF4, CTM, HSF4, CTM, MIP, AQPO, CRYAB, CRYA2, CTPP2, CRYBBl, CRYGD, CRYG4, CRYBB2, CRYB2, CRYGC, CRYG3, CCL, CRYAA, CRYAL, GJA8, CX50, GAEL, GJA3, CX46, CZP3, CAE3, CCMl, CAM, KRIT1); Corneal clouding and dystrophy (APOA1, TGFBI, CSD2, CDGG1, CSD, BIGH3, CDG2, TACSTD2, TROP2, MlSl, VSXL, RINX, PPCD, PPD, KTCN, COL8A2, FECD, PPCD2, PIP5K3, CFD); Cornea plana congenital (KERA, CNA2); Glaucoma (MYOC, TIGR, GLC1A, JOAG, GPOA, OPTN, GLC1E, FIP2, HYPL, NRP, CYP1BL, GLC3A, OPAL, NTG, NPG, CYP1B1, GLC3A); Leber congenital amaurosis (CRB1, RP12, CRX, CORD2, CRD, RPGRIP1, LCA6, CORD9, RPE65, RP20, AIPLl, LCA4, GUCY2D, GUC2D, LCA1, CORD6, RDH12, LCA3); Macular dystrophy (ELOVL4, ADMD, STGD2, STGD3, RDS, RP7, PRPH2, PRPH, AVMD, AOFMD, VMD2).

Table C:

CELLULAR FUNCTION	GENES
PL3K/AKT Signaling	PRKCE; ITGAM; ITGA5; IRAKI; PRKAA2; EIF2AK2;
	PTEN; EIF4E; PRKCZ; GRK6; MAPK1; TSC1; PLK1;
	AKT2; IKBKB; PIK3CA; CDK8; CDKN1B; NFKB2; BCL2;
	PIK3CB; PPP2R1A; MAPK8; BCL2L1; MAPK3; TSC2;

	ITGA1; KRAS; EIF4EBP1; RELA; PRKCD; NOS3;
	PRKAA1; MAPK9; CDK2; PPP2CA; PIM1; ITGB7;
	YWHAZ; ILK; TP53; RAF1; IKBKG; RELB; DYRK1A;
	CDKN1A; ITGB1; MAP2K2; JAK1; AKT1; JAK2; PIK3R1;
	CHUK; PDPK1; PPP2R5C; CTNNB1; MAP2K1; NFKB1;
	PAK3; ITGB3; CCND1; GSK3A; FRAP1; SFN; ITGA2;
	TTK; CSNK1A1; BRAF; GSK3B; AKT3; FOXO1; SGK;
	HSP90AA1; RPS6KB1
ERK/MAPK Signaling	PRKCE; ITGAM; ITGA5; HSPB1; IRAK1; PRKAA2;
	EIF2AK2; RAC1; RAP1A; TLN1; EIF4E; ELK1; GRK6;
	MAPK1; RAC2; PLK1; AKT2; PIK3CA; CDK8; CREB1;
	PRKCI; PTK2; FOS; RPS6KA4; PIK3CB; PPP2R1A;
	PIK3C3; MAPK8; MAPK3; ITGA1; ETS1; KRAS; MYCN;
	EIF4EBP1; PPARG; PRKCD; PRKAA1; MAPK9; SRC;
	CDK2; PPP2CA; PIM1; PIK3C2A; ITGB7; YWHAZ;
	PPP1CC; KSR1; PXN; RAF1; FYN; DYRK1A; ITGB1;
	MAP2K2; PAK4; PIK3R1; STAT3; PPP2R5C; MAP2K1;
	PAK3; ITGB3; ESR1; ITGA2; MYC; TTK; CSNK1A1;
	CRKL; BRAF; ATF4; PRKCA; SRF; STAT1; SGK
Glucocorticoid Receptor	RAC1; TAF4B; EP300; SMAD2; TRAF6; PCAF; ELK1;
Signaling	MAPK1; SMAD3; AKT2; IKBKB; NCOR2; UBE2I;
	PIK3CA; CREB1; FOS; HSPA5; NFKB2; BCL2;
	MAP3K14; STAT5B; PIK3CB; PIK3C3; MAPK8; BCL2L1;
	MAPK3; TSC22D3; MAPK10; NRIP1; KRAS; MAPK13;
	RELA; STAT5A; MAPK9; NOS2A; PBX1; NR3C1;
	PIK3C2A; CDKN1C; TRAF2; SERPINE1; NCOA3;
	MAPK14; TNF; RAF1; IKBKG; MAP3K7; CREBBP;
	CDKN1A; MAP2K2; JAK1; IL8; NCOA2; AKT1; JAK2;
	PIK3R1; CHUK; STAT3; MAP2K1; NFKB1; TGFBR1;
	ESR1; SMAD4; CEBPB; JUN; AR; AKT3; CCL2; MMP1;
	STAT1; IL6; HSP90AA1
Axonal Guidance Signaling	PRKCE; ITGAM; ROCK1; ITGA5; CXCR4; ADAM12;
	IGF1; RAC1; RAP1A; EIF4E; PRKCZ; NRP1; NTRK2;
	ARHGEF7; SMO; ROCK2; MAPK1; PGF; RAC2;
	PTPN11; GNAS; AKT2; PIK3CA; ERBB2; PRKCI; PTK2;
	CFL1; GNAQ; PIK3CB; CXCL12; PIK3C3; WNT11;
	PRKD1; GNB2L1; ABL1; MAPK3; ITGA1; KRAS; RHOA;
	PRKCD; PIK3C2A; ITGB7; GLI2; PXN; VASP; RAF1;
	FYN; ITGB1; MAP2K2; PAK4; ADAM17; AKT1; PIK3R1;
	GLI1; WNT5A; ADAM10; MAP2K1; PAK3; ITGB3;
	CDC42; VEGFA; ITGA2; EPHA8; CRKL; RND1; GSK3B;
	AKT3; PRKCA
Ephrin Receptor	PRKCE; ITGAM; ROCK1; ITGA5; CXCR4; IRAK1;

Signaling	
	PRKAA2; EIF2AK2; RAC1; RAP1A; GRK6; ROCK2;
	MAPK1; PGF; RAC2; PTPN11; GNAS; PLK1; AKT2;
	DOK1; CDK8; CREB1; PTK2; CFL1; GNAQ; MAP3K14;
	CXCL12; MAPK8; GNB2L1; ABL1; MAPK3; ITGA1;
	KRAS; RHOA; PRKCD; PRKAA1; MAPK9; SRC; CDK2;
	PIM1; ITGB7; PXN; RAF1; FYN; DYRK1A; ITGB1;
	MAP2K2; PAK4; AKT1; JAK2; STAT3; ADAM10;
	MAP2K1; PAK3; ITGB3; CDC42; VEGFA; ITGA2;
	EPHA8; TTK; CSNK1A1; CRKL; BRAF; PTPN13; ATF4;
	AKT3; SGK
Actin Cytoskeleton	ACTN4; PRKCE; ITGAM; ROCK1; ITGA5; IRAK1;
Signaling	PRKAA2; EIF2AK2; RAC1; INS; ARHGEF7; GRK6;
	ROCK2; MAPK1; RAC2; PLK1; AKT2; PIK3CA; CDK8;
	PTK2; CFL1; PIK3CB; MYH9; DIAPH1; PIK3C3; MAPK8;
	F2R; MAPK3; SLC9A1; ITGA1; KRAS; RHOA; PRKCD;
	PRKAA1; MAPK9; CDK2; PIM1; PIK3C2A; ITGB7;
	PPP1CC; PXN; VIL2; RAF1; GSN; DYRK1A; ITGB1;
	MAP2K2; PAK4; PIP5K1A; PIK3R1; MAP2K1; PAK3;
	ITGB3; CDC42; APC; ITGA2; TTK; CSNK1A1; CRKL;
	BRAF; VAV3; SGK
Huntington's Disease	PRKCE; IGF1; EP300; RCOR1; PRKCZ; HDAC4; TGM2;
Signaling	MAPK1; CAPNS1; AKT2; EGFR; NCOR2; SP1; CAPN2;
	PIK3CA; HDAC5; CREB1; PRKCI; HSPA5; REST;
	GNAQ; PIK3CB; PIK3C3; MAPK8; IGF1R; PRKD1;
	GNB2L1; BCL2L1; CAPN1; MAPK3; CASP8; HDAC2;
	HDAC7A; PRKCD; HDAC11; MAPK9; HDAC9; PIK3C2A;
	HDAC3; TP53; CASP9; CREBBP; AKT1; PIK3R1;
	PDPK1; CASP1; APAF1; FRAP1; CASP2; JUN; BAX;
	ATF4; AKT3; PRKCA; CLTC; SGK; HDAC6; CASP3
Apoptosis Signaling	PRKCE; ROCK1; BID; IRAK1; PRKAA2; EIF2AK2; BAK1;
	BIRC4; GRK6; MAPK1; CAPNS1; PLK1; AKT2; IKBKB;
	CAPN2; CDK8; FAS; NFKB2; BCL2; MAP3K14; MAPK8;
	BCL2L1; CAPN1; MAPK3; CASP8; KRAS; RELA;
	PRKCD; PRKAA1; MAPK9; CDK2; PIM1; TP53; TNF;
	RAF1; IKBKG; RELB; CASP9; DYRK1A; MAP2K2;
	CHUK; APAF1; MAP2K1; NFKB1; PAK3; LMNA; CASP2;
	BIRC2; TTK; CSNK1A1; BRAF; BAX; PRKCA; SGK;
	CASP3; BIRC3; PARP1
B Cell Receptor Signaling	RAC1; PTEN; LYN; ELK1; MAPK1; RAC2; PTPN11;
	AKT2; IKBKB; PIK3CA; CREB1; SYK; NFKB2; CAMK2A;
	MAP3K14; PIK3CB; PIK3C3; MAPK8; BCL2L1; ABL1;
	MAPK3; ETS1; KRAS; MAPK13; RELA; PTPN6; MAPK9;

	EGR1; PIK3C2A; BTK; MAPK14; RAF1; IKBKG; RELB;
	MAP3K7; MAP2K2; AKT1; PIK3R1; CHUK; MAP2K1;
	NFKB1; CDC42; GSK3A; FRAP1; BCL6; BCL10; JUN;
	GSK3B; ATF4; AKT3; VAV3; RPS6KB1
Leukocyte Extravasation Signaling	ACTN4; CD44; PRKCE; ITGAM; ROCK1; CXCR4; CYBA;
	RAC1; RAP1A; PRKCZ; ROCK2; RAC2; PTPN11;
	MMP14; PIK3CA; PRKCI; PTK2; PIK3CB; CXCL12;
	PIK3C3; MAPK8; PRKD1; ABL1; MAPK10; CYBB;
	MAPK13; RHOA; PRKCD; MAPK9; SRC; PIK3C2A; BTK;
	MAPK14; NOX1; PXN; VIL2; VASP; ITGB1; MAP2K2;
	CTNND1; PIK3R1; CTNNB1; CLDN1; CDC42; F11R; ITK;
	CRKL; VAV3; CTTN; PRKCA; MMP1; MMP9
Integrin Signaling	ACTN4; ITGAM; ROCK1; ITGA5; RAC1; PTEN; RAP1A;
	TLN1; ARHGEF7; MAPK1; RAC2; CAPNS1; AKT2;
	CAPN2; PIK3CA; PTK2; PIK3CB; PIK3C3; MAPK8;
	CAV1; CAPN1; ABL1; MAPK3; ITGA1; KRAS; RHOA;
	SRC; PIK3C2A; ITGB7; PPP1CC; ILK; PXN; VASP;
	RAF1; FYN; ITGB1; MAP2K2; PAK4; AKT1; PIK3R1;
	TNK2; MAP2K1; PAK3; ITGB3; CDC42; RND3; ITGA2;
	CRKL; BRAF; GSK3B; AKT3
Acute Phase Response Signaling	IRAK1; SOD2; MYD88; TRAF6; ELK1; MAPK1; PTPN11;
	AKT2; IKBKB; PIK3CA; FOS; NFKB2; MAP3K14;
	PIK3CB; MAPK8; RIPK1; MAPK3; IL6ST; KRAS;
	MAPK13; IL6R; RELA; SOCS1; MAPK9; FTL; NR3C1;
	TRAF2; SERPINE1; MAPK14; TNF; RAF1; PDK1;
	IKBKG; RELB; MAP3K7; MAP2K2; AKT1; JAK2; PIK3R1;
	CHUK; STAT3; MAP2K1; NFKB1; FRAP1; CEBPB; JUN;
	AKT3; IL1R1; IL6
PTEN Signaling	ITGAM; ITGA5; RAC1; PTEN; PRKCZ; BCL2L11;
	MAPK1; RAC2; AKT2; EGFR; IKBKB; CBL; PIK3CA;
	CDKN1B; PTK2; NFKB2; BCL2; PIK3CB; BCL2L1;
	MAPK3; ITGA1; KRAS; ITGB7; ILK; PDGFRB; INSR;
	RAF1; IKBKG; CASP9; CDKN1A; ITGB1; MAP2K2;
	AKT1; PIK3R1; CHUK; PDGFRA; PDPK1; MAP2K1;
	NFKB1; ITGB3; CDC42; CCND1; GSK3A; ITGA2;
	GSK3B; AKT3; FOXO1; CASP3; RPS6KB1
p53 Signaling	PTEN; EP300; BBC3; PCAF; FASN; BRCA1; GADD45A;
	BIRC5; AKT2; PIK3CA; CHEK1; TP53INP1; BCL2;
	PIK3CB; PIK3C3; MAPK8; THBS1; ATR; BCL2L1; E2F1;
	PMAIP1; CHEK2; TNFRSF10B; TP73; RB1; HDAC9;
	CDK2; PIK3C2A; MAPK14; TP53; LRDD; CDKN1A;
	HIPK2; AKT1; PIK3R1; RRM2B; APAF1; CTNNB1;
	SIRT1; CCND1; PRKDC; ATM; SFN; CDKN2A; JUN;
	SNAI2; GSK3B; BAX; AKT3

Aryl Hydrocarbon Receptor	HSPB1; EP300; FASN; TGM2; RXRA; MAPK1; NQO1;
Signaling	NCOR2; SP1; ARNT; CDKN1B; FOS; CHEK1;
	SMARCA4; NFKB2; MAPK8; ALDH1A1; ATR; E2F1;
	MAPK3; NRIP1; CHEK2; RELA; TP73; GSTP1; RB1;
	SRC; CDK2; AHR; NFE2L2; NCOA3; TP53; TNF;
	CDKN1A; NCOA2; APAF1; NFKB1; CCND1; ATM; ESR1;
	CDKN2A; MYC; JUN; ESR2; BAX; IL6; CYP1B1;
	HSP90AA1
Xenobiotic Metabolism	PRKCE; EP300; PRKCZ; RXRA; MAPK1; NQO1;
Signaling	NCOR2; PIK3CA; ARNT; PRKCI; NFKB2; CAMK2A;
	PIK3CB; PPP2R1A; PIK3C3; MAPK8; PRKD1;
	ALDH1A1; MAPK3; NRIP1; KRAS; MAPK13; PRKCD;
	GSTP1; MAPK9; NOS2A; ABCB1; AHR; PPP2CA; FTL;
	NFE2L2; PIK3C2A; PPARGC1A; MAPK14; TNF; RAF1;
	CREBBP; MAP2K2; PIK3R1; PPP2R5C; MAP2K1;
	NFKB1; KEAP1; PRKCA; EIF2AK3; IL6; CYP1B1;
	HSP90AA1
SAPK/JNK Signaling	PRKCE; IRAK1; PRKAA2; EIF2AK2; RAC1; ELK1;
	GRK6; MAPK1; GADD45A; RAC2; PLK1; AKT2; PIK3CA;
	FADD; CDK8; PIK3CB; PIK3C3; MAPK8; RIPK1;
	GNB2L1; IRS1; MAPK3; MAPK10; DAXX; KRAS;
	PRKCD; PRKAA1; MAPK9; CDK2; PIM1; PIK3C2A;
	TRAF2; TP53; LCK; MAP3K7; DYRK1A; MAP2K2;
	PIK3R1; MAP2K1; PAK3; CDC42; JUN; TTK; CSNK1A1;
	CRKL; BRAF; SGK
PPAr/RXR Signaling	PRKAA2; EP300; INS; SMAD2; TRAF6; PPARA; FASN;
	RXRA; MAPK1; SMAD3; GNAS; IKBKB; NCOR2;
	ABCA1; GNAQ; NFKB2; MAP3K14; STAT5B; MAPK8;
	IRS1; MAPK3; KRAS; RELA; PRKAA1; PPARGC1A;
	NCOA3; MAPK14; INSR; RAF1; IKBKG; RELB; MAP3K7;
	CREBBP; MAP2K2; JAK2; CHUK; MAP2K1; NFKB1;
	TGFBR1; SMAD4; JUN; IL1R1; PRKCA; IL6; HSP90AA1;
	ADIPOQ
NF-KB Signaling	IRAK1; EIF2AK2; EP300; INS; MYD88; PRKCZ; TRAF6;
	TBK1; AKT2; EGFR; IKBKB; PIK3CA; BTRC; NFKB2;
	MAP3K14; PIK3CB; PIK3C3; MAPK8; RIPK1; HDAC2;
	KRAS; RELA; PIK3C2A; TRAF2; TLR4; PDGFRB; TNF;
	INSR; LCK; IKBKG; RELB; MAP3K7; CREBBP; AKT1;
	PIK3R1; CHUK; PDGFRA; NFKB1; TLR2; BCL10;
	GSK3B; AKT3; TNFAIP3; IL1R1
Neuregulin Signaling	ERBB4; PRKCE; ITGAM; ITGA5; PTEN; PRKCZ; ELK1;
	MAPK1; PTPN11; AKT2; EGFR; ERBB2; PRKCI;
	CDKN1B; STAT5B; PRKD1; MAPK3; ITGA1; KRAS;

	PRKCD; STAT5A; SRC; ITGB7; RAF1; ITGB1; MAP2K2;
	ADAM17; AKT1; PIK3R1; PDPK1; MAP2K1; ITGB3;
	EREG; FRAP1; PSEN1; ITGA2; MYC; NRG1; CRKL;
	AKT3; PRKCA; HSP90AA1; RPS6KB1
Wnt & Beta catenin	CD44; EP300; LRP6; DVL3; CSNK1E; GJA1; SMO;
Signaling	AKT2; PIN1; CDH1; BTRC; GNAQ; MARK2; PPP2R1A;
	WNT11; SRC; DKK1; PPP2CA; SOX6; SFRP2; ILK;
	LEF1; SOX9; TP53; MAP3K7; CREBBP; TCF7L2; AKT1;
	PPP2R5C; WNT5A; LRP5; CTNNB1; TGFBR1; CCND1;
	GSK3A; DVL1; APC; CDKN2A; MYC; CSNK1A1; GSK3B;
	AKT3; SOX2
Insulin Receptor Signaling	PTEN; INS; EIF4E; PTPN1; PRKCZ; MAPK1; TSC1;
	PTPN11; AKT2; CBL; PIK3CA; PRKCI; PIK3CB; PIK3C3;
	MAPK8; IRS1; MAPK3; TSC2; KRAS; EIF4EBP1;
	SLC2A4; PIK3C2A; PPP1CC; INSR; RAF1; FYN;
	MAP2K2; JAK1; AKT1; JAK2; PIK3R1; PDPK1; MAP2K1;
	GSK3A; FRAP1; CRKL; GSK3B; AKT3; FOXO1; SGK;
	RPS6KB1
IL-6 Signaling	HSPB1; TRAF6; MAPKAPK2; ELK1; MAPK1; PTPN11;
	IKBKB; FOS; NFKB2; MAP3K14; MAPK8; MAPK3;
	MAPK10; IL6ST; KRAS; MAPK13; IL6R; RELA; SOCS1;
	MAPK9; ABCB1; TRAF2; MAPK14; TNF; RAF1; IKBKG;
	RELB; MAP3K7; MAP2K2; IL8; JAK2; CHUK; STAT3;
	MAP2K1; NFKB1; CEBPB; JUN; IL1R1; SRF; IL6
Hepatic Cholestasis	PRKCE; IRAK1; INS; MYD88; PRKCZ; TRAF6; PPARA;
	RXRA; IKBKB; PRKCI; NFKB2; MAP3K14; MAPK8;
	PRKD1; MAPK10; RELA; PRKCD; MAPK9; ABCB1;
	TRAF2; TLR4; TNF; INSR; IKBKG; RELB; MAP3K7; IL8;
	CHUK; NR1H2; TJP2; NFKB1; ESR1; SREBF1; FGFR4;
	JUN; IL1R1; PRKCA; IL6
IGF-1 Signaling	IGF1; PRKCZ; ELK1; MAPK1; PTPN11; NEDD4; AKT2;
	PIK3CA; PRKCI; PTK2; FOS; PIK3CB; PIK3C3; MAPK8;
	IGF1R; IRS1; MAPK3; IGFBP7; KRAS; PIK3C2A;
	YWHAZ; PXN; RAF1; CASP9; MAP2K2; AKT1; PIK3R1;
	PDPK1; MAP2K1; IGFBP2; SFN; JUN; CYR61; AKT3;
	FOXO1; SRF; CTGF; RPS6KB1
NRF2-mediated Oxidative	PRKCE; EP300; SOD2; PRKCZ; MAPK1; SQSTM1;
Stress Response	NQO1; PIK3CA; PRKCI; FOS; PIK3CB; PIK3C3; MAPK8;
	PRKD1; MAPK3; KRAS; PRKCD; GSTP1; MAPK9; FTL;
	NFE2L2; PIK3C2A; MAPK14; RAF1; MAP3K7; CREBBP;
	MAP2K2; AKT1; PIK3R1; MAP2K1; PPIB; JUN; KEAP1;
	GSK3B; ATF4; PRKCA; EIF2AK3; HSP90AA1

Hepatic Fibrosis/Hepatic	EDN1; IGF1; KDR; FLT1; SMAD2; FGFR1; MET; PGF;
Stellate Cell Activation	SMAD3; EGFR; FAS; CSF1; NFKB2; BCL2; MYH9;
	IGF1R; IL6R; RELA; TLR4; PDGFRB; TNF; RELB; IL8;
	PDGFRA; NFKBl; TGFBR1; SMAD4; VEGFA; BAX;
	IL1R1; CCL2; HGF; MMP1; STAT1; IL6; CTGF; MMP9
PPAR Signaling	EP300; INS; TRAF6; PPARA; RXRA; MAPKl; IKBKB;
	NCOR2; FOS; NFKB2; MAP3K14; STATSB; MAPK3;
	NRIPl; KRAS; PPARG; RELA; STAT5A; TRAF2;
	PPARGC1A; PDGFRB; TNF; INSR; RAF1; iKBKG;
	RELB; MAP3K7; CREBBP; MAP2K2; CHUK; PDGFRA;
	MAP2K1; NFKBl; JUN; IL1R1; HSP90AA1
Fc Epsiion RI Signaling	PRKCE; RAC1; PRKCZ; LYN; MAPKl; RAC2; PTPN11;
	AKT2; PIK3CA; SYK; PRKCI; PIK3CB; PIK3C3; MAPK8;
	PRKD1; MAPK3; MAPKIQ; KRAS; MAPKl 3; PRKCD;
	MAPK9; PIK3C2A; BTK; MAPKl 4; TNF; RAF1; FYN;
	MAP2K2; AKTl; PIK3R1 ; PDPKl; MAP2KI ; AKT3;
	VAV3; PRKCA
G-Protein Coupled	PRKCE; RAP1A; RGS16; MAPKl ; GNAS; AKT2; IKBKB;
Receptor Signaling	PIK3CA; CREB1; GNAQ; NFKB2; CAMK2A; PIK3CB;
	PIK3C3; MAPK3; KRAS; RELA; SRC; PIK3C2A; RAF1;
	IKBKG; RELB; FYN; MAP2K2; AKT1; PIK3R1; CHUK;
	PDPKl; STAT3; MAP2K1; NFKBl; BRAF; ATF4; AKT3;
	PRKCA
Inositol Phosphate	PRKCE; IRAKI; PRKAA2; EIF2AK2; PTEN; GRK6;
Metabolism	MAPKl; PLK1 ; AKT2; PIK3CA; CDK8; PIK3CB; PIK3C3;
	MAPK8; MAPK3; PRKCD; PRKAA1; MAPK9; CDK2;
	PIM1; PIK3C2A; DYRKIA; MAP2K2; PIP5K1A; PIK3R1;
	MAP2K1; PAK3; ATM; TTK; CSNKIAI; BRAF; SGK
PDGF Signaling	EIF2AK2; ELK1; ABL2; MAPKl; PIK3CA; FOS; PIK3CB;
	PIK3C3; MAPK8; CAV1; ABLl; MAPK3; KRAS; SRC;
	PIK3C2A; PDGFRB; RAF I; MAP2K2; JAK1; JAK2;
	PIK3R1; PDGFRA; STAT3; SPHK1; MAP2K1; MYC;
	JUN; CRKL; PRKCA; SRF; STAT1; SPHK2
VEGF Signaling	ACTN4; ROCK1; KDR; FLTl; ROCK2; MAPKl; PGF;
	AKT2; PIK3CA; ARNT; PTK2; BCL2; PIK3CB; PIK3C3;
	BCL2L1; MAPK3; KRAS; HIF1A; N0S3; PIK3C2A; PXN;
	RAF1; MAP2K2; ELAVL1; AKT1; PIK3R1; MAP2K1; SFN;
	VEGFA; AKT3; FOXOl; PRKCA
Natural Killer Cell Signaling	PRKCE; RACl; PRKCZ; MAPKl; RAC2; PTPN11;
	K1R2DL3; AKT2; PIK3CA; SYK; PRKCI; PIK3CB;
	PIK3C3; PRKD1; MAPK3; KRAS; PRKCD; PTPN6;
	PIK3C2A; LCK; RAF1; FYN; MAP2K2; PAK4; AKTl;
	PIK3R1; MAP2K1; PAK3; AKT3; VAV3; PRKCA

Cell Cycle: G1/S	HDAC4; SMAD3; SUV39H1; HDAC5; CDKN1B; BTRC;
Checkpoint Regulation	ATR; ABL1; E2F1; HDAC2; HDAC7A; RB1; HDAC11;
	HDAC9; CDK2; E2F2; HDAC3; TP53; CDKN1A; CCND1;
	E2F4; ATM; RBL2; SMAD4; CDKN2A; MYC; NRG1;
	GSK3B; RBL1; HDAC6
T Cell Receptor Signaling	RAC1; ELK1; MAPK1; IKBKB; CBL; PIK3CA; FOS;
	NFKB2; PIK3CB; PIK3C3; MAPK8; MAPK3; KRAS;
	RELA; PIK3C2A; BTK; LCK; RAF1; IKBKG; RELB; FYN;
	MAP2K2; PIK3R1; CHUK; MAP2K1; NFKB1; ITK; BCL10;
	JUN; VAV3
Death Receptor Signaling	CRADD; HSPB1; BID; BIRC4; TBK1; IKBKB; FADD;
	FAS; NFKB2; BCL2; MAP3K14; MAPK8; RIPK1; CASP8;
	DAXX; TNFRSF10B; RELA; TRAF2; TNF; IKBKG; RELB;
	CASP9; CHUK; APAF1; NFKB1; CASP2; BIRC2; CASP3;
	BIRC3
FGF Signaling	RAC1; FGFR1; MET; MAPKAPK2; MAPK1; PTPN11;
	AKT2; PIK3CA; CREB1; PIK3CB; PIK3C3; MAPK8;
	MAPK3; MAPK13; PTPN6; PIK3C2A; MAPK14; RAF1;
	AKT1; PIK3R1; STAT3; MAP2K1; FGFR4; CRKL; ATF4;
	AKT3; PRKCA; HGF
GM-CSF Signaling	LYN; ELK1; MAPK1; PTPN11; AKT2; PIK3CA; CAMK2A;
	STAT5B; PIK3CB; PIK3C3; GNB2L1; BCL2L1; MAPK3;
	ETS1; KRAS; RUNX1; PIM1; PIK3C2A; RAF1; MAP2K2;
	AKT1; JAK2; PIK3R1; STAT3; MAP2K1; CCND1; AKT3;
	STAT1
Amyotrophic Lateral	BID; IGF1; RAC1; BIRC4; PGF; CAPNS1; CAPN2;
Sclerosis Signaling	PIK3CA; BCL2; PIK3CB; PIK3C3; BCL2L1; CAPN1;
	PIK3C2A; TP53; CASP9; PIK3R1; RAB5A; CASP1;
	APAF1; VEGFA; BIRC2; BAX; AKT3; CASP3; BIRC3
JAK/Stat Signaling	PTPN1; MAPK1; PTPN11; AKT2; PIK3CA; STAT5B;
	PIK3CB; PIK3C3; MAPK3; KRAS; SOCS1; STAT5A;
	PTPN6; PIK3C2A; RAF1; CDKN1A; MAP2K2; JAK1;
	AKT1; JAK2; PIK3R1; STAT3; MAP2K1; FRAP1; AKT3;
	STAT1
Nicotinate and Nicotinamide	PRKCE; IRAK1; PRKAA2; EIF2AK2; GRK6; MAPK1;
Metabolism	PLK1; AKT2; CDK8; MAPK8; MAPK3; PRKCD; PRKAA1;
	PBEF1; MAPK9; CDK2; PIM1; DYRK1A; MAP2K2;
	MAP2K1; PAK3; NT5E; TTK; CSNK1A1; BRAF; SGK
Chemokine Signaling	CXCR4; ROCK2; MAPK1; PTK2; FOS; CFL1; GNAQ;
	CAMK2A; CXCL12; MAPK8; MAPK3; KRAS; MAPK13;
	RHOA; CCR3; SRC; PPP1CC; MAPK14; NOX1; RAF1;
	MAP2K2; MAP2K1; JUN; CCL2; PRKCA

IL-2 Signaling	ELK1; MAPK1; PTPN11; AKT2; PIK3CA; SYK; FOS;
	STAT5B; PIK3CB; PIK3C3; MAPK8; MAPK3; KRAS;
	SOCS1; STAT5A; PIK3C2A; LCK; RAF1; MAP2K2;
	JAK1; AKT1; PIK3R1; MAP2K1; JUN; AKT3
Synaptic Long Term Depression	PRKCE; IGF1; PRKCZ; PRDX6; LYN; MAPK1; GNAS;
	PRKCI; GNAQ; PPP2R1A; IGF1R; PRKD1; MAPK3;
	KRAS; GRN; PRKCD; NOS3; NOS2A; PPP2CA;
	YWHAZ; RAF1; MAP2K2; PPP2R5C; MAP2K1; PRKCA
Estrogen Receptor Signaling	TAF4B; EP300; CARM1; PCAF; MAPK1; NCOR2;
	SMARCA4; MAPK3; NRIP1; KRAS; SRC; NR3C1;
	HDAC3; PPARGC1A; RBM9; NCOA3; RAF1; CREBBP;
	MAP2K2; NCOA2; MAP2K1; PRKDC; ESR1; ESR2
Protein Ubiquitination Pathway	TRAF6; SMURF1; BIRC4; BRCA1; UCHL1; NEDD4;
	CBL; UBE2I; BTRC; HSPA5; USP7; USP10; FBXW7;
	USP9X; STUB1; USP22; B2M; BIRC2; PARK2; USP8;
	USP1; VHL; HSP90AA1; BIRC3
IL-10 Signaling	TRAF6; CCR1; ELK1; IKBKB; SP1; FOS; NFKB2;
	MAP3K14; MAPK8; MAPK13; RELA; MAPK14; TNF;
	IKBKG; RELB; MAP3K7; JAK1; CHUK; STAT3; NFKB1;
	JUN; IL1R1; IL6
VDR/RXR Activation	PRKCE; EP300; PRKCZ; RXRA; GADD45A; HES1;
	NCOR2; SP1; PRKCI; CDKN1B; PRKD1; PRKCD;
	RUNX2; KLF4; YY1; NCOA3; CDKN1A; NCOA2; SPP1;
	LRP5; CEBPB; FOXO1; PRKCA
TGF-beta Signaling	EP300; SMAD2; SMURF1; MAPK1; SMAD3; SMAD1;
	FOS; MAPK8; MAPK3; KRAS; MAPK9; RUNX2;
	SERPINE1; RAF1; MAP3K7; CREBBP; MAP2K2;
	MAP2K1; TGFBR1; SMAD4; JUN; SMAD5
Toll-like Receptor Signaling	IRAK1; EIF2AK2; MYD88; TRAF6; PPARA; ELK1;
	IKBKB; FOS; NFKB2; MAP3K14; MAPK8; MAPK13;
	RELA; TLR4; MAPK14; IKBKG; RELB; MAP3K7; CHUK;
	NFKB1; TLR2; JUN
p38 MAPK Signaling	HSPB1; IRAK1; TRAF6; MAPKAPK2; ELK1; FADD; FAS;
	CREB1; DDIT3; RPS6KA4; DAXX; MAPK13; TRAF2;
	MAPK14; TNF; MAP3K7; TGFBR1; MYC; ATF4; IL1R1;
	SRF; STAT1
Neurotrophin/TRK Signaling	NTRK2; MAPK1; PTPN11; PIK3CA; CREB1; FOS;
	PIK3CB; PIK3C3; MAPK8; MAPK3; KRAS; PIK3C2A;
	RAF1; MAP2K2; AKT1; PIK3R1; PDPK1; MAP2K1;
	CDC42; JUN; ATF4
FXR/RXR Activation	INS; PPARA; FASN; RXRA; AKT2; SDC1; MAPK8;
	APOB; MAPK10; PPARG; MTTP; MAPK9; PPARGC1A;

	TNF; CREBBP; AKT1; SREBF1; FGFR4; AKT3; FOXO1
Synaptic Long Term	PRKCE; RAP1A; EP300; PRKCZ; MAPK1; CREB1;
Potentiation	PRKCI; GNAQ; CAMK2A; PRKD1; MAPK3; KRAS;
	PRKCD; PPP1CC; RAF1; CREBBP; MAP2K2; MAP2K1;
	ATF4; PRKCA
Calcium Signaling	RAP1A; EP300; HDAC4; MAPK1; HDAC5; CREB1;
	CAMK2A; MYH9; MAPK3; HDAC2; HDAC7A; HDAC11;
	HDAC9; HDAC3; CREBBP; CALR; CAMKK2; ATF4;
	HDAC6
EGF Signaling	ELK1; MAPK1; EGFR; PIK3CA; FOS; PIK3CB; PIK3C3;
	MAPK8; MAPK3; PIK3C2A; RAF1; JAK1; PIK3R1;
	STAT3; MAP2K1; JUN; PRKCA; SRF; STAT1
Hypoxia Signaling in the	EDN1; PTEN; EP300; NQO1; UBE2I; CREB1; ARNT;
Cardiovascular System	HIF1A; SLC2A4; NOS3; TP53; LDHA; AKT1; ATM;
	VEGFA; JUN; ATF4; VHL; HSP90AA1
LPS/IL-1 Mediated Inhibition	IRAK1; MYD88; TRAF6; PPARA; RXRA; ABCA1;
of RXR Function	MAPK8; ALDH1A1; GSTP1; MAPK9; ABCB1; TRAF2;
	TLR4; TNF; MAP3K7; NR1H2; SREBF1; JUN; IL1R1
LXR/RXR Activation	FASN; RXRA; NCOR2; ABCA1; NFKB2; IRF3; RELA;
	NOS2A; TLR4; TNF; RELB; LDLR; NR1H2; NFKB1;
	SREBF1; IL1R1; CCL2; IL6; MMP9
Amyloid Processing	PRKCE; CSNK1E; MAPK1; CAPNS1; AKT2; CAPN2;
	CAPN1; MAPK3; MAPK13; MAPT; MAPK14; AKT1;
	PSEN1; CSNK1A1; GSK3B; AKT3; APP
IL-4 Signaling	AKT2; PIK3CA; PIK3CB; PIK3C3; IRS1; KRAS; SOCS1;
	PTPN6; NR3C1; PIK3C2A; JAK1; AKT1; JAK2; PIK3R1;
	FRAP1; AKT3; RPS6KB1
Cell Cycle: G2/M DNA	EP300; PCAF; BRCA1; GADD45A; PLK1; BTRC;
Damage Checkpoint	CHEK1; ATR; CHEK2; YWHAZ; TP53; CDKN1A;
Regulation	PRKDC; ATM; SFN; CDKN2A
Nitric Oxide Signaling in the	KDR; FLT1; PGF; AKT2; PIK3CA; PIK3CB; PIK3C3;
Cardiovascular System	CAV1; PRKCD; NOS3; PIK3C2A; AKT1; PIK3R1;
	VEGFA; AKT3; HSP90AA1
Purine Metabolism	NME2; SMARCA4; MYH9; RRM2; ADAR; EIF2AK4;
	PKM2; ENTPD1; RAD51; RRM2B; TJP2; RAD51C;
	NT5E; POLD1; NME1
cAMP-mediated Signaling	RAP1A; MAPK1; GNAS; CREB1; CAMK2A; MAPK3;
	SRC; RAF1; MAP2K2; STAT3; MAP2K1; BRAF; ATF4
Mitochondrial Dysfunction	SOD2; MAPK8; CASP8; MAPK10; MAPK9; CASP9;
	PARK7; PSEN1; PARK2; APP; CASP3
Notch Signaling	HES1; JAG1; NUMB; NOTCH4; ADAM17; NOTCH2;

	PSEN1; NOTCH3; NOTCH1; DLL4
Endoplasmic Reticulum	HSPA5; MAPK8; XBP1; TRAF2; ATF6; CASP9; ATF4;
Stress Pathway	EIF2AK3; CASP3
Pyrimidine Metabolism	NME2; AICDA; RRM2; EIF2AK4; ENTPD1; RRM2B;
	NT5E; POLD1; NME1
Parkinson's Signaling	UCHL1; MAPK8; MAPK13; MAPK14; CASP9; PARK7;
	PARK2; CASP3
Cardiac & Beta Adrenergic	GNAS; GNAQ; PPP2R1A; GNB2L1; PPP2CA; PPP1CC;
Signaling	PPP2R5C
Glycolysis/Gluconeogenesis	HK2; GCK; GPI; ALDH1A1; PKM2; LDHA; HK1
Interferon Signaling	IRF1; SOCS1; JAK1; JAK2; IFITM1; STAT1; IFIT3
Sonic Hedgehog Signaling	ARRB2; SMO; GLI2; DYRK1A; GLI1; GSK3B; DYRK1B
Glycerophospholipid	PLD1; GRN; GPAM; YWHAZ; SPHK1; SPHK2
Metabolism	
Phospholipid Degradation	PRDX6; PLD1; GRN; YWHAZ; SPHK1; SPHK2
Tryptophan Metabolism	SIAH2; PRMT5; NEDD4; ALDH1A1; CYP1B1; SIAH1
Lysine Degradation	SUV39H1; EHMT2; NSD1; SETD7; PPP2R5C
Nucleotide Excision Repair	ERCC5; ERCC4; XPA; XPC; ERCC1
Pathway	
Starch and Sucrose	UCHL1; HK2; GCK; GPI; HK1
Metabolism	
Aminosugars Metabolism	NQO1; HK2; GCK; HK1
Arachidonic Acid	PRDX6; GRN; YWHAZ; CYP1B1
Metabolism	
Circadian Rhythm Signaling	CSNK1E; CREB1; ATF4; NR1D1
Coagulation System	BDKRB1; F2R; SERPINE1; F3
Dopamine Receptor	PPP2R1A; PPP2CA; PPP1CC; PPP2R5C
Signaling	
Glutathione Metabolism	IDH2; GSTP1; ANPEP; IDH1
Glycerolipid Metabolism	ALDH1A1; GPAM; SPHK1; SPHK2
Linoleic Acid Metabolism	PRDX6; GRN; YWHAZ; CYP1B1
Methionine Metabolism	DNMT1; DNMT3B; AHCY; DNMT3A
Pyruvate Metabolism	GLO1; ALDH1A1; PKM2; LDHA
Arginine and Proline	ALDH1A1; NOS3; NOS2A
Metabolism	
Eicosanoid Signaling	PRDX6; GRN; YWHAZ
Fructose and Mannose	HK2; GCK; HK1
Metabolism	

Galactose Metabolism	HK2; GCK; HK1
Stiibene, Coimiarine and	PRDX6; PRDX1; TYR
Lignin Biosynthesis	
Antigen Presentation	CALR; B2M
Pathway	
Biosynthesis of Steroids	NQOl; DHCR7
Butanoate Metabolism	ALDH1A1; NLGN1
Citrate Cycle	IDH2; IDHl
Fatty Acid Metabolism	ALDH1A1; CYP1B1
Glycerophospholipid	PRDX6; CHKA
Metabolism	
Histidine Metabolism	PRMT5; ALDH1A1
Inositol Metabolism	EROIL; APEXI
Metabolism of Xenobiotics	GSTP1 ; CYPiBl
by Cytochrome p450	
Methane Metabolism	PRDX6; PRTJX1
Phenylalanine Metabolism	PRDX6; PRDX1
Propanoate Metabolism	ALDH1A1; LDHA
Selenoamino Acid	PRMT5; AHCY
Metabolism	
Sphingolipid Metabolism	SPHK1; SPHK2
Aminophosphonate	PRMT5
Metabolism	
Androgen and Estrogen	PRMT5
Metabolism	
Ascorbate and Aldarate	ALDH1A1
Metabolism	
Bile Acid Biosynthesis	ALDHIAI
Cysteine Metabolism	LDHA
Fatty Acid Biosynthesis	FASN
Glutamate Receptor	GNB2L1
Signaling	
NRF2-mediated Oxidative	PRDX1
Stress Response	
Pentose Phosphate	GPI
Pathway	
Pentose and Glucuronate	UCHLl
Interconversions	
Retinol Metabolism	ALDHIAI
Riboflavin Metabolism	TYR
Tyrosine Metabolism	PRMT5, TYR
Ubiquinone Biosynthesis	PRMT5

Valine, Leucine and	ALDH1A1
Isoleucine Degradation	
Glycine, Serine and	CHKA
Threonine Metabolism	
Lysine Degradation	ALDH1A1
Pain/Taste	TRPM5; TRPA1
Pain	TRPVI7; TRPC5; TRPC6; TRPC1; Cnrl; cnr2; Grk2;
	Trpal; Pome; Cgrp; Crf; Pka; Era; Nr2b; TRPM5; Prkaca;
	Prkacb; Prkarla; Prkar2a
Mitochondrial Function	AIF; CytC; SMAC (Diablo); Aifm-1; Aifin-2
Developmental Neurology	BMP-4; Chordin (Chrd); Noggin (Nog); WNT (Wnt2;
	Wnt2b; Wnt3a; Wnt4; Wnt5a; Wnt6; Wnt7b; Wnt8b;
	Wnt9a; Wnt9b; WntlOa; WntlOb; Wntl6); beta-catenin;
	Dkk-1; Frizzled related proteins; Otx-2; Gbx2; FGF-8;
	Reelin; Dab1; une-86 (Pou4fl or Brn3a); Numb; Rein

[00369] Embodiments of the invention also relate to methods and compositions related to knocking out genes, amplifying genes and repairing particular mutations associated with DNA repeat instability and neurological disorders (Robert D. Wells, Tetsuo Ashizawa, Genetic instabilities and Neurological Diseases, Second Edition, Academic Press, Oct 13, 2011 - Medical). Specific aspects of tandem repeat sequences have been found to be responsible for more than twenty human diseases (New insights into repeat instability: role of RNA*DNA hybrids. Mclvor EI, Polak U, Napieraia M. RNA Biol. 2010 Sep-Oct;7(5):551-8). The CRISPR-Cas system may be harnessed to correct these defects of genomic instability.

[0G370] A further aspect of the invention relates to utilizing the CRISPR-Cas system for correcting defects in the EMP2A and EMP2B genes that have been identified to be associated with Lafora disease. Lafora disease is an autosomal recessive condition which is characterized by progressive myoclonus epilepsy which may start as epileptic seizures in adolescence. A few cases of the disease may be caused by mutations in genes yet to be identified. The disease causes seizures, muscle spasms, difficulty walking, dementia, and eventually death. There is currently no therapy that has proven effective against disease progression. Other genetic abnormalities associated with epilepsy may also be targeted by the CRISPR-Cas system and the underlying genetics is further described in Genetics of Epilepsy and Genetic Epilepsies, edited by Giuliano Avanzini, Jeffrey L. Noebels, Mariani Foundation Paediatric Neurology:20; 2009).

[00371] In yet another aspect of the invention, the CRISPR-Cas system may be used to correct ocular defects that arise from several genetic mutations further described in Genetic Diseases of the Eye, Second Edition, edited by Elias I. Traboulsi, Oxford University Press, 2012.

[00372] Several further aspects of the invention relate to correcting defects associated with a wide range of genetic diseases which are further described on the website of the National Institutes of Health under the topic subsection Genetic Disorders (website at health.nih.gov/topic/GeneticDisorders). The genetic brain diseases may include but are not limited to Adrenoleukodystrophy, Agenesis of the Corpus Callosum, Aicardi Syndrome, Alpers' Disease, Alzheimer's Disease, Barth Syndrome, Batten Disease, CADASIL, Cerebellar Degeneration, Fabry's Disease, Gerstmann-Siraussler-Scheinker Disease, Huntington's Disease and other Triplet Repeat Disorders, Leigh's Disease, Lesch-Nyhan Syndrome, Menkes Disease, Mitochondrial Myopathies and NINDS Colpocephaly. These diseases are further described on the website of the National Institutes of Health under the subsection Genetic Brain Disorders.

[00373] In some embodiments, the condition may be neoplasia. In some embodiments, where the condition is neoplasia, the genes to be targeted are any of those listed in Table A (in this case PTEN asn so forth). In some embodiments, the condition may be Age-related Macular Degeneration. In some embodiments, the condition may be a Schizophrenic Disorder. In some embodiments, the condition may be a Trinucleotide Repeat Disorder. In some embodiments, the condition may be Fragile X Syndrome. In some embodiments, the condition may be a Secretase Related Disorder. In some embodiments, the condition may be a Prion - related disorder. In some embodiments, the condition may be ALS. In some embodiments, the condition may be a drug addiction. In some embodiments, the condition may be Autism. In some embodiments, the condition may be Alzheimer's Disease. In some embodiments, the condition may be inflammation. In some embodiments, the condition may be Parkinson's Disease.

[00374] Examples of proteins associated with Parkinson's disease include but are not limited to a-synuclein, DJ~1, LRRK2, PINK1, Parkin, UCHL1, Synphilin-1, and NURR1.

[00375] Examples of addiction-related proteins may include ABAT for example.

[00376] Examples of inflammation-related proteins may include the monocyte chemoattractant protein-1 (MCP1) encoded by the Ccr2 gene, the C-C chemokine receptor type 5 (CCR5) encoded by the Ccr5 gene, the IgG receptor IIB (FCGR2b, also termed CD32) encoded

by the Fcgr2b gene, or the Fc epsilon Rig (FCERlg) protein encoded by the Fcerlg gene, for example.

[00377] Examples of cardiovascular diseases associated proteins may include IL1B (interleukin 1, beta), XDH (xanthine dehydrogenase), TP53 (tumor protein p53), PTG18 (prostaglandin I2 (prostacyclin) synthase), MB (myoglobin), IL4 (interleukin 4), ANGPTl (angiopoietin 1), ABCG8 (ATP-binding cassette, sub-family G (WHITE), member 8), or CTSK (cathepsin K), for example.

[00378] Examples of Alzheimer's disease associated proteins may include the very low density lipoprotein receptor protein (VLDLR) encoded by the VLDLR gene, the ubiquitin-like modifier activating enzyme 1 (UBA1) encoded by the UBA 1 gene, or the NEDD8-activating enzyme E1 catalytic subunit protein (UBE1C) encoded by the UBA3 gene, for example.

[00379] Examples of proteins associated Autism Spectrum Disorder may include the benzodiazapine receptor (peripheral) associated protein 1 (BZRAP1) encoded by the BZRAP! gene, the AF4/FMR2 family member 2 protein (AFF2) encoded by the AFF2 gene (also termed MFR2), the fragile X mental retardation autosomal homolog 1 protein (FXR1) encoded by the FXR1 gene, or the fragile X mental retardation autosomal homolog 2 protein (FXR2) encoded by the FXR2 gene, for example.

[00380] Examples of proteins associated Macular Degeneration may include the ATP-binding cassette, sub-family A (ABC1) member 4 protein (ABCA4) encoded by the ABCR gene, the apolipoprotein E protein (APOE) encoded by the APOE gene, or the chemokine (C-C motif) Ligand 2 protein (CCL2.) encoded by the CCL2 gene, for example.

[00381] Examples of proteins associated Schizophrenia may include NRG1, ErbB4, CPLX1, TPH1, TPH2, NRXNl, GSK3A, BDNF, DISCI, GSK3B, and combinations thereof.

[00382] Examples of proteins involved in tumor suppression may include ATM (ataxia telangiectasia mutated), ATR (ataxia telangiectasia and Rad3 related), EGFR (epidermal growth factor receptor), ERBB2 (v-erb-b2 erythroblastic leukemia viral oncogene homolog 2), ERBB3 (v-erb-b2 erythroblastic leukemia viral oncogene homolog 3), ERBB4 (v-erb-b2 erythroblastic leukemia viral oncogene homolog 4), Notch 1, Notcli2, Notch 3, or Notch 4, for example.

[00383] Examples of proteins associated with a secretase disorder may include PSENEN (presenilin enhancer 2 homolog (C. eiegans)), CTSB (cathepsin B), PSEN1 (presenilin 1), APP (amyloid beta (A4) precursor protein), APH1B (anterior pharynx defective 1 homolog B (C.

elegans)), PSEN2 (presenilin 2 (Alzheimer disease 4)), or BACE1 (beta-site APP-cleaving enzyme 1), for example.

[00384] Examples of proteins associated with Amyotrophic Lateral Sclerosis may include SOD! (superoxide dismutase 1), ALS2 (amyotrophic lateral sclerosis 2), FUS (fused in sarcoma), TARDBP (TAR DNA binding protein), VAGFA (vascular endothelial growth factor A), VAGFB (vascular endothelial growth factor B), and VAGFC (vascular endothelial growth factor C), and any combination thereof.

[00385] Examples of proteins associated with prion diseases may include SODl (superoxide dismutase 1), ALS2 (amyotrophic lateral sclerosis 2), FUS (fused in sarcoma), TARDBP (TAR DNA binding protein), VAGFA (vascular endothelial growth factor A), VAGFB (vascular endothelial growth factor B), and VAGFC (vascular endothelial growth factor C), and any combination thereof.

[00386] Examples of proteins related to neurodegenerative conditions in prion disorders may include A2M (Alpha-2-Macroglobulin), AATF (Apoptosis antagonizing transcription factor), ACPP (Acid phosphatase prostate), ACTA2 (Actin alpha 2 smooth muscle aorta), ADAM22 (ADAM metallopeptidase domain), ADORA3 (Adenosine A3 receptor), or ADRA1D (Alpha-1D adrenergic receptor for Alpha-1D adrenoreceptor), for example.

[00387] Examples of proteins associated with Immunodeficiency may include A2M [alpha-2-macroglobulin]; AANAT [arylalkylamine N-acetyltransferase] ; ABCA1 [ATP-binding cassette, sub-family A (ABC!), member !]; ABCA2 [ATP-binding cassette, sub-family A (ABCl), member 2]; or ABCA3 [ATP-binding cassette, sub-family A (ABCl), member 3]; for example.

[00388] Examples of proteins associated with Trinucleotide Repeat Disorders include AR (androgen receptor), FMR1 (fragile X mental retardation 1), HTT (huntingtin), or DMPK (dystrophia myotonica-protein kinase), FXN (frataxin), ATXN2 (ataxin 2), for example.

[00389] Examples of proteins associated with Neurotransmission Disorders include SST (somatostatin), NOS! (nitric oxide synthase 1 (neuronal)), ADRA2A (adrenergic, aipha-2A-, receptor), ADRA2C (adrenergic, alpha-2C-, receptor), TACR1 (tachykinin receptor 1), or HTR2c (5-hydroxytryptamine (serotonin) receptor 2C), for example.

[00390] Examples of neurodevelopmental-associated sequences include A2BP! [ataxin 2-binding protein 1], AADAT [aminoadipate aminotransferase], AANAT [arylalkylamine N-acety!transferase], ABAT [4-aminobutyrate aminotransferase], ABCA! [ATP-binding cassette.

sub-family A (ABC1), member 1], or ABCA13 [ATP-binding cassette, sub-family A (ABC1), member 13], for example.

[00391] Further examples of preferred conditions treatable with the present system include may be selected from: Aicardi-Goutieres Syndrome; Alexander Disease; Allan-Herndon-Dudley Syndrome; POLG-Related Disorders; Alpha-Mannosidosis (Type II and III); Alstrom Syndrome; Angelman; Syndrome; Ataxia-Telangiectasia; Neuronal Ceroid-Lipofuscinoses; Beta-Thalassemia; Bilateral Optic Atrophy and (infantile) Optic Atrophy Type 1; Retinoblastoma (bilateral); Canavan Disease; Cerebrooculofacioskeletal Syndrome 1 [COFS1]; Cerebrotendinous Xanthomatosis; Cornelia de Lange Syndrome; MAPT-Related Disorders; Genetic Prion Diseases; Dravet Syndrome; Early-Onset Familial Alzheimer Disease; Friedreich Ataxia [FRDA]; Fryns Syndrome; Fucosidosis; Fukuyama Congenital Muscular Dystrophy; Galactosialidosis; Gaucher Disease; Organic Acidemias; Hemophagocytic Lymphohistiocytosis; Hutchinson-Gilford Progeria Syndrome; Mucolipidosis II; Infantile Free Sialic Acid Storage Disease; PLA2G6-Associated Neurodegeneration; Jervell and Lange-Nielsen Syndrome; Junctional Epidermolysis Bullosa; Huntington Disease; Kxabbe Disease (Infantile); Mitochondrial DNA-Associated Leigh Syndrome and NARP; Lesch-Nyhan Syndrome; LIS1-Associated Lissencephaly; Lowe Syndrome; Maple Syrup Urine Disease; MECP2 Duplication Syndrome; ATP7A-Related Copper Transport Disorders; LAMA2-Related Muscular Dystrophy; Arylsulfatase A Deficiency; Mucopolysaccharidosis Types I, II or III; Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum; Neurodegeneration with Brain Iron Accumulation Disorders; Acid Sphingomyelinase Deficiency; Niemann-Pick Disease Type C; Glycine Encephalopathy; ARX-Related Disorders; Urea Cycle Disorders; COLlAl/2-ReIated Osteogenesis Imperfecta; Mitochondrial DNA Deletion Syndromes; PLP1-Related Disorders; Perry Syndrome; Pheian-McDermid Syndrome; Glycogen Storage Disease Type II (Pompe Disease) (Infantile); MAPT-Related Disorders; MECP2-Related Disorders; Rhizomelic Chondrodysplasia Punctata Type 1; Roberts Syndrome; Sandhoff Disease; Schindler Disease - Type 1; Adenosine Deaminase Deficiency; Smith-Lemli-Opitz Syndrome; Spinal Muscular Atrophy; Infantile-Onset Spinocerebellar Ataxia; Hexosaminidase A Deficiency; Thanatophoric Dysplasia Type 1; Collagen Type VI-Related Disorders; Usher Syndrome Type I; Congenital Muscular Dystrophy; Wolf-Hirschhorn Syndrome; Lysosomal Acid Lipase Deficiency; and Xeroderma Pigmentosurn.

[00392] As will be apparent, it is envisaged that the present system can be used to target any polynucleotide sequence of interest. Some examples of conditions or diseases that might be usefully treated using the present system are included in the Tables above and examples of genes currently associated with those conditions are also provided there. However, the genes exemplified are not exhaustive.

[00393] Aspects of the invention also encompass delivery of engineered and optimized CRISPR-Cas systems. Cas9 and one or more guide RNA can be delivered using adeno associated virus (AAV), lentivirus, adenovirus or other plasmid or viral vector types, in particular, using formulations and doses from, for example, US Patents Nos. 8,454,972 (formulations, doses for adenovirus), 8,404,658 (formulations, doses for AAV) and 5,846,946 (formulations, doses for DNA plasmids) and from clinical trials and publications regarding the clinical trials involving lentivirus, AAV and adenovirus. For examples, for AAV, the route of administration, formulation and dose can be as in US Patent No. 8,454,972 and as in clinical trials involving AAV. For Adenovirus, the route of administration, formulation and dose can be as in US Patent No. 8,404,658 and as in clinical trials involving adenovirus. For plasmid delivery, the route of administration, formulation and dose can be as in US Patent No 5,846,946 and as in clinical studies involving plasmids. Doses may be based on or extrapolated to an average 70 kg individual, and can be adjusted for patients, subjects, mammals of different weight and species. Frequency of administration is within the ambit of the medical or veterinary practitioner (e.g., physician, veterinarian), depending on usual factors including the age, sex, general health, other conditions of the patient or subject and the particular condition or symptoms being addressed.

[00394] The viral vectors can be injected into the tissue of interest. For cell-type specific genome modification, the expression of Cas9 can be driven by a cell-type specific promoter. For example, liver-specific expression might use the Albumin promoter and neuron-specific expression might use the Synapsin I promoter.

Transgenic animals and plants

[00395] Transgenic animals are also provided. Preferred examples include animals comprising Cas9, in terms of polynucleotides encoding Cas9 or the protein itself. Mice, rats and rabbits are preferred. To generate transgenic mice with the constructs, as exemplified herein one may inject pure, linear DNA into the pronucleus of a zygote from a pseudo pregnant female, e.g.

a CB56 female. Founders may then be identified, genotyped, and backcrossed to CB57 mice. The constructs may then be cloned and optionally verified, for instance by Sanger sequencing. Knock outs are envisaged where for instance one or more genes are knocked out in a model. However, are knockins are also envisaged (alone or in combination). An example knockin Cas9 mouse was generated and this is exemplified, but Cas9 knockins are preferred. To generate a Cas9 knock in mice one may target the same constitutive and conditional constructs to the Rosa26 locus, as described herein (Figs. 25A-B and 26). Methods of US Patent Publication Nos. 20120017290 and 201 10265198 assigned to Sangamo Biosciences, Inc. directed to targeting the Rosa locus may be modified to utilize the CRISPR Cas system of the present invention. In another embodiment, the methods of US Patent Publication No. 20130236946 assigned to Cellectis directed to targeting the Rosa locus may also be modified to utilize the CRISPR Cas system of the present invention.

[00396] Utility of the conditional Cas9 mouse: Applicants have shown in 293 cells that the Cas9 conditional expression construct can be activated by co-expression with Cre. Applicants also show that the correctly targeted R1 mESCs can have active Cas9 when Cre is expressed. Because Cas9 is followed by the P2A peptide cleavage sequence and then EGFP Applicants identify successful expression by observing EGFP. Applicants have shown Cas9 activation in mESCs. This same concept is what makes the conditional Cas9 mouse so useful. Applicants may cross their conditional Cas9 mouse with a mouse that ubiquitously expresses Cre (ACTB-Cre line) and may arrive at a mouse that expresses Cas9 in every cell. It should only take the delivery of chimeric RNA to induce genome editing in embryonic or adult mice. Interestingly, if the conditional Cas9 mouse is crossed with a mouse expressing Cre under a tissue specific promoter, there should only be Cas9 in the tissues that also express Cre. This approach may be used to edit the genome in only precise tissues by delivering chimeric RNA to the same tissue.

[00397] As mentioned above, transgenic animals are also provided, as are transgenic plants, especially crops and algae. The transgenic plants may be useful in applications outside of providing a disease model. These may include food or feed production through expression of, for instance, higher protein, carbohydrate, nutrient or vitamin levels than would normally be seen in the wildtype. In this regard, transgenic plants, especially pulses and tubers, and animals, especially mammals such as livestock (cows, sheep, goats and pigs), but also poultry and edible insects, are preferred.

[00398] Transgenic algae or other plants such as rape may be particularly useful in the production of vegetable oils or biofuels such as alcohols (especially methanol and ethanol), for instance. These may be engineered to express or overexpress high levels of oil or alcohols for use in the oil or biofuel industries.

Adeno associated virus (AAV)

[00399] In terms of *in vivo* delivery, AAV is advantageous over other viral vectors for a couple of reasons:

[00400] Low toxicity (this may be due to the purification method not requiring ultra centrifugation of cell particles that can activate the immune response)

[00401] Low probability of causing insertional mutagenesis because it doesn't integrate into the host genome.

[00402] AAV has a packaging limit of 4.5 or 4.75 Kb. This means that Cas9 as well as a promoter and transcription terminator have to be all fit into the same viral vector. Constructs larger than 4.5 or 4.75 Kb will lead to significantly reduced virus production. SpCas9 is quite large, the gene itself is over 4.1 Kb, which makes it difficult for packing into AAV. Therefore embodiments of the invention include utilizing homologs of Cas9 that are shorter. For example:

Species	Cas9 Size
Corynebacter diphtheriae	3252
Eubacterium ventriosum	3321
Streptococcus pasteurianus	3390
Lactobacillus farciminis	3378
Sphaerochaeta globus	3537
Azospirillum B510	3504
Gluconaeetobacter diazotrophicus	3150
Neisseria cinerea	3246
Roseburia intestinalis	3420
Parvibaculum lavamentivorans	3111
Staphylococcus aureus	3159
Nitratifraetor salsuginis DSM 16511	3396
Campylobacter lari CF89-12	3009
Streptococcus thermophilus LMD-9	3396

[00403] These species are therefore, in general, preferred Cas9 species. Applicants have shown delivery and *in vivo* mouse brain Cas9 expression data.

[00404] Two ways to package Cas9 coding nucleic acid molecules, e.g., DNA, into viral vectors to mediate genome modification *in vivo* are preferred:

To achieve NHEJ-mediated gene knockout:

Single virus vector:

Vector containing two or more expression cassettes:

Promoter-Cas9 coding nucleic acid molecule -terminator

Promoter-gRNA 1-terminator

Promoter-gRNA2-terminator

Promoter-gRNA(N)-terminator (up to size limit of vector)

Double virus vector:

Vector 1 containing one expression cassette for driving the expression of Cas9

Promoter-Cas9 coding nucleic acid molecule-terminator

Vector 2 containing one more expression cassettes for driving the expression of one or more guideRNAs

Promoter-gRNA] -terminator

Promoter-gRNA(N)-terminator (up to size limit of vector)

[00405] To mediate homology-directed repair: In addition to the single and double virus vector approaches described above, an additional vector is used to deliver a homology-direct repair template.

[00406] Promoter used to drive Cas9 coding nucleic acid molecule expression can include: AAV ITR can serve as a promoter: this is advantageous for eliminating the need for an additional promoter element (which can take up space in the vector). The additional space freed up can be used to drive the expression of additional elements (gRNA, etc.). Also, ITR activity is relatively weaker, so can be used to reduce toxicity due to over expression of Cas9.

[00407] For ubiquitous expression, can use promoters: CMV, CAG, CBh, PGK, SV40, Ferritin heavy or light chains, etc.

[00408] For brain expression, can use promoters: Synapsinl for all neurons, CaMKJIalpha for excitatory neurons, GAD67 or GAD65 or VGAT for GABAergic neurons, etc.

[00409] For liver expression, can use Albumin promoter.

[00410] For lung expression, can use SP-B.

[00411] For endothelial cells, can use ICAM.

[00412] For hematopoietic cells can use IFNbeta or CD45.

[00413] For Osteoblasts can use OG-2.

[00414] Promoter used to drive guide RNA can include:

Pol III promoters such as U6 or H1

Use of Pol II promoter and intronic cassettes to express gRNA.

[00415] As to AAV, the AAV can be AAV1, AAV2, AAV5 or any combination thereof. One can select the AAV of the AAV with regard to the cells to be targeted; e.g., one can select AAV serotypes 1, 2, 5 or a hybrid or capsid AAV1, AAV2, AAV5 or any combination thereof for targeting brain or neuronal cells; and one can select AAV4 for targeting cardiac tissue. AAV8 is useful for delivery to the liver. The above promoters and vectors are preferred individually.

[00416] RNA delivery is also a useful method of *in vivo* delivery. It is possible to deliver Cas9 and gRNA (and, for instance, HR repair template) into cells using liposomes or nanoparticles. Thus delivery of the CRISPR enzyme, such as a Cas9 and/or deliver}' of the RNAs of the invention may be in RNA form and via microvesicles, liposomes or nanoparticles. For example, Cas9 mRNA and gRNA can be packaged into liposomal particles for delivery *in vivo.* Liposomal transfection reagents such as lipofectamine from Life Technologies and other reagents on the market can effectively deliver RNA molecules into the liver.

[00417] Enhancing NHEJ or HR efficiency is also helpful for delivery. It is preferred that NHEJ efficiency is enhanced by co-expressing end-processing enzymes such as Trex2 (Dumitrache et al. Genetics. 2011 August; 188(4): 787-797). it is preferred that HR efficiency is increased by transiently inhibiting NHEJ machineries such as Ku70 and Ku86. HR efficiency can also be increased by co-expressing prokaryotic or eukaryotic homologous recombination enzymes such as RecBCD, RecA.

[00418] Various means of delivery are described herein, and further discussed in this section.

[00419] Viral delivery: The CRISPR enzyme, for instance a Cas9, and/or any of the present RNAs, for instance a guide RNA, can be delivered using adeno associated virus (AAV), lentivirus, adenovirus or other viral vector types, or combinations thereof. Cas9 and one or more guide RNAs can be packaged into one or more viral vectors. In some embodiments, the viral vector is delivered to the tissue of interest by, for example, an intramuscular injection, while other times the viral delivery is via intravenous, transdermal, intranasal, oral, mucosal, or other delivery methods. Such delivery may be either via a single dose, or multiple doses. One skilled in the art understands that the actual dosage to be delivered herein may vary greatly depending upon a variety of factors, such as the vector chose, the target cell, organism, or tissue, the general

condition of the subject to be treated, the degree of transformation/modification sought, the administration route, the administration mode, the type of transformation/modification sought, etc.

[00420] Such a dosage may further contain, for example, a carrier (water, saline, ethanol, glycerol, lactose, sucrose, calcium phosphate, gelatin, dextran, agar, pectin, peanut oil, sesame oil, etc.), a diluent, a pharmaceutically-acceptable carrier (e.g., phosphate-buffered saline), a pharmaceutically-acceptable excipient, an adjuvant to enhance antigenicity, an immunostimulatory compound or molecule, and/or other compounds known in the art. The adjuvant herein may contain a suspension of minerals (alum, aluminum hydroxide, aluminum phosphate) on which antigen is adsorbed; or water-in-oil emulsion in which antigen solution is emulsified in oil (MF-59, Freund's incomplete adjuvant), sometimes with the inclusion of killed mycobacteria (Freund's complete adjuvant) to further enhance antigenicity (inhibits degradation of antigen and/or causes influx of macrophages). Adjuvants also include immunostimulatory molecules, such as cytokines, costimulatory molecules, and for example, immunostimulatory DNA or RNA molecules, such as CpG oligonucleotides. Such a dosage formulation is readily ascertainable by one skilled in the art. The dosage may further contain one or more pharmaceutically acceptable salts such as, for example, a mineral acid salt such as a hydrochloride, a hydrobromide, a phosphate, a sulfate, etc.; and the salts of organic acids such as acetates, propionates, malonates, benzoates, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, gels or gelling materials, flavorings, colorants, microspheres, polymers, suspension agents, etc. may also be present herein. In addition, one or more other conventional pharmaceutical ingredients, such as preservatives, humectants, suspending agents, surfactants, antioxidants, anticaking agents, fillers, chelating agents, coating agents, chemical stabilizers, etc. may also be present, especially if the dosage form is a reconstitutable form. Suitable exemplary ingredients include microcrystalline cellulose, carboxymethylcellulose sodium, polysorbate 80, phenylethyl alcohol, chlorobutanol, potassium sorbate, sorbic acid, sulfur dioxide, propyl gallate, the parabens, ethyl vanillin, glycerin, phenol, parachlorophenol, gelatin, albumin and a combination thereof. A thorough discussion of pharmaceutically acceptable excipients is available in REMINGTON'S PHARMACEUTICAL SCIENCES (Mack Pub. Co., N.J. 1991) which is incorporated by reference herein.

[00421] In an embodiment herein the delivery is via an adenovirus, which may be at a single booster dose containing at least 1 x 10^3 particles (also referred to as particle units, pu) of adenoviral vector. In an embodiment herein, the dose preferably is at least about 1 x 10° particles (for example, about 1 x 10^6-1 x 10^{12} particles), more preferably at least about 1 x 10^7 particles, more preferably at least about 1 x 10^8 particles (e.g., about 1 x 10^8-1 x 10^{11} particles or about 1 x 10^8-1 x 10^{12} particles), and most preferably at least about 1 x 10^9 particles (e.g., about 1* x 10^9-1 x 10^{10} particles or about 1 x 10^9-1 x 10^{12} particles), or even at least about 1 x 10^{10} particles (e.g., about 1 x 10^{10}-1 x 10^{12} particles) of the adenoviral vector. Alternatively, the dose comprises no more than about 1 x 10^{14} particles, preferably no more than about 1 x 10° particles, even more preferably no more than about 1 x 10^{12} particles, even more preferably no more than about 1 x 10^{11} particles, and most preferably no more than about 1 x 10^{10} particles (e.g., no more than about 1 x 10^9 articles). Thus, the dose may contain a single dose of adenoviral vector with, for example, about 1 x 10^6 particle units (pu), about 2 x 10° pu, about 4 x 10° pu, about 1 x 10^7 pu, about 2 x 10^7 pu, about 4 x 10^7 pu, about 1 x 10^8 pu, about 2 x 10^8 pu, about 4 x 10^8 pu, about 1 x 10^9 pu, about 2 x 10^9 pu, about 4 x 10^9 pu, about 1 x 10^{10} pu, about 2 x 10^{10} pu, about 4 x 10^{10} pu, about 1 x 10^{11} pu, about 2 x 10^{11} pu, about 4 x 10^{11} pu, about 1 x 10^{12} pu, about 2 x 10^{12} pu, or about 4 x 10^{12} pu of adenoviral vector. See, for example, the adenoviral vectors in U.S. Patent No. 8,454,972 B2 to Nabel, et. al, granted on June 4, 2013; incorporated by reference herein, and the dosages at col 29, lines 36-58 thereof. In an embodiment herein, the adenovirus is delivered via multiple doses.

[00422] In an embodiment herein, the delivery is via an AAV. A therapeutically effective dosage for in vivo delivery of the AAA" to a human is believed to be in the range of from about 20 to about 50 ml of saline solution containing from about 1 x 10^{10} to about 1 x 10^{10} functional AAV/ml solution. The dosage may be adjusted to balance the therapeutic benefit against any side effects. In an embodiment herein, the AAV dose is generally in the range of concentrations of from about 1 x 10^5 to 1 x 10^{50} genomes AAV, from about 1 x 10^8 to 1 x 10^{20} genomes AAV, from about 1 x 10^{10} to about 1 x 10^{16} genomes, or about 1 x 10^{11} to about 1 x 10^{16} genomes AAV. A human dosage may be about 1 x 10^{13} genomes AAV. Such concentrations may be delivered in from about 0.001 ml to about 100 ml, about 0.05 to about 50 ml, or about 10 to about 25 ml of a carrier solution. Other effective dosages can be readily established by one of ordinary skill in the art through routine trials establishing dose response curves. See, for example, U.S. Patent No. 8,404,658 B2 to Hajjar, et al., granted on March 26, 2013, at col. 27, lines 45-60.

[00423] In an embodiment herein the delivery is via a plasmid. In such plasmid compositions, the dosage should be a sufficient amount of plasmid to elicit a response. For instance, suitable quantities of plasmid DNA in plasmid compositions can be from about 0.1 to about 2 mg, or from about 1 μg to about 10 μg.

[00424] The doses herein are based on an average 70 kg individual. The frequency of administration is within the ambit of the medical or veterinary practitioner (e.g., physician, veterinarian), or scientist skilled in the art.

Lentivirus

[00425] Lentiviruses are complex retroviruses that have the ability to infect and express their genes in both mitotic and post-mitotic cells. The most commonly known lentivirus is the human immunodeficiency virus (HIV), which uses the envelope glycoproteins of other viruses to target a broad range of cell types.

[00426] Lentiviruses may be prepared as follows. After cloning pCasES10 (which contains a lentiviral transfer plasmid backbone), HEK293FT at low passage (p=5) were seeded in a T-75 flask to 50% confluence the day before transfection in DMEM with 10% fetal bovine serum and without antibiotics. After 20 hours, media was changed to OptiMEM (serum-free) media and transfection was done 4 hours later. Cells were transfected with 10 μg of lentiviral transfer plasmid (pCasES10) and the following packaging plasmids: 5 μg of pMD2.G (VSV-g pseudotype), and 7.5ug of psPAX2 (gag/pol/rev/tat). Transfection was done in 4mL OptiMEM with a cationic lipid delivery agent (50uL Lipofectamine 2000 and 100ul Plus reagent). After 6 hours, the media was changed to antibiotic-free DMEM with 10% fetal bovine serum.

[00427] Lentivirus may be purified as follows. Viral supernatants were harvested after 48 hours. Supernatants were first cleared of debris and filtered through a 0.45um low protein binding (PVDF) filter. They were then spun in a ultracentrifuge for 2 hours at 24,000 rpm. Viral pellets were resuspended in 50ul of DMEM overnight at 4C. They were then aliquotted and immediately frozen at -80C.

[00428] In another embodiment, minimal non-primate lentiviral vectors based on the equine infectious anemia virus (EIAV) are also contemplated, especially for ocular gene therapy (see, e.g., Balagaan, J Gene Med 2006; 8: 275 - 285, Published online 21 November 2005 in Wiley

InterScience (www.interscience.wiley.com). DOT 10.1002/jgm.845). In another embodiment, RetinoStat®, an equine infectious anemia virus-based lentiviral gene therapy vector that expresses angiostatic proteins endostain and angiostatin that is delivered via a subretinal injection for the treatment of the web form of age-related macular degeneration is also contemplated (see, e.g., Binley et al., HUMAN GENE THERAPY 23:980-991 (September 2012)) may be modified for the CRISPR-Cas system of the present invention.

[00429] In another embodiment, self-inactivating lentiviral vectors with an siRNA targeting a common exon shared by HIV tat/rev, a nucleolar-localizing TAR decoy, and an anti-CCR5-specific hammerhead ribozyme (see, e.g., DiGiusto et al. (2010) Sci Transl Med 2:36ra43) may be used/and or adapted to the CRISPR-Cas system of the present invention. A minimum of 2.5 x 10^6 CD34+ cells per kilogram patient weight may be collected and prestimulated for 16 to 20 hours in X-VIVO 15 medium (Lonza) containing 2mML-glutamine, stem cell factor (100 ng/ml), Flt-3 ligand (Flt-3L) (100 ng/ml), and thrombopoietin (10 ng/ml) (CellGenix) at a density of 2 x 10° cells/ml. Prestimulated cells may be transduced with lentiviral at a multiplicity of infection of 5 for 16 to 24 hours in 75~cm^2 tissue culture flasks coated with fibronectin (25 mg/cm^2) (RetroNectin,T'akara Bio Inc.).

[00430] Lentiviral vectors have been disclosed as in the treatment for Parkinson's Disease, see, e.g., US Patent Publication No. 20120295960 and US Patent Nos. 7303910 and 7351585. Lentiviral vectors have also been disclosed for the treatment of ocular diseases, see e.g., US Patent Publication Nos. 20060281180, 20090007284, US20110117189; US20090017543; US20070054961, US20100317109. Lentiviral vectors have also been disclosed for delivery to the train, see, e.g., US Patent Publication Nos. US20110293571; US20110293571, US20040013648, US20070025970, US20090111106 and US Patent No. US7259015.

RNA delivery

[00431] RNA delivery: The CRISPR enzyme, for instance a Cas9, and/or any of the present RNAs, for instance a guide RNA, can also be delivered in the form of RNA. Cas9 mRNA can be generated using *in vitro* transcription. For example, Cas9 mRNA can be synthesized using a PGR cassette containing the following elements: T7_promoter-kozak sequence (GCCACC)-Cas9-3' UTR from beta globin-polyA tail (a string of 120 or more adenines). The cassette can be used for transcription by T7 polymerase. Guide RNAs can also be transcribed using in vitro transcription from a cassette containing T7_promoter-GG-guide RNA sequence.

[00432] To enhance expression and reduce toxicity, the CRISPR enzyme and/or guide RNA can be modified using pseudo-U or 5-Methyl-C.

[00433] mRNA delivery methods are especially promising for liver delivery currently. In particular, for AAV8 is particularly preferred for delivery to the liver.

Nanoparticles

[00434] CRISPR enzyme mRNA and guide RNA may be delivered simultaneously using nanoparticles or lipid envelopes.

[00435] For example, Su X, Fricke J, Kavanagh DG, Irvine DJ ("In vitro and in vivo mRNA delivery using lipid-enveloped pH-responsive polymer nanoparticles" Mol Pharm. 2011 Jun 6;8(3):774-87. doi: 10.1021/mpl00390w. Epub 2011 Apr 1) describes biodegradable core-shell structured nanoparticles with a poly(β-amino ester) (PBAE) core enveloped by a phospholipid bilayer shell. These were developed for in vivo mRNA delivery. The pH-responsive PBAE component was chosen to promote endosome disruption, while the lipid surface layer was selected to minimize toxicity of the polycation core. Such are, therefore, preferred for delivering RNA of the present invention.

[00436] In one embodiment, nanoparticles based on self assembling bioadhesive polymers are contemplated, which may be applied to oral delivery of peptides, intravenous delivery of peptides and nasal delivery of peptides, all to the brain. Other embodiments, such as oral absorption and ocular deliver of hydrophobic drugs are also contemplated. The molecular envelope technology involves an engineered polymer envelope which is protected and delivered to the site of the disease (see, e.g., Mazza, M. et al. ACSNano, 2013. 7(2): 1016-1026; Slew, A., et al. Mol Pharm, 2012. 9(1): 14-28; Lalatsa, A., et al. J Contr Rel, 2012. 161(2):523-36; Lalatsa, A., et al., Mol Pharm, 2012. 9(6): 1665-80; Lalatsa, A., et al. Mol Pharm, 2012. 9(6): 1764-74; Garrett, N.L., et al. J Biophotonics, 2012. 5(5-6):458-68; Garrett, N.L., et al. J Raman Spect, 2012. 43(5):681-688; Ahmad, S., et al. J Royal Soc Interface 2010. 7:8423-33; Uehegbu, I.F. Expert Opin Drug Deiiv, 2006. 3(5):629-40; Qu, X.,et al. Biomacromolecules, 2006. 7(12):3452-9 and Uehegbu, LF., et al. Int J Pharm, 2001. 224:185-199). Doses of about 5 mg/kg are contemplated, with single or multiple doses, depending on the target tissue.

[00437] In one embodiment, nanoparticles that can deliver RNA to a cancer cell to stop tumor growth developed by Dan Anderson's lab at MIT may be used/and or adapted to the CRISPR Cas system of the present invention. In particular, the Anderson lab developed fully automated,

combinatorial systems for the synthesis, purification, characterization, and formulation of new biomaterials and nanoformulations. See, e.g., Alabi et al., Proc Natl Acad Sci U S A. 2013 Aug 6;110(32):12881-6; Zhang et al., Adv Mater. 2013 Sep 6;25(33):4641-5; Jiang et al, Nano Lett. 2013 Mar 13;13(3):1059-64; Karagiannis et al, ACS Nano. 2012 Oct 23;6(10):8484-7; Whitehead et al, ACS Nano. 2012 Aug 28;6(8):6922-9 and Lee et al., Nat Nanotechnol. 2012 Jun 3;7(6):389-93.

[00438] US patent application 201 10293703 relates to lipidoid compounds are also particularly useful in the administration of polynucleotides, which may be applied to deliver the CRISPR Cas system of the present invention. In one aspect, the aminoalcohol lipidoid compounds are combined with an agent to be delivered to a cell or a subject to form microparticles, nanoparticles, liposomes, or micelles. The agent to be delivered by the particles, liposomes, or micelles may be in the form of a gas, liquid, or solid, and the agent may be a polynucleotide, protein, peptide, or small molecule. The minoalcohol lipidoid compounds may be combined with other aminoalcohol lipidoid compounds, polymers (synthetic or natural), surfactants, cholesterol, carbohydrates, proteins, lipids, etc. to form the particles. These particles may then optionally be combined with a pharmaceutical excipient to form a pharmaceutical composition.

[00439] US Patent Publication No. 01 10293703 also provides methods of preparing the aminoalcohol lipidoid compounds. One or more equivalents of an amine are allowed to react with one or more equivalents of an epoxide-terminated compound under suitable conditions to form an aminoalcohol lipidoid compound of the present invention. In certain embodiments, all the amino groups of the amine are fully reacted with the epoxide-terminated compound to form tertiary amines. In other embodiments, all the amino groups of the amine are not fully reacted with the epoxide-terminated compound to form tertiary amines thereby resulting in primary or secondary amines in the aminoalcohol lipidoid compound. These primary or secondary amines are left as is or may be reacted with another electrophile such as a different epoxide-terminated compound. As will be appreciated by one skilled in the art, reacting an amine with less than excess of epoxide-terminated compound will result in a plurality of different aminoalcohol lipidoid compounds with various numbers of tails. Certain amines may be fully functionalized with two epoxide-derived compound tails while other molecules will not be completely functionalized with epoxide-derived compound tails. For example, a diamine or polyamine may

include one, two, three, or four epoxide-derived compound tails off the various amino moieties of the molecule resulting in primary, secondary, and tertiary amines. In certain embodiments, all the amino groups are not fully functionalized. In certain embodiments, two of the same types of epoxide-terminated compounds are used. In other embodiments, two or more different epoxide-terminated compounds are used. The synthesis of the aminoalcohol lipidoid compounds is performed with or without solvent, and the synthesis may be performed at higher temperatures ranging from 30.-100 C , preferably at approximately 50.-90 C. The prepared aminoalcohol lipidoid compounds may be optionally purified. For example, the mixture of aminoalcohol lipidoid compounds may be purified to yield an aminoalcohol lipidoid compound with a particular number of epoxide-derived compound tails. Or the mixture may be purified to yield a particular stereo- or regioisomer. The aminoalcohol lipidoid compounds may also be alkylated using an alkyl halide (e.g., methyl iodide) or other alkylating agent, and/or they may be acylated.

[00440] US Patent Publication No. 0110293703 also provides libraries of aminoalcohol lipidoid compounds prepared by the inventive methods. These aminoalcohol lipidoid compounds may be prepared and/or screened using high-throughput techniques involving liquid handlers, robots, microliter plates, computers, etc. In certain embodiments, the aminoalcohol lipidoid compounds are screened for their ability to transfect polynucleotides or other agents (e.g., proteins, peptides, small molecules) into the cell.

[00441] US Patent Publication No. 20130302401 relates to a class of poly(beta-amino alcohols) (PBAAs) has been prepared using combinatorial polymerization. The inventive PBAAs may be used in biotechnology and biomedical applications as coatings (such as coatings of films or multilayer films for medical devices or implants), additives, materials, excipients, non-biofouling agents, micropatterning agents, and cellular encapsulation agents. When used as surface coatings, these PBAAs elicited different levels of inflammation, both in vitro and in vivo, depending on their chemical structures. The large chemical diversity of this class of materials allowed us to identify polymer coatings that inhibit macrophage activation in vitro. Furthermore, these coatings reduce the recruitment of inflammatory cells, and reduce fibrosis, following the subcutaneous implantation of carboxylated polystyrene microparticles. These polymers may be used to form polyelectrolyte complex capsules for cell encapsulation. The invention may also have many other biological applications such as antimicrobial coatings, DNA or siRNA delivery,

and stem cell tissue engineering. The teachings of US Patent Publication No. 20130302401 may be applied to the CRISPR Cas system of the present invention.

[00442] In another embodiment, lipid nanoparticles (LNPs) are contemplated. In particular, an antitransthyretin small interfering RNA encapsulated in lipid nanoparticles (see, e.g., Coelho et al, N Engl J Med 2013;369:819-29) may be applied to the CRISPR Cas system of the present invention. Doses of about 0.01 to about 1 mg per kg of body weight administered intravenously are contemplated. Medications to reduce the risk of infusion-related reactions are contemplated, such as dexamethasone, acetampmophen, diphenhydramine or cetirizine, and ranitidine are contemplated. Multiple doses of about 0.3 mg per kilogram every 4 weeks for five doses are also contemplated.

[00443] LNPs have been shown to be highly effective in delivering siRNAs to the liver (see, e.g., Tabemero et al, Cancer Discovery, April 2013, Vol. 3, No. 4, pages 363-470) and are therefore contemplated for delivering CRISPR Cas to the liver. A dosage of about four doses of 6 mg/kg of the LNP every two weeks may be contemplated. Tabemero et al. demonstrated that tumor regression was observed after the first 2 cycles of LNPs dosed at 0.7 mg/kg, and by the end of 6 cycles the patient had achieved a partial response with complete regression of the lymph node metastasis and substantial shrinkage of the liver tumors. A complete response was obtained after 40 doses in this patient, who has remained in remission and completed treatment after receiving doses over 26 months. Two patients with RCC and extrahepatic sites of disease including kidney, lung, and lymph nodes that were progressing following prior therapy with VEGF pathway inhibitors had stable disease at all sites for approximately 8 to 12 months, and a patient with PNET and liver metastases continued on the extension study for 18 months (36 doses) with stable disease.

[00444] However, the charge of the LNP must be taken into consideration. As cationic lipids combined with negatively charged lipids to induce nonbilayer structures that facilitate intracellular delivery. Because charged LNPs are rapidly cleared from circulation following intravenous injection, ionizable cationic lipids with pKa values below 7 were developed (see, e.g., Rosin et al, Molecular Therapy, vol. 19, no. 12, pages 1286-2200, Dec. 2011). Negatively charged polymers such as siRNA oligonucleotides may be loaded into LNPs at low pH values (e.g., pH 4) where the ionizable lipids display a positive charge. However, at physiological pH values, the LNPs exhibit a low surface charge compatible with longer circulation times. Four

species of ionizabie eationie lipids have been focused upon, namely 1,2-dilmeoyl~3-dimethylammonium-propane (DLinDAP), l,2-dilinoleyloxy-3-N,N-dimethylaminopropane (DLinDMA), l,2-dilinoleyloxy-keto-N,N-dimethyl-3-aminopropane (DLinKDMA), and 1,2-dilmoIeyl-4-(2-dimethylaminoethyl)-[l,3]-dioxoiane (DLmKC2-DMA). It has been shown that LNP siRNA systems containing these lipids exhibit remarkably different gene silencing properties in hepatocytes in vivo, with potencies varying according to the series DLinKC2-DMA>DLinKDMA>DLinDMA>>DLinDAP employing a Factor VII gene silencing model (see, e.g., Rosin et al, Molecular Therapy, vol. 19, no. 12, pages 1286-2200, Dec. 2011). A dosage of 1 µg/ml levels may be contemplated, especially for a formulation containing DLinKC2-DMA.

[00445] Preparation of LNPs and CRISPR Cas encapsulation may be used/and or adapted from Rosin et al, Molecular Therapy, vol. 19, no. 12, pages 1286-2200, Dec. 2011). The eationie lipids 1,2-dilineoyl-3-dimethylarnmonium-propane (DLinDAP), 1,2-dilinoleyloxy-3-N,N-dimethylaminopropane (DLinDMA), 1,2-dilinoleyloxyketo-N,N-dimethyl-3-aminopropane (DLinK-DMA), l,2-dilmoieyl-4~(2-dimethylaminoethyl)~[L3]-dioxoiaiie (DLinKC2-DMA), (3-o~[2" -(methoxypolyethyleneglycol 2000) succmoyl]-l ,2-dimyristoyl-sn-glycol (PEG-S-DMG), and R-3-[(co-methoxy-poly(ethylene glycol)2000) carbamoyl]-l,2-dimyristyloxlpropyl-3-amine (PEG-C-DOMG) may be provided by Tekmira Pharmaceuticals (Vancouver, Canada) or synthesized. Cholesterol may be purchased from Sigma (St Louis, MO). The specific CRISPR Cas RNA may be encapsulated in LNPs containing DLinDAP, DLinDMA, DLinK-DMA, and DLinKC2-DMA (eationie lipid:DSPC:CHOL: PEGS-DMG or PEG-C-DOMG at 40:10:40:10 molar ratios). When required, 0.2% SP-DiOC18 (mvitrogen, Burlington, Canada) may be incorporated to assess cellular uptake, intracellular delivery, and biodistribution. Encapsulation may be performed by dissolving lipid mixtures comprised of eationie lipid:DSPC:cholesterol:PEG-c-DOMG (40:10:40:10 molar ratio) in ethanol to a final lipid concentration of 10 mmol/l. This ethanol solution of lipid may be added drop-wise to 50 mmol/1 citrate, pH 4.0 to form multilamellar vesicles to produce a final concentration of 30% ethanol vol/vol. Large unilamellar vesicles may be formed following extrusion of multilamellar vesicles through two stacked 80 nm Nuclepore polycarbonate filters using the Extruder (Northern Lipids, Vancouver, Canada). Encapsulation may be achieved by adding RNA dissolved at 2 mg/ml in 50 mmol/1 citrate, pH 4.0 containing 30% ethanol vol/vol drop-wise to extruded preformed large unilamellar vesicles and incubation at 31 °C for 30 minutes with constant mixing to a final

RNA/lipid weight ratio of 0.06/1 wt/wt. Removal of ethanol and neutralization of formulation buffer were performed by dialysis against phosphate-buffered saline (PBS), pH 7.4 for 16 hours using Spectra/Por 2 regenerated cellulose dialysis membranes. Nanoparticle size distribution may be determined by dynamic light scattering using a NICOMP 370 particle sizer, the vesicle/intensity modes, and Gaussian fitting (Nicomp Particle Sizing, Santa Barbara, CA). The particle size for all three LNP systems may be -70 nm in diameter. siRNA encapsulation efficiency may be determined by removal of free siRNA using VivaPureD MiniH columns (Sartorius Stedim Biotech) from samples collected before and after dialysis. The encapsulated RNA may be extracted from the eluted nanoparticles and quantified at 260 nm. siRNA to lipid ratio was determined by measurement of cholesterol content in vesicles using the Cholesterol E enzymatic assay from Wako Chemicals USA (Richmond, VA).

[ΘΘ446] Preparation of large LNPs may be used/and or adapted from Rosin et al, Molecular Therapy, vol. 19, no. 12, pages 1286-2200, Dec. 2011. A lipid premix solution (20.4 mg/ml total lipid concentration) may be prepared in ethanol containing DLinKC2-DMA, DSPC, and cholesterol at 50:10:38.5 molar ratios. Sodium acetate may be added to the lipid premix at a molar ratio of 0.75:1 (sodium acetate:DLinKC2-DMA). The lipids may be subsequently hydrated by combining the mixture with 1.85 volumes of citrate buffer (10 mmol/1, pH 3.0) with vigorous stirring, resulting in spontaneous liposome formation in aqueous buffer containing 35% ethanol. The liposome solution may be incubated at 37 °C to allow for time-dependent increase in particle size. Aliquots may be removed at various times during incubation to investigate changes in liposome size by dynamic light scattering (Zetasizer Nano ZS, Malvern Instruments, Worcestershire, UK). Once the desired particle size is achieved, an aqueous PEG lipid solution (stock = 10 mg/ml PEG-DMG in 35% (vol/vol) ethanol) may be added to the liposome mixture to yield a final PEG molar concentration of 3.5% of total lipid. Upon addition of PEG-lipids, the liposomes should their size, effectively quenching further growth. RNA may then be added to the empty liposomes at an siRNA to total lipid ratio of approximately 1:10 (wt:wt), followed by incubation for 30 minutes at 37 °C to form loaded LNPs. The mixture may be subsequently dialyzed overnight in PBS and filtered with a 0.45-μm syringe filter.

[00447] Spherical Nucleic Acid (SNA™) constructs and other nanoparticles (particularly gold nanoparticles) are also contemplate as a means to delivery CRISPR/Cas system to intended targets. Significant data show that AuraSense Therapeutics' Spherical Nucleic Acid (SNA™)

constructs, based upon nucleic acid-functionalized gold nanoparticles, are superior to alternative platforms based on multiple key success factors, such as:

[00448] High in vivo stability. Due to their dense loading, a majority of cargo (DNA or siRNA) remains bound to the constructs inside cells, conferring nucleic acid stability and resistance to enzymatic degradation.

[00449] Deliverability. For all cell types studied (e.g., neurons, tumor cell lines, etc.) the constructs demonstrate a transfection efficiency of 99% with no need for carriers or transfection agents.

[00450] Therapeutic targeting. The unique target binding affinity and specificity of the constructs allow exquisite specificity for matched target sequences (i.e., limited off-target effects).

[00451] Superior efficacy. The constructs significantly outperform leading conventional transfection reagents (Lipofectamine 2000 and Cytofectm).

[00452] Low toxicity. The constructs can enter a variety of cultured cells, primary cells, and tissues with no apparent toxicity.

[00453] No significant immune response. The constructs elicit minimal changes in global gene expression as measured by whole-genome microarray studies and cytokine-specific protein assays.

[00454] Chemical tailorability. Any number of single or combinatorial agents (e.g., proteins, peptides, small molecules) can be used to tailor the surface of the constructs.

[00455] This platform for nucleic acid-based therapeutics may be applicable to numerous disease states, including inflammation and infectious disease, cancer, skin disorders and cardiovascular disease.

[00456] Citable literature includes: Cutler et al.,. J. Am. Chem. Soc. 2011 133:9254-9257, Hao et al., Small. 2011 7:3158-3162, Zhang et al., ACS Nano. 2011 5:6962-6970, Cutler et al, J. Am. Chem. Soc. 2012 134:1376-1391, Young et al.,. Nano Lett. 2012 12:3867-71, Zheng et al, Proc. Natl. Acad. Sci. USA. 2012 109:11975-80, Mirkin, Nanomedicine 2012 7:635-638 Zhang et al., J. Am. Chem. Soc. 2012 134:16488-1691, Weintraub, Nature 2013 495:S14-S16, Choi et al., Proc. Natl. Acad. Sci. USA. 2013 110(19):7625-7630, Jensen et al., Sci. Transl. Med. 5, 209ral52 (2013) and Mirkin, et al, Small, doi.org/10.1002/smil.201302143.

[00457] Self-assembling nanoparticles with siRNA may be constructed with polyethyleneimine (PEI) that is PEGylated with an Arg-Gly-Asp (RGD) peptide ligand attached at the distal end of the polyethylene glycol (PEG), for example, as a means to target tumor neovasculature expressing integrins and used to deliver siRNA inhibiting vascular endothelial growth factor receptor-2 (VEGF R2.) expression and thereby tumor angiogenesis (see, e.g., Schiffelers et al., Nucleic Acids Research, 2004, Vol. 32, No. 19). Nanoplexes may be prepared by mixing equal volumes of aqueous solutions of cationic polymer and nucleic acid to give a net molar excess of ionizable nitrogen (polymer) to phosphate (nucleic acid) over the range of 2 to 6. The electrostatic interactions between cationic polymers and nucleic acid resulted in the formation of polyplexes with average particle size distribution of about 100 nm, hence referred to here as nanoplexes. A dosage of about 100 to 200 mg of CRISPR Cas is envisioned for delivery in the self-assembling nanoparticles of Schiffelers et al.

[00458] The nanoplexes of Bartlett et al. (PNAS, September 25, 2007,vol. 104, no. 39) may also be applied to the present invention. The nanoplexes of Bartlett et al. are prepared by mixing equal volumes of aqueous solutions of cationic polymer and nucleic acid to give a net molar excess of ionizable nitrogen (polymer) to phosphate (nucleic acid) over the range of 2 to 6. The electrostatic interactions between cationic polymers and nucleic acid resulted in the formation of polyplexes with average particle size distribution of about 100 nm, hence referred to here as nanoplexes. The DOTA-siRNA of Bartlett et al. was synthesized as follows: 1,4,7,10-tetraazacyclododecane- 1,4,7,10-tetraacetic acid mono(N-hydroxysuccinimide ester) (DOTA-NHSester) was ordered from Macrocyclics (Dallas, TX). The amine modified RNA sense strand with a 100-fold molar excess of DOTA-NBS-ester in carbonate buffer (pH 9) was added to a microcentrifuge tube. The contents were reacted by stirring for 4 h at room temperature. The DOTA-RNAsense conjugate was ethanol-precipitated, resuspended in water, and annealed to the unmodified antisense strand to yield DOTA-siRNA. All liquids were pretreated with Chelex-100 (Bio-Rad, Hercules, CA) to remove trace metal contaminants. Tf-targeted and nontargeted siRNA nanoparticles may be formed by using cyclodextrin-containing polycations. Typically, nanoparticles were formed in water at a charge ratio of 3 (+/-) and an siRNA concentration of 0.5 g/liter. One percent of the adamantane-PEG molecules on the surface of the targeted nanoparticles were modified with Tf (adamantane-PEG-Tf). The nanoparticles were suspended in a 5% (wt/vol) glucose carrier solution for injection.

[00459] Davis et al. (Nature, Vol 464, 15 April 2010) conducts a siRNA clinical trial that uses a targeted nanoparticle-de livery system (clinical trial registration number NCT00689065). Patients with solid cancers refractory to standard-of-care therapies are administered doses of targeted nanoparticles on days 1, 3, 8 and 10 of a 21-day cycle by a 30-min intravenous infusion. The nanoparticles consist of a synthetic delivery system containing: (1) a linear, cyclodextrin-based polymer (CDP), (2) a human transferrin protein (TF) targeting ligand displayed on the exterior of the nanoparticle to engage TF receptors (TFR) on the surface of the cancer cells, (3) a hydrophilic polymer (polyethylene glycol (PEG) used to promote nanoparticle stability in biological fluids), and (4) siRNA designed to reduce the expression of the RRM2 (sequence used in the clinic was previously denoted siR2B+5). The TFR has long been known to be upregulated in malignant cells, and RRM2 is an established anti-cancer target. These nanoparticles (clinical version denoted as CALAA-01) have been shown to be well tolerated in multi-dosing studies in non-human primates. Although a single patient with chronic myeloid leukaemia has been administered siRNAby liposomal delivery, Davis et al.'s clinical trial is the initial human trial to systemicaliy deliver siRNA with a targeted delivery system and to treat patients with solid cancer. To ascertain whether the targeted delivery system can provide effective delivery of functional siRNA to human tumours, Davis et al. investigated biopsies f om three patients from three different dosing cohorts; patients A, B and C, all of whom had metastatic melanoma and received CALAA-01 doses of 18, 24 and 30 mg m^{-2} siRNA, respectively. Similar doses may also be contemplated for the CRISPR Cas system of the present invention. The deliver)' of the invention may be achieved with nanoparticles containing a linear, cyclodextrin-based polymer (CDP), a human transferrin protein (TF) targeting ligand displayed on the exterior of the nanoparticle to engage TF receptors (TFR) on the surface of the cancer cells and/or a hydrophilic polymer (for example, polyethylene glycol (PEG) used to promote nanoparticle stability in biological fluids).

Exosomes

[00460] Exosomes are endogenous nano-vesicles that transport RNAs and proteins which can deliver short interfering (si)RNA to the brain in mice. To reduce immunogenicity, Alvarez-Erviti et al. (2011, Nat Biotechnol 29: 341) used self-derived dendritic cells for exosome production. Targeting was achieved by engineering the dendritic ceils to express Lamp2b, an exosomal membrane protein, fused to the neuron-specific RVG pep†ide3. Purified exosomes were loaded

with exogenous siRNA by electroporation. Intravenously injected RVG-targeted exosomes delivered GAPDH siRNA specifically to neurons, microglia, oligodendrocytes in the brain, resulting in a specific gene knockdown. Pre-exposure to RVG exosomes did not attenuate knockdown, and non-specific uptake in other tissues was not observed. The therapeutic potential of exosome-mediated siRNA delivery was demonstrated by the strong mRNA (60%) and protein (62%) knockdown of BACE1, a therapeutic target in Alzheimer's disease.

[00461] To obtain a pool of immunologically inert exosomes, Alvarez-Erviti et al. harvested bone marrow from inbred C57BL/6 mice with a homogenous major histocompatibility complex (MHC) haplotype. As immature dendritic cells produce large quantities of exosomes devoid of T-cell activators such as MHC-II and CD86, Alvarez-Erviti et al. selected for dendritic cells with granulocyte/macrophage-colony stimulating factor (GM-CSF) for 7 d. Exosomes were purified from the culture supernatant the following day using well-established ultracentrifugation protocols. The exosomes produced were physically homogenous, with a size distribution peaking at 80 nm in diameter as determined by nanoparticle tracking analysis (NTA) and electron microscopy. Aivarez-Endti et al. obtained 6-12 µg of exosomes (measured based on protein concentration) per 10^6 cells.

[00462] Next, Aivarez-Endti et al. investigated the possibility of loading modified exosomes with exogenous cargoes using electroporation protocols adapted for nanoscale applications. As electroporation for membrane particles at the nanometer scale is not well-characterized, nonspecific Cy5-labeled siRNA was used for the empirical optimization of the electroporation protocol. The amount of encapsulated siRNA was assayed after ultracentrifugation and lysis of exosomes. Electroporation at 400 V and 125 µF resulted in the greatest retention of siRNA and was used for all subsequent experiments.

[00463] Alvarez-Erviti et al. administered 150 µg of each BACE1 siRNA encapsulated in 150 µg of RVG exosomes to normal C57BL/6 mice and compared the knockdown efficiency to four controls: untreated mice, mice injected with RVG exosomes only, mice injected with BACE1 siRNA complexed to an in vivo cationic liposome reagent and mice injected with BACE1 siRNA complexed to RVG-9R, the RVG peptide conjugated to 9 D-arginines that electrostatically binds to the siRNA. Cortical tissue samples were analyzed 3 d after administration and a significant protein knockdown (45%. $P < 0.05$, versus 62%, $P < 0.01$) in both siRNA-RVG-9R-treated and siRNARVG exosome-treated mice was observed, resulting from a significant decrease in

BACE1 mRNA levels (66% [+ or -] **15%,** P < 0.001 and 61% [+ or -] **13%** respectively, P < 0.01). Moreover, Applicants demonstrated a significant decrease **(55%,** P < 0.05) in the total [beta]-amyloid 1-42 levels, a main component of the amyloid plaques in Alzheimer's pathology, in the RVG-exosome-treated animals. The decrease observed was greater than the β-amyloid 1-40 decrease demonstrated in normal mice after intraventricular injection of BACE1 inhibitors. Alvarez-Erviti et al. carried out 5'-rapid amplification of cDNA ends (RACE) on BACE1 cleavage product, which provided evidence of RNAi-mediated knockdown by the siRNA.

[00464] Finally, Alvarez-Erviti et al. investigated whether siRNA-RVG exosomes induced immune responses in vivo by assessing IL-6, IP-10, TNFa and IFN-a serum concentrations. Following siRNA-RVG exosome treatment, nonsignificant changes in all cytokines were registered similar to siRNA-transfection reagent treatment in contrast to siRN.A~RVG-9R, which potently stimulated IL-6 secretion, confirming the immunologically inert profile of the exosome treatment. Given that exosomes encapsulate only 20% of siRNA, delivery with RVG-exosome appears to be more efficient than **RVG-9R** delivery as comparable niRNA knockdown and greater protein knockdown was achieved with fivefold less siRNA without the corresponding level of immune stimulation. This experiment demonstrated the therapeutic potential of RVG-exosome technology, which is potentially suited for long-term silencing of genes related to neurodegenerative diseases. The exosome delivery system of Alvarez-Erviti et al. may be applied to deliver the CRISPR-Cas system of the present invention to therapeutic targets, especially neurodegenerative diseases. A dosage of about 100 to 1000 mg of CRISPR Cas encapsulated in about 100 to 1000 mg of RVG exosomes may be contemplated for the present invention.

[00465] El-Andaloussi et al. (Nature Protocols 7,2112-2126(2012)) discloses how exosomes derived from cultured cells can be harnessed for delivery of siRNA in vitro and in vivo. This protocol first describes the generation of targeted exosomes through transfection of an expression vector, comprising an exosomal protein fused with a peptide ligand. Next, El-Andaloussi et al. explain how to purify and characterize exosomes from transfected cell supernatant. Next, El-Andaloussi et al. detail cnicial steps for loading siRNA into exosomes. Finally, El-Andaloussi et al. outline how to use exosomes to efficiently deliver siRNA in vitro and in vivo in mouse brain. Examples of anticipated results in which exosome-mediated siRNA delivery is evaluated by functional assays and imaging are also provided. The entire protocol takes ~3 weeks. Delivery or

administration according to the invention may be performed using exosomes produced from self-derived dendritic cells.

[00466] In another embodiment, the plasma exosomes of Wahlgren et al. (Nucleic Acids Research, 2012, Vol. 40, No. 17 e130) are contemplated. Exosomes are nano-sized vesicles (30-90nm in size) produced by many cell types, including dendritic ceils (DC), B cells, T cells, mast cells, epithelial cells and tumor cells. These vesicles are formed by inward budding of late endosomes and are then released to the extracellular environment upon fusion with the plasma membrane. Because exosomes naturally carry RNA between cells, this property might be useful in gene therapy.

[00467] Exosomes from plasma are prepared by centrifugation of buffy coat at 900g for 20 min to isolate the plasma followed by harvesting cell supernatants, centrifuging at 300g for 10 min to eliminate cells and at 16 500g for 30 min followed by filtration through a 0.22 mm filter. Exosomes are pelleted by ultracentrifugation at 120 000g for70 min. Chemical transfection of siRNA into exosomes is carried out according to the manufacturer's instructions in RNAi Buman/Mouse Starter Kit (Quiagen, Hilden, Germany). siRNA is added to 100 ml PBS at a final concentration of 2 mmoi/ml. After adding HiPerFect transfection reagent, the mixture is incubated for 10 min at RT. In order to remove the excess of micelles, the exosomes are re-isolated using aidehyde/sulfate latex beads. The chemical transfection of CRISPR Cas into exosomes may be conducted similarly to siRNA. The exosomes may be co-cultured with monocytes and lymphocytes isolated from the peripheral blood of healthy donors. Therefore, it may be contemplated that exosomes containing CRISPR Cas may be introduced to monocytes and lymphocytes of and autologously reintroduced into a human. Accordingly, delivery or administration according to the invention may beperformed using plasma exosomes.

Liposomes

[00468] Delivery or administration according to the invention can be performed with liposomes. Liposomes are spherical vesicle structures composed of a uni- or multilamellar lipid bilayer surrounding internal aqueous compartments and a relatively impermeable outer lipophilic phospholipid bilayer. Liposomes have gained considerable attention as drug delivery carriers because they are biocompatible, nontoxic, can deliver both hydrophilie and lipophilic drug molecules, protect their cargo from degradation by plasma enzymes, and transport their load across biological membranes and the blood brain barrier (BBB) (see, e.g., Spuch and Navarro,

Journal of Drug Delivery, vol. 2011, Article ID 469679, 12 pages, 2011. doi: 10.1155/2011Z469679 for review).

[00469] Liposomes can be made from several different types of lipids; however, phospholipids are most commonly used to generate liposomes as drug carriers. Although liposome formation is spontaneous when a lipid film is mixed with an aqueous solution, it can also be expedited by applying force in the form of shaking by using a homogenizer, sonicator, or an extrusion apparatus (see, e.g., Spuch and Navarro, Journal of Drug Delivery, vol. 2011, Article ID 469679, 12 pages, 2011. doi:10.1155/2011/469679 for review).

[00470] Several other additives may be added to liposomes in order to modify their structure and properties. For instance, either cholesterol or sphingomyelin may be added to the liposomal mixture in order to help stabilize the liposomal structure and to prevent the leakage of the liposomal inner cargo. Further, liposomes are prepared from hydrogenated egg phosphatidylcholine or egg phosphatidylcholine, cholesterol, and dicetyl phosphate, and their mean vesicle sizes were adjusted to about 50 and 100 nm. (see, e.g., Spuch and Navarro, Journal of Drug Deliver}', vol. 2011, Article ID 469679, 12 pages, 2011. doi:10.1155/2011/469679 for review).

[00471] Conventional liposome formulation is mainly comprised of natural phospholipids and lipids such as l,2-distearoryl-sn-glycero-3-phosphatidyl choline (DSPC), sphingomyelin, egg phosphatidylcholines and monosialoganglioside. Since this formulation is made up of phospholipids only, liposomal formulations have encountered many challenges, one of the ones being the instability in plasma. Several attempts to overcome these challenges have been made, specifically in the manipulation of the lipid membrane. One of these attempts focused on the mampulation of cholesterol. Addition of cholesterol to conventional formulations reduces rapid release of the encapsulated bioactive compound into the plasma or 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (DOPE) increases the stability (see, e.g., Spuch and Navarro, Journal of Drug Delivery, vol. 2011, Article ID 469679, 12 pages, 2011. doi:10.1155/2011/469679 for review).

[00472] In a particularly advantageous embodiment, Trojan Horse liposomes (also known as Molecular Trojan Horses) are desirable and protocols may be found at http://cshprotoa>is.cshfp.org/content/2010/4/pdb.prot5407.1ong. These particles allow delivery of a transgene to the entire brain after an intravascular injection. Without being bound by limitation.

it is believed that neutral lipid particles with specific antibodies conjugated to surface allow crossing of the blood brain barrier via endocytosis. Applicant postulates utilizing Trojan Horse Liposomes to deliver the CRISPR family of nucleases to the brain via an intravascular injection, which would allow whole brain transgenic animals without the need for embryonic manipulation. About 1-5 g of DNA may be contemplated for in vivo administration in liposomes.

[00473] In another embodiment, the CRISPR Cas system may be administered in liposomes, such as a stable nucleie-acid-lipid particle (SNALP) (see, e.g., Morrissey et **al.**, Nature Biotechnology, Vol. 23, No. 8, August 2005). Daily intravenous injections of about 1, 3 or 5 mg/kg/day of a specific CRISPR Cas targeted in a SNALP are contemplated. The daily treatment may be over about three days and then weekly for about five weeks. In another embodiment, a specific CRISPR Cas encapsulated SNALP) administered by intravenous injection to at doses of abpit 1 or 2.5 mg/kg are also contemplated (see, e.g., Zimmerman et al., Nature Letters, Vol. 441, 4 May 2006). The SNALP formulation may contain the lipids 3-N-[(wmethoxypoly(ethylene glycol) 2000) carbamoyl] -1,2-dimyristyloxy-propylamine (PEG-C-DMA), 1,2-dilinoieyloxy-N,N-dimethyi-3-aminopropane (DLmDMA), 1,2-distearoyl-sn-glyeero-3-phosphocholine (DSPC) and cholesterol, in a 2:40:10:48 molar per cent ratio (see, e.g., Zimmerman et al., Nature Letters, Vol. 441, 4 May 2006).

[00474] In another embodiment, stable nucleic-acid-lipid particles (SNALPs) have proven to be effective delivery molecules to highly vascularized HepG2-derived liver tumors but not in poorly vascularized HCT-116 derived liver tumors (see, e.g., Li, Gene Therapy (2012) 19, 775-780). The SNALP liposomes may be prepared by formulating D-Lin-DMA and PEG-C-DMA with distearoylphosphatidylcholine (DSPC), Cholesterol and siRNA using a 25:1 lipid/siRNA ratio and a 48/40/10/2 molar ratio of Cholesterol/D-Lin-DMA/DSPC/PEG-C-DMA. The resulted SNALP liposomes are about 80-100 nm in size.

[00475] In yet another embodiment, a SNALP may comprise synthetic cholesterol (Sigma-Aldrich, St Louis, MO, USA), dipalmitoylphosphatidylcholine (Avanti Polar Lipids, Alabaster, AL, USA), 3-N-[(w-methoxy polyiethylene glycol)2000)carbamoyl]-l,2-dimyrestyloxypropylamine, and cationic l,2-dilinoleyloxy-3-N,NdimethylaminopiOpane (see, e.g., Geisbert et al, Lancet 2010; 375: 1896-905). A dosage of about 2 mg/kg total CRISPR Cas per dose administered as, for example, a bolus intravenous infusion may be contemplated.

[00476] In yet another embodiment, a SNALP may comprise synthetic cholesterol (Sigma-Aldrich), l,2-distearoyl-sn-glycero-3-phosphocholine (DSPC; Avanti Polar Lipids inc.), PEG-cDMA, and l,2-dilinoleyloxy-3-(N;N-dimethyl)aminopropane (DLinDMA) (see, e.g., Judge, J. Clin. invest. 119:661-673 (2009)). Formulations used for in vivo studies may comprise a final lipid/RNA mass ratio of about 9:1.

[00477] The safety profile of RNAi nanomedicines has been reviewed by Barros and Gollob of Alnylam Pharmaceuticals (see, e.g., Advanced Drug Delivery Reviews 64 (2012) 1730-1737). The stable nucleic acid lipid particle (SNALP) is comprised of four different lipids — an ionizable lipid (DLinDMA) that is cationic at low pH, a neutral helper lipid, cholesterol, and a diffusible polyethylene glycol (PEG)-lipid. The particle is approximately 80 nm in diameter and is charge-neutral at physiologic pH. During formulation, the ionizable lipid serves to condense lipid with the anionic siRNA during particle formation. When positively charged under increasing!)' acidic endosomal conditions, the ionizable lipid also mediates the fusion of SNALP with the endosomal membrane enabling release of siRNA into the cytoplasm. The PEG-lipid stabilizes the particle and reduces aggregation during formulation, and subsequently provides a neutral hydrophilic exterior that improves pharmacokinetic properties.

[00478] To date, two clinical programs have been initiated using SNALPsiRNA formulations. Tekmira Pharmaceuticals recently completed a phase I single-dose study of SNALP-ApoB in adult volunteers with elevated LDL cholesterol. ApoB is predominantly expressed in the liver and jejunum and is essential for the assembly and secretion of VLDL and LDL. Seventeen subjects received a single dose of SNALP-ApoB (dose escalation across 7 dose levels). There was no evidence of liver toxicity (anticipated as the potential dose-limiting toxicity based on preclinical studies). One (of two) subjects at the highest dose experienced flu-like symptoms consistent with immune system stimulation, and the decision was made to conclude the trial.

[00479] Alnylam Pharmaceuticals has similarly advanced ALN-TTR01, which employs the SNALP technology described above and targets hepatocyte production of both mutant and wild-type TTR to treat TTR amyloidosis (ATTR). Three ATTR syndromes have been described: familial amyloidotic polyneuropathy (FAP) and familial amyloidotic cardiomyopathy (FAC) — both caused by autosomal dominant mutations in TTR; and senile systemic amyloidosis (SSA) cause by wildtype TTR. A placebo-controlled, single dose-escalation phase I trial of ALN-TTR01 was recently completed in patients with ATTR. ALN-TTR01 was administered as a 15-

minute IV infusion to 31 patients (23 with study drug and 8 with placebo) within a dose range of 0.01 to 1.0 mg/kg (based on siRNA). Treatmentwaswell tolerated with no significant increases in liver function tests. Infusion-related reactions were noted in 3 of 23 patients at>0.4 mg/kg; all responded to slowing of the infusion rate and all continued on study. Minimal and transient elevations of semm cytokines IL-6, IP-10 and IL-lra were noted in two patients at the highest dose of 1 mg/kg (as anticipated from preclinical and NHP studies). Lowering of serum TTR, the expected pharmacodynamics effect of ALN-TTR01, was observed at 1 mg/kg.

[00480] In yet another embodiment, a SNALP may be made by solubilizing a cationic lipid, DSPC, cholesterol and PEG-lipid were solubilized in ethanol at a molar ratio of 40: 10:40: 10, respectively (see, Semple et al., Nature Niotechnology, Volume 28 Number 2 February 2010, pp. 172-177). The lipid mixture was added to an aqueous buffer (50 mM citrate, pH 4) with mixing to a final ethanol and lipid concentration of 30% (vol/vol) and 6.1 mg/ml, respectively, and allowed to equilibrate at 22 °C for 2 min before extrusion. The hydrated lipids were extmded through two stacked 80 nm pore-sized filters (Nuclepore) at 22 °C using a Lipex Extruder (Northern Lipids) until a vesicle diameter of 70-90 nm, as determined by dynamic light scattering analysis, was obtained. This generally required 1-3 passes. The siRNA (solubilized in a 50 mM citrate, pH 4 aqueous solution containing 30% ethanol) was added to the pre-equilibrated (35 °C) vesicles at a rate of ~5 ml/min with mixing. After a final target siRNA/lipid ratio of 0.06 (wt/wt) was reached, the mixture was incubated for a further 30 min at 35 °C to allow vesicle reorganization and encapsulation of the siRNA. The ethanol was then removed and the external buffer replaced with PBS (155 mM NaCL 3 mM Na2HP04, I mM KH2P04, pH 7.5) by either dialysis or tangential flow diafiltration. siRNA were encapsulated in SNALP using a controlled step-wise dilution method process. The lipid constituents of KC2-SNALP were DLin-KC2-DMA (cationic lipid), dipalmitoylphosphatidylcholine (DPPC; Avanti Polar Lipids), synthetic cholesterol (Sigma) and PEG-C-DMA used at a molar ratio of 57.1:7.1 :34.3:1.4. Upon formation of the loaded particles, SNALP were dialyzed against PBS and filter sterilized through a 0.2 μm filter before use. Mean particle sizes were 75-85 nm and 90-95% of the siRNA was encapsulated within the lipid particles. The final siRNA/lipid ratio in formulations used for in vivo testing was ~0.15 (wt/wt). LNP-siRNA systems containing Factor VII siRNA were diluted to the appropriate concentrations in sterile PBS immediately before use and the formulations

were administered intravenously through the lateral tail vein in a total volume of 10 ml/kg. This method may he extrapolated to the CRISPR Cas system of the present invention.

Other Lipids

[00481] Other cationic lipids, such as amino lipid 2,2-dilmoley[-4-dimethylaminoethyl-[l ,3]~dioxolane (DLin-KC2-DMA) may be utilized to encapsulate CRISPR Cas similar to SiRNA (see, e.g., Jayaraman, Angew. Chem. Int. Ed. 2012, 51, 8529 -8533). A preformed vesicle with the following lipid composition may be contemplated: amino lipid, distearoylphosphatidyichoime (DSPC), cholesterol and (R)~2,3~bis(octadecyloxy) propyl-1-(methoxy polyiethylene glycol)2000)propylcarbamate (PEG-lipid) in the molar ratio 40/10/40/10, respectively, and a FVII siRNA/total lipid ratio of approximately 0.05 (w/w). To ensure a narrow particle size distribution in the range of 70-90 ran and a low polydispersity index of 0.11_0.04 (n=56), the particles may be extruded up to three times through 80 nm membranes prior to adding the CRISPR Cas RNA. Particles containing the highly potent amino lipid 16 may be used, in which the molar ratio of the four lipid components 16, DSPC, cholesterol and PEG-lipid (50/10/38.5/1.5) which may be further optimized to enhance in vivo activity.

[00482] Michael S D Kormann et al. ("Expression of therapeutic proteins after delivery of chemically modified mRNA in mice: Nature Biotechnology, Volume:29, Pages: 154-157 (2011) Published online 09 January 2011) describes the use of lipid envelopes to deliver RNA. Use of lipid envelopes is also preferred in the present invention.

[00483] In another embodiment, lipids may be formulated with the CRISPR Cas system of the present invention to form lipid nanoparticles (LNPs). Lipids include, but are not limited to, DLin-KC2-DMA4, C12-200 and eolipids disteroylphosphatidyl choline, cholesterol, and PEG-DMG may be formulated with CRISPR Cas instead of siRNA (see, e.g., Novobrantseva, Molecular Therapy-Nucleic Acids (2012) 1, e4; doi:10.1038/mtna.2011.3) using a spontaneous vesicle formation procedure. The component molar ratio may be about 50/10/38.5/1.5 (DLin-KC2-DMA or C12-200/disteroylphosphatidyl choline/cholesterol/PEG-DMG). The final lipid:siRNA weight ratio may be ~12:1 and 9:1 in the case of DLin-KC2-DMA and C12-200 lipid nanoparticles (LNPs), respectively. The formulations may have mean particle diameters of ~80 nm with >90% entrapment efficiency. A 3 mg/kg dose may be contemplated.

[00484] Tekmira has a portfolio of approximately 95 patent families, in the U.S. and abroad, that are directed to various aspects of LNPs and LNP formulations (see, e.g., U.S. Pat. Nos. 7,982,027; 7,799,565; 8,058,069; 8,283,333; 7,901,708; 7,745,651; 7,803,397; 8,101,741; 8,188,263; 7,915,399; 8,236,943 and 7,838,658 and European Pat. Nos .1766035; 1519714; 1781593 and 1664316), ail of which may be used/and or adapted to the present invention.

[00485] The CRISPR Cas system may be delivered encapsulated in PLGA Microspheres such as that further described in US published applications 20130252281 and 20130245107 and 20130244279 (assigned to Moderna Therapeutics) which relate to aspects of formulation of compositions comprising modified nucleic acid molecules which may encode a protein, a protein precursor, or a partially or fully processed form of the protein or a protein precursor. The formulation may have a molar ratio 50:10:38.5:1.5-3.0 (cationic lipidifusogenic lipid:cholesterol:PEG lipid). The PEG lipid may be selected from, but is not limited to PEG-c-DOMG, PEG-DMG. The fusogenic lipid may be DSPC. See also, Schnim et al., Delivery and Formulation of Engineered Nucleic Acids, US published application 20120251618.

[00486] Nanomerics' technology addresses bioavailability challenges for a broad range of therapeutics, including low molecular weight hydrophobic drugs, peptides, and nucleic acid based therapeutics (plasmid, siRNA, miRNA). Specific administration routes for which the technology has demonstrated clear advantages include the oral route, transport across the blood-brain-barrier, delivery to solid tumours, as well as to the eye. See, e.g., Mazza et al, 2013, ACS Nano. 2013 Feb 26;7(2):1016-26; Uchegbu and Slew, 2013, J Pharm Sci. 102(2):305-10 and Laiatsa et al, 2012, J Control Release. 2012 Jul 20;161(2):523-36.

[00487] US Patent Publication No. 20050019923 describes cationic dendrimers for delivering bioactive molecules, such as polynucleotide molecules, peptides and polypeptides and/or pharmaceutical agents, to a mammalian body. The dendrimers are suitable for targeting the delivery of the bioactive molecules to, for example, the liver, spleen, lung, kidney or heart. Dendrimers are synthetic 3-dimensional macromolecules that are prepared in a step-wise fashion from simple branched monomer units, the nature and functionality of which can be easily controlled and varied. Dendrimers are synthesised from the repeated addition of building blocks to a multifunctional core (divergent approach to synthesis), or towards a multifunctional core (convergent approach to synthesis) and each addition of a 3-dimensional shell of building blocks leads to the formation of a higher generation of the dendrimers. Polypropyienrmme dendrimers

start from a diaminobutane core to which is added twice the number of amino groups by a double Michael addition of acrylonitrile to the primary amines followed by the hydrogenation of the nitriles. This results in a doubling of the amino groups. Polypropylenimine dendrimers contain 100% protonable nitrogens and up to 64 terminal amino groups (generation 5, DAB 64). Protonable groups are usually amine groups which are able to accept protons at neutral pH. The use of dendrimers as gene delivery agents has largely focused on the use of the polyamidoamine. and phosphorous containing compounds with a mixture of amine/amide or N--P(0_2)S as the conjugating units respectively with no work being reported on the use of the lower generation polypropylenimine dendrimers for gene delivery. Polypropylenimine dendrimers have also been studied as pH sensitive controlled release systems for drug delivery and for their encapsulation of guest molecules when chemically modified by peripheral amino acid groups. The cytotoxicity and interaction of polypropylenimine dendrimers with DNA as well as the transfection efficacy of DAB 64 has also been studied.

[0488] US Patent Publication No. 20050019923 is based upon the observation that, contrary to earlier reports, cationic dendrimers, such as polypropylenimine dendrimers, display suitable properties, such as specific targeting and low toxicity, for use in the targeted delivery of bioactive molecules, such as genetic material. In addition, derivatives of the cationic dendrimer also display suitable properties for the targeted delivery of bioactive molecules. See also, Bioactive Polymers, US published application 20080267903, which discloses "Various polymers, including cationic polyamine polymers and dendrimeric polymers, are shown to possess anti-proliferative activity, and may therefore be useful for treatment of disorders characterised by undesirable cellular proliferation such as neoplasms and tumours, inflammatory disorders (including autoimmune disorders), psoriasis and atherosclerosis. The polymers may be used alone as active agents, or as delivery vehicles for other therapeutic agents, such as drug molecules or nucleic acids for gene therapy. In such cases, the polymers' own intrinsic anti-tumour activity may complement the activity of the agent to be delivered."

Supercharged proteins

[0489] Supercharged proteins are a class of engineered or naturally occurring proteins with unusually high positive or negative net theoretical charge. Both supernegatively and superpositively charged proteins exhibit a remarkable ability to withstand thermally or chemically induced aggregation. Superpositively charged proteins are also able to penetrate mammalian cells. Associating cargo with these proteins, such as plasmid DNA, siRNA, or other proteins, can enable the functional delivery of these macromolecules into mammalian cells both in vitro and in vivo. David Liu's lab reported the creation and characterization of supercharged proteins in 2007 (Lawrence et al., 2007, journal of the American Chemical Society 129, 101 10-101 12).

[00490] The nonviral delivery of siRNA and plasmid DNA into mammalian cells are valuable both for research and therapeutic applications (Akinc et al., 2010, Nat. Biotech. 26, 561-569). Purified +36 GFP protein (or other superposi lively charged protein) is mixed with siRNAs in the appropriate serum-free media and allowed to complex prior addition to cells. Inclusion of serum al this stage inhibits formation of the supercharged protein-siRNA complexes and reduces the effectiveness of the treatment. The following protocol has been found to be effective for a variety of cell lines (McNaughton et al, 2009, Proc. Natl. Acad. Sci. USA 106, 6111-6116). However, pilot experiments varying the dose of protein and siRNA should be performed to optimize the procedure for specific ceil lines.

(1) One day before treatment, plate *I* x 10^5 cells per well in a 48-well plate.

(2) On the day of treatment, dilute purified +36 GFP protein in serumfree media to a final concentration 200nM. Add siRNA to a final concentration of 50nM. Vortex to mix and incubate at room temperature for lOmin.

(3) During incubation, aspirate media from cells and wash once with PBS.

(4) Following incubation of +36 GFP and siRNA, add the protein-siRNA complexes to cells.

(5) Incubate cells with complexes at 37 C for 4h.

(6) Following incubation, aspirate the media and wash three times with 20 U/mL heparin PBS. Incubate cells with serum-containing media for a further 48h or longer depending upon the assay for knockdown.

(7) Analyze cells by immunoblot, qPCR, phenotypic assay, or other appropriate method.

[00491] David Liu's lab has further found +36 GFP to be an effective plasmid delivery reagent in a range of cells. As plasmid DNA is a larger cargo than siRNA, proportionately more +36 GFP protein is required to effectively complex plasmids. For effective plasmid delivery Applicants have developed a variant of +36 GFP bearing a C-terminal HA2 peptide tag, a known

endosome-disrupting peptide derived from the influenza virus hemagglutinin protein. The following protocol has been effective in a variety of cells, but as above it is advised that plasmid DNA and supercharged protein doses be optimized for specific cell lines and delivery applications.

(1) One day before treatment, plate 1 x 10^5 per well in a 48-well plate.

(2) On the day of treatment, dilute purified p36 GFP protein in serumfree media to a final concentration 2 niM. Add Img of plasmid DNA. Vortex to mix and incubate at room temperature for lOmin.

(3) During incubation, aspirate media from cells and wash once with PBS.

(4) Following incubation of p36 GFP and plasmid DNA, gently add the protein-DNA complexes to cells.

(5) Incubate cells with complexes at 37 C for 4h.

(6) Following incubation, aspirate the media and wash with PBS. Incubate cells in serum-containing media and incubate for a further 24-48h.

(7) Analyze plasmid delivery (e.g., by plasmid-driven gene expression) as appropriate.

[00492] See also, e.g., McNaughton et al, Proc. Natl. Acad. Sci. USA 106, 6111-6116 (2009); Cronican et al., ACS Chemical Biology 5, 747-752 (2010); Cronican et al.. Chemistry & Biology 18, 833-838 (2011); Thompson et al, Methods in Enzymology 503, 293-319 (2012); Thompson, D.B., et al, Chemistry & Biology 19 (7), 831-843 (2012). The methods of the super charged proteins may be used and/or adapted for delivery of the CRISPR Cas system of the present invention.

Cell penetrating peptides

[00493] In yet another embodiment, cell penetrating peptides (CPPs) are contemplated for the delivery of the CRISPR Cas system. CPPs are short peptides that facilitate cellular uptake of various molecular cargo (from nanosize particles to small chemical molecules and large fragments of DNA). The term "cargo" as used herein includes but is not limited to the group consisting of therapeutic agents, diagnostic probes, peptides, nucleic acids, antisense oligonucleotides, plasmids, proteins, nanoparticles, liposomes, chromophores, small molecules and radioactive materials. In aspects of the invention, the cargo may also comprise any component of the CRISPR Cas system or the entire functional CRISPR Cas system. Aspects of

the present invention further provide methods for delivering a desired cargo into a subject comprising: (a) preparing a complex comprising the cell penetrating peptide of the present invention and a desired cargo, and (b) orally, intraarticularly, intraperitoneally, intrathecally, intrarterially, intranasally, intraparenchymally, subcutaneously, intramuscularly, intravenously, dermally, intrarectally, or topically administering the complex to a subject. The cargo is associated with the peptides either through chemical linkage via covalent bonds or through non-covalent interactions.

[00494] The function of the CPPs are to deliver the cargo into cells, a process that commonly occurs through endocytosis with the cargo delivered to the endosomes of living mammalian cells. Cell-penetrating peptides are of different sizes, amino acid sequences, and charges but all CPPs have one distinct characteristic, which is the ability to translocate the plasma membrane and facilitate the delivery of various molecular cargoes to the cytoplasm or an organelle. CPP translocation may be classified into three main entry mechanisms: direct penetration in the membrane, endocytosis-mediated entry, and translocation through the formation of a transitory structure. CPPs have found numerous applications in medicine as drug delivery agents in the treatment of different diseases including cancer and virus inhibitors, as well as contrast agents for cell labeling. Examples of the latter include acting as a carrier for GFP, MRI contrast agents, or quantum dots. CPPs hold great potential as *in vitro* and *in vivo* delivery vectors for use in research and medicine. CPPs typically have an amino acid composition that either contains a high relative abundance of positively charged amino acids such as lysine or arginine or has sequences that contain an alternating pattern of polar/charged amino acids and non-polar, hydrophobic amino acids. These two types of structures are referred to as polycationic or amphipathic, respectively. A third class of CPPs are the hydrophobic peptides, containing only apolar residues, with low net charge or have hydrophobic amino acid groups that are crucial for cellular uptake. One of the initial CPPs discovered was the trans-activating transcriptional activator (Tat) from Human Immunodeficiency Virus 1 (HIV-1) which was found to be efficiently taken up from the surrounding media by numerous cell types in culture. Since then, the number of known CPPs has expanded considerably and small molecule synthetic analogues with more effective protein transduction properties have been generated. CPPs include but are not limited to Penetratin, Tat (48-60), Transportan, and (R-AhX-R_4) (Ahx=aminohexanoyl).

[00495] As described in U.S. patent 8,372,951, there is provided a CPP derived from eosinophil cationic protein (ECP) which exhibits highly cell-penetrating efficiency and low toxicity. Aspects of delivering the CPP with its cargo into a vertebrate subject are also provided. Further aspects of CPPs and their delivery are described in U. S. patents 8,575,305; 8;6!4,194 and 8,044,019.

[00496] That CPPs can be employed to deliver the CRISPR-Cas system is also provided in the manuscript "Gene disruption by cell-penetrating peptide-mediated delivery of Cas9 protein and guide RNA", by Suresh Ramakrishna, Abu-Bonsrah Kwaku Dad, Jagadish Beloor, et ah Genome Res. 2014 Apr 2. [Epub ahead of print], incorporated by reference in its entirety, wherein it is demonstrated that treatment with CPP-conjugated recombinant Cas9 protein and CPP-complexed guide RNAs lead to endogenous gene disruptions in human cell lines. In the paper the Cas9 protein was conjugated to CPP via a thioether bond, whereas the guide RNA was complexed with CPP, forming condensed, positively charged nanoparticles. It was shown that simultaneous and sequential treatment of human cells, including embryonic stem cells, dermal fibroblasts, HEK293T cells, HeLa cells, and embryonic carcinoma cells, with the modified Cas9 and guide RNA led to efficient gene disruptions with reduced off-target mutations relative to plasmid transfections.

Implantable devices

[00497] In another embodiment, implantable devices are also contemplated for delivery of the CRISPR Cas system. For example, US Patent Publication 201 10195123 discloses an implantable medical device which elutes a drag locally and in prolonged period is provided, including several types of such a device, the treatment modes of implementation and methods of implantation. The device comprising of polymeric substrate, such as a matrix for example, that is used as the device body, and drugs, and in some cases additional scaffolding materials, such as metals or additional polymers, and materials to enhance visibility and imaging. The selection of drag is based on the advantageous of releasing drug locally and in prolonged period, where drug is released directly to the extracellular matrix (ECM) of the diseased area such as tumor, inflammation, degeneration or for symptomatic objectives, or to injured smooth muscle cells, or for prevention. One kind of drug is the gene silencing drugs based on RNA interference (RNAi), including but not limited to si RNA, sh RNA, or antisense RNA/DNA, ribozyme and nucleoside analogs. Therefore, this system may be used/and or adapted to the CRISPR Cas system of the present invention. The

modes of implantation in some embodiments are existing implantation procedures that are developed and used today for other treatments, including brachytherapy and needle biopsy. In such cases the dimensions of the new implant described in this invention are similar to the original implant. Typically a few devices are implanted during the same treatment procedure.

[0498] As described in US Patent Publication 20110195123, there is provided a drug delivery implantable or insertable system, including systems applicable to a cavity such as the abdominal cavity and/or any other type of administration in which the drug delivery system is not anchored or attached, comprising a biostable and/or degradable and/or bioabsorbable polymeric substrate, which may for example optionally be a matrix. It should be noted that the term "insertion" also includes implantation. The drug delivery system is preferably implemented as a "Loder" as described in US Patent Publication 20110195123.

[0499] The polymer or plurality of polymers are biocompatible, incorporating an agent and/or plurality of agents, enabling the release of agent at a controlled rate, wherein the total volume of the polymeric substrate, such as a matrix for example, in some embodiments is optionally and preferably no greater than a maximum volume that permits a therapeutic level of the agent to be reached. As a non-limiting example, such a volume is preferably within the range of 0.1 mm^3 to 1000 mm^3, as required by the volume for the agent load. The Loder may optionally be larger, for example when incorporated with a device whose size is determined by functionality, for example and without limitation, a knee joint, an intra-uterine or cervical ring and the like.

[0500] The drug delivery system (for delivering the composition) is designed in some embodiments to preferably employ degradable polymers, wherein the main release mechanism is bulk erosion; or in some embodiments, non degradable, or slowly degraded polymers are used, wherein the main release mechanism is diffusion rather than bulk erosion, so that the outer part functions as membrane, and its internal part functions as a drug reservoir, which practically is not affected by the surroundings for an extended period (for example from about a week to about a few months). Combinations of different polymers with different release mechanisms may also optionally be used. The concentration gradient at the surface is preferably maintained effectively constant during a significant period of the total drug releasing period, and therefore the diffusion rate is effectively constant (termed "zero mode" diffusion). By the term "constant" it is meant a diffusion rate that is preferably maintained above the lower threshold of therapeutic effectiveness, but which may still optionally feature an initial burst and/or fluctuate, for example increasing and decreasing to a certain degree. The diffusion rate is preferably so maintained for a prolonged period, and it can be considered constant to a certain level to optimize the therapeutically effective period, for example the effective silencing period.

[00501] The drug delivery system optionally and preferably is designed to shield the nucleotide based therapeutic agent from degradation, whether chemical in nature or due to attack from enzymes and other factors in the body of the subject.

[00502] The drug delivery system as described in US Patent Publication 201 10195123 is optionally associated with sensing and/or activation appliances that are operated at and/or after implantation of the device, by non and/or minimally invasive methods of activation and/or acceleration/deceleration, for example optionally including but not limited to thermal heating and cooling, laser beams, and ultrasonic, including focused ultrasound and/or RF (radiofrequency) methods or devices.

[00503] According to some embodiments of US Patent Publication 201 10195123, the site for local delivery may optionally include target sites characterized by high abnormal proliferation of cells, and suppressed apoptosis, including tumors, active and or chronic inflammation and infection including autoimmune diseases states, degenerating tissue including muscle and nervous tissue, chronic pain, degenerative sites, and location of bone fractures and other wound locations for enhancement of regeneration of tissue, and injured cardiac, smooth and striated muscle. The site for local delivery also may optionally include sites enabling performing preventive activities including pregnancy, prevention of infection and aging.

[00504] The site for implantation of the composition, or target site, preferably features a radius, area and/or volume that is sufficiently small for targeted local delivery. For example, the target site optionally has a diameter in a range of from about 0.1 mm to about 5 cm.

[00505] The location of the target site is preferably selected for maximum therapeutic efficacy. For example, the composition of the drug delivery system (optionally with a device for implantation as described above) is optionally and preferably implanted within or in the proximity of a tumor environment, or the blood supply associated thereof

[00506] For example the composition (optionally with the device) is optionally implanted within or in the proximity to pancreas, prostate, breast, liver, via the nipple, within the vascular system and so forth.

[00507] The target location is optionally selected from the group consisting of (as non-limiting examples only, as optionally any site within the body may be suitable for implanting a Loder): 1. brain at degenerative sites like in Parkinson or Alzheimer disease at the basal ganglia, white and gray matter; 2. spine as in the case of amyotrophic lateral sclerosis (ALS); 3. uterine cervix to prevent HPV infection; 4. active and chronic inflammatory joints; 5. dermis as in the case of psoriasis; 6. sympathetic and sensoric nervous sites for analgesic effect; 7. Intra osseous implantation; 8. acute and chronic infection sites; 9. Intra vaginal; 10. Inner ear—auditory system, labyrinth of the inner ear, vestibular system; 11. Intra tracheal; 12. Intra-cardiac; coronary, epicardiac; 13. urinary bladder; 14. biliary system; 15. parenchymal tissue including and not limited to the kidney, liver, spleen; 16. lymph nodes; 17. salivary glands; 18. dental gums; 19. Intra-articular (into joints); 20. Intra-ocular; 21. Brain tissue; 22. Brain ventricles; 23. Cavities, including abdominal cavity (for example but without limitation, for ovary cancer); 24. Intra esophageal and 25. Intra rectal.

[00508] Optionally insertion of the system (for example a device containing the composition) is associated with injection of material to the ECM at the target site and the vicinity of that site to affect local pH and/or temperature and/or other biological factors affecting the diffusion of the drug and/or drug kinetics in the ECM, of the target site and the vicinity of such a site.

[00509] Optionally, according to some embodiments, the release of said agent could be associated with sensing and/or activation appliances that are operated prior and/or at and/or after insertion, by non and/or minimally invasive and/or else methods of activation and/or acceleration/deceleration, including laser beam, radiation, thermal heating and cooling, and ultrasonic, including focused ultrasound and/or RF (radiofrequency) methods or devices, and chemical activators.

[00510] According to other embodiments of US Patent Publication 201 10195123, the drug preferably comprises a gene silencing biological RNAi drag, for example for localized cancer cases in breast, pancreas, brain, kidney, bladder, lung, and prostate as described below. Moreover, many drugs other than siRNA are applicable to be encapsulated in Loder, and can be used in association with this invention, as long as such drags can be encapsulated with the Loder substrate, such as a matrix for example. Such drags include approved drugs that are delivered today by methods other than of this invention, including Amphotericin B for fungal infection; antibiotics such as in osteomyelitis; pain killers such as narcotics; and degenerative such as in

Alzheimer or Parkinson diseases in a Loder implanted in the vicinity of the spine in the case of back pain. Such a system may be used and/or adapted to deliver the CRISPR Cas system of the present invention.

[00511] For example, for specific applications such as prevention of growth or regrowth of smooth muscle cells (that are injured during a stenting procedure and as a result tend to proliferate), the drug may optionally be siRNA that silence smooth muscle cells, including H19 silencing, or a drug selected from the group consisting of taxol, rapamycin and rapamycin-analogs. In such cases the Loder is preferably either a Drug Eluting Stent (DES), with prolonged release at constant rate, or a dedicated device that is implanted separately, in association to the stent. All of this may be used/and or adapted to the CRISPR Cas system of the present invention.

[00512] As another example of a specific application, neuro and muscular degenerative diseases develop due to abnormal gene expression. Local delivery of silencing RNAs may have therapeutic properties for interfering with such abnormal gene expression. Local delivery of anti apoptotic, anti inflammatory and anti degenerative drugs including small drugs and macromolecules may also optionally be therapeutic. In such cases the Loder is applied for prolonged release at constant rate and/or through a dedicated device that is implanted separately. All of this may be used and/or adapted to the CRISPR Cas system of the present invention.

[00513] As yet another example of a specific application, psychiatric and cognitive disorders are treated with gene modifiers. Gene knockdown with silencing RNA is a treatment option. Loders locally delivering nucleotide based agents to central nervous system sites are therapeutic options for psychiatric and cognitive disorders including but not limited to psychosis, bi-polar diseases, neurotic disorders and behavioral maladies. The Loders could also deliver locally drugs including small drugs and macromolecules upon implantation at specific brain sites. All of this may be used and/or adapted to the CRISPR Cas system of the present invention.

[00514] As another example of a specific application, silencing of innate and/or adaptive immune mediators at local sites enables the prevention of organ transplant rejection. Local delivery of silencing RNAs and immunomodulating reagents with the Loder implanted into the transplanted organ and/or the implanted site renders local immune suppression by repelling immune cells such as CDS activated against the transplanted organ. All of this may be used/and or adapted to the CRISPR Cas system of the present invention.

[00515] As another example of a specific application, vascular growth factors including VEGFs and angiogenin and others are essential for neovascularization. Local delivery of the factors, peptides, peptidomimetics, or suppressing their repressors is an important therapeutic modality; silencing the repressors and local delivery of the factors, peptides, macromolecules and small drugs stimulating angiogenesis with the Loder is therapeutic for peripheral, systemic and cardiac vascular disease.

[00516] The method of insertion, such as implantation, may optionally already be used for other types of tissue implantation and/or for insertions and/or for sampling tissues, optionally without modifications, or alternatively optionally only with non-major modifications in such methods. Such methods optionally include but are not limited to brachytherapy methods, biopsy, endoscopy with and/or without ultrasound, such as ERCP, stereotactic methods into the brain tissue, Laparoscopy, including implantation with a laparoscope into joints, abdominal organs, the bladder wall and body cavities.

CRISPR enzyme mRNA and guide RNA

[00517] CRISPR enzyme mRNA and guide RNA might also be delivered separately. CRISPR enzyme mRNA can be delivered prior to the guide RNA to give time for CRISPR enzyme to be expressed. CRISPR enzyme mRNA might be administered 1-12 hours (preferably around 2-6 hours) prior to the administration of guide RNA.

[00518] Alternatively, CRISPR enzyme mRNA and guide RNA can be administered together. Advantageously, a second booster dose of guide RNA can be administered 1-12 hours (preferably around 2-6 hours) after the initial administration of CRISPR enzyme mRNA + guide RNA.

[00519] Additional administrations of CRISPR enzyme mRNA and/or guide RNA might be useful to achieve the most efficient levels of genome modification.

[00520] For minimization of toxicity and off-target effect, it will be important to control the concentration of CRISPR enzyme mRNA and guide RNA delivered. Optimal concentrations of CRISPR enzyme mRNA and guide RNA can be detennined by testing different concentrations in a cellular or animal model and using deep sequencing the analyze the extent of modification at potential off-target genomic loci. For example, for the guide sequence targeting 5'-**GAGTCCGAGCAGAAGAAGAA-3'** in the **EMX1** gene of the human genome, deep sequencing can be used to assess the level of modification at the following two off-target loci, 1:

5'-GAGTCCTAGCAGGAGAAGAA-3 ' and 2: 5'-GAGTCTAAGCAGAAGAAGAA-3'. The concentration that gives the highest level of on-target modification while minimizing the level of off-target modification should be chosen for in vivo delivery.

Crystallization of CRISPR-Cas9 and Characterization of Crystal Structure

[00521] The crystals of the invention can be obtained by techniques of protein crystallography, including batch, liquid bridge, dialysis, vapor diffusion and hanging drop methods. Generally, the crystals of the invention are grown by dissolving substantially pure CRISPR-Cas9 and a nucleic acid molecule to which it binds in an aqueous buffer containing a precipitant at a concentration just below that necessary to precipitate. Water is removed by controlled evaporation to produce precipitating conditions, which are maintained until crystal growth ceases.

[00522] Uses of the Crystals, Crystal Structure and Atomic Structure Co-Ordinates: The crystals of the invention, and particularly the atomic structure co-ordinates obtained therefrom, have a wide variety of uses. The crystals and structure co-ordinates are particularly useful for identifying compounds (nucleic acid molecules) that bind to CRISPR-Cas9, and CRISPR-Cas9s that can bind to particular compounds (nucleic acid molecules). Thus, the structure co-ordinates described herein can be used as phasing models in determining the crystal structures of additional synthetic or mutated CRISPR-Cas9s, Cas9s, nickases, binding domains. The provision of the crystal structure of CRISPR-Cas9 complexed with a nucleic acid molecule as in the herein Crystal Structure Table and the Figures provide the skilled artisan with a detailed insight into the mechanisms of action of CRISPR-Cas9. This insight provides a means to design modified CRISPR-Cas9s, such as by attaching thereto a functional group, such as a repressor or activator. While one can attach a functional group such as a repressor or activator to the N or C terminal of CRISPR-Cas9, the crystal structure demonstrates that the N terminal seems obscured or hidden, whereas the C terminal is more available for a functional group such as repressor or activator. Moreover, the crystal structure demonstrates that there is a flexible loop between approximately CRISPR-Cas9 *(S. pyogenes)* residues 534-676 which is suitable for attachment of a functional group such as an activator or repressor. Attachment can be via a linker, e.g., a flexible glycine-serine (GlyGlyGlySer) or (GGGS)$_3$ or a rigid alpha-helical linker such as (Ala(GluAlaAlaAlaLys)Ala). In addition to the flexible loop there is also a nuclease or H3 region, an H2 region and a helical region. By "helix" or "helical", is meant a helix as known in

the art, including, but not limited to an alpha-helix. Additionally, the term helix or helical may also be used to indicate a c-terminal helical element with an N-terminal turn.

[00523] The provision of the crystal structure of CRISPR-Cas9 complexed with a nucleic acid molecule allows a novel approach for drug or compound discovery, identification, and design for compounds that can bind to CRISPR-Cas9 and thus the invention provides tools useful in diagnosis, treatment, or prevention of conditions or diseases of multicellular organisms, e.g., algae, plants, invertebrates, fish, amphibians, reptiles, avians, mammals; for example domesticated plants, animals (e.g., production animals such as swine, bovine, chicken; companion animal such as felines, canines, rodents (rabbit, gerbil, hamster); laboratory animals such as mouse, rat), and humans. Accordingly, the invention provides a computer-based method of rational design of CRISPR-Cas9 complexes. This rational design can comprise: providing the structure of the CRISPR-Cas9 complex as defined by some or all (e.g., at least 2 or more, e.g., at least 5, advantageously at least 10, more advantageously at least 50 and even more advantageously at least 100 atoms of the structure) co-ordinates in the herein Crystal Structure Table and/or in Figure(s); providing a structure of a desired nucleic acid molecule as to which a CRISPR-Cas9 complex is desired; and fitting the structure of the CRISPR-Cas9 complex as defined by some or all co-ordinates in the herein Crystal Structure Table and/or in Figures to the desired nucleic acid molecule, including in said fitting obtaining putative modification(s) of the CRISPR-Cas9 complex as defined by some or all co-ordinates in the herein Crystal Structure Table and/or in Figures for said desired nucleic acid molecule to bind for CRISPR-Cas9 complex(es) involving the desired nucleic acid molecule. The method or fitting of the method may use the co-ordinates of atoms of interest of the CRISPR-Cas9 complex as defined by some or all co-ordinates in the herein Crystal Structure Table and/or in Figures which are in the vicinity of the active site or binding region (e.g., at least 2 or more, e.g., at least 5, advantageously at least 10, more advantageously at least 50 and even more advantageously at least 100 atoms of the structure) in order to model the vicinity of the active site or binding region. These co-ordinates may be used to define a space which is then screened "in silico" against a desired or candidate nucleic acid molecule. Thus, the invention provides a computer-based method of rational design of CRISPR-Cas9 complexes. This method may include: providing the co-ordinates of at least two atoms of the herein Crystal Structure Table ("selected co-ordinates"); providing the structure of a candidate or desired nucleic acid molecule; and

fitting the structure of the candidate to the selected co-ordinates. In this fashion, the skilled person may also fit a functional group and a candidate or desired nucleic acid molecule. For example, providing the structure of the CRISPR-Cas9 complex as defined by some or all (e.g., at least 2 or more, e.g., at least 5, advantageously at least 10, more advantageously at least 50 and even more advantageously at least 100 atoms of the structure) co-ordinates in the herein Crystal Structure Table and/or in Figure(s); providing a structure of a desired nucleic acid molecule as to which a CRISPR-Cas9 complex is desired; fitting the structure of the CRISPR-Cas9 complex as defined by some or all co-ordinates in the herein Crystal Structure Table and/or in Figures to the desired nucleic acid molecule, including in said fitting obtaining putative modification(s) of the CRISPR~Cas9 complex as defined by some or all co-ordinates in the herein Crystal Structure Table and/or in Figures for said desired nucleic acid molecule to bind for CR1SPR-Cas9 complex(es) involving the desired nucleic acid molecule; selecting putative fit CR1SPR-Cas9—desired nucleic acid molecule complex(es), fitting such putative fit CRISPR-Cas9—desired nucleic acid molecule complex(es) to the functional group (e.g., activator, repressor), e.g., as to locations for situating the functional group (e.g., positions within the flexible loop) and/or putative modifications of the putative fit CRISPR-Cas9—desired nucleic acid molecule complex(es) for creating locations for situating the functional group. As alluded to, the invention can be practiced using co-ordinates in the herein Crystal Structure Table and/or in Figures which are in the vicinity of the active site or binding region; and therefore, the methods of the invention can employ a sub-domain of interest of the CR1SPR-Cas9 complex. Methods of the invention can be practiced using coordinates of a domain or sub-domain. The methods can optionally include synthesizing the candidate or desired nucleic acid molecule and/or the CRISPR-Cas9 systems from the "in silico" output and testing binding and/or activity of "wet" or actual a functional group linked to a "wet" or actual CR1SPR-Cas9 system bound to a "wet" or actual candidate or desired nucleic acid molecule. The methods can include synthesizing the CRISPR-Cas9 systems (including a functional group) from the "in silico" output and testing binding and/or activity of "wet" or actual a functional group linked to a "wet" or actual CRISPR-Cas9 system bound to an *in vivo* "wet" or actual candidate or desired nucleic acid molecule, e.g., contacting "wet" or actual CR1SPR-Cas9 system including a functional group from the "in silico" output with a cell containing the desired or candidate nucleic acid molecule. These methods can include observing the cell or an organism containing the cell for a desired reaction, e.g., reduction of symptoms or condition or disease. The step of providing the structure of a candidate nucleic acid molecule may involve selecting the compound by computationally screening a database containing nucleic acid molecule data, e.g., such data as to conditions or diseases. A 3-D descriptor for binding of the candidate nucleic acid molecule may be derived from geometric and functional constraints derived from the architecture and chemical nature of the CRISPR-Cas9 complex or domains or regions thereof from the herein crystal stmcture. In effect, the descriptor can be a type of virtual modification's) of the CRISPR-Cas9 complex crystal structure herein for binding CRISPR-Cas9 to the candidate or desired nucleic acid molecule. The descriptor may then be used to interrogate the nucleic acid molecule database to ascertain those nucleic acid molecules of the database that have putativeiy good binding to the descriptor. The herein "wet" steps can then be performed using the descriptor and nucleic acid molecules that have putativeiy good binding.

[00524] "Fitting" can mean determining, by automatic or semi-automatic means, interactions between at least one atom of the candidate and at least one atom of the CRISPR-Cas9 complex and calculating the extent to which such an interaction is stable. Interactions can include attraction, repulsion, brought about by charge, steric considerations, and the like. A "sub-domain" can mean at least one, e.g., one, two, three, or four, complete element(s) of secondary stmcture. Particular regions or domains of the CRISPR-Cas9 include those identified in the herein Crystal Stmcture Table and the Figures.

[00525] In any event, the determination of the three-dimensional structure of CRISPR-cas 9 *(S. pyogenes* Cas9) complex provides a basis for the design of new and specific nucleic acid molecules that bind to CRJSPR-cas 9 (e.g., *S. pyogenes* Cas9), as well as the design of new CRISPR-Cas9 systems, such as by way of modification of the CRISPR-Cas9 system to bind to various nucleic acid molecules, by way of modification of the CRISPR-Cas9 system to have linked thereto to any one or more of various functional groups that may interact with each other, with the CRISPR~Cas9 (e.g., an inducible system that provides for self-activation and/or self-termination of function), with the nucleic acid molecule nucleic acid molecules (e.g., the functional group may be a regulatory or functional domain which may be selected from the group consisting of a transcriptional repressor, a transcriptional activator, a nuclease domain, a DNA methyl transferase, a protein acetyltransferase, a protein deacetylase, a protein methyltransferase, a protein deaminase, a protein kinase, and a protein phosphatase; and, in some

aspects, the functional domain is an epigenetic regulator; see, e.g., Zhang et al., US Patent No. 8,507,272, and it is again mentioned that it and all documents cited herein and all appln cited documents are hereby incorporated herein by reference), by way of modification of Cas9, by way of novel mckases). Indeed, the herewith CRISPR-Cas9 (*S. pyogenes* Cas9) crystal structure has a multitude of uses. For example, from knowing the three-dimensional structure of CRISPR-Cas9 (*S. pyogenes* Cas9) crystal structure, computer modelling programs may be used to design or identify different molecules expected to interact with possible or confirmed sites such as binding sites or other structural or functional features of the CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9). Compound that potentially bind ("binder") can be examined through the use of computer modeling using a docking program. Docking programs are known; for example GRAM, DOCK or AUTODOCK (see Walters et al. Drug Discovery Today, vol. 3, no. 4 (1998), 160-178, and Dunbrack et al. Folding and Design 2 (1997), 27-42). This procedure can include computer fitting of potential binders ascertain how well the shape and the chemical structure of the potential binder will bind to a CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9). Computer-assisted, manual examination of the active site or binding site of a CRISPR~Cas9 system (e.g., *S. pyogenes* Cas9) may be performed. Programs such as GRID (P. Goodford, J. Med. Chem, 1985, 28, 849-57)—a program that determines probable interaction sites between molecules with various functional groups—may also be used to analyze the active site or binding site to predict partial structures of binding compounds. Computer programs can be employed to estimate the attraction, repulsion or steric hindrance of the two binding partners, e.g., CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9) and a candidate nucleic acid molecule or a nucleic acid molecule and a candidate CR1SPR-Cas9 system (e.g., *S. pyogenes* Cas9); and the CRISPR-Cas9 crystral structure (*S. pyogenes* Cas9) herewith enables such methods. Generally, the tighter the fit, the fewer the steric hindrances, and the greater the attractive forces, the more potent the potential binder, since these properties are consistent with a tighter binding constant. Furthermore, the more specificity in the design of a candidate CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9), the more likely it is that it will not interact with off-target molecules as well. Also, "wet" methods are enabled by the instant invention. For example, in an aspect, the invention provides for a method for determining the structure of a binder (e.g., target nucleic acid molecule) of a candidate CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9) bound to the candidate CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9), said method comprising, (a) providing a first crystal of a candidate CRISPR~Cas9 system *(S. pyogenes* Cas9) according to the invention or a second crystal of a candidate a candidate CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9), (h) contacting the first crystal or second crystal with said binder under conditions whereby a complex may form; and (c) determining the structure of said a candidate (e.g., CR1SPR-Cas9 system (e.g., *S. pyogenes* Cas9) or CRISPR-Cas9 system *(S. pyogenes* Cas9) complex. The second crystal may-have essentially the same coordinates discussed herein, however due to minor alterations in CRISPR-Cas9 system (e.g., from the Cas9 of such a system being e.g., *S. pyogenes* Cas9 versus being *S. pyogenes* Cas9), wherein "e.g., *S. pyogenes* Cas9" indicates that the Cas9 is a Cas9 and can be of or derived from *S. pyogenes* or an ortholog thereof), the crystal may form in a different space group.

[00526] The invention further involves, in place of or in addition to "in silico" methods, other "wet" methods, including high throughput screening of a binder (e.g., target nucleic acid molecule) and a candidate CRISPR~Cas9 system (e.g., *S. pyogenes* Cas9), or a candidate binder (e.g., target nucleic acid molecule) and a CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9), or a candidate binder (e.g., target nucleic acid molecule) and a candidate CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9) (the foregoing CRISPR-Cas9 system(s) with or without one or more functional group(s)), to select compounds with binding activity. Those pairs of binder and CRISPR-Cas9 system which show binding activity may be selected and further crystallized with the CRJSPR-Cas9 crystal having a structure herein, e.g., by co-crystallization or by soaking, for X-ray analysis. The resulting X-ray structure may be compared with that of the herein Crystal Structure Table and the information in the Figures for a variety of purposes, e.g., for areas of overlap. Having designed, identified, or selected possible pairs of binder and CR1SPR-Cas9 system by determining those which have favorable fitting properties, e.g., predicted strong attraction based on the pairs of binder and CRISPR-Cas9 crystal structure data herein, these possible pairs can then be screened by "wet" methods for activity. Consequently, in an aspect the invention can involve: obtaining or synthesizing the possible pairs; and contacting a binder (e.g., target nucleic acid molecule) and a candidate CRISPR-Cas9 system (e.g., *S. pyogenes* Cas9), or a candidate binder (e.g., target nucleic acid molecule) and a CRJSPR-Cas9 system (e.g., *S. pyogenes* Cas9), or a candidate binder (e.g., target nucleic acid molecule) and a candidate CRJSPR-Cas9 system (e.g., *S. pyogenes* Cas9) (the foregoing CRISPR-Cas9 system(s) with or without one or more functional group(s)) to determine ability to bind. In the latter step, the

contacting is advantageously under conditions to determine function. Instead of, or in addition to, performing such an assay, the invention may comprise: obtaining or synthesizing complex(es) from said contacting and analyzing the compiex(es), e.g., by X-ray diffraction or NMR or other means, to determine the ability to bind or interact. Detailed structural information can then be obtained about the binding, and in light of this information, adjustments can be made to the structure or functionality of a candidate CRISPR-Cas9 system or components thereof. These steps may be repeated and re-repeated as necessary. Alternatively or additionally, potential CRJSPR-Cas9 systems from or in the foregoing methods can be with nucleic acid molecules in vivo, including without limitation by way of administration to an organism (including non-human animal and human) to ascertain or confirm function, including whether a desired outcome (e.g., reduction of symptoms, treatment) results therefrom.

[00527] The invention further involves a method of determining three dimensional structures of CRISPR-cas systems or complex(es) of unknown structure by using the structural co-ordinates of the herein Crystal Structure Table and the information in the Figures. For example, if X-ray crystaliographic or NMR spectroscopic data are provided for a CRISPR-cas system or complex of unknown crystal structure, the structure of a CRISPR-Cas9 complex as defined in the herein Crystal Structure Table and the Figures may be used to interpret that data to provide a likely structure for the unknown system or complex by such techniques as by phase modeling in the case of X-ray crystallography. Thus, an inventive method can comprise: aligning a representation of the CRISPR-cas system or complex having an unknown crystral structure with an analogous representation of the CRISPR-cas(9) system and complex of the crystal structure herein to match homologous or analogous regions (e.g., homologous or analogous sequences); modeling the structure of the matched homologous or analogous regions (e.g., sequences) of the CRISPR-cas system or complex of unknown crystal structure based on the structure as defined in the herein Crystal Structure Table and/or in the Figures of the corresponding regions (e.g., sequences); and, determining a conformation (e.g. taking into consideration favorable interactions should be formed so that a low energy conformation is formed) for the unknown crystal structure which substantially preserves the structure of said matched homologous regions. "Homologous regions" describes, for example as to amino acids, amino acid residues in two sequences that are identical or have similar, e.g., aliphatic, aromatic, polar, negatively charged, or positively charged, side-chain chemical groups. Homologous regions as ot nucleic acid molecules can

include at least 85% or 86% or 87% or 88% or 89% or 90% or 91% or 92% or 93% or 94% or 95% or 96% or 97% or 98% or 99% homology or identity. identical and similar regions are sometimes described as being respectively "invariant" and "conserved" by those skilled in the art. Advantageously, the first and third steps are performed by computer modeling. Homology modeling is a technique that is well known to those skilled in the art (see, e.g., Greer, Science vol. 228 (1985) 1055, and Blundell et al. Eur J Biochem vol 172 (1988), 513). The computer representation of the conserved regions of the CRISPR-Cas9 crystral structure herein and those of a CRISPR-cas system of unknown crystral structure aid in the prediction and determination of the crystral structure of the CRISPR-cas system of unknown crystal structure.

[00528] Further still, the aspects of the invention which employ the CRISPR~Cas9 crystral structure in silico may be equally applied to new CRISPR-cas crystral structures divined by using the herein CRISPR-Cas9 crystral structure. In this fashion, a library of CRISPR-cas crystral structures can be obtained. Rational CRISPR-cas system design is thus provided by the instant invention. For instance, having determined a conformation or crystral structure of a CRISPR-cas system or complex, by the methods described herein, such a conformation may be used in a computer-based methods herein for determining the conformation or crystal structure of other CRISPR-cas systems or complexes whose crystral structures are yet unkown. Data from all of these crystal structures can be in a database, and the herein methods can be more robust by having herein comparisons involving the herein crystral structure or portions thereof be with respect to one or more crystal structures in the library. The invention further provides systems, such as computer systems, intended to generate structures and/or perform rational design of a CRISPR-cas system or complex. The system can contain: atomic co-ordinate data according to the herein Crystal Structure Table and the Figures or be derived therefrom e.g., by modeling, said data defining the three-dimensional structure of a CRISPR-cas system or complex or at least one domain or sub-domain thereof, or structure factor data therefor, said structure factor data being derivable from the atomic co-ordinate data of the herein Crystal Structure Table and the Figures. The invention also involves computer readable media with: atomic co-ordinate data according to the herein Crystal Structure Table and/or the Figures or derived therefrom e.g., by homology modeling, said data defining the three-dimensional structure of a CRISPR-cas system or complex or at least one domain or sub-domain thereof, or structure factor data therefor, said structure factor data being derivable from the atomic co-ordinate data of the herein Crystal

Structure Table and/or the Figures. "Computer readable media" refers to any media which can be read and accessed directly by a computer, and includes, but is not limited to: magnetic storage media; optical storage media; electrical storage media; cloud storage and hybrids of these categories. By providing such computer readable media, the atomic co-ordinate data can be routinely accessed for modeling or other "in silico" methods. The invention further comprehends methods of doing business by providing access to such computer readable media, for instance on a subscription basis, via the Internet or a global communication/computer network; or, the computer system can be available to a user, on a subscription basis. A "computer system" refers to the hardware means, software means and data storage means used to analyze the atomic co-ordinate data of the present invention. The minimum hardware means of computer-based systems of the invention may comprise a central processing unit (CPU), input means, output means, and data storage means. Desirably, a display or monitor is provided to visualize structure data. The invention further comprehends methods of transmitting information obtained in any method or step thereof described herein or any information described herein, e.g., via telecommunications, telephone, mass communications, mass media, presentations, internet, email, etc. The crystal stmctures of the invention can be analyzed to generate Fourier electron density map(s) of CRISPR-cas systems or complexes; advantageously, the three-dimensional structure being as defined by the atomic co-ordinate data according to the herein Crystal Structure Table and'or the Figures. Fourier electron density maps can be calculated based on X-ray diffraction patterns. These maps can then be used to determine aspects of binding or other interactions. Electron density maps can be calculated using known programs such as those from the CCP4 computer package (Collaborative Computing Project, No. 4. The CCP4 Suite: Programs for Protein Crystallography, Acta Crystallographica, D50, 1994, 760-763). For map visualization and model building programs such as "QUANTA" (1994, San Diego, Calif.: Molecular Simulations, Jones et al., Acta Crystallography A47 (1991), 110-119) can be used.

[00529] The herein Crystal Structure Table (see Example 8) gives atomic co-ordinate data for a CR1SPR-Cas9 *(S. pyogenes)*, and lists each atom by a unique number; the chemical element and its position for each amino acid residue (as determined by electron density maps and antibody sequence comparisons), the amino acid residue in which the element is located, the chain identifier, the number of the residue, co-ordinates (e.g., X, Y, Z) which define with respect to the crystallographic axes the atomic position (in angstroms) of the respective atom, the occupancy of

the atom in the respective position, "B", isotropic displacement parameter (in angstroms^2) which accounts for movement of the atom around its atomic center, and atomic number. See also Example 12, the text herein and the Figures.

[00530] In particular embodiments of the invention, the conformational variations in the crystal structures of the CRISPR-Cas9 system or of components of the CRISPR-Cas9 provide important and critical information about the flexibility or movement of protein structure regions relative to nucleotide (RNA or DNA) structure regions that may be important for CRISPR-Cas system function. The structural information provided for Cas9 (e.g. S. pyogenes Cas9) as the CRISPR enzyme in the present application may be used to further engineer and optimize the CRISPR-Cas system and this may be extrapolated to interrogate structure-function relationships in other CRISPR enzyme systems as well. An aspect of the invention relates to the crystal structure of S. pyogenes Cas9 in complex with sgRNA and its target DNA at 2.4 **A** resolution. The structure revealed a bilobed architecture composed of target recognition and nuclease lobes, accommodating a sgRNA:DNA duplex in a positively-charged groove at their interface. The recognition lobe is essential for sgRNA and DNA binding and the nuclease lobe contains the HNH and RuvC nuclease domains, which are properly positioned for the cleavage of complementary and non-complementary strands of the target DNA, respectively. This high-resolution structure and the functional analyses provided herein elucidate the molecular mechanism of RNA-guided DNA targeting by Cas9, and provides an abundance of information for generating optimized CRISPR-Cas systems and components thereof.

[00531] In particular embodiments of the invention, the crystal structure provides a critical step towards understanding the molecular mechanism of RNA-guided DNA targeting by Cas9. The structural and functional analyses herein provide a useful scaffold for rational engineering of Cas9~based genome modulating technologies and may provide guidance as to Cas9-mediated recognition of PAM sequences on the target DNA or mismatch tolerance between the sgRNA:DNA duplex. Aspects of the invention also relate to truncation mutants, e.g. an S. pyogenes Cas9 truncation mutant may facilitate packaging of Cas9 into size-constrained viral vectors for in vivo and therapeutic applications. Similarly, future engineering of the PAM Interacting (PI) domain may allow programing of PAM specificity, improve target site recognition fidelity, and increase the versatility of the Cas9 genome engineering platform.

[00532] The invention comprehends optimized functional CRISPR-Cas enzyme systems. In particular the CRISPR enzyme comprises one or more mutations that converts it to a DNA binding protein to which functional domains exhibiting a function of interest may be recruited or appended or inserted or attached. In certain embodiments, the CRISPR enzyme comprises one or more mutations which include but are not limited to DIOA, E762A, H840A, N854A, N863A or D986A (based on the amino acid position numbering of a S. pyogenes Cas9) and/or the one or more mutations is in a RuvCl or HNH domain of the CRISPR enzyme or is a mutation as otherwise as discussed herein. In some embodiments, the CRISPR enzyme has one or more mutations in a catalytic domain, wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the enzyme further comprises a functional domain.

[00533] The structural information provided herein allows for interrogation of sgRNA (or chimeric RNA) interaction with the target DNA and the CRISPR enzyme (e.g. Cas9) permitting engineering or alteration of sgRNA structure to optimize functionality of the entire CRISPR-Cas system. For example, loops of the sgRNA may be extended, without colliding with the Cas9 protein by the insertion of distinct RNA loop(s) or disctinct sequence(s) that may recruit adaptor proteins that can bind to the distinct RNA loop(s) or distinct sequence(s). The adaptor proteins may include but are not limited to orthogonal RNA-binding protein / aptamer combinations that exist within the diversity of bacteriophage coat proteins. A list of such coat proteins includes, but is not limited to: Qβ, F2, GA, fr, JP501, M12, R17, BZ13, JP34, JP500, KU1, M11, MX1, TW18, VK, SP, FI, ID2, NL95, TW19, AP205, ϕCb5, ϕCb8r, ϕCb12r, ϕCb23r, 7s and PRR1. These adaptor proteins or orthogonal RNA binding proteins can further recruit effector proteins or fusions which comprise one or more functional domains. In some embodiments, the functional domain may be selected from the group consisting of: transposase domain, integrase domain, recombinase domain, resolvase domain, invertase domain, protease domain, DNA methyl transferase domain, DNA hydroxylmethylase domain, DNA demethylase domain, histone acetylase domain, histone deacetylases domain, nuclease domain, repressor domain, activator domain, nuclear-localization signal domains, transcription-regulatory protein (or transcription complex recruiting) domain, cellular uptake activity associated domain, nucleic acid binding domain, antibody presentation domain, histone modifying enzymes, recruiter of histone modifying enzymes; inhibitor of histone modifying enzymes, histone methyltransferase, histone

demethylase, histone kinase, histone phosphatase, histone ribosylase, histone deribosylase, histone ubiquitinase, histone deubiquitinase, histone biotinase and histone tail protease.

In some preferred embodiments, the functional domain is a transcriptional activation domain, preferably VP64. In some embodiments, the functional domain is a transcription repression domain, preferably KRAB. In some embodiments, the transcription repression domain is SID, or concatemers of SID (eg SID4X). In some embodiments, the functional domain is an epigenetic modifying domain, such that an epigenetic modifying enzyme is provided. In some embodiments, the functional domain is an activation domain, which may be the P65 activation domain.

[00534] The invention will now be further described by way of the following non-limiting examples.

EXAMPLES

[00535] The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion. The present examples, along with the methods described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses which are encompassed within the spirit of the invention as defined by the scope of the claims will occur to those skilled in the art.

Example 1: CRISPR Compiex Activity in the Nucleus of a Eukaryotic Cell

[00536] An example type II CRISPR system is the type II CRISPR locus from *Streptococcus pyogenes* SF370, which contains a cluster of four genes Cas9, Casl, Cas2, and Csnl, as well as two non-coding RNA elements, tracrRNA and a characteristic array of repetitive sequences (direct repeats) interspaced by short stretches of non-repetitive sequences (spacers, about 30bp each). In this system, targeted DNA double-strand break (DSB) is generated in four sequential steps (Figure 2A). First, two non-coding RNAs, the pre-crRNA array and tracrRNA, are transcribed from the CRISPR locus. Second, tracrRNA hybridizes to the direct repeats of pre-crRNA, which is then processed into mature crRNAs containing individual spacer sequences. Third, the mature crRNA:tracrRNA complex directs Cas9 to the DNA target consisting of the protospacer and the corresponding PAM via heteroduplex formation between the spacer region of the crRNA and the protospacer DNA. Finally, Cas9 mediates cleavage of target DNA

upstream of PAM to create a DSB within the protospacer (Figure 2A). This example describes an example process for adapting this RNA-programmable nuclease system to direct CRISPR complex activity in the nuclei of eukaryotic cells.

[00537] *Cell culture and transfection*

[00538] Human embryonic kidney (HEK) cell line HEK 293FT (Life Technologies) was maintained in Dulhecco's modified Eagle's Medium (DMEM) supplemented with 10% fetal bovine serum (HyClone), 2mM GlutaMAX (Life Technologies), lOOU/mL penicillin, and lQGjig/mL streptomycin at 37°C with 5% C0$_2$ incubation. Mouse neuro2A (N2A) cell line (ATCC) was maintained with DMEM supplemented with 5% fetal bovine serum (HyClone), 2mM GlutaMAX (Life Technologies), lOGU/mL penicillin, and 10Qjig/mL streptomycin at 37°C with 5% C0$_2$.

[00539] HEK 293FT or N2A cells were seeded into 24-well plates (Corning) one day prior to transfection at a density of 200,000 cells per well. Cells were transfected using Lipofectamine 2000 (Life Technologies) following the manufacturer's recommended protocol. For each well of a 24-weil plate a total of 800ng of plasmids were used.

[00540] *Surveyor assay and sequencing analysis for genome modification*

[00541] HEK 293FT or N2A cells were transfected with plasmid DNA as described above. After transfection, the cells were incubated at 37°C for 72 hours before genomic DNA extraction. Genomic DNA was extracted using the QuickExtract DNA extraction kit (Epicentre) following the manufacturer's protocol. Briefly, cells were resuspended in QuickExtract solution and incubated at 65°C for 15 minutes and 98°C for 10 minutes. Extracted genomic DNA was immediately processed or stored at -20°C.

[00542] The genomic region surrounding a CRISPR target site for each gene was PGR amplified, and products were purified using QiaQuick Spin Column (Qiagen) following manufacturer's protocol. A total of 400ng of the purified PCJR products were mixed with 2μ1 10X Taq polymerase PGR buffer (Enzymatics) and ultrapure water to a final volume of 20ul, and subjected to a re-annealing process to enable beteroduplex formation: 95°C for lOmin, 95°C to 85°C ramping at - 2°C/s, 85°C to 25°C at - 0.25°C/s, and 25°C hold for 1 minute. After re-annealing, products were treated with Surveyor nuclease and Surveyor enhancer S (Transgenomics) following the manufacturer's recommended protocol, and analyzed on 4-20% Novex TBE poly-acrylamide gels (Life Technologies). Gels were stained with SYBR Gold

DNA stain (Life Technologies) for 30 minutes and imaged with a Gel Doc gel imaging system (Bio-rad). Quantification was based on relative band intensities, as a measure of the fraction of cleaved DNA. Figure 7 provides a schematic illustration of this Surveyor assay.

[00543] Restriction fragment length polymorphism assay for detection of homologous recombination.

[00544] HEK 293FT and N2A cells were transfected with plasmid DNA, and incubated at 37°C for 72 hours before genomic DNA extraction as described above. The target genomic region was PGR amplified using primers outside the homology amis of the homologous recombination (HR) template. PGR products were separated on a 1% agarose gel and extracted with MinElute GelExtraction Kit (Qiagen). Purified products were digested with HindIII (Fermentas) and analyzed on a 6% Novex TBE poly-acrylamide gel (Life Technologies).

[00545] RNA secondary structure prediction and analysis

[00546] RNA secondary structure prediction was performed using the online webserver RNAfold developed at Institute for Theoretical Chemistiy at the University of Vienna, using the centroid structure prediction algorithm (see e.g. A.R. Gruber et al, 2008, Cell 106(1): 23-24; and PA Carr and GM Church, 2009, Nature Biotechnology 27(12): 1151-62).

[00547] RNA purification

[00548] HEK 293FT cells were maintained and transfected as stated above. Cells were harvested by trypsinization followed by washing in phosphate buffered saline (PBS). Total cell RNA was extracted with TRI reagent (Sigma) following manufacturer's protocol. Extracted total RNA was quantified using Naonodrop (Thermo Scientific) and normalized to same concentration.

[00549] *Northern blot analysis ofcrRNA and tracrRNA expression in mammalian cells*

[00550] RNAs were mixed with equal volumes of 2X loading buffer (Ambion), heated to 95°C for 5 min, chilled on ice for 1 min, and then loaded onto 8% denaturing poiyaeryl amide gels (SequaGel, National Diagnostics) after pre-running the gel for at least 30 minutes. The samples were electrophoresed for 1.5 hours at 40W limit. Afterwards, the RNA was transferred to Hybond N+ membrane (GE Healthcare) at 300 mA in a semi-dry transfer apparatus (Bio-rad) at room temperature for 1.5 hours. The RNA was crosslinked to the membrane using autocrosslink button on Stratagene UV Crosslinker the Stratalinker (Stratagene). The membrane was pre-hybridized in ULTRAhyb-Oligo Hybridization Buffer (Ambion) for 30 min with

rotation at 42°C, and probes were then added and hybridized overnight. Probes were ordered from IDT and labeled with [gamma-^{32}P] ATP (Perkin Elmer) with T4 polynucleotide kinase (New England Biolabs). The membrane was washed once with pre-warmed (42°C) 2xSSC, 0.5% SDS for 1 min followed by two 30 minute washes at 42°C. The membrane was exposed to a phosphor screen for one hour or overnight at room temperature and then scanned with a phosphorimager (Typhoon).

[00551] *Bacterial CRISPR system construction and evaluation*

[00552] CRISPR locus elements, including tracrRNA, *Cas9*, and leader were PCR amplified from *Streptococcus pyogenes* SF370 genomic DNA with flanking homology arms for Gibson Assembly. Two *Bsal* type IIS sites were introduced in between **two** direct repeats to facilitate easy insertion of spacers (Figure 8). PCR products were cloned into EcoRV-digested pACYC184 downstream of the tet promoter using Gibson Assembly Master Mix (NEB). Other endogenous CRISPR system elements were omitted, with the exception of the last 50bp of Csn2. Oligos (Integrated DNA Technology) encoding spacers with complimentary overhangs were cloned into the feal-digested vector pDCOOO (NEB) and then ligated with T7 ligase (Enzymatics) to generate pCRISPR plasmids. Challenge plasmids containing spacers with PAM

[00553] expression in mammalian cells (expression constructs illustrated in Figure 6A, with functionality as determined by results of the Surveyor assay shown in Figure 6B). Transcription start sites are marked as +1, and transcription terminator and the sequence probed by northern blot are also indicated. Expression of processed tracrRNA was also confirmed by Northern blot. Figure 6C shows results of a Northern blot analysis of total RNA extracted from 293FT cells transfected with U6 expression constructs carrying long or short tracrRNA, as well as SpCas9 and DR-EMX1(1)-DR. Left and right panels are from 293FT cells transfected without or with SpRNase III, respectively. U6 indicate loading control blotted with a probe targeting human U6 snRNA. Transfection of the short tracrRNA expression construct led to abundant levels of the processed form of tracrRNA (~75bp). Very low amounts of long tracrRNA are detected on the Northern blot.

[00554] To promote precise transcriptional initiation, the RNA polymerase III-based U6 promoter was selected to drive the expression of tracrRNA (Figure 2C). Similarly, a U6 promoter-based construct was developed to express a pre-crRNA array consisting of a single spacer flanked by two direct repeats (DRs, also encompassed by the term "tracr-mate

sequences"; Figure 2C). The initial spacer was designed to target a 33-base-pair (bp) target site (30-bp protospacer plus a 3-bp CRJSPR motif (PAM) sequence satisfying the NGG recognition motif of Cas9) in the human *EMXl* locus (Figure 2C), a key gene in the development of the cerebral cortex.

[00555] To test whether heterologous expression of the CRISPR system (SpCas9, SpRNase III, tracrRNA, and pre-crRNA) in mammalian cells can achieve targeted cleavage of mammalian chromosomes, HEK 293FT cells were transfected with combinations of CRISPR components. Since DSBs in mammalian nuclei are partially repaired by the non-homologous end joining (NHEJ) pathway, which leads to the formation of indels, the Surveyor assay was used to detect potential cleavage activity at the target *EMXl* locus (Figure 7) (see e.g. Guschin *et aL*, 2010, Methods Mol Biol 649: 247). Co-transfection of all four CRISPR components was able to induce up to 5.0% cleavage in the protospacer (see Figure 2D). Co-transfection of all CRISPR components minus SpRNase III also induced up to 4.7% indel in the protospacer, suggesting that there may be endogenous mammalian RNases that are capable of assisting with crRNA maturation, such as for example the related Dicer and Drosha enzymes. Removing any of the remaining three components abolished the genome cleavage activity of the CRISPR system (Figure 2D). Sanger sequencing of amplicons containing the target locus verified the cleavage activity: in 43 sequenced clones, 5 mutated alleles (11.6%) were found. Similar experiments using a variety of guide sequences produced indel percentages as high as 29% (see Figures 3-6, 10, and 11). These results define a three-component system for efficient CRISPR-mediated genome modification in mammalian cells. To optimize the cleavage efficiency, Applicants also tested whether different isoforms of tracrRNA affected the cleavage efficiency and found that, in this example system, only the short (89-bp) transcript form was able to mediate cleavage of the human *EMXl* genomic locus (Figure 6B).

[00556] Figure 12 provides an additional Northern blot analysis of crRNA processing in mammalian cells. Figure 12A illustrates a schematic showing the expression vector for a single spacer flanked by two direct repeats (DR-EMXl(l)-DR). The 30bp spacer targeting the human EMXl locus protospacer 1 (see Figure 6) and the direct repeat sequences are shown in the sequence beneath Figure 12A. The line indicates the region whose reverse-complement sequence was used to generate Northern blot probes for EMX1(1) crRNA detection. Figure 12B shows a Northern blot analysis of total RNA extracted from 293FT cells transfected with U6

expression constructs carrying DR-EMX1(1)-DR. Left and right panels are from 293FT cells transfected without or with SpRNase HI respectively. DR-EMX1(1)-DR was processed into mature crRNAs only in the presence of SpCas9 and short tracrRNA and was not dependent on the presence of SpRNase III. The mature crRNA detected from transfected 293FT total RNA is ~33bp and is shorter than the 39-42bp mature crRNA from *S. pyogenes.* These results demonstrate that a CR1SPR system can be transplanted into eukaryotic cells and reprogrammed to facilitate cleavage of endogenous mammalian target polynucleotides.

[00557] Figure 2 illustrates the bacterial CRISPR system described in this example. Figure 2A illustrates a schematic showing the CRISPR locus 1 from *Streptococcus pyogenes* SF370 and a proposed mechanism of CRISPR-mediated DNA cleavage by this system. Mature crRNA processed from the direct repeat-spacer array directs Cas9 to genomic targets consisting of complimentary protospacers and a protospacer-adjacent motif (PAM). Upon target-spacer base pairing, Cas9 mediates a double-strand break in the target DNA. Figure 2B illustrates engineering of *S. pyogenes* Cas9 (SpCas9) and RNase III (SpRNase III) with nuclear localization signals (NLSs) to enable import into the mammalian nucleus. Figure 2C illustrates mammalian expression of SpCas9 and SpRNase III driven by the constitutive EFla promoter and tracrRNA and pre-crRNA array (DR-Spacer-DR) driven by the RNA Pol3 promoter U6 to promote precise transcription initiation and termination. A protospacer from the human *EMXl* locus with a satisfactory PAM sequence is used as the spacer in the pre-crRNA array. Figure 2D illustrates surveyor nuclease assay for SpCas9-mediated minor insertions and deletions. SpCas9 was expressed with and without SpRNase III, tracrRNA, and a pre-crRNA array carrying the *EMXl*-target spacer. Figure 2E illustrates a schematic representation of base pairing between target locus and *EMXl*-targeting crRNA, as well as an example chromatogram showing a micro deletion adjacent to the SpCas9 cleavage site. Figure 2F illustrates mutated alleles identified from sequencing analysis of 43 clonal amplicons showing a variety of micro insertions and deletions. Dashes indicate deleted bases, and non-aligned or mismatched bases indicate insertions or mutations. Scale bar = 10μm.

[00558] To further simplify the three-component system, a chimeric crRNA-tracrRNA hybrid design was adapted, where a mature crRNA (comprising a guide sequence) may be fused to a partial tracrRNA via a stem-loop to mimic the natural crRNA:tracrRNA duplex. To increase co-delivery efficiency, a bicistronic expression vector was created to drive co-expression of a

chimeric RNA and SpCas9 in transfected cells. In parallel, the bicistronic vectors were used to express a pre-crRNA (DR-guide sequence-DR) with SpCas9, to induce processing into crRNA with a separately expressed tracrRNA (compare Figure 11B top and bottom). Figure 8 provides schematic illustrations of bicistronic expression vectors for pre-crRNA array (Figure 8A) or chimeric crRNA (represented by the short line downstream of the guide sequence insertion site and upstream of the EF1α promoter in Figure 8B) with hSpCas9, showing location of various elements and the point of guide sequence insertion. The expanded sequence around the location of the guide sequence insertion site in Figure 8B also shows a partial DR sequence (GTTTAGAGCTA) and a partial tracrRNA sequence (TAGCAAGTTAAAATAAGGCTAGTCCGTTTTT). Guide sequences can be inserted between BbsI sites using annealed oligonucleotides. Sequence design for the oligonucleotides are shown below the schematic illustrations in Figure 8, with appropriate ligation adapters indicated. WPRE represents the Woodchuck hepatitis virus post-transcriptional regulatory element. The efficiency of chimeric RNA-mediated cleavage was tested by targeting the same *EMX1* locus described above. Using both Surveyor assay and Sanger sequencing of amplicons, Applicants confirmed that the chimeric RNA design facilitates cleavage of human *EMX1* locus with approximately a 4.7% modification rate (Figure 3).

[00559] Generalizability of CRISPR-mediated cleavage in eukaryotic cells was tested by targeting additional genomic loci in both human and mouse cells by designing chimeric RNA targeting multiple sites in the human *EMX1* and *PVALB*, as well as the mouse *Th* loci. Figure 13 illustrates the selection of some additional targeted protospacers in human *PVALB* (Figure 13A) and mouse *Th* (Figure 13B) loci. Schematics of the gene loci and the location of three protospacers within the last exon of each are provided. The underlined sequences include 30bp of protospacer sequence and 3bp at the 3' end corresponding to the PAM sequences. Protospacers on the sense and anti-sense strands are indicated above and below the DNA sequences, respectively. A modification rate of 6.3% and 0.75% was achieved for the human *PVALB* and mouse *Th* loci respectively, demonstrating the broad applicability of the CRISPR system in modifying different loci across multiple organisms (Figure 5). While cleavage was only detected with one out of three spacers for each locus using the chimeric constructs, all target sequences were cleaved with efficiency of indel production reaching 27% when using the co-expressed pre-crRNA arrangement (Figures 6 and 13).

[00560] Figure 11 provides a further illustration that SpCas9 can be reprogrammed to target multiple genomic loci in mammalian cells. Figure 11A provides a schematic of the human *EMX1* locus showing the location of five protospacers, indicated by the underlined sequences. Figure 11B provides a schematic of the pre-crRNA/trcrRNA complex showing hybridization between the direct repeat region of the pre-crRNA and tracrRNA (top), and a schematic of a chimeric RNA design comprising a 20bp guide sequence, and tracr mate and tracr sequences consisting of partial direct repeat and tracrRNA sequences hybridized in a hairpin structure (bottom). Results of a Surveyor assay comparing the efficacy of Cas9-mediated cleavage at five protospacers in the human *EMX1* locus is illustrated in Figure 11C. Each protospacer is targeted using either processed pre-crRNA/tracrRNA complex (crRNA) or chimeric RNA (chiRNA).

[00561] Since the secondary structure of RNA can be crucial for intermolecular interactions, a structure prediction algorithm based on minimum free energy and Boltzmann-weighted structure ensemble was used to compare the putative secondary structure of all guide sequences used in the genome targeting experiment (see e.g. Gruber *et al,* 2008, Nucleic Acids Research, 36: WTO). Analysis revealed that in most cases, the effective guide sequences in the chimeric crRNA context were substantially free of secondary structure motifs, whereas the ineffective guide sequences were more likely to form internal secondary structures that could prevent base pairing with the target protospacer DNA. It is thus possible that variability in the spacer secondary structure might impact the efficiency of CRISPR-mediated interference when using a chimeric crRNA.

[00562] Further vector designs for SpCas9 are shown in Figure 22, which illustrates single expression vectors incorporating a U6 promoter linked to an insertion site for a guide oligo, and a Cbh promoter linked to SpCas9 coding sequence. The vector shown in Figure 22b includes a tracrRNA coding sequence linked to an H1 promoter.

[00563] In the bacterial assay, all spacers facilitated efficient CRISPR interference (Figure 3C). These results suggest that there may be additional factors affecting the efficiency of CRISPR activity in mammalian cells.

[00564] To investigate the specificity of CRISPR-mediated cleavage, the effect of single-nucleotide mutations in the guide sequence on protospacer cleavage in the mammalian genome was analyzed using a series of *EMX1*-targeting chimeric crRNAs with single point mutations (Figure 3A). Figure 3B illustrates results of a Surveyor nuclease assay comparing the cleavage

efficiency of Cas9 when paired with different mutant chimeric RNAs. Single-base mismatch up to 12-bp 5' of the PAM substantially abrogated genomic cleavage by SpCas9, whereas spacers with mutations at farther upstream positions retained activity against the original protospacer target (Figure 3B). In addition to the PAM, SpCas9 has single-base specificity within the last 12-bp of the spacer. Furthermore, CRISPR is able to mediate genomic cleavage as efficiently as a pair of TALE nucleases (TALEN) targeting the same ***EMXl*** protospacer. Figure 3C provides a schematic showing the design of TALENs targeting *EMX1*, and Figure 3D shows a Surveyor gel comparing the efficiency of TALEN and Cas9 (n=***S***).

[00565] Having established a set of components for achieving CRISPR-mediated gene editing in mammalian cells through the error-prone NHEJ mechanism, the ability of CRISPR to stimulate homologous recombination (HR), a high fidelity gene repair pathway for making precise edits in the genome, was tested. The wild type SpCas9 is able to mediate site-specific DSBs, which can be repaired through both NHEJ and HR. In addition, an aspartate-to-alanine substitution (DIOA) in the RuvC I catalytic domain of SpCas9 was engineered to convert the nuclease into a nickase (SpCas9n; illustrated in Figure 4A) (see e.g. Sapranausaks ***et** al*, 2011, Nucleic Acids Research, 39: 9275; Gasiunas ***et** al*, 2012, Proc. Natl. Acad. Sci. USA, 109:E2579), such that nicked genomic DNA undergoes the high-fidelity homology-directed repair (HDR). Surveyor assay confirmed that SpCas9n does not generate indels at the *EMXl* protospacer target. As illustrated in Figure 4B, co-expression of *EMX1*-targeting chimeric crRNA with SpCas9 produced indels in the target site, whereas co-expression with SpCas9n did not (n=3). Moreover, sequencing of 327 amplicons did not detect any indels induced by SpCas9n. The same locus was selected to test CRISPR-mediated HR by co-transfecting HEK 293FT cells with the chimeric RNA targeting *EMXl*, hSpCas9 or hSpCas9n, as well as a HR template to introduce a pair of restriction sites (*///'*miIII and *Nhel)* near the protospacer. Figure 4C provides a schematic illustration of the HR strategy, with relative locations of recombination points and primer annealing sequences (arrows). SpCas9 and SpCas9n indeed catalyzed integration of the HR template into the *EMXl* locus. PCR amplification of the target region followed by restriction digest with ***HindUl*** revealed cleavage products corresponding to expected fragment sizes (arrow's in restriction fragment length polymorphism gel analysis shown in Figure 4D), with SpCas9 and SpCas9n mediating similar levels of HR efficiencies. Applicants further verified HR using Sanger sequencing of genomic amplicons (Figure 4E). These results

demonstrate the utility of CRISPR for facilitating targeted gene insertion in the mammalian genome. Given the 14-bp (12-bp from the spacer and 2-bp from the PAM) target specificity of the wild type SpCas9, the availability of a nickase can significantly reduce the likelihood of off-target modifications, since single strand breaks are not substrates for the error-prone NHEJ pathway.

[00566] Expression constructs mimicking the natural architecture of CRISPR loci with arrayed spacers (Figure 2A) were constructed to test the possibility of multiplexed sequence targeting. Using a single CRISPR array encoding a pair of *EMX1*- and *PVALB*-targeting spacers, efficient cleavage at both loci was detected (Figure 4F, showing both a schematic design of the crRNA array and a Surveyor blot showing efficient mediation of cleavage). Targeted deletion of larger genomic regions through concurrent DSBs using spacers against two targets within *EMXl* spaced by 119bp was also tested, and a 1.6% deletion efficacy (3 out of 182 amplicons; Figure 4G) was detected. This demonstrates that the CRISPR system can mediate multiplexed editing within a single genome.

Example 2: CRISPR system modifications and alternatives

[00567] The ability to use RNA to program sequence-specific DNA cleavage defines a new class of genome engineering tools for a variety of research and industrial applications. Several aspects of the CRISPR system can be further improved to increase the efficiency and versatility of CRISPR targeting. Optimal Cas9 activity may depend on the availability of free Mg^{2+} at levels higher than that present in the mammalian nucleus (see e.g. Jinek *et ai,* 2012, Science, 337:816), and the preference for an NGG motif immediately downstream of the protospacer restricts the ability to target on average every 12-bp in the human genome (Figure 9, evaluating both plus and minus strands of human chromosomal sequences). Some of these constraints can be overcome by exploring the diversity of CRISPR loci across the microbial metagenome (see e.g. Makarova *et ai,* 2011, Nat Rev Microbiol, 9:467). Other CRISPR loci may be transplanted into the mammalian cellular milieu by a process similar to that described in Example 1. For example, Figure 10 illustrates adaptation of the Type II CRISPR system from CRISPR 1 of *Streptococcus thermophilus* LMD-9 for heterologous expression in mammalian cells to achieve CRISPR-mediated genome editing. Figure 10A provides a Schematic illustration of CRISPR 1 from *S. thermophilus* LMD-9. Figure 10B illustrates the design of an expression system for the *S. thermophilus* CRISPR system. Human codon-optimized *hStCas9* is expressed using a

constitutive EF1α promoter. Mature versions of tracrRNA and crRNA are expressed using the U6 promoter to promote precise transcription initiation. Sequences from the mature crRNA and tracrRNA are illustrated. A single base indicated by the lower case "a" in the crRNA sequence is used to remove the poiyU sequence, which serves as a RNA pollll transcriptional terminator. Figure 10C provides a schematic showing guide sequences targeting the human *EMX1* locus. Figure 10D shows the results of hStCas9-mediated cleavage in the target locus using the Surveyor assay. RNA guide spacers 1 and 2 induced 14% and 6.4%, respectively. Statistical analysis of cleavage activity across biological replica at these two protospacer sites is also provided in Figure 5. Figure 14 provides a schematic of additional protospacer and corresponding PAM sequence targets of the *S. thermophilus* CRISPR system in the human *EMXl* locus. Two protospacer sequences are highlighted and their corresponding PAM sequences satisfying NNAGAAW motif are indicated by underlining 3' with respect to the corresponding highlighted sequence. Both protospacers target the anti-sense strand.

Example 3: Sample target sequence selection algorithm

[00568] A software program is designed to identify candidate CRISPR target sequences on both strands of an input DNA sequence based on desired guide sequence length and a CRISPR motif sequence (PAM) for a specified CRISPR enzyme. For example, target sites for Cas9 from *S.pyogenes,* with PAM sequences NGG, may be identified by searching for 5'-N_x-NGG-3' both on the input sequence and on the reverse-complement of the input. Likewise, target sites for Cas9 of *S. thermophilics* CRISPR!, with PAM sequence NNAGAAW, may be identified by searching for 5'-N_x-NNAGAAW-3' both on the input sequence and on the reverse-complement of the input. Likewise, target sites for Cas9 of *S. thermophilics* CRISPR3, with PAM sequence NGGNG, may be identified by searching for 5'-N_x-NGGNG-3' both on the input sequence and on the reverse-complement of the input. The value "x" in N_x may be fixed by the program or specified by the user, such as 20.

[00569] Since multiple occurrences in the genome of the DNA target site may lead to nonspecific genome editing, after identifying all potential sites, the program filters out sequences based on the number of times they appear in the relevant reference genome. For those CRISPR enzymes for which sequence specificity is determined by a 'seed' sequence, such as the 1l-12bp 5' from the PAM sequence, including the PAM sequence itself, the filtering step may be based on the seed sequence. Thus, to avoid editing at additional genomic loci, results are filtered based

on the number of occurrences of the seed:PAM sequence in the relevant genome. The user may be allowed to choose the length of the seed sequence. The user may also be allowed to specify the number of occurrences of the seed:PAM sequence in a genome for purposes of passing the filter. The default is to screen for unique sequences. Filtration level is altered by changing both the length of the seed sequence and the number of occurrences of the sequence in the genome. The program may in addition or alternatively provide the sequence of a guide sequence complementary to the reported target sequence(s) by providing the reverse complement of the identified target sequence(s). An example visualization of some target sites in the human genome is provided in Figure 18.

[00570] Further details of methods and algorithms to optimize sequence selection can be found in U.S. application Serial No. 61/064,798 (Attorney docket 44790.1 1.2022; Broad Reference BI-20 12/084); incorporated herein by reference.

Example 4: Evaluation of multiple chimeric crRNA-tracrRNA hybrids

[00571] This example describes results obtained for chimeric RNAs (chiRNAs; comprising a guide sequence, a tracr mate sequence, and a tracr sequence in a single transcript) having tracr sequences that incorporate different lengths of wild-type tracrRNA sequence. Figure 16a illustrates a schematic of a bicistronic expression vector for chimeric RNA and Cas9. Cas9 is driven by the CBh promoter and the chimeric RNA is driven by a U6 promoter. The chimeric guide RNA consists of a 20bp guide sequence (Ns) joined to the tracr sequence (running from the first "U" of the lower strand to the end of the transcript), which is truncated at various positions as indicated. The guide and tracr sequences are separated by the tracr-mate sequence GUUUUAGAGCUA followed by the loop sequence GAAA. Results of SURVEYOR assays tor Cas9-mediated indels at the human *EMXl* and *PVALB* loci are illustrated in Figure 16b and 16c, respectively. Arrows indicate the expected SURVEYOR fragments. ChiRNAs are indicated by their "+n" designation, and crRNA refers to a hybrid RNA where guide and tracr sequences are expressed as separate transcripts. Quantification of these results, performed in triplicate, are illustrated by histogram in Figures 17a and 17b, corresponding to Figures 16b and 16c, respectively ("N.D." indicates no indels detected). Protospacer IDs and their corresponding genomic target, protospacer sequence, PAM sequence, and strand location are provided in Table D. Guide sequences were designed to be complementary to the entire protospacer sequence in

the case of separate transcripts in the hybrid system, or only to the underlined portion in the case of chimeric RNAs.

Table D:

protospacer ID	genomic target	protospacer sequence (5' to 3')	PAM	strand
1	*EMX1*	GGACATCGATGTCACCTCCAATGACTAGGG	TGG	+
2	*EMX1*	CATTGGAGGTGACATCGATGTCCTCCCCAT	TGG	-
3	*EMX1*	GGAAGGGCCTGAGTCCGAGCAGAAGAAGAA	GGG	+
4	*PVALB*	GGTGGCGAGAGGGGCCGAGATTGGGTGTTC	AGG	+
5	*PVALB*	ATGCAGGAGGGTGGCGAGAGGGGCCGAGAT	TGG	+

[00572] Further details to optimize guide sequences can be found in U.S. application Serial No. 61/836,127 (Attorney docket 44790.08.2022; Broad Reference BI-2013/004G); incorporated herein by reference.

[00573] Initially, three sites within the EMXl locus in human HEK 293FT cells were targeted. Genome modification efficiency of each chiRNA was assessed using the SURVEYOR nuclease assay, which detects mutations resulting from DNA double-strand breaks (DSBs) and their subsequent repair by the non-homologous end joining (NHEJ) DNA damage repair pathway. Constructs designated chiRNA(+n) indicate that up to the +n nucleotide of wild-type tracrRNA is included in the chimeric RNA construct, with values of 48, 54, 67, and 85 used for n. Chimeric RNAs containing longer fragments of wild-type tracrRNA (chiRNA(+67) and ehiRNA(+85)) mediated DNA cleavage at all three EMXl target sites, with chiRNA(+85) in particular demonstrating significantly higher levels of DNA cleavage than the corresponding crRNA/tracrRNA hybrids that expressed guide and tracr sequences in separate transcripts (Figures 16b and 17a). Two sites in the PVALB locus that yielded no detectable cleavage using the hybrid system (guide sequence and tracr sequence expressed as separate transcripts) were also targeted using chiRNAs. chiRNA(+67) and chiRNA(+85) were able to mediate significant cleavage at the two PVALB protospacers (Figures 16c and 17b).

For all five targets in the EMXl and PVALB loci, a consistent increase in genome modification efficiency with increasing tracr sequence length was observed. Without wishing to be bound by any theory, the secondary structure formed by the 3' end of the tracrRNA may play a role in enhancing the rate of CRJSPR complex formation.

Example 5: Cas9 diversity

[00574] The CRISPR-Cas system is an adaptive immune mechanism against invading exogenous DNA employed by diverse species across bacteria and archaea. The type II CRISPR-Cas9 system consists of a set of genes encoding proteins responsible for the "acquisition" of foreign DNA into the CRISPR locus, as well as a set of genes encoding the "execution" of the DNA cleavage mechanism; these include the DNA nuclease (Cas9), a non-coding transactivating cr-RNA (tracrRNA), and an array of foreign DNA-derived spacers flanked by direct repeats (crRNAs). Upon maturation by Cas9, the tracRNA and crRNA duplex guide the Cas9 nuclease to a target DNA sequence specified by the spacer guide sequences, and mediates double-stranded breaks in the DNA near a short sequence motif in the target DNA that is required for cleavage and specific to each CRISPR-Cas system. The type II CRISPR-Cas systems are found throughout the bacterial kingdom and highly diverse in in Cas9 protein sequence and size, tracrRNA and crRNA direct repeat sequence, genome organization of these elements, and the motif requirement for target cleavage. One species may have multiple distinct CRISPR-Cas systems.

[00575] Applicants evaluated 207 putative Cas9s from bacterial species identified based on sequence homology to known Cas9s and structures orthologous to known subdomains, including the HNH endonuclease domain and the RuvC endonuclease domains [information from the Eugene Koonin and Kira Makarova]. Phylogenetic analysis based on the protein sequence conservation of this set revealed five families of Cas9s, including three groups of large Cas9s (-1400 amino acids) and two of small Cas9s (~1100 amino acids) (see Figures 19 and 20A-F).

[0G576] Further details of Cas9s and mutations of the Cas9 enzyme to convert into a nickase or DNA binding protein and use of same with altered functionality can be found in U.S. application Serial Nos 61/836,101 and 61/835,936 (Attorney docket 44790.09.2022 and 4790.07.2022 and Broad Reference BI-2013/004E and B1-2013/004F respectively) incorporated herein by reference.

Example 6: Cas9 orthologs

[00577] Applicants analyzed Cas9 orthologs to identify the relevant PAM sequences and the corresponding chimeric guide RNA. Having an expanded set of PAMs provides broader targeting across the genome and also significantly increases the number of unique target sites and provides potential for identifying novel Cas9s with increased levels of specificity in the genome.

[00578] The specificity of Cas9 orthologs can be evaluated by testing the ability of each Cas9 to tolerate mismatches between the guide RNA and its DNA target. For example, the specificity of SpCas9 has been characterized by testing the effect of mutations in the guide RNA on cleavage efficiency. Libraries of guide RNAs were made with single or multiple mismatches between the guide sequence and the target DNA. Based on these findings, target sites for SpCas9 can be selected based on the following guidelines:

[00579] To maximize SpCas9 specificity for editing a particular gene, one should choose a target site within the locus of interest such that potential 'off-target' genomic sequences abide by the following four constraints: First and foremost, they should not be followed by a PAM with either 5'-NGG or NAG sequences. Second, their global sequence similarity to the target sequence should be minimized. Third, a maximal number of mismatches should lie within the PAM-proximal region of the off-target site. Finally, a maximal number of mismatches should be consecutive or spaced less than four bases apart.

[00580] Similar methods can be used to evaluate the specificity of other Cas9 orthologs and to establish criteria for the selection of specific target sites within the genomes of target species. As mentioned previously phylogenetic analysis based on the protein sequence conservation of this set revealed five families of Cas9s, including three groups of large Cas9s (-1400 amino acids) and two of small Cas9s (-1 100 amino acids) (see Figures 19 and 20A-F). Further details on Cas orthologs can be found in U.S. application Serial Nos 61/836,101 and 61/835,936 (Attorney docket 44790.09.2022 and 4790.07.2022 and Broad Reference BI-2013/004E and BI-2013/004F respectively) incorporated herein by reference.

Example 7: Engineering of Plants (Micro-algae) using Cas9 to target and manipulate plant genes

[00581] Methods of delivering Cas9

[00582] Method 1: Applicants deliver Cas9 and guide RNA using a vector that expresses Cas9 under the control of a constitutive promoter such as Hsp70A-Rbc S2 or Beta2-tubulin.

[00583] Method 2: Applicants deliver Cas9 and T7 polymerase using vectors that expresses Cas9 and T7 polymerase under the control of a constitutive promoter such as Hsp70A-Rbc S2 or Beta2-tubulin. Guide RNA will be delivered using a vector containing T7 promoter driving the guide RNA.

[00584] Method 3: Applicants deliver Cas9 mRNA and in vitro transcribed guide RNA to algae cells. RNA can be in vitro transcribed. Cas9 mRNA will consist of the coding region for Cas9 as well as 3'UTR from Cop1 to ensure stabilization of the Cas9 mRNA.

[00585] For Homologous recombination, Applicants provide an additional homology directed repair template.

[00586] Sequence for a cassette driving the expression of Cas9 under the control of beta-2 tubulin promoter, followed by the 3' UTR of Cop1.

[00587] **TCTTTCTTGCGCTATGACACTTCCAGCAAAAGGTAGGGCGGGCTGCGAGA CGGCTTCCCGGCGCTGCATGCAACACCGATGATGCTTCGACCCCCCGAAGCTCCTTC GGGGCTGCATGGGCGCTCCGATGCCGCTCCAGGGCGAGCGCTGTTTAAATAGCCAG** GCCCCCGATTGCAAAGACATTATAGCGAGCTACCAAAGCCATATTCAAACACCTAG ATCACTACCACTTCTACACAGGCCACTCGAGCTTGTGATCGCACTCCGCTAAGGGGG CGCGTGTTTGCCTGTTCGTTTGAGTCACAACCGGCAAACATGTACGGCATACGGATTGTTGGA GATTACGCTTCGCCGAAGAAAAAGCGCAAGGTCGAAGCGTCCGACAAGAAGTACAG CATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGT **ACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATC AAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCAC CCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGC** TATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCAC AGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCAT CTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACC **ACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTG**ATCTAT CTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTG AACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAA CCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCC TGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCC GGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGAC CCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCA AGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTAC GCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATC CTGAGAGTGAACACCG AGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAG

ATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGC
TGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGC
TACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCT
GGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTG
CTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGG
AGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAA
CCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCT
GGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATC
ACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCAT
CGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGC
ACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATAC
GTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCA
TCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAG
GACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGAT
CGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAA
GGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCC
TGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCAC
CTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGG
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CACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCA
GGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGA
AGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGG
CACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGA
AGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGA
GCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACG
AGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAA
CTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTT
CTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGG
GCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGG
CGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAA

GGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAG
CTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGAT
GAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCC
TGAAGTCCAA(GCI 'GGTGTCCGATTI '(XXGGAA{GGAT'T!X'CAGTTTI 'ACAAAGTGCGCG
AGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACC
GCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAA
GGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCT
ACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACC
CTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGG
GGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCA
TG{CX(A A<T!XiAAT\ TCGTxGAAAAAGACXXGA<G**r**]G {A<A(AG(=(G{i( ]'r(-A{i(AAA
GAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTG
GGACCCTAAGAAGTACGGCGGCTTCGACAGCCXXACCGTGGCCTATTCTGTGCTGGT
GGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTG
CTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCT
GGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGT
ACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAA
CTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTG
GCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCT
<TT!I 'G!XGGAA{CAGCACAAGCA CTA CXTxGGACGAGATCA TXXGAGCAGATXAGCGAGT
TCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACA
ACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTT
ACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGAC
CGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAG
CATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACAGCC
CCAAGAAGAAGAGAAAGGTGGAGGCCAGCTAAGGATCCGGCAAGACTGGCCCCGC
TTGGCAACGCAACAGTGAGCCCCTCCCTAGTGTGTT^^GGGATGTGACTATGTATTC
GTGTGTTGGCCAACGGGTCAACCCGAACAGATTGATACCCGCCTTGGCATTTCCTGT
CAGAATGTAACGTCAGTTGATGGTACT

[0588] Sequence for a cassette driving the expression of T7 polymerase under the control of beta-2 tubulin promoter, followed by the 3' UTR of Cop1:

[00589] **TCTTTCTTGCGCTATGACACTTCCAGCAAAAGGTAGGGCGGGCTGCGAGA** CGGCTTCCCGGCGCTGCATGCAACACCGATGATGCTTCGACCCCCCGAAGCTCCTTC GGGGCTGCATGGGCGCTCCGATGCCGCTCCAGGGCGAGCGCTGTTTAAATAGCCAG GCGCGCCGATTCCAAAGACATTATAGCGAGCTACCAAAGCCATATTCAAACACCTAG ATCACTACCACTTCTACACAGGCCACTCGAGCTTGTGATCGCACTCCGCTAAGGGGG **CGCCTCTTCCTCTTCGTTTCAGTCACAACCCGCAAACatgcctaagaagaagaggaaggttaacacgatt** aacatcgctaagaacgacttctctgacatcgaactggctgctatcccgttcaacactctggctgaccattacggtgagcgtttagctcgcgaa cagttggcccttgagcatgagtcttacgagatgggtgaagcacgcttccgcaagatgtttgagcgtcaacttaaagctggtgaggttgcggat aacgctgccgccaagcctctcatcactaccctactccctaagatgattgcacgcatcaacgactggtttgaggaagtgaaagctaagcgcg gcaagcgcccgacagcciiccagitccigcaagaaatcaagccggaagccgiagcgtacatcaccatiaagaccactctggcttgcctaac cagtgctgacaatacaaccgttcaggctgtagcaagcgcaatcggtcgggccattgaggacgaggctcgcttcggtcgtatccgtgacctt gaagctaagcacttcaagaaaaacgttgaggaacaactcaacaagcgcgtagggcacgtctacaagaaagcatttatgcaagitgtcgag gctgacatgctctctaagggtctactcggtggcgaggcgtggtcttcgtggcataaggaagactctattcatgtaggagtacgctgcatcgag atgctcattgagtcaaccggaatggttagcttacaccgccaaaatgctggcgtagiaggtcaagactctgagactatcgaactcgcacctga atacgctgaggctatcgcaacccgtgcaggtgcgctggctggcatctctccgatgttccaaccttgcgtagttcctcctaagccg^^gactgg cattactggtggtggctattgggctaacggtcgtcgtcctctggcgctggtgcgtactcacagtaagaaagcactgatgcgctacgaagacg tttacatgcctgaggtgtacaaagcgattaacattgcgcaaaacaccgcatggaaaatcaacaagaaagtcctagcggtegccaacgtaatc accaagtggaagcattgtccggtcgaggacatccctgcgattgagcgtgaagaactcccgatgaaaccggaagacatcgacatgaatcct gaggctctcaccgcgtggaaacgtgctgccgctgctgtgtaccgcaaggacaaggctcgcaagtctcgccgtatcagccttgagttcatgc ttgagcaagccaataagtttgctaaccataaggccatctggttcccttacaacatggactggcgcggtcgtgtttacgctgtgtcaatgttcaac ccgcaaggtaacgatatgaccaaaggactgctiacgctggcgaaaggtaaaccaatcggtaaggaaggttactactggctgaaaatccac ggtgcaaactgtgcgggtgtcgacaaggttccgttccctgagcgcatcaagttcattgaggaaaaccacgagaacatcatggcttgcgctaa gtctccactggagaacacttggtgggctgagcaagattctccgttctgcttccttgcgttctgctttgagtacgctggggtacagcaccacggc ctgagctataactgctcccttccgctggcgtttgac^^gtcttgctctggcatccagcacttctccgcgatgctccgagatgaggtaggtggtc gcgcggttaacttgcttcctagtgaaaccgttcaggacatctacgggattgttgctaagaaagtcaacgagattctacaagcagacgcaatca atgggaccgataacgaagtagttaccgtgaccgatgagaacactggtgaaatctctgagaaagtcaagctgggcactaaggcactggctg gtcaatggctggcttacggtgttactcgcagtgtgactaagcgttcagtcatgacgctggcttacgggtccaaagagttcggcttccgtcaac aagtgctggaagataccattcagccagctattgattccggcaagggtctgatgttcactcagccgaatcaggctgctggatacatggctaag ctgatttgggaatctgtgagcgtgacggtggtagctgcggttgaagcaatgaactggcttaagtctgctgctaagctgctggctgctgaggtc aaagataagaagactggagagattcttcgcaagcgitgcgctgtgcattgggtaactcctgatggittccctgtgtggcaggaatacaagaa gcctattcagacgcgcttgaacctgatgttcctcggtcagttccgcttacagcctaccattaacaccaacaaagatagcgagattgatgcaca

caaacaggagtctggtatcgctcctaac^ gtacacagccaagacggtagccaccttcgtaagactgtagtgtgggcacacgagaagtac ggaatcgaatcttttgcactgattcacgactccttcggtacgattccggctgacgctgcgaacctgttcaaagcagtgcgcgaaactatggttg acacatatgagtcttgtgatgtactggctgatttctacgaccagttcgctgaccagttgcacgagtctcaattggacaaaatgccagcacttcc ggctaaaggtaacttgaacctccgtgacatcttagagtcggacttcgcgttcgcgtaaGGATCCGGCAAGACTGGCCCC GCTTGGCAACGCAACAGTGAGCCCCTCCCTAGTGTGTTTGGGGATGTGACTATGTAT TCGTGTGTTTGGCCAACGGGTCAACCCGAACAGATTGATACCCGCCTTGGCATTTCCT GTCAGAATGTAACGTCAGTTGATGGTACT

[00590] Sequence of guide RNA driven by the T7 promoter (T7 promoter, Ns represent targeting sequence):

[00591] gaaatTAATACGACTCACTATANNNNNNNNNNNNNNNNNNNNgttttagagctaGA AAtagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgctttttt

[00592] Gene delivery:

[00593] Chiamydomonas reinhardtii strain CC-124 and CC-125 from the Chlamydomonas Resource Center will be used for electroporation. Electroporation protocol follows standard recommended protocol from the GeneArt Chlamydomonas Engineering kit.

[00594] Also, Applicants generate a line of Chlamydomonas reinhardtii that expresses Cas9 constitutively. This can be done by using pChlamyl (linearized using Pvul) and selecting for hygromycin resistant colonies. Sequence for pChlamyl containing Cas9 is below. In this way to achieve gene knockout one simply needs to deliver RNA for the guideRNA. For homologous recombination Applicants deliver guideRNA as well as a linearized homologous recombination template.

[00595] pChlamyl-Cas9:

[00596] TGCGGTATTTCACACCGCATCAGGTGGCACTTTTCGGGGAAATGTGCGCG GAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGATT ATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAAT CTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGC ACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTG TAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCG CGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAG GGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTG TTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGC

CATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCC
GGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTC
ATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTT
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GTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAA
AAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGC
TGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTT
TACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAA
AGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATT
ATTGAAGCATTTATCAGGGTTATTGTCTCATGACCAAAATCCCTTAACGTGAGTTTTC
GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTT
TTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGT
TTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAG
AGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAA
GAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGTT
GCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGAT
AAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCG
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AGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCG
GGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGA
GCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGC
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AGTGAGCGAGGAAGCGGTCGCTGAGGCTTGACATGATTGGTGCGTATGTTTGTATGA
AGCTACAGGACTGATTTGGCGGGCTATGAGGGCGGGGGAAGCTCTGGAAGGGCCGC
GATGGGGCGCGCGGCGTCCAGAAGGCGCCATACGGCCCGCTGGCGGCACCCATCCG
GTATAAAAGCCCGCGACCCCGAACGGTGACCTCCACTTTCAGCGACAAACGAGCAC
TTATACATACGCGACTATTCTGCCGCTATACATAACCACTCAGCTAGCTTAAGATCC
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AAACCGGCCAGGGGGCCTATGTTCTTTACTTTTTTACAAGAGAAGTCACTCAACATC
TTAAAATGGCCAGGTGAGTCGACGAGCAAGCCCGGCGGATCAGGCAGCGTGCTTGC
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GATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGA
GGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGC
TGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCG
ACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCC
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GAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACC
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CATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGA
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CCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTAT
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CTAGTGTGTTTGGGGATGTGACTATGTATTCGTGTGTTGGCCAACGGGTCAACCCGA
ACAGATTGATACCCGCCTTGGCATTTCCTGTCAGAATGTAACGTCAGTTGATGGTAC
T.

[00597] For all modified Chlamydomonas reinhardtii cells, Applicants use PCR, SURVEYOR nuclease assay, and DNA sequencing to verify successful modification.

Example 8: Crystal Structure

[00598] Figures 23A-M provide: various views of the CRISPR-cas complex crystal structure (A-I), chemieric RNA architecture from the crystal structure (J-K), an interaction schematic from the crystal structure (L) and a topology schematic from the crystal structure (M).

[00599] Figures 23J-K concern a SpCas9 sgRNA structural study, and Figures 26A-B also pertain to sgRNA mutations. SpCas9 sgRNAs were mutated to investigate contribution of specific bases or groups of bases to activity. These include mutations in the direct repeat (DR) and tracrRNA regions of the sgRNA, divided into: stem 1 (base-pairing region between DR and tracrRNA), bulge (un-paired bases between DR and tracrRNA), loop 1 (artificial GAAA connector between DR and tracrRNA), linker 1 (between stem 1 and stem 2), stem 2 (first hairpin formed by tracrRNA tail), loop 2 (loop in between stem 2), stem 3 (second, or last

hairpin formed by tracrRNA tail), and loop 3 (loop in between stem 3). Mutations were chosen based on predicted secondary structure as well as secondary structure as illustrated in Figures 23A-M, especially Figure 23J. In addition, three (3) sgRNA scaffolds were designed to incorporate MS2 loops in loop regions for interaction/binding to recruit functional domains fused to MBP. sgRNAs were synthesized as U6::PCR amplicon and tested in co-transfection with wildtype SpCas9.

[00600] 400ng of Cas9 plasmid, 100ng of sgRNA into 200,000 HEK 293FT cells with Lipofectamine 2000; DNA was harvested 3 days post-transfection for SURVEYOR analysis.

[00601] The invention thus comprehends the invention comprehends a CRISPR-cas9 (S. pyogenes) system having a crystal having the structure defined by the co-ordinates of following Cystral Structure Table (the CRISPR-cas9 crystal structure).

```
REMARK   PHEKIX  refinement
REMARK
REMARK   ******************      INPUT  FILES AND  LABELS   ******************************
REMARK   Reflections  :
REMARK     file  name        :
/net6/nisimasu/eas9/native03_24/phx/Ref     ine_4/ca.¾9_2 3_ref ine__data .mtz
REMARK     labels            : ['I -obs , SIGI-obs ']
REMARK   R-free  flags:
REMARK     file  name        :
/net6/nisimasv./cas9/native03   _24/phx/Ref ine_4/cas9 _23_refine _data. mtz
REMARK     label             : R-free-flags
REMARK     test_flag_value:  1
REMARK   Model  file name(s) :
REMARK     /net6/nisimasu/cas9/native03    _24/phx/cas9 _23_refine _5-coot-l .pdb
REMARK
REMARK   *******************      REFINEMENT    SUMMARY:   QUICK   FACTS   ******************
REMARK   Start:  r_work  = 0.2333  r_free  = 0.2681  bonds  = 0.009  angles  = 1.224
REMARK   Final:  r_work  = 0.2287  r_free  - 0.2727  bonds  = 0.008  angles  = 1.195
REMARK   ***************************************************************************
REMARK
REMARK   ******************      REFINEMENT    STATISTICS    STEP  BY STEP  ******************
REMARK   leading  digit,  like  1_, means  number  of macro-cycle
REMARK   0     : statistics  at the  very  beginning  when  nothing  is done  yet
REMARK   l_bSS  : bulk  solvent  correction  and/or  (anisotropic)  scaling
REMARK   1_xyz : refinement  of coordinates
REMARK   l__adp : refinement  of ADPs  (Atomic  Displacement  Parameters)
REMARK   ----------------------------------------------------------------------------
REMARK    R-factors,  x-ray  target  values  and  norm  of gradient  of x-ray  target
REMARK    stage      r-work  r-free   xray__target__w   xray_ta rget_t
REMARK      θ     :  0..4183  0.3996    3.183623e+00     3.249901e+00
REMARK      1_bss:   0.,2333  0.2681    2.986992e+00     3,103838e+00
REMARK   1_settarget :  0.2333  0.2681    5.570105e-02    7,188160e-02
REMARK   1_addcbetar :  0.2333  0.2681    5.570105e-02    7.188160e-02
REMARK   l_we right :  0.2333  0.2681    5,570105e-02     7,I88160e-02
REMARK   l_xyzrec  :  0..2301  0.2756    5.160978e-02     7.597045e-02
REMARK      1_adp :  0..2297  0,2750    5.053688e-02     7.559149e~02
REMARK      2__bss :  0.I304  0.2755    5,085887e-02     7,576964e-02
REMARK   2 settarget:  0.2304  0.2755    3.030450e+00    3.133267e+00
REMARK   2~weight:    0.2304  0.2755    3.030450e+00     3.1332675+00
REMARK   2__xyzrec :  0.2319  0.2724    3,002038e+00     3,I14623e+00
REMARK      2_adp :  0.2308  0.2735    2.983982e+00     3,111742e+00
REMARK      3_bss :  0.2301  0.2722    2.986422e÷00     3.I13812e+00
REMARK   3_settarget :  0.2301  0.2722    2.986422e+00    3.113812e+00
REMARK   3_weight:    0.2301  0.2722    2.986422e+00     3,113812e+00
REMARK   3_xyzrec :  0.2296  0.2720    2.982246e+00     3.U2724e+00
REMARK      3_adp :  0.2311  0.2740    2.983885e+00     3.113561e+00
REMARK        end.:  0.2287  0.2727    2,980889e÷00     3,I14524e+00
REMARK   ----------------------------------------------------------------------------
REMARK    stage      <pher >    fom    a-ipha        beta
REMARK      0     :  40..667  0.6489   0.0924       375. 058
REMARK      1_bss:   34.. 679  0.7169   0.8687       159.107
REMARK   1_settarget :  34.679  0.7169   0,8687       159. 107
REMARK   l_addcbetar :  34.679  0.7169   0.8687       159.107
REMARK   1_weight:    34.. 679  0.7169   0.8687       159.107
REMARK   l_xyzrec. :  35,,930  0.7024   0.8546       168.565
REMARK      l_adp :  35.. 994  0.7018   0.8670       168.273
REMARK      2_bss:   36..236  0.6986   0,8407       168. 452
REMARK   2__settarget:  36. 236  0.6986   0.8407       168.452
REMARK   2_-weight :  36..236  0.6986   0.8407       168. 452
REMARK   2_xyzrec :  35..526  0.7068   0,8488       163.909
REMARK      2_adp:   35..506  0.7069   0.8267       164 .124
REMARK      3__b3s:   35..216  0.7106   0.8544       164.060
REMARK   3_settarget :  35.216  0.7106   0.8544       164.060
```

```
REMARK   3_weight:    35.216  0.7106    0.8544        164.060
REMARK   3_xyzrec :   35.053  0.7127    0,8566        164.509
REMARK      3_adp:    35.140  0.7117    0.8257        165.334
REMARK        end :   35.132  0.7117    0.8548        163.891
REMARK   ----------------------------------------------------------------------------
REMARK    stage          angl     bond     chir     dihe     plan     repu    geom_target
REMARK      0     :    I.224   0.009    0.053   16.866    0.005    4.103     1.366ie--01
REMARK      1_bss:     i.224   0.009    0.053   16.866    0.005    4.103     1.366ie-01
REMARK   1_set target  :   1.224   0.009   0.053   16. 866   0.005   4.103    1.3661e- -01
REMARK   1_addcbe tar:    1.224   0.009   0,053   16. 866   0.005   4,103    i.37S3e- -01
REMARK   1_weight  :    i.224   0.009    0.053   16.866    0.005    4.103     1.3753e-01
REMARK   1_xyzrec  :    i.197   0.009    0.046   16.893    0.005    4.102     1.2487e-01
REMARK      1_adp:      1.197   0.009    0.046   16.893    0.005    4.102      .2487e-01
REMARK      2_bss :     1.197   0.009    0.046   16.893    0.005    4.102     1.2487e--01
REMARK   2_settarget   :   1.197   0.009   0.046   16. 893   0.005   4.102    l,2487e- -01
REMARK   2_weight:      1.197   0.009    0.046   16.893    0.005    4.102     1.2485e-01
REMARK   2_xyzrec  :    1.200   0.008    0.047   16.800    0.005    4.105     1.1966e-01
REMARK      2_adp:      i.200   0.008    0.047   16.800    0.005    4.105     1.1966e-01
REMARK      3_bss:      1.200   0.008    0.047   16.800    0.005    4.105     1.1966e-01
REMARK   3_settarget   :   1.200   0.008   0,047   16. 800   0.005   4,105    1.I966e- -01
REMARK   3_weight  :    i.200   0.008    0.047   16.800    0.005    4.105     1.1992e-01
REMARK   3_xyzrec  :    i.195   0.008    0.047   16.785    0.005    4.106     1.1995e-01
REMARK      3_adp:      I.195   0.008    0.047   16.785    0.005    4.106     1.1995e--01
REMARK        end :     i.195   0.008    0,047   16.785    0.005    4.106     1.1995e-01
REMARK   ----------------------------------------------------------------------------
REMARK                              Maximal deviations:
REMARK    stage          angl     bond     chir     dihe     plan     repu       !grad!
REMARK      0     :   16.300   0.091    0,409170  .819    0.060    1.791     3.589oe-02
REMARK      1_bss :   16.300   0.091    0.409170  .819    0.060    1.791     3.5698e-02
REMARK   1_settarget   :  16. 300   0.091   0.409170.   819    0.060   1.791    3.5898e- 02
REMARK   1_addcbe tar :   16. 300   0.091   0.409170.   819    0.060   1.791    3,S821e-  02
REMARK   1_weight  :  16.300   0.091    0.409170.819     0.060    1.791     3.5821e-02
REMARK   1_xyzrec  :  13.201   0.098    0.380173.670     0.070    2.099     2.2688e-02
REMARK      1_adp:    13.201   0.098    0,380173.670     0.070    2.099     2.2688e-02
REMARK      2_bss :   13.201   0.098    0.380173.670     0.070    2.099     2.2688e-02
REMARK   2_settarget   :  13. 201   0.098   0,380173.   670    0.070   2,099    2.2688e- 02
REMARK   2_weight:    13.201   0.098    0,380173.670     0.070    2.099     2.2685e-02
REMARK   2_xyzrec:    13.522   0.083    0.397172  .158    0.058    2.078     2.2398e-02
REMARK      2_adp:    13.522   0.083    0.397172.158     0.058    2.078     2,2398e-02
REMARK      3_bss:    13.522   0.083    0.397.172.158    0.058    2.078     2.2398e-02
REMARK   3_settarget   :  13. 522   0.083   0.397172.   158    0.058   2.078    2,2398e~  02
REMARK   3_weight  :  13.522   0.083    0.397172.158     0.058    2.078     2.2446e-02
REMARK   3_xyzrec  :  14.311   0.081    0.393172.025     0.057    2.054     2.2726e-02
REMARK      3_adp:    14.311   0.081    0,393172.025     0.057    2.054     2.2726e-02
REMARK        end:    14.311   0.081    0.393172.025     0.057    2.054     2.2726e-02
REMARK   ----------------------------------------------------------------------------
REMARK               !-----overal 1-----|---macromolecule----j------solvent -------|
REMARK     stage       b_max    b_min   b_ave   b_max   b_min   b_ave   b_maK   b_rain   b_ave
REMARK      0     : 160.43    28.85   71.22  160.43   28.85   71.30   81.67   30.00   51.94
REMARK      1_bss: 160.43    28.85   71,22  160.43   28.85   71.30   81.67   30.00   51.94
REMARK   1_settarget: 160.43   28.85   71.22  160.43   28.85   71.30   81.67   30.00   51.94
REMARK   1_addcbe tar: 160.43   28.85   71.22  160.43   28.85   71.30   81.67   30.00   51.94
REMARK   1_weight  : 160.43    28.85   71,22  160.4 3   28.85   71.30   81.67   30.00   51.94
REMARK   1 xyzrec  : 160.43    28.85   71.22  160.43   28.85   71.30   81.67   30.00   51.94
REMARK      1_adp: 161.86    28.35   71.48  161.8 6   28.35   71.56   76.67   37.13   51.11
REMARK      2_bss : 161.86    28.35   71,48  161.86   28.35   71.56   76.67   37.13   51.11
REMARK   2_settarget:    161.86   28.35   71.48  161.86   28.35   71.56   76.67   37.13   51.11
REMARK   2_weight  : 161.86    28.35   71.48  161.8 6   28.35   71.56   76.67   37.13   51.11
REMARK   2_xyzrec  : 161.86    28.35   71.48  161.86    28.35   71.56   76.67   37.13   51.11
REMARK      2_adp  : 161.72    27.70   70,86  161.72    27.70   70. 95   83.20   35.10   51.05
REMARK      3_bss: 161.72    27.70   70. 86  161.72    27.70   70. 95   83.20   35.10   51.05
REMARK   3_settarget:    161.72   27.70   70.86  161.72   27.70   70.95   83.20   35.10   51.0 5
REMARK   3_weight: 161. 72   27.70   70, 86  161.72    27.70   70.95   83.20   35.10   51.05
```

```
REMARK   3_xyzrec: 161.72    27.70    70.86  161.72    27.70    70.95    83.20    35.10    51.05
REMARK      3_adp: 160.38    27.42    69,33  160.38    27.42    69.42    81. 92   31.44    49.95
REMARK        end: 160.38    27.42    69.33  160.38    27.42    69.42    81. 92   31.4 4   49.95
REMARK ----------------------------------------------------------------------------------------
REMARK  stage          Deviat ;.i.on of  ref ined.
REMARK                 model  from  start- model
REMARK                   max        min      mean
REMARK      0     :     0.000      0 .000     0.000
REMARK      1_bss:      0.000      0 .000     0.000
REMARK   1_settarget  :     0 .000     0.000      0 ,000
REMARK   1_addcbetar  :     0 .000     0.000      0 .000
REMARK   1_weight :     0 .000      0 .000     0.000
REMARK   1_xyzrec  :    1 .645      0 .002     0.094
REMARK      1_adp :     1 .645      0 .002     0.0 94
REMARK      2Joss:      1 .645      0 .002     0.0 94
REMARK   2_settarget   :    1 .645     0.002      0.094
REMARK   2__weight :    1.645      0 .002     0.0 94
REMARK   2_xyz.rec :    1.564      0 .001     0.062
REMARK      2__adp:     1.564      0 .001     0.062
REMARK      3_bss:      1.564      0 .001     0.062
REMARK   3_setta .rget :    1 .564     0.001      0 .062
REMARK   3_weight:      1.564      0 .001     0.0 62
REMARK   3_xyzrec:      1.660      0 .001     0.068
REMARK      3_adp :     1 .660      0 .001     0.0 68
REMARK        end :     1 .660      0 .001     0.0 68
REMARK ------------------------------------------------------------------------
REMARK MODEL   CONTENT.
REMARK  ELEMENT          ATOM   RECORD   COUNT     OCCUPANCY    SUM
REMARK        P                              234             234.00
REMARK        C                            14252           14252.00
REMARK        S                               37              37.00
REMARK        0                             5241            5241 ,00
REMARK        N                             4105            4105.00
REMARK     TOTAL                           23869           23869.00
REMARK -----------------------------------------------------------------------
REMARK r_free _flags  .md5 .hexdigest    524 86022af  bddl8 92776b3e20dl  fccb4
REMARK
REMARK IF THIS  FILE  IS FOR  PDB  DEPOSITION:    REMOVE   ALL  FROM  THIS  LINE  UP.
REMARK   3
REMARK   3 REFINEMENT   .
REMARK   3    PROGRAM        : PHENIX   (phenix. refine:   1.8.3 _1479)
REMARK   3    AUTHORS        : Adams, Afonine,  Burnley,  Chen, Davis,Echols,  Gi.ld.ea,
REMARK   3                   : Gopal,  Gros, Grosse-Kunstleve,    Keadd. Hung, Immorrriino,
REMARK   3                   : Ioerger,  McCoy,McKee,  Moriartv,   Pai, Read, Richardson,
REMARK   3                   : Richardson,Romo, Sacchettini   ,Sauter,  Smith,  Storoni,
REMARK   3                   : Terw ilIiger,Zwar t
REMARK   3
REMARK   3  REFINEMENT  TARGET  : ML
REMARK   3
REMARK   3  DATA  USED  IN  REFINEMENT.
REMARK   3   RESOLUTION   RANGE  HIGH   (ANGSTROMS)   : 2.400
REMARK   3   RESOLUTION   RANGE  LOW    (ANGSTROMS)   : 46 .701
REMARK   3   MIN (FOBS / SIGMR_FOBS  )                : 1 ,96
REMARK   3   COMPLETENESS    FOR  RANGE          (%)  : 98.45
REMARK   3   NUMBER   OF  REFLECTIONS                 : 147138
REMARK   3   NUMBER   OF  REFLECTIONS    (NON-ANOMALOUS   ) : 147138
REMARK   3
REMARK   3  FIT  TO  DATA. USED  IN  REFINEMENT,
REMARK   3   R  VALUE        (WORKING  + TEST  SET)  : 0.2292
REMARK   3   R  VALUE               (WORKING  SET)   : 0.2287
REMARK   3   FREE  R  VALUE                          : 0.2 727
REMARK   3   FREE  R  VALUE  TEST  SET  SIZE    (%)  : 1.20
REMARK   3   FREE  R  VALUE  TEST  SET  COUNT        : 1764
```

```
REMARK   3
REMARK   3  FIT TO DATA USED IN REFINEMENT  (IN BINS }.
REMARK   3   BIN  RESOLUTION  RANGE   COMPL .   NWORK  NFREE   RWORK  RFREE
REMARK   3     1 46..7097 -  5.6402    0 ..98   11173    136  0.1784 0.1955
REMARK   3     2  5 ,,6402 -  4,4779    0,99    11296    136  0.1963 0.2500
REMARK   3     3  4.4779 -  3.9122    0.99    11265    137  0.2028 0.2244
REMARK   3     4  3 ..9122 -  3.5546    0 ..99   11271    137  0.2226 0.3028
REMARK   3     5  3 ,,5546 -  3,2999    0,99    11153    136  0.2451 0.3052
REMARK   3     6  3 ..2999 -  3.1054    0 ..99   11275    136  0.2661 0.3084
REMARK   3     7  3 ,1054 -  2.9499    0 ..99   11123    136  0.2853 0.3308
REMARK   3     8  2.,9499 -  2.8215    0 ,.98   11224    135  0.2929 0.3928
REMARK   3     9  2,8215 -  2.7129    0 ..98   11150    136  0.2981 0.3419
REMARK   3    10  2,7129 -  2.6193    0,98    11162    136  0.3059 0.3756
REMARK   3    11  2..6193 -  2.5374    0 ..98   11133    135  0.3217 0.3694
REMARK   3    12  2,5374 -  2,4649    0 ,.98   11116    135  0.3351 0.3945
REMARK   3    13  2.4649 -  2.4000    0 ..98   11033    133  0.3470 0.3895
REMARK   3
REMARK   3  BULK SOLVENT MODELLING .
REMARK   3   METHOD USED        : FLAT BULK SOLVENT MODEL
REMARK   3   SOLVENT RADIUS     : 1.11
REMARK   3   SHRINKAGE RADIUS   : 0.90
REMARK   3   GRID STEP FACTOR   : 4.00
REMARK   3
REMARK   3  ERROR ESTIMATES.
REMARK   3   COORDINATE ERROR (MAXIMUM-LIKELIHOOD BASED)     : 0.45
REMARK   3   PHASE ERROR (DEGREES , MAXIMUM-LIKELIHOOD BASED) : 35.13
REMARK   3
REMARK   3  STRUCTURE FACTORS CALCULATION ALGORITHM : FFT
REMARK   3
REMARK   3  DEVIATIONS FROM IDEAL VALUES.
REMARK   3                 RMSD      MAX    COUNT
REMARK   3   BOND      :   0.008    0.081   24696
REMARK   3   ANGLE     :   1.195   14.311   34572
REMARK   3   CHIRALITY :   0.047    0.393    4125
REMARK   3   PLANARITY :   0.005    0.057    3568
REMARK   3   DIHEDRAL  :  16.785  172.025    9579
REMARK   3   MIN N0N30NDED DISTANCE : 2.054
REMARK   3
REMARK   3  MOL PROBITY STATISTICS,
REMARK   3   ALL-ATOM CLASKSCORE  : 9.29
REMARK   3   RAMACHANDRAN PLOT:
REMARK   3     OUTLIERS : 0.79 %
REMARK   3     ALLOWED  : 7.27 %
REMARK   3     FAVORED  : 91.94 %
REMARK   3   ROTAMER OUTLIERS  : 7.46 %
REMARK   3   CBETA DEVIATIONS  : 0
REMARK   3
REMARK   3  ATOMIC DISPLACEMENT PARAMETERS.
REMARK   3   WILSON B : 59,56
REMARK   3   RMS (B_ISO_OR_EQUIVALENT _BONDED) : 4.09
REMARK   3   ATOMS          NUMBER OF ATOMS
REMARK   3                    ISO.  ANISO.
REMARK   3    ALL         :  23869     0
REMARK   3    ALL (NO H ) :  23869     0
REMARK   3    SOLVENT     :    101     0
REMARK   3    NON-SOLVENT :  23768     0
REMARK   3    HYDROGENS   :      0     0
REMARK   3
CRYST1   76.711  105.692  126.815  97.68  98.43 100.31 P 1
SCALE 1    0,013036  0.002370  0.002353        0.00000
SCALE 2    0.000000  0.009617  0.001602        0.00000
SCALES     0.000000  0.000000  0.008081        0.00000
ATOM      1  O   LYS A   3     -6,852  51.606 -17,925  1.00 84.57           O
```

ATOM	2	N	LYS	A	3	-6.495	49.272	-16.515	1.00	86.17	N
ATOM	3	CA	LYS	A	3	-7.583	49.348	-17.492	1.00	87.06	C
ATOM	4	C	LYS	A	3	-7.504	50.633	-18.320	1.00	84.64	C
ATOM	5	CB	LYS	A	3	-8.949	49.249	-16.801	1.00	77.43	c
ATOM	6	O	LYS	A	4	-10.418	52.058	-20.996	I.00	82.35	0
ATOM	7	N	LYS	A	4	-8.178	50.622	-19.469	1.00	81.04	N
ATOM	8	CA	LYS	A	4	-8.087	51.707	-20.442	1.00	78.21	c
ATOM	9	C	LYS	A	4	-9.376	52.528	-20.508	I.00	78.42	c
ATOM	10	CB	LYS	A	4	-7.751	51.144	-21.829	1.00	74.60	c
ATOM	11	O	TYR	A	5	-9.289	56.162	-21.449	1.00	61.89	0
ATOM	12	N	TYR	A	5	-9.295	53.764	-20.035	I.00	73.68	N
ATOM	13	CA	TYR	A	5	-10.461	54.641	-19.995	1.00	65.53	C
ATOM	14	C	TYR	*A*	5	-10.380	55.757	-21.025	1.00	62.17	C
ATOM	15	CB	TYR	A	5	-10.618	55.250	-18.601	1.00	60.26	c
ATOM	16	CG	TYR	A	5	-9.626	56.352	-18.318	1.00	63.62	c
ATOM	17	CD1	TYR	A	5	-8.270	56.078	-18.205	1.00	61.48	c
ATOM	18	*CD2*	TYR	A	5	-10.043	57.680	-18.178	1.00	60.86	c
ATOM	19	CE1	TYR	A	5	-7.350	57.087	-17.948	I.00	64.63	c
ATOM	20	CE2	TYR	A	5	-9.126	58.697	-17.922	1.00	58.87	c
ATOM	21	CZ	TYR	A	5	-7.783	58.396	-17.808	1.00	63.09	c
ATOM	22	OH	TYR	A	5	-6.860	59.392	-17.564	I.00	63.66	0
ATOM	23	N	SER	A	6	-11.540	56.275	-21.410	1.00	64.32	N
ATOM	24	CA	SER	A	6	-11.563	57.487	-22.218	1.00	64.81	c
ATOM	25	C	SER	A	6	-12.416	58.627	-21.624	I.00	57.95	c
ATOM	26	O	SER	A	6	-13.393	58.397	-20.903	1.00	54.94	0
ATOM	27	CB	SER	*A*	6	-12.033	57.149	-23.633	1.00	62.65	c
ATOM	28	OG	SER	A	6	-10.907	56.947	-24.478	I.00	65.58	0
ATOM	29	N	ILE	A	7	-12.022	59.856	-21.943	1.00	59.93	N
ATOM	30	CA	ILE	*A*	7	-12.723	61.054	-21.488	1.00	53.57	c
ATOM	31	c	ILE	A	7	-13.332	61.844	-22.634	1.00	55.81	c
ATOM	32	O	ILE	A	7	-12.625	62.274	-23.543	1.00	57.60	0
ATOM	33	CB	ILE	A	7	-11.789	62.011	-20.753	1.00	57.06	c
ATOM	34	CGI	ILE	A	7	-10.974	61.286	-19.703	1.00	51.86	c
ATOM	35	CG2	ILE	A	7	-12.577	63.182	-20.135	I.00	61.29	c
ATOM	36	CD1	ILE	A	7	-9.788	62.098	-19.278	1.00	59.83	c
ATOM	37	N	GLY	A	8	-14.636	62.063	-22.582	1.00	52.53	N
ATOM	38	CA.	GLY	A	8	-15.256	63.038	-23.466	I.00	54.40	c
ATOM	39	C	GLY	A	8	-15.432	64.411	-22.817	1.00	56.88	c
ATOM	40	O	GLY	*A*	8	-15.439	64.528	-21.592	1.00	52.45	0
ATOM	41	N	LEU	A	9	-15.587	65.446	-23.644	I.00	55.80	N
ATOM	42	CA	LEU	A	9	-15.687	66.827	-23.163	1.00	52.69	C
ATOM	43	C	LEU	*A*	9	-16.695	67.669	-23.958	1.00	54.15	c
ATOM	44	O	LEU	A	9	-16.631	67.732	-25.186	1.00	55.12	0
ATOM	45	CB	LEU	A	9	-14.316	67.508	-23.216	1.00	48.99	c
ATOM	46	CG	LEU	A	9	-13.189	66.869	-22.396	1.00	48.86	c
ATOM	47	CD1	LEU	A	9	-11.839	67.478	-22.758	1.00	37.45	c
ATOM	48	CD2	LEU	A	9	-13.464	66.995	-20.900	I.00	46.82	c
ATOM	49	N	ALA	A	10	-17.612	68.332	-23.265	1.00	45.53	N
ATOM	50	CA	ALA	A	10	-18.543	69.213	-23.942	1.00	49.53	c
ATOM	51	C	ALA	A	10	-18.347	70.661	-23.500	I.00	49.91	c
ATOM	52	O	ALA	A	10	-18.857	71.085	-22.469	1.00	47.09	0
ATOM	53	CB	ALA	A	10	-19.961	68.765	-23.694	1.00	52.67	c
ATOM	54	N	ILE	A	11	-17.587	71.410	-24.286	I.00	51.48	N
ATOM	55	CA	ILE	A	11	-17.288	72.796	-23.954	1.00	50.46	c
ATOM	56	C	ILE	*A*	11	-18.343	73.795	-24.455	1.00	50.05	c
ATOM	57	O	ILE	A	11	-18.650	73.845	-25.643	I.00	56.39	0
ATOM	58	CB	ILE	A	11	-15.932	73.206	-24.522	1.00	48.70	c
ATOM	59	CGI	ILE	*A*	11	-14.955	72.038	-24.434	1.00	47.33	c
ATOM	60	CG2	ILE	A	11	-15.402	74.390	-23.774	1.00	49.00	c
ATOM	61	CD1	ILE	A	11	-13.580	72.392	-24.901	1.00	50.66	c
ATOM	62	N	GLY	A	12	-18.892	74.578	-23.531	1.00	47.11	N
ATOM	63	CA	GLY	A	12	-19.804	75.669	-23.848	1.00	47.61	c
ATOM	64	C	GLY	A	12	-19.322	76.965	-23.213	I.00	46.13	c

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ATOM     65  O   GLY A  12     -18.211  77.029 -22.707  1.00 48.69           O
ATOM     66  O   THR A  13     -19.618  80.244 -20.510  1.00 55.02           O
ATOM     67  N   THR A  13     -20.140  78.006 -23.249  1.00 51.65           N
ATOM     68  CA  THR A  13     -19.742  79.308 -22.692  1.00 48.23           c
ATOM     69  C   THR A  13     -20.136  79.411 -21.227  1.00 45.99           C
ATOM     70  CB  THR A  13     -20.360  80.490 -23.463  1.00 50.01           C
ATOM     71  OG1 THR A  13     -21.715  80.189 -23.808  1.00 51.86           O
ATOM     72  CG2 THR A  13     -19.594  80.752 -24.726  1.00 55.66           C
ATOM     73  O   ASN A  14     -21.794  76.775 -17.708  1.00 43.59           O
ATOM     74  N   ASN A  14     -21.031  78.542 -20.783  1.00 43.11           N
ATOM     75  CA  ASN A  14     -21.357  78.465 -19.380  1.00 40.57           C
ATOM     76  C   ASN A  14     -21.268  77.047 -18.781  1.00 40.89           C
ATOM     77  CB  ASN A  14     -22.740  79.067 -19.195  1.00 43.14           C
ATOM     78  CG  ASN A  14     -22.808  80.469 -19.747  1.00 44.19           c
ATOM     79  OD1 ASN A  14     -23.083  80.673 -20.930  1.00 55.09           0
ATOM     80  ND2 ASN A  14     -22.480  81.444 -18.915  1.00 42.57           N
ATOM     81  O   SER A  15     -19.101  74.060 -20.763  1.00 45.29           O
ATOM     82  N   SER A  15     -20.584  76.138 -19.461  1.00 41.88           N
ATOM     83  CA  SER A  15     -20.547  74.767 -18.970  1.00 42.67           C
ATOM     84  c   SER A  15     -19.429  73.928 -19.586  1.00 42.48           c
ATOM     85  CB  SER A  15     -21.900  74.072 -19.199  1.00 43.19           c
ATOM     86  OG  SER A  15     -22.297  74.133 -20.565  1.00 48.23           0
ATOM     87  O   VAL A  16     -18.556  70.366 -17.594  1.00 39.92           0
ATOM     88  N   VAL A  16     -18.831  73.082 -18.760  1.00 37.38           N
ATOM     89  CA  VAL A  16     -17.993  71.999 -19.265  1.00 43.04           c
ATOM     90  C   VAL A  16     -18.555  70.673 -18.790  1.00 41.68           c
ATOM     91  CB  VAL A  16     -16.529  72.108 -18.828  1.00 36.60           c
ATOM     92  CGI VAL A  16     -15.751  70.931 -19.383  1.00 43.90           c
ATOM     93  CG2 VAL A  16     -15.932  73.399 -19.303  1.00 34.97           c
ATOM     94  N   GLY A  17     -19.082  69.916 -19.742  1.00 48.15           N
ATOM     95  CA  GLY A  17     -19.490  68.547 -19.488  1.00 49.97           C
ATOM     96  C   GLY A  17     -18.327  67.577 -19.647  1.00 45.61           c
ATOM     97  O   GLY A  17     -17.479  67.743 -20.536  1.00 46.12           0
ATOM     98  N   TRP A  18     -18.272  66.582 -18.771  1.00 46.44           N
ATOM     99  CA  TRP A  18     -17.190  65.592 -18.831  1.00 54.14           c
ATOM    100  c   TRP A  18     -17.684  64.206 -18.416  1.00 52.40           c
ATOM    101  0   TRP A  18     -18.591  64.080 -17.594  1.00 53.51           0
ATOM    102  CB  TRP A  18     -16.014  66.023 -17.940  1.00 51.68           c
ATOM    103  CG  TRP A  18     -16.447  66.257 -16.544  1.00 51.86           c
ATOM    104  CD1 TRP A  18     -16.954  67.407 -16.032  1.00 47.72           c
ATOM    105  CD2 TRP A  18     -16.460  65.305 -15.481  1.00 51.80           c
ATOM    106  NE1 TRP A  18     -17.275  67.238 -14.707  1.00 50.21           N
ATOM    107  CE2 TRP A  18     -16.979  65.952 -14.346  1.00 52.39           c
ATOM    108  CE3 TRP A  18     -16.084  63.964 -15.382  1.00 55.41           C
ATOM    109  ca2 TRP A  18     -17.124  65.308 -13.124  1.00 53.43           c
ATOM    110  CZ3 TRP A  18     -16.231  63.327 -14.167  1.00 53.37           c
ATOM    111  CH2 TRP A  18     -16.739  63.992 -13.057  1.00 49.43           c
ATOM    112  N   ALA A  19     -17.077  63.168 -18.981  1.00 53.20           N
ATOM    113  CA  ALA A  19     -17.430  61.797 -18.629  1.00 51.14           c
ATOM    114  c   ALA A  19     -16.259  60.869 -18.865  1.00 54.16           c
ATOM    115  0   ALA A  19     -15.529  61.013 -19.847  1.00 56.96           0
ATOM    116  CB  ALA A  19     -18.628  61.329 -19.414  1.00 54.56           c
ATOM    117  N   VAL A  20     -16.075  59.937 -17.937  1.00 52.67           N
ATOM    118  CA  VAL A  20     -15.041  58.920 -18.038  1.00 58.65           c
ATOM    119  C   VAL A  20     -15.656  57.594 -18.510  1.00 59.05           c
ATOM    120  O   VAL A  20     -16.689  57.145 -17.999  1.00 57.31           0
ATOM    121  CB  VAL A  20     -14.335  58.715 -16.699  1.00 56.98           c
ATOM    122  CGI VAL A  20     -13.279  57.626 -16.817  1.00 58.12           c
ATOM    123  CG2 VAL A  20     -13.714  60.006 -16.247  1.00 54.28           c
ATOM    124  N   ILE A  21     -15.024  56.972 -19.489  1.00 57.13           N
ATOM    125  CA  ILE A  21     -15.646  55.834 -20.159  1.00 62.37           C
ATOM    126  c   ILE A  21     -14.721  54.620 -20.228  1.00 63.65           c
ATOM    127  0   ILE A  21     -13.518  54.777 -20.455  1.00 64.09           0
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ATOM     128  CB   ILE A   21      -16.104   56.264  -21.559   1.00 60.20           C
ATOM     129  CGI  ILE A   21      -17.598   56.562  -21.535   1.00 63.28           C
ATOM     130  CG2  ILE A   21      -15.763   55.243  -22.622   1.00 63.73           C
ATOM     131  GDI  ILE A   21      -18.091   57.207  -22.802   1.00 69.12           C
ATOM     132  N    THR A   22      -15.285   53.431  -19.984   I.00 65.26           N
ATOM     133  CA   THR A   22      -14.577   52.146  -20.154   1.00 68.63           C
ATOM     134  C    THR A   22      -14.847   51.514  -21.512   1.00 70.08           C
ATOM     135  0    THR A   22      -15.743   51.945  -22.238   I.00 67.79           0
ATOM     136  CB   THR A   22      -14.980   51.092  -19.096   1.00 65.50           C
ATOM     137  OG1  THR A   22      -16.404   50.896  -19.125   1.00 64.92           0
ATOM     138  CG2  THR A   22      -14.530   51.507  -17.714   I.00 60.20           C
ATOM     139  O    ASP A   23      -16.082   49.313  -24.533   1.00 75.47           0
ATOM     140  N    ASP A   23      -14.092   50.457  -21.814   1.00 77.30           N
ATOM     141  CA   ASP A   23      -14.230   49.677  -23.057   1.00 73.77           C
ATOM     142  C    ASP A   23      -15.670   49.320  -23.382   1.00 70.82           C
ATOM     143  CB   ASP A   23      -13.433   48.370  -22.975   1.00 75.99           C
ATOM     144  CG   ASP A   23      -11.950   48.585  -22.745   1.00 77.77           C
ATOM     145  OD1  ASP A   23      -11.349   49.478  -23.386   I.00 80.48           0
ATOM     146  OD2  ASP A   23      -11..385   47.831  -21.922   1.00 78.63           0
ATOM     147  N    GLU A   24      -16.431   49.010  —Z2.347   1.00 72.11           N
ATOM     148  CA.  GLU A   24      -17.793   48.540  -2.2.509   I.00 72.21           C
ATOM     149  C    GLU A   24      -18.746   49.719  -22.687   1.00 73.94           C
ATOM     150  O    GLU A   24      -19.972   49.548  —Z2.728   1.00 75.11           0
ATOM     151  CB   GLU A   24      -18.186   47.680  -21.302   I.00 82.71           C
ATOM     152  CG   GLU A   24      -17.173   47.715  -20.118   1.00 83.09           C
ATOM     153  CD   GLU A   24      -15.960   46.787  -20..303   1.00 83.44           C
ATOM     154  OE1  GLU A   24      -16.162   45.563  -20.508   I.00 84..34           0
ATOM     155  OE2  GLU A   24      -14.808   47.285  -20.234   1.00 78.82           0
ATOM     156  N    TYR A   25      -18.152   50.910  -22.809   1.00 70.52           N
ATOM     157  CA   TYR A   25      -18.863   52.179  -22.894   1.00 66.59           C
ATOM     158  C    TYR A   25      -19.612   52.486  -21.614   1.00 68.56           C
ATOM     159  O    TYR A   25      -20.615   53.201  -21.633   1.00 70.19           0
ATOM     160  CB   TYR A   25      -19.842   52.198  -24.058   1.00 70.51           C
ATOM     161  CG   TYR A   25      -19.201   51.985  -25.394   I.00 72.08           C
ATOM     162  CD1  TYR A   25      -18.312   52.910  -25.916   1.00 67.16           C
ATOM     163  CD2  TYR A   25      -19.497   50.857  -26.145   1.00 75.88           C
ATOM     164  CE1  TYR A   25      -17.725   52.709  -27.149   I.00 69.95           C
ATOM     165  CE2  TYR A   25      -18.918   50.647  -27.372   1.00 77.42           C
ATOM     166  CZ   TYR A   25      -18.038   51.571  -27.872   1.00 75.92           C
ATOM     167  OH   TYR A   25      -17.478   51..337  -29.103   I.00 77.63           0
ATOM     168  O    LYS A   26      -17.918   53.803  -18.781   1.00 58.18           0
ATOM     169  N    LYS A   26      -19.106   51.959  -20.506   1.00 64.18           N
ATOM     170  CA   LYS A   26      -19.680   52.197  -19.191   1.00 66.21           C
ATOM     171  C    LYS A   26      -19.058   53.411  -18.493   1.00 61.37           C
ATOM     172  CB   LYS A   26      -19.500   50.958  -18..310   1.00 70.89           C
ATOM     173  N    VAL A   27      -19.803   53.987  -17.558   1.00 56.80           N
ATOM     174  CA.  VAL A   27      -19.226   54.972  -16.658   I.00 51.50           C
ATOM     175  C    VAL A   27      -18.874   54.348  -15..308   1.00 50.09           C
ATOM     176  O    VAL A   27      -19.748   53.920  -14.566   1.00 57.58           0
ATOM     177  CB   VAL A   27      -20.169   56.164  -16.438   I.00 59.58           C
ATOM     178  CGI  VAL A   27      -19.545   57.151  -15.472   1.00 56.56           C
ATOM     179  CG2  VAL A   27      -20.496   56.849  -17.773   1.00 57.39           C
ATOM     180  N    PRO A   28      -17.579   54.311  -14.981   I.00 47.31           N
ATOM     181  CA   PRO A   28      -17.073   53.892  -13.669   1.00 49.84           C
ATOM     182  C    PRO A   28      -17.778   54.524  -12.476   1.00 58.91           C
ATOM     183  O    PRO A   28      -18.527   55.492  -12.607   I.00 63.78           0
ATOM     184  CB   FRO A   28      -15.605   54.350  -13.692   1.00 56.48           C
ATOM     185  CG   PRO A   28      -15.231   54.388  -15.142   1.00 51.55           C
ATOM     186  CD   PRO A   28      -16.495   54.626  -15.932   1.00 51.28           C
ATOM     187  N    SER A   29      -17.535   53.936  -11.306   1.00 67.86           N
ATOM     188  CA   SER A   29      -17.815   54.546  -10.007   1.00 50.68           C
ATOM     189  C    SER A   29      -16.514   54.517   -9.244   1.00 55.70           C
ATOM     190  O    SER A   29      -15.679   53.667   -9.503   I.00 66.74           0
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ATOM	191	CB	SER	A	29	-18.864	53.776	-9.199	1.00	59.20	C
ATOM	192	OG	SER	A	29	--20.096	53.630	-9.859	1.00	61.34	O
ATOM	193	N	LYS	A	30	-16.337	55.440	-8..308	1.00	63.00	N
ATOM	194	CA	LYS	A	30	-15.332	55.290	-7.260	1.00	59.60	C
ATOM	195	C	LYS	A	30	-15.900	55.849	-5.949	1.00	62.28	C
ATOM	196	O	LYS	A	30	-16.714	56.799	-5.945	1.00	64.22	0
ATOM	197	CE	LYS	A	30	-14.013	55.978	-7.624	1.00	54.09	C
ATOM	198	CG	LYS	A	30	-13.254	55.332	-8.773	1.00	59.72	C
ATOM	199	CD	LYS	A	30	-11.879	55.956	-8.946	1.00	65.70	C
ATOM	200	CE	LYS	A	30	-11.052	55.249	-10.017	1.00	68.34	C
ATOM	201	NZ	LYS	A	30	-11.310	53.777	-10.050	1.00	79.94	N
ATOM	202	N	LYS	A	31	-15.510	55.218	-4.847	1.00	55.63	N
ATOM	203	CA	LYS	A	31	-15.774	55.740	-3.522	1.00	54.54	C
ATOM	204	C	LYS	A	31	-14.723	56.792	-3.266	1.00	60.61	C
ATOM	205	O	LYS	A	31	-13.524	56.542	-3.469	1.00	61.06	0
ATOM	206	CB	LYS	A	31	-15.714	54.652	-2.458	1.00	62.25	C
ATOM	207	CG	LYS	A	31	-16.856	53.650	-2.510	1.00	70.86	C
ATOM	208	CD	LYS	A	31	-16.433	52.317	-1.913	1.00	76.14	C
ATOM	209	CE	LYS	A	31	-17.556	51.319	-1.988	1.00	84.96	C
ATOM	210	NZ	LYS	A	31	-18.543	51.529	-0.900	1.00	89.99	N
ATOM	211	N	PHE	A	32	-15.172	57.971	-2.843	1.00	56.46	N
ATOM	212	CA	PHE	A	32	-14.275	59.111	-2.682	1.00	59.34	C
ATOM	213	C	PHE	A	32	-14.196	59.558	-1.249	1.00	59.21	C
ATOM	214	0	PHE	A	32	-15.211	59.643	-0.564	1.00	61.45	0
ATOM	215	CB	PHE	A	32	-14.723	60.290	-3.551	1.00	53.77	C
ATOM	216	CG	PHE	A	32	-14.391	60.126	-5.003	1.00	53.60	C
ATOM	217	CD1	PHE	A	32	-13.125	60.410	-5.466	1.00	49.20	C
ATOM	218	CD2	PHE	A	32	-15.344	59.671	-5.899	1.00	52.67	C
ATOM	219	CE1	PHE	A	32	-12.813	60.255	-6.804	1.00	51.77	C
ATOM	220	CE2	PHE	A	32	-15.037	59.516	-7.227	1.00	52.47	C
ATOM	221	CZ	PHE	A	32	-13.771	59.812	-7.680	1.00	51.06	C
ATOM	222	N	LYS	A	33	-12.986	59.862	-0.804	1.00	56.96	N
ATOM	223	CA	LYS	A	33	-12.795	60.388	0.540	1.00	60.18	C
ATOM	224	C	LYS	A	33	-13.470	61.770	0.727	1.00	60.08	C
ATOM	225	O	LYS	A	33	-13.386	62.658	-0.126	1.00	52.61	0
ATOM	226	CB	LYS	A	33	-11.301	60.469	0.850	1.00	56.72	C
ATOM	227	CG	LYS	A	33	-10.955	61.178	2.143	1.00	62.76	C
ATOM	228	CD	LYS	A	33	-9.468	61.476	2.200	1.00	64.89	C
ATOM	229	CE	LYS	A	33	-8.669	60.191	2.167	1.00	69.92	C
ATOM	230	NZ	LYS	A	33	-8.891	59.406	3.407	1.00	67.46	N
ATOM	231	N	VAL	A	34	-14.137	61.917	1.864	1.00	59.95	N
ATOM	232	CA	VAL	A	34	-14.727	63.178	2.292	1.00	6.1.22	C
ATOM	233	C	VAL	A	34	-13.930	63.814	3.453	1.00	62.61	C
ATOM	234	O	VAL	A	34	-13.510	63.123	4.382	1.00	61.47	0
ATOM	235	CB	VAL	A	34	-16.173	62.963	2.732	1.00	63.44	C
ATOM	236	CGI	VAL	A	34	-16.801	64.271	3.163	1.00	64.10	C
ATOM	237	CG2	VAL	A	34	-16.964	62.302	1.614	1.00	60.59	C
ATOM	238	N	LEU	A	35	-13.707	65.124	3.395	1.00	55.62	N
ATOM	239	CA	LEU	A	35	-12.986	65.802	4.466	1.00	58.70	C
ATOM	240	C	LEU	A	35	-13.952	66.562	5.368	1.00	58.12	C
ATOM	241	O	LEU	A	35	-15.173	66.372	5.284	1.00	60.33	0
ATOM	242	CB	LEU	A	35	-11.919	66.729	3.891	1.00	53.22	C
ATOM	243	CG	LEU	A	35	-10.932	65.921	3.051	1.00	51.60	C
ATOM	244	CD1	LEU	A	35	-9.777	66.744	2.543	1.00	43.94	C
ATOM	245	CD2	LEU	A	35	-10.436	64.765	3.889	1.00	58.53	C
ATOM	246	O	GLY	A	36	-14.235	66.549	8.874	1.00	64.24	0
ATOM	247	N	GLY	A	36	-13.404	67.368	6.273	1.00	56.38	N
ATOM	248	CA	GLY	A	36	-14.225	68.202	7.139	1.00	6.1.11	C
ATOM	249	C	GLY	A	36	-14.577	67.663	8.513	1.00	61.85	C
ATOM	250	O	ASM	A	37	-17.396	67.054	11.818	1.00	66.00	0
ATOM	251	N	ASN	A	37	-15.282	68.471	9.291	1.00	66.08	N
ATOM	252	CA	ASN	A	37	-15.583	68.111	10.666	1.00	62.97	C
ATOM	253	C	ASM	A	37	-16.720	67.098	10.794	1.00	61.51	C

ATOM	254	CB	ASN	A	37	-15.919	69.383	11.469	1.00	52.12	c
ATOM	255	CG	ASM	A	37	-17.202	70.089	10.980	1.00	60.09	c
ATOM	256	OD1	ASN	A	37	-17.867	69.638	10.052	1.00	61.31	0
ATOM	257	ND2	ASN	A	37	-17.550	71.200	11.628	1.00	62.05	N
ATOM	258	O	TH.R	A	38	-17.264	63.412	9.966	I.00	61.03	O
ATOM	259	N	THR	A	38	-16.937	66.277	9.770	1.00	64.19	N
ATOM	260	CA	THR	A	38	-18.238	65.598	9.636	1.00	72.01	c
ATOM	261	C	TH.R	A	38	-18.285	64.070	9.875	I.00	64.77	c
ATOM	262	CB	THR	A	38	-18.826	65.874	8.225	1.00	73.63	c
ATOM	263	OG1	THR	A	38	-20.228	65.586	8.215	1.00	68.57	0
ATOM	264	CG2	THR	A	38	-18.092	65.043	7.150	I.00	65.04	c
ATOM	265	O	ASP	A	39	-20.784	60.455	8.649	1.00	77.75	0
ATOM	266	N	ASP	*A*	39	-19.511	63.550	9.971	1.00	74.66	N
ATOM	267	CA	ASP	A	39	-19.824	62.121	10.125	1.00	79.95	c
ATOM	268	C	ASP	A	39	-19.941	61.353	8.791	1.00	79.13	c
ATOM	269	CB	ASP	A	39	-21.147	61.956	10.895	1.00	78.92	c
ATOM	270	CG	ASP	A	39	-20.945	61.555	12.348	1.00	89.07	c
ATOM	271	OD1	ASP	A	39	-20.090	62.164	13.030	I.00	93.56	0
ATOM	272	OD2	ASP	A	39	-21.648	60.626	12.808	1.00	90.20	0
ATOM	273	O	ARG	A	40	-17.196	62.195	5.758	1.00	66.06	0
ATOM	274	N	ARG	A	40	-19.111	61.710	7.819	I.00	73.55	N
ATOM	275	CA	ARG	A	40	-19.158	61.090	6.503	1.00	69.26	c
ATOM	276	c	ARG	A	40	-17.763	61.124	5.931	1.00	65.29	c
ATOM	277	CB	ARG	A	40	-20.142	61.823	5.603	I.00	71.78	c
ATOM	278	CG	ARG	A	40	-20.332	61.218	4.221	1.00	69.94	c
ATOM	279	CD	ARG	*A*	40	-21.472	61.952	3.512	1.00	72.19	c
ATOM	280	NE	ARG	A	40	-22.276	61.069	2.673	I.00	70.45	N
ATOM	281	CZ	ARG	A	40	-23.536	61.310	2.333	1.00	67.59	c
ATOM	282	NH1	ARG	*A*	40	-24.146	62.412	2.753	1.00	68.58	N
ATOM	283	NH2	ARG	A	40	-24.187	60.444	1.572	1.00	68.15	N
ATOM	284	O	HIS	A	41	-14.280	59.593	3.559	1.00	57.93	O
ATOM	285	N	HIS	A	41	-17.187	59.960	5.660	1.00	70.29	N
ATOM	286	CA	HIS	A	41	-15.743	59.910	5.431	1.00	68.54	c
ATOM	287	C	HIS	A	41	-15.415	59.458	4.025	I.00	62.35	c
ATOM	288	CB	HIS	A	41	-15.075	59.009	6.483	1.00	69.24	c
ATOM	289	CG	HIS	A	41	-15.380	59.422	7.895	1.00	76.82	c
ATOM	290	ND1	HIS	A	41	-16.501	58.986	8.573	I.00	80.98	N
ATOM	291	CD2	HIS	A	41	-14.741	60.271	8.735	1.00	75.54	C
ATOM	292	CE1	HIS	*A*	41	-16.532	59.540	9.773	1.00	77.96	C
ATOM	293	NE2	HIS	A	41	-15.475	60.324	9.896	I.00	78.42	N
ATOM	294	O	SER	A	42	-18.624	58.332	2.009	1.00	56.23	O
ATOM	295	N	SER	*A*	42	-16.430	58.948	3.342	1.00	59.48	N
ATOM	296	CA	SER	A	42	-16.262	58.493	1.980	1.00	54.83	c
ATOM	297	C	SER	A	42	-17.617	58.465	1.318	1.00	53.91	C
ATOM	298	CB	SER	A	42	-15.594	57.117	1.948	1.00	57.20	c
ATOM	299	OG	SER	A	42	-16.369	56.176	1.227	1.00	58.88	0
ATOM	300	O	ILE	A	43	-17.809	57.981	-2.710	I.00	55.52	0
ATOM	301	N	ILE	A	43	-17.659	58.606	-0.007	1.00	49.28	N
ATOM	302	CA	ILE	A	43	-18.941	58.661	-0.707	1.00	58.17	c
ATOM	303	C	ILE	A	43	-18.886	58.032	-2.105	I.00	56.13	c
ATOM	304	CB	ILE	A	43	-19.438	60.140	-0.815	1.00	58.31	c
ATOM	305	CGI	ILE	A	43	-20.957	60.205	-0.991	1.00	55.77	c
ATOM	306	CG2	ILE	A	43	-18.699	60.871	-1.913	I.00	57.70	c
ATOM	307	CD1	ILE	A	43	-21.508	61.630	-0.987	1.00	60.72	c
ATOM	308	O	LYS	*A*	44	-21.587	58.529	-5.014	1.00	68.90	0
ATOM	309	N	LYS	A	44	-20.038	57.560	-2.604	I.00	47.79	N
ATOM	310	CA	LYS	A	44	-20.122	56.951	-3.937	1.00	57.38	c
ATOM	311	C	LYS	*A*	44	-20.519	57.909	-5.056	1.00	59.03	c
ATOM	312	CB	LYS	A	44	-21.112	55.778	-3.932	1.00	62.75	c
ATOM	313	O	LYS	A	45	-18.506	57.728	-8.787	1.00	54.37	0
ATOM	314	N	LYS	A	45	-19.674	58.003	-6.078	1.00	64.23	N
ATOM	315	CA	LYS	A	45	-19.955	58.888	-7.214	1.00	62.03	c
ATOM	316	C	LYS	A	45	-19.580	58.328	-8.593	I.00	60.01	c

ATOM	317	CB	LYS	A	45	-19.246	60.230	-7.001	1.00	61.22	c
ATOM	318	CG	LYS	A	45	--20,094	61.224	-8,210	1,00	61.31	C
ATOM	319	CD	LYS	A	45	-19.232	62,192	-5.451	1,00	60,33	c
ATOM	320	CE	LYS	A	45	-20.092	63:082	-4.556	1.00	56.47	c
ATOM	321	NZ	LYS	A	45	-19.217	64.134	-3,989	1,00	64.49	N
ATOM	322	O	ASN	A	46	-19.275	60,338	-11..387	1,00	57,94	O
ATOM	323	N	ASN	A	46	-20.476	58,563	-9.549	1,00	58,04	N
ATOM	324	CA.	ASM	A	46	-20,252	58.207	-10,941	1,00	52.55	C
ATOM	325	C	ASN	A	46	-19.241	59,136	-11:601	1,00	54.06	C
ATOM	326	CE	ASN	A	46	-21.576	58,228	-11.699	1,00	54,31	c
ATOM	327	CG	ASN	A	46	-22,566	57.199	-11,173	I,00	63.30	c
ATOM	328	OD1	ASN	A	46	-22.192	56.067	-10:826	1,00	63.20	0
ATOM	329	ND2	ASN	A	46	-23.838	57,577	-11.127	1,00	57,76	N
ATOM	330	O	LEU	A	47	-17.367	59:967	-15.416	1.00	59.46	O
ATOM	331	N	LEU	A	47	-18,333	58.584	-12,393	1,00	56.16	N
ATOM	332	CA	LEU	A	47	-17..337	59,396	-13.077	1,00	52,49	C
ATOM	333	c	LEU	A	47	-17.909	60:085	-14.317	1.00	56.35	c
ATOM	334	CB	LEU	A	47	-16,131	58.532	-13,449	1,00	56.67	c
ATOM	335	CG	LEU	A	47	-14.915	58,664	-12.533	1,00	52,62	c
ATOM	336	CD1	LEU	A	47	-15.311	58,439	-11.087	1,00	59,35	c
ATOM	337	CD2	LEU	A	47	-13,782	57.727	-12,938	1,00	60.51	c
ATOM	338	O	ILE	A	48	-20:494	62,980	-13:241	1,00	56.45	0
ATOM	339	N	ILE	A	48	-19.022	60,790	-14.116	1,00	55,08	N
ATOM	340	CA	ILE	A	48	-19,606	61.705	-15,093	I,00	54.82	C
ATOM	341	C	ILE	A	48	-20:062	63.008	-14:390	1,00	55.35	C
ATOM	342	CB	ILE	A	48	-20.802	61,061	-15.808	1,00	52,21	C
ATOM	343	CGI	ILE	A	48	-21,241	61.897	-17,002	I,00	52.54	C
ATOM	344	CG2	ILE	A	48	-21,969	60.859	-14,847	1,00	51.65	c
ATOM	345	GDI	ILE	A	48	-22.408	61,295	-17.766	1,00	51,89	c
ATOM	346	O	GLY	A	49	-20:543	66:504	-16,572	1.00	51.38	0
ATOM	347	N	GLY	A	49	-19,963	64.150	-15,056	1,00	47.85	N
ATOM	348	CA	GLY	A	49	-20.457	65,368	-14.447	1,00	52,18	C
ATOM	349	c	GLY	A	49	-20.546	66:596	-15.341	1.00	52.12	c
ATOM	350	O	ALA	A	50	-20,887	70..353	-13,440	1,00	47.79	0
ATOM	351	N	ALA	A	50	-20.615	67,762	-14.708	1,00	49,90	N
ATOM	352	CA	ALA	A	50	-20.743	69,018	-15.431	1,00	45,63	c
ATOM	353	C	ALA	A	50	-20,384	70.213	-14,555	1,00	44.78	c
ATOM	354	CB	ALA	A	50	-22:143	69:159	-15:962	1,00	48.99	c
ATOM	355	O	LEU	A	51	-19.878	73,686	-16.249	1,00	41,52	0
ATOM	356	N	LEU	A	51	-19,490	71.052	-15,057	I,00	41.63	N
ATOM	357	CA	LEU	A	51	-19,159	72.304	-14,400	1,00	44.88	C
ATOM	358	C	LEU	A	51	-19.957	73,478	-15.041	1,00	44,40	C
ATOM	359	CB	LEU	A	51	-17:647	72:565	-14.476	1.00	40.73	c
ATOM	360	CG	LEU	A	51	-17,206	73.884	-13,853	1,00	43.83	c
ATOM	361	GD1	LEU	A	51	-17.433	73,853	-12.338	1,00	42,55	c
ATOM	362	CD2	LEU	A	51	-15.768	74:206	-14.216	1.00	37.81	c
ATOM	363	O	LEU	A	52	-20,371	76.695	-13,037	1,00	43.12	0
ATOM	364	N	LEU	A	52	-20.744	74,203	-14.235	1,00	41,48	N
ATOM	365	CA	LEU	A	52	-21.484	75,391	-14.709	1,00	40,32	c
ATOM	366	C	LEU	A	52	-20,815	76.645	-14,189	1,00	40.91	c
ATOM	367	CB	LEU	A	52	-22:951	75:371	-14:260	1,00	35.83	c
ATOM	368	CG	LEU	A	52	-23.629	73,999	-14.340	1,00	49,14	c
ATOM	369	GDI	LEU	A	52	-25,104	74.014	-13,861	I,00	40.87	c
ATOM	370	CD2	LEU	A	52	-23:499	73.412	-15:751	1,00	43.19	c
ATOM	371	O	PHE	A	53	-21.435	79,906	-16.422	1,00	40,66	0
ATOM	372	N	PHE	A	53	-20,733	77.659	-15,035	I,00	41.51	N
ATOM	373	CA	PHE	A	53	-20,205	78.952	-14,619	1,00	39.56	C
ATOM	374	C	PHE	A	53	-20.889	80,088	-15.335	1,00	43,04	c
ATOM	375	CB	PHE	A	53	-18:706	79:024	-14.874	1.00	40.25	c
ATOM	376	CG	PHE	A	53	-18,288	78.494	-16,212	1,00	35.14	c
ATOM	377	GD1	PHE	A	53	-18.014	77,150	-16..385	1,00	41,67	c
ATOM	378	CD2	PHE	A	53	-18.128	79:342	-17.288	1.00	41.06	c
ATOM	379	CE1	PHE	A	53	-17,605	76.647	-17,609	1,00	38.99	c

ATOM	380	CE2	PHE	A	53	-17.724	78.850	-18.529	1.00	42.29	c
ATOM	381	CZ	PHE	A	53	-17.461	77.496	-18.682	1.00	40.95	C
ATOM	382	O	ASP	A	54	-19.006	82.497	-16.247	1.00	42.43	0
ATOM	383	N	ASP	A	54	-20.835	81.260	-14.715	1.00	42.24	N
ATOM	384	CA.	ASP	A	54	-21.216	82.508	-15.334	1.00	36.55	C
ATOM	385	C	ASP	A	54	-20.182	82.866	-16.381	1.00	40.45	C
ATOM	386	CB	ASP	A	54	-21.309	83.625	-14.286	1.00	40.10	c
ATOM	387	CG	ASP	A	54	-22.365	83.357	-13.260	1.00	46.92	c
ATOM	388	OD1	ASP	A	54	-23.263	82.548	-13.553	1.00	53.11	0
ATOM	389	OD2	ASP	A	54	-22.317	83.939	-12.161	1.00	52.18	0
ATOM	390	O	SER	A	55	-18.811	85.815	-17.561	1.00	41.56	0
ATOM	391	N	SER	A	55	-20.599	83.626	-17.390	1.00	41.06	N
ATOM	392	CA	SER	A	55	-19.776	83.905	-18.566	1.00	45.09	C
ATOM	393	c	SER	A	55	-18.643	84.861	-18.298	1.00	44.11	c
ATOM	394	CB	SER	A	55	-20.643	84.480	-19.697	1.00	43.53	c
ATOM	395	OG	SER	A	55	-22.006	84.287	-19.399	1.00	47.20	0
ATOM	396	O	GLY	A	56	-17.390	86.701	-20.831	1.00	51.53	0
ATOM	397	N	GLY	A	56	-17.495	84.613	-18.935	1.00	48.39	N
ATOM	398	CA	GLY	A	56	-16.400	85.565	-18.956	1.00	42.08	C
ATOM	399	c	GLY	A	56	-16.743	86.794	-19.782	1.00	51.38	c
ATOM	400	0	GLU	A	57	-14.259	89.551	-20.417	1.00	46.34	0
ATOM	401	N	GLU	A	57	-16.294	87.956	-19.318	1.00	44.47	N
ATOM	402	CA	GLU	A	57	-16.595	89.211	-19.975	1.00	40.45	c
ATOM	403	C	GLU	A	57	-15.414	89.767	-20.758	1.00	40.57	c
ATOM	404	CB	GLU	A	57	-17.055	90.249	-18.931	1.00	41.06	c
ATOM	405	CG	GLU	A	57	-18.239	89.752	-18.112	1.00	44.02	c
ATOM	406	CD	GLU	A	57	-18.741	90.754	-17.060	1.00	50.78	c
ATOM	407	OE1	GLU	A	57	-18.026	91.713	-16.687	1.00	54.86	0
ATOM	408	OE2	GLU	A	57	-19.871	90.573	-16.583	1.00	58.67	0
ATOM	409	O	THR	A	58	-14.899	92.797	-20.522	1.00	42.18	0
ATOM	410	N	THR	A	58	-15.717	90.506	-21.807	1.00	40.48	N
ATOM	411	CA	THR	A	58	-14.731	91.351	-22.458	1.00	43.49	c
ATOM	412	c	THR	A	58	-14.285	92.504	-21.561	1.00	41.40	c
ATOM	413	CB	THR	A	58	-15.292	91.947	-23.767	1.00	42.70	c
ATOM	414	OG1	THR	A	58	-16.410	92.787	-23.452	1.00	37.65	0
ATOM	415	CG2	THR	A	58	-15.744	90.828	-24.706	1.00	35.12	c
ATOM	416	O	ALA	A	59	-12.832	96.677	-21.260	1.00	43.43	0
ATOM	417	N	ALA	A	59	-13.217	93.157	-21.992	1.00	38.31	N
ATOM	418	CA	ALA	A	59	-12.639	94.263	-21.260	1.00	42.21	c
ATOM	419	C	ALA	A	59	-13.237	95.610	-21.724	1.00	41.54	c
ATOM	420	CB	ALA	A	59	-11.125	94.253	-21.420	1.00	32.33	c
ATOM	421	O	GLU	A	60	-15.181	98.885	-22.217	1.00	37.80	0
ATOM	422	N	GLU	A	60	-14.217	95.539	-22.618	1.00	41.38	N
ATOM	423	CA	GLU	A	60	-14.806	96.730	-23.235	1.00	46.21	c
ATOM	424	C	GLU	A	60	-15.504	97.714	-22.252	1.00	39.53	c
ATOM	425	CB	GLU	A	60	-15.801	96.314	-24.315	1.00	41.05	c
ATOM	426	CG	GLU	A	60	-16.653	97.478	-24.766	1.00	41.17	c
ATOM	427	CD	GLU	A	60	-17.068	97.385	-26.222	1.00	53.23	c
ATOM	428	OE1	GLU	A	60	-16.456	96.599	-26.978	1.00	56.84	0
ATOM	429	OE2	GLU	A	60	-18.002	98.114	-26.610	1.00	61.87	0
ATOM	430	N	ALA	A	61	-16.456	97.212	-21.479	1.00	36.79	N
ATOM	431	CA	ALA	A	61	-17.125	98.006	-20.472	1.00	39.93	c
ATOM	432	C	ALA	A	61	-16.117	98.647	-19.488	1.00	38.65	c
ATOM	433	O	ALA	A	61	-16.326	99.750	-19.015	1.00	44.78	0
ATOM	434	CB	ALA	A	61	-18.155	97.136	-19.720	1.00	31.90	c
ATOM	435	N	THR	A	62	-15.027	97.950	-19.199	1.00	43.26	N
ATOM	436	CA	THR	A	62	-14.042	98.400	-18.238	1.00	34.47	c
ATOM	437	C	THR	A	62	-13.208	99.500	-18.871	1.00	36.56	c
ATOM	438	O	THR	A	62	-12.857	100.479	-18.214	1.00	40.82	0
ATOM	439	CB	THR	A	62	-13.179	97.204	-17.751	1.00	38.66	c
ATOM	440	OG1	THR	A	62	-13.987	96.330	-16.951	1.00	40.08	0
ATOM	441	CG2	THR	A	62	-11.981	97.641	-16.931	1.00	39.48	c
ATOM	442	N	ARG	A	63	-12.943	99.383	-20.162	1.00	39.49	N

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ATOM      443  CA   ARG  A   63      --12.166  100.396  -20.892   1.00  38.82           C
ATOM      444  C    ARG  A   63      --12.943  101.717  -21.158   1.00  35.71           C
ATOM      445  O    ARG  A   63      -12..378  102.803  -21.011   1.00  41.90           0
ATOM      446  CB   ARG  A   63      -11.656    99.801  -22.223   1.00  37.49           C
ATOM      447  CG   ARG  A   63      -10.953   100.786  -23.133   1.00  36.55           C
ATOM      448  CD   ARG  A   63      -10.527   100.162  -24.460   1.00  38.38           C
ATOM      449  NE   ARG  A   63      -11.647    99.917  -25.370   1.00  40.81           N
ATOM      450  CZ   ARG  A   63      -12.133    98.719  -25.719   1.00  42.16           C
ATOM      451  NH1  ARG  A   63      -13.154    98.652  -26.557   1.00  43.21           N
ATOM      452  NH2  ARG  A   63      -11.623    97.588  -25.244   1.00  39.23           N
ATOM      453  N    LEU  A   64      -14.208   101.631  -21.560   1.00  35.90           N
ATOM      454  CA   LEU  A   64      -15.050   102.846  -21.713   1.00  34.46           C
ATOM      455  C    LEU  A   64      -15.092   103.653  -20.438   1.00  32.10           C
ATOM      456  O    LEU  A   64      -14.871   104.853  -20.453   1.00  39.98           O
ATOM      457  CB   LEU  A   64      -16.463   102.475  -22.140   1.00  32.44           C
ATOM      458  CG   LEU  A   64      -16.415   101.823  -23.536   1.00  46.06           C
ATOM      459  CD1  LEU  A   64      -17.759   101.276  -23.961   1.00  45.31           C
ATOM      460  CD2  LEU  A   64      -15.864   102.781  -24.595   1.00  37.94           C
ATOM      461  N    LYS  A   65      -15.296   102.990  -19..307   1.00  39.07           N
ATOM      462  CA   LYS  A   65      -15.323   103.704  -18.031   1.00  34.09           C
ATOM      463  C    LYS  A   65      -13.966   104.307  -17.672   1.00  38..35           C
ATOM      464  O    LYS  A   65      -13.912   105.457  -17.227   1.00  38.38           O
ATOM      465  CB   LYS  A   65      -15.828   102.787  -16.927   1.00  33.01           C
ATOM      466  CG   LYS  A   65      -17.265   102.428  -17.148   1.00  27.42           C
ATOM      467  CD   LYS  A   65      -17.790   101.402  -16.195   1.00  37.88           C
ATOM      468  CE   LYS  A   65      -19.282   101.227  -16.424   1.00  45.14           C
ATOM      469  NZ   LYS  A   65      -19.730    99.896  -15.984   1.00  55..32           N
ATOM      470  N    ARG  A   66      -12.879   103.571  -17.929   1.00  38.13           N
ATOM      471  CA   ARG  A   66      -11.527   104.055  -17.648   1.00  35.44           C
ATOM      472  C    ARG  A   66      -11.278   105.395  -18.341   1.00  37.39           C
ATOM      473  O    ARG  A   66      -10.807   106.378  -17.737   1.00  41.01           0
ATOM      474  CB   ARG  A   66      -10.479   103.009  -18.095   1.00  38.31           C
ATOM      475  CG   ARG  A   66       -9.020   103.333  -17.749   1.00  38.94           C
ATOM      476  CD   ARG  A   66       -7.967   102..329  -18.393   1.00  43.06           C
ATOM      477  NE   ARG  A   66       -8.465   100.962  -18.470   1.00  36.24           N
ATOM      478  CZ   ARG  A   66       -8.503   100.265  -19.586   1.00  39.15           C
ATOM      479  NH1  ARG  A   66       -8.987    99.044  -19.588   1.00  41.23           N
ATOM      480  NH2  ARG  A   66       -8.050   100.789  -20.705   1.00  40.65           N
ATOM      481  N    THR  A   67      -11.617   105.417  -19.616   1.00  34.83           N
ATOM      482  CA   THR  A   67      -11.419   106.564  -20.474   1.00  34.78           C
ATOM      483  C    THR  A   67      -12.357   107.742  -20.097   1.00  40.97           C
ATOM      484  O    THR  A   67      -11.960   108.901  -20.123   1.00  41.32           O
ATOM      485  CB   THR  A   67      -11.632   106.114  -21.914   1.00  38.48           C
ATOM      486  OG1  THR  A   67      -10.369   106.107  -22.580   1.00  54.40           0
ATOM      487  CG2  THR  A   67      -12.578   106.978  -22.641   1.00  36.99           C
ATOM      488  N    ALA  A   68      -13.583   107.415  -19.699   1.00  39.04           N
ATOM      489  CA.  ALA  A   68      -14.510   108..390  -19.164   1.00  35.74           C
ATOM      490  C    ALA  A   68      -14.016   108.949  -17.838   1.00  39.54           C
ATOM      491  O    ALA  A   68      -14.246   110.123  -17.526   1.00  38.51           O
ATOM      492  CB   ALA  A   68      -15.892   107.767  -18.993   1.00  31.84           C
ATOM      493  N    ARG  A   69      -13.340   108.118  -17.038   1.00  38.94           N
ATOM      494  CA   ARG  A   69      -12.782   108.626  -15.784   1.00  38.97           C
ATOM      495  C    ARG  A   69      -11.686   109.646  -16.091   1.00  36.83           C
ATOM      496  O    ARG  A   69      -11.639   110.715  -15.482   1.00  44.81           0
ATOM      497  CB   ARG  A   69      -12.237   107.511  -14.924   1.00  39.94           C
ATOM      498  CG   ARG  A   69      -13.169   106.966  -13.888   1.00  34.99           C
ATOM      499  CD   ARG  A   69      -12.341   105.999  -13.061   1.00  42.20           C
ATOM      500  NE   ARG  A   69      -12.626   104.617  -13.413   1.00  47.45           N
ATOM      501  CZ   ARG  A   69      -11.784   103.773  -13.960   1.00  38.38           C
ATOM      502  NH1  ARG  A   69      -10.525   104.121  -14.205   1.00  46.89           N
ATOM      503  NH2  ARG  A   69      -12.214   102.566  -14.234   1.00  42.76           N
ATOM      504  N    ARG  A   70      -10.852   109.365  -17.079   1.00  36.24           N
ATOM      505  CA.  ARG  A   70       -9.819   110..338  -17.399   1.00  39.81           C
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ATOM   506  C   ARG A  70    -10.430 111.663 -17.828  1.00 43.34     C
ATOM   507  O   ARG A  70     -9.946 112.723 -17.468  1.00 47.29     O
ATOM   508  CB  ARG A  70     -8.885 109.819 -18.495  1.00 36.89     C
ATOM   509  CG  ARG A  70     -8.058 108.608 -18.058  1.00 35.18     C
ATOM   510  CD  ARG A  70     -7.032 108.198 -19.130  1.00 42.28     C
ATOM   511  NE  ARG A  70     -6.282 106.986 -18.747  1.00 46.73     N
ATOM   512  CZ  ARG A  70     -6.253 105.857 -19.461  1.00 43.84     C
ATOM   513  NH1 ARG A  70     -6.928 105.764 -20.591  1.00 41.51     N
ATOM   514  NH2 ARG A  70     -5.557 104.812 -19.039  1.00 46.30     N
ATOM   515  N   ARG A  71    -11.500 111.584 -18.598  1.00 42.61     N
ATOM   516  CA  ARG A  71    -12.014 112.733 -19.298  1.00 41.12     C
ATOM   517  C   ARG A  71    -12.744 113.697 -18.357  1.00 38.30     C
ATOM   518  O   ARG A  71    -12.587 114.903 -18.463  1.00 43.33     O
ATOM   519  CB  ARG A  71    -12.908 112.268 -20.444  1.00 39.89     C
ATOM   520  CG  ARG A  71    -12.165 112.226 -21.749  1.00 33.95     C
ATOM   521  CD  ARG A  71    -13.091 112.034 -22.876  1.00 34.75     C
ATOM   522  NE  ARG A  71    -13.850 110.801 -22.703  1.00 49.32     N
ATOM   523  CZ  ARG A  71    -15.041 110.570 -23.255  1.00 54.97     C
ATOM   524  NH1 ARG A  71    -15.651 109.401 -23.037  1.00 50.26     N
ATOM   525  NH2 ARG A  71    -15.623 111.512 -24.017  1.00 47.26     N
ATOM   526  N   TYR A  72    -13.485 113.155 -17.404  1.00 35.85     N
ATOM   527  CA  TYR A  72    -13.994 113.942 -16.304  1.00 35.00     C
ATOM   528  C   TYR A  72    -12.889 114.626 -15.466  1.00 43.12     C
ATOM   529  0   TYR A  72    -13.018 115.798 -15.117  1.00 47.30     0
ATOM   530  CB  TYR A  72    -14.882 113.078 -15.413  1.00 35.43     C
ATOM   531  CG  TYR A  72    -16.292 112.847 -15.957  1.00 42.40     C
ATOM   532  CD1 TYR A  72    -17.075 113.911 -16.457  1.00 35.36     C
ATOM   533  CD2 TYR A  72    -16.841 111.573 -15.975  1.00 40.74     C
ATOM   534  CE1 TYR A  72    -18.352 113.690 -16.940  1.00 34.07     C
ATOM   535  CE2 TYR A  72    -18.110 111.356 -16.452  1.00 41.64     C
ATOM   536  CZ  TYR A  72    -18.862 112.424 -16.927  1.00 39.72     C
ATOM   537  OH  TYR A  72    -20.108 112.157 -17.391  1.00 37.40     0
ATOM   538  N   THR A  73    -11.802 113.920 -15.158  1.00 44.82     N
ATOM   539  CA  THR A  73    -10.663 114.548 -14.494  1.00 41.92     C
ATOM   540  C   THR A  73    -10.156 115.733 -15.325  1.00 42.58     C
ATOM   541  O   THR A  73    -10.022 116.842 -14.817  1.00 44.27     0
ATOM   542  CB  THR A  73     -9.548 113.506 -14.221  1.00 47.98     C
ATOM   543  OG1 THR A  73     -9.777 112.932 -12.933  1.00 53.84     0
ATOM   544  CG2 THR A  73     -8.134 114.108 -14.253  1.00 43.19     C
ATOM   545  N   ARG A  74     -9.942 115.506 -16.613  1.00 43.70     N
ATOM   546  C   ARG A  74    -10.442 117.683 -17.796  1.00 50.38     C
ATOM   547  CA  ARG A  74     -9.429 116.534 -17.508  1.00 40.30     C
ATOM   548  O   ARG A  74    -10.042 118.836 -17.969  1.00 50.62     0
ATOM   549  CB  ARG A  74     -8.971 115.881 -18.816  1.00 37.97     C
ATOM   550  CG  ARG A  74     -7.722 114.961 -18.658  1.00 45.02     C
ATOM   551  CD  ARG A  74     -7.443 114.014 -19.860  1.00 44.64     C
ATOM   552  NE  ARG A  74     -6.388 113.053 -19.554  1.00 46.01     N
ATOM   553  CZ  ARG A  74     -6.079 111.984 -20.289  1.00 50.55     C
ATOM   554  NH1 ARG A  74     -6.743 111.685 -21.404  1.00 46.01     N
ATOM   555  NH2 ARG A  74     -5.096 111.190 -19.892  1.00 53.43     N
ATOM   556  N   ARG A  75    -11.738 117.392 -17.854  1.00 45.18     N
ATOM   557  C   ARG A  75    -12.639 119.373 -16.795  1.00 44.11     C
ATOM   558  CA  ARG A  75    -12.708 118.482 -18.032  1.00 45.86     C
ATOM   559  O   ARG A  75    -12.524 120.583 -16.894  1.00 47.22     0
ATOM   560  CB  ARG A  75    -14.132 117.951 -18.246  1.00 38.78     C
ATOM   561  CG  ARG A  75    -15.116 118.963 -18.800  1.00 39.15     C
ATOM   562  CD  ARG A  75    -16.564 118.443 -18.792  1.00 35.65     C
ATOM   563  NE  ARG A  75    -17.063 118.117 -17.455  1.00 34.90     N
ATOM   564  CZ  ARG A  75    -18.275 117.626 -17.219  1.00 36.55     C
ATOM   565  NH1 ARG A  75    -19.100 117.437 -18.229  1.00 35.62     N
ATOM   566  NH2 ARG A  75    -18.662 117.298 -15.994  1.00 27.92     N
ATOM   567  N   LYS A  76    -12.660 118.763 -15.623  1.00 41.82     N
ATOM   568  C   LYS A  76    -11.212 120.319 -14.422  1.00 54.95     C
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ATOM	569	CA	LYS	A	76	-12.512	119.525	-14.412	1.00	42.56	C
ATOM	570	O	LYS	A	76	-11.208	121.494	-14.052	1.00	56.29	O
ATOM	571	CB	LYS	A	76	-12.568	118.610	-13.202	1.00	48.12	C
ATOM	572	CG	LYS	A	76	-11.894	119.163	-11.969	1.00	47.39	C
ATOM	573	CD	LYS	A	76	-12.600	118.646	-10.724	I.00	48.57	C
ATOM	574	CE	LYS	A	76	-12.948	117.144	-10.812	1.00	50.97	C
ATOM	575	NZ	LYS	A	76	-14.169	116.806	-9.964	1.00	45.03	N
ATOM	576	N	ASM	A	77	-10.115	119.706	-14.874	I.00	52.37	N
ATOM	577	C	ASN	A	77	-8.933	121.708	-15.772	1.00	52.46	C
ATOM	578	CA	ASN	A	77	-8.860	120.450	-14.923	1.00	50.20	C
ATOM	579	O	ASM	A	77	-8.489	122.756	-15.336	I.00	58.17	0
ATOM	580	CB	ASN	A	77	-7.731	119.557	-15.403	1.00	49.88	C
ATOM	581	CG	ASN	A	77	-7.297	118.603	-14.336	1.00	52.71	C
ATOM	582	OD1	ASN	A	77	-7.737	118.734	-13.197	1.00	57.83	0
ATOM	583	ND2	ASN	A	77	-6.441	117.633	-14.678	1.00	51.04	N
ATOM	584	N	AP.G	A	78	-9.510	12.1.591	-16.965	1.00	53.34	N
ATOM	585	C	ARG	A	78	-10.305	123.922	-17.191	1.00	55.27	C
ATOM	586	CA.	ARG	A	78	-9.711	122.701	-17.888	I.00	45.4.1	C
ATOM	587	O	ARG	A	78	-9.881	125.057	-17.410	1.00	60.02	O
ATOM	588	CB	ARG	A	78	-10.646	122.281	-19.022	1.00	53.93	C
ATOM	589	CG	ARG	A	78	-9.991	121.769	-20.296	I.00	47.40	C
ATOM	590	CD	ARG	A	78	-10.979	121.829	-21.452	1.00	45.55	C
ATOM	591	NE	ARG	A	78	-11.355	120.493	-21.849	1.00	59.54	N
ATOM	592	CZ	ARG	A	78	-12.585	120.001	-21.824	I.00	52.87	C
ATOM	593	NH1	ARG	A	78	-13.606	120.748	-21.455	1.00	56.71	N
ATOM	594	NH2	ARG	A	78	-12.783	118.752	-22.199	1.00	56.21	N
ATOM	595	N	ILE	A	79	-11.304	123.679	-16.356	I.00	55.59	N
ATOM	596	C	ILE	A	79	-10.984	125.351	-14.613	1.00	55.71	C
ATOM	597	CA	ILE	A	79	-11.946	124.748	-15.616	1.00	54.11	C
ATOM	598	O	ILE	A	79	-10.828	126.576	-14.543	1.00	57.15	O
ATOM	599	CB	ILE	A	79	-13.194	124.249	-14.899	1.00	54.24	C
ATOM	600	CGI	ILE	A	79	-14.254	123.918	-15.933	1.00	49.28	C
ATOM	601	CG2	ILE	A	79	-13.754	125.338	-13.993	1.00	50.58	C
ATOM	602	CD1	ILE	A	79	-14.717	125.169	-16.680	I.00	53.44	C
ATOM	603	N	LEU	A	80	-10..339	124.470	-13.851	1.00	56.13	N
ATOM	604	C	LEU	A	80	-8.188	125.645	-13.499	1.00	59.98	C
ATOM	605	CA.	LEU	A	80	-9.328	124.843	-12.866	I.00	59.97	C
ATOM	606	O	LEU	A	80	-7.633	126.540	-12.867	1.00	57.07	O
ATOM	607	CB	LEU	A	80	-8.758	123.598	-12.180	1.00	54.23	C
ATOM	608	CG	LEU	A	80	-9.637	122.797	-11.224	I.00	54.58	C
ATOM	609	CD1	LEU	A	80	-8.849	121.605	-10.656	1.00	57.30	C
ATOM	610	CD2	LEU	A	80	-10.187	123.661	-10.112	1.00	53.16	C
ATOM	611	N	TYR	A	81	-7.834	125.308	-14.735	1.00	57.27	N
ATOM	612	C	TYR	A	81	-7.294	127.479	-15.696	1.00	64.98	C
ATOM	613	CA	TYR	A	81	-6.807	126.049	-15.449	1.00	59.30	C
ATOM	614	O	TYR	A	81	-6.499	128.418	-15.767	1.00	71.65	O
ATOM	615	CB	TYR	A	81	-6.456	125.386	-16.783	I.00	55.68	C
ATOM	616	CG	TYR	A	81	-5.720	124.051	-16.717	1.00	62.39	C
ATOM	617	CD1	TYR	A	81	-4.960	123.687	-15.612	1.00	64.66	C
ATOM	618	CD.2	TYR	A	81	-5.764	123.169	-17.789	I.00	58.53	C
ATOM	619	CE1	TYR	A	81	-4.284	122.466	-15.577	1.00	60.78	C
ATOM	620	CE2	TYR	A	81	-5.097	121.963	-17.765	1.00	56.32	C
ATOM	621	CZ	TYR	A	81	-4.358	121.609	-16.666	I.00	62.22	C
ATOM	622	OH	TYR	A	81	-3.695	120.387	-16.667	1.00	61.93	0
ATOM	623	N	LEU	A	82	-8.603	127.650	-15.832	1.00	62.56	N
ATOM	624	C	LEU	A	82	-9.397	129.717	-14.874	I.00	62.15	C
ATOM	625	CA	LEU	A	82	-9.133	128.963	-16.153	1.00	60.44	C
ATOM	626	O	LEU	A	82	-9.342	130.943	-14.851	1.00	65.37	O
ATOM	627	CB	LEU	A	82	-10.409	128.859	-16.981	1.00	60.34	C
ATOM	628	CG	LEU	A	82	-11.150	130.143	-17.400	1.00	58.21	C
ATOM	629	CD1	LEU	A	82	-10.556	1.30.761	-18.664	1.00	51.12	C
ATOM	630	CD2	LEU	A	82	-12.625	129.843	-17.586	1.00	53.67	C
ATOM	631	N	GLN	A	83	-9.683	128.981	-13.806	I.00	60.66	N

ATOM	632	C	GLN	A	83	--8..638	130..129	-11 .939	1 .00	70..27	C
ATOM	633	CA	GLN	A	83	-9,,937	129..604	-12,,515	1,00	61 .28	C
ATOM	634	O	GLN	A	83	-8..632	131.,099	-11 .173	1 ,00	69,,13	0
ATOM	635	CB	GLN	A	83	-10..597	128.,625	-11 .543	1 .00	57 .98	C
ATOM	636	CG	GLN	A	83	-12,,078	128. 453	-11 ,805	1 ,00	59.,33	C
ATOM	637	CD	GLN	A	83	-12. .741	127,516	-10 .833	1 ,00	59,,45	C
ATOM	638	OE1	GLN	A	83	-12. .149	127,122	-9..836	1,00	63,,22	0
ATOM	639	NE2	GLN	A	83	-13.,982	127 .148	-11 ,117	1,00	60..18	N
ATOM	640	N	GLU	A	84	-7.539	129..482	-12.,319	1,00	65..73	N
ATOM	641	C	GLU	A	84	-5..988	131.,317	-12..521	1,00	66,.92	C
ATOM	642	CA	GLU	A	84	-6.,223	129..942	-11 ,922	I,00	65..50	C
ATOM	643	O	GLU	A	84	-5..784	132..284	-11 ,800	1,00	69..29	0
ATOM	644	CB	GLU	A	84	-5. 131	128,966	-12.367	1,00	59,00	C
ATOM	645	N	ILE	A	85	-6..052	131.,389	-13.,844	1.00	65..11	N
ATOM	646	C	ILE	A	85	-9,618	133..781	-14,058	1,00	67 .42	C
ATOM	647	CA	ILE	A	85	-5..788	1.32.,615	-14.576	1,00	66,,00	C
ATOM	648	O	ILE	A	85	-6..167	134.,912	-14 .068	1.00	72 .70	0
ATOM	649	CB	ILE	A	85	-6.,034	132. 398	-16,076	1,00	64,79	C
ATOM	650	CGI	ILE	A	85	-4.948	131.,469	-16.638	1,00	72,07	C
ATOM	651	CG2	ILE	A	85	-6..060	133.,716	-16..833	1,00	67,91	C
ATOM	652	CD1	ILE	A	85	-5,088	131. 164	-18.,126	1,00	71 ,79	C
ATOM	653	O	PHE	A	86	-9.116	135..753	-11 ,058	1,00	74 .19	0
ATOM	654	N	PHE	A	86	-7.806	133.,480	-13..550	1,00	70,.81	N
ATOM	655	CA	PHE	A	86	-8.,728	134..487	-13.,043	I,00	71 .34	C
ATOM	656	C	PHE	A	86	-8..540	134..796	-11 ,558	1,00	72 .85	C
ATOM	657	CB	PHE	A	86	-10. 181	134.,037	-13 .262	1,00	68,97	C
ATOM	658	CG	PHE	A	86	-10.,810	134..584	-14,502	I,00	67 .34	C
ATOM	659	CD2	PHE	A	86	-11 ,934	135..384	-14,422	1,00	65..77	C
ATOM	660	GDI	PHE	A	86	-10. 298	134.,284	-15. 748	1,00	69,34	C
ATOM	661	CE2	PHE	A	86	-12..528	135.,883	-15.,562	1.00	64.27	C
ATOM	662	CEl	PHE	A	86	-10,,891	134..785	-16,892	1,00	66..89	C
ATOM	663	CZ	PHE	A	86	-12.007	1.35.,583	-16.795	1,00	62,14	C
ATOM	664	O	SER	A	87	-8..247	135.,933	-8.,008	1.00	82 .74	0
ATOM	665	N	SER	A	87	-7,757	133. 980	-10.,860	1,00	71,63	N
ATOM	666	CA	SER	A	87	-7.672	1.34.,036	-9..390	1,00	76,,88	C
ATOM	667	C	SER	A	87	-7.443	135.,438	-8..810	1,00	81,48	C
ATOM	668	CB	SER	A	87	-6.,550	133. 127	-8.,898	1,00	76.,37	C
ATOM	669	OG	SER	A	87	-5..288	133..700	-9,213	1,00	76..86	0
ATOM	670	O	A.SN	A	88	-7.623	138.,928	-7.998	1,00	81,24	0
ATOM	671	N	ASN	A	88	-6.,333	136.055	-9.,212	I,00	79.26	N
ATOM	672	CA	ASM	A	88	-5.,944	137..373	-8,,720	1,00	83..29	C
ATOM	673	C	ASN	A	88	-7.026	138.,404	-8. 943	1,00	81,57	C
ATOM	674	CB	ASN	A	88	-4.660	137.,850	-9.,404	1.00	79..60	C
ATOM	675	CG	ASM	A	88	-3.,453	137..038	-9,,007	1,00	76..96	C
ATOM	676	OD1	ASN	A	88	-3...380	1.36,513	-7.893	1,00	78,,48	0
ATOM	677	ND2	ASN	A	88	-2.489	136,933	-9.,916	1.00	79..80	N
ATOM	678	O	GLU	A	89	-10.,437	140. 367	-10.,218	1,00	85.,50	O
ATOM	679	N	GLU	A	89	-7.268	1.38.,676	-10.218	1,00	79,,47	N
ATOM	680	CA	GLU	A	89	-8..182	139.,718	-10..629	1,00	74,74	C
ATOM	681	C	GLU	A	89	-9.,630	139. 444	-10.,228	1,00	78.,97	C
ATOM	682	CB	GLU	A	89	-8.,067	139.,923	-12.,135	1,00	71 .64	C
ATOM	683	CG	GLU	A	89	-6..708	140,,483	-12..563	1,00	78,.23	C
ATOM	684	CD	GLU	A	89	-6.,612	142 .017	-12.,474	I,00	79 .90	C
ATOM	685	OE1	GLU	A	89	-7,570	142..676	-12.,002	1,00	80..77	0
ATOM	686	OE2	GLU	A	89	-5. 572	142.,565	-12.888	1,00	77,09	0
ATOM	687	O	MET	A	90	-12.,416	138..490	-7,321	I,00	83..45	0
ATOM	688	N	MET	A	90	-9.,965	138..200	-9,,878	1,00	81 .51	N
ATOM	689	CA	MET	A	90	-11.313	137 ,899	-9. 370	1,00	82,05	C
ATOM	690	C	MET	A	90	-11 .378	138.,114	-7,864	1.00	82 .31	C
ATOM	691	CB	MET	A	90	-11 ,748	136..462	-9,,697	1,00	74 .64	C
ATOM	692	CG	MET	A	90	-12.751	1.36,329	-10.855	1,00	76,,41	C
ATOM	693	SD	MET	A	90	-14 .360	137.,157	-10..633	1.00	72 .38	S
ATOM	694	CE	MET	A	90	-14 ,756	136. 696	-8.,955	1,00	66.,62	C

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ATOM     695  O    ALA  A  91     -10.863 139.885  -4.289  1.00 80.18          O
ATOM     696  N    ALA  A  91     -10.261 137.877  -7.187  1.00 83.70          N
ATOM     697  CA   ALA  A  91     -10.211 138.078  -5.749  1.00 86.16          C
ATOM     698  C    ALA  A  91     -10.491 139.553  -5.413  1.00 83.22          C
ATOM     699  CB   ALA  A  91      -8.868 137.634  -5.209  1.00 77.59          C
ATOM     700  O    LYS  A  92     -12.624 143.022  -5.807  1.00 82.38          0
ATOM     701  N    LYS  A  92     -10.327 140.417  -6.414  1.00 79.94          N
ATOM     702  CA.  LYS  A  92     -10.584 141.848  -6.281  1.00 83.43          C
ATOM     703  C    LYS  A  92     -12.057 142.203  -6.525  1.00 79.48          C
ATOM     704  CB   LYS  A  92      -9.691 142.640  -7.248  1.00 81.94          C
ATOM     705  CG   LYS  A  92      -8.191 142.423  -7.052  1.00 74.45          C
ATOM     706  CD   LYS  A  92      -7.368 143.145  -8.116  1.00 75.05          C
ATOM     707  CE   LYS  A  92      -5.876 142.843  -7.965  1.00 73.95          C
ATOM     708  NZ   LYS  A  92      -5.023 143.405  -9.059  1.00 73.13          N
ATOM     709  O    VAL  A  93     -16.024 141.724  -6.475  1.00 72.30          O
ATOM     710  N    VAL  A  93     -12.672 141.589  -7.533  1.00 78.25          N
ATOM     711  CA   VAL  A  93     -14.070 141.869  -7.870  1.00 80.12          C
ATOM     712  C    VAL  A  93     -15.063 141.135  -6.961  1.00 80.79          C
ATOM     713  CB   VAL  A  93     -14.372 141.499  -9.331  1.00 78.07          C
ATOM     714  CGI  VAL  A  93     -15.814 141.831  -9.677  1.00 76.06          C
ATOM     715  CG2  VAL  A  93     -13.421 142.226 -10.254  1.00 81.49          C
ATOM     716  O    ASP  A  94     -14.237 137.123  -5.931  1.00 86.98          0
ATOM     717  N    ASP  A  94     -14.834 139.841  -6.752  1.00 82.06          N
ATOM     718  CA   ASP  A  94     -15.655 139.045  -5.838  1.00 80.61          C
ATOM     719  C    ASP  A  94     -14.794 137.955  -5.229  1.00 81.82          C
ATOM     720  CB   ASP  A  94     -16.866 138.429  -6.550  1.00 78.18          C
ATOM     721  CG   ASP  A  94     -17.911 137.883  -5.573  1.00 79.36          C
ATOM     722  OD1  ASP  A  94     -17.576 137.638  -4.388  1.00 79.34          0
ATOM     723  OD2  ASP  A  94     -19.073 137.692  -5.997  1.00 78.77          0
ATOM     724  O    ASP  A  95     -13.550 134.726  -2.902  1.00 87.46          0
ATOM     725  N    ASP  A  95     -14.689 137.958  -3.913  1.00 81.35          N
ATOM     726  CA   ASP  A  95     -13.733 137.092  -3.254  1.00 85.44          C
ATOM     727  C    ASP  A  95     -14.302 135.695  -3.016  1.00 81.99          C
ATOM     728  CB   ASP  A  95     -13.292 137.723  -1.930  1.00 88.44          C
ATOM     729  CG   ASP  A  95     -14.458 137.956  -0.983  1.00 91.17          C
ATOM     730  OD2  ASP  A  95     -14.228 138.012   0.245  1.00 97.92          0
ATOM     731  OD1  ASP  A  95     -15.608 138.081  -1.470  1.00 90.99          0
ATOM     732  O    SER  A  96     -17.781 132.730  -3.556  1.00 77.24          0
ATOM     733  N    SER  A  96     -15.625 135.591  -2.947  1.00 76.94          N
ATOM     734  CA   SER  A  96     -16.264 134.330  -2.586  1.00 78.49          C
ATOM     735  C    SER  A  96     -17.047 133.701  -3.748  1.00 77.97          C
ATOM     736  CB   SER  A  96     -17.190 134.548  -1.398  1.00 70.20          C
ATOM     737  OG   SER  A  96     -18.279 135.366  -1.774  1.00 73.46          0
ATOM     738  O    PHE  A  97     -18.018 131.469  -6.468  1.00 68.80          0
ATOM     739  N    PHE  A  97     -16.890 134.275  -4.940  1.00 75.64          N
ATOM     740  CA   PHE  A  97     -17.556 133.803  -6.153  1.00 70.22          C
ATOM     741  C    PHE  A  97     -17.170 132.365  -6.499  1.00 71.54          C
ATOM     742  CB   PHE  A  97     -17.222 134.724  -7.319  1.00 68.97          C
ATOM     743  CG   PHE  A  97     -17.717 134.238  -8.656  1.00 64.27          C
ATOM     744  CD1  PHE  A  97     -19.063 134.058  -8.884  1.00 63.91          C
ATOM     745  CD2  PHE  A  97     -16.829 134.004  -9.698  1.00 69.78          C
ATOM     746  CE1  PHE  A  97     -19.516 133.637 -10.122  1.00 65.28          C
ATOM     747  CE2  PHE  A  97     -17.264 133.576 -10.943  1.00 60.63          C
ATOM     748  CZ   PHE  A  97     -18.609 133.394 -11.156  1.00 64.83          C
ATOM     749  N    PHE  A  98     -15.894 132.151  -6.821  1.00 67.06          N
ATOM     750  CA   PHE  A  98     -15.397 130.810  -7.121  1.00 62.35          C
ATOM     751  C    PHE  A  98     -15.786 129.832  -6.029  1.00 66.02          C
ATOM     752  O    PHE  A  98     -16.159 128.706  -6.316  1.00 65.97          0
ATOM     753  CB   PHE  A  98     -13.890 130.823  -7.320  1.00 56.09          C
ATOM     754  CG   PHE  A  98     -13.473 131.308  -8.677  1.00 55.78          C
ATOM     755  CD1  PHE  A  98     -14.332 131.189  -9.761  1.00 55.35          C
ATOM     756  CD2  PHE  A  98     -12.231 131.891  -8.873  1.00 53.89          C
ATOM     757  CE1  PHE  A  98     -13.950 131.634 -11.027  1.00 56.62          C
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ATOM     758   CE2   PHE  A   98     -11 .843    132..345   -10..127    1,00   57.44         C
ATOM     759   CZ    PHE  A   98     --12.,700   132..215   -11 ,206    1,00   57.21         C
ATOM     760   N     HIS  A   99     -15.758     1.30.,279  - 4.781     1.00   7.1 ,75       N
ATOM     761   CA    HIS  A   99     -16..207    129.,445   -3..675     1,00   70..15        C
ATOM     762   C     HIS  A   99     -17 ,687    129. 120   -3.,785     1,00   67.63         C
ATOM     763   O     HIS  A   99     -18.123     128,044    -3...394    1.00   65,.35        0
ATOM     764   CB    HIS  A   99     -15..944    130.,131   - 2.339     1,00   79,.57        C
ATOM     765   CG    HIS  A   99     -14 ,527    .130. 036  - 1 ,869    1,00   80..82        C
ATOM     766   ND1   HIS  A   99     -14.165     129.,324   -0.,745     1,00   84.05         N
ATOM     767   CD2   HIS  A   99     -13..386    130.,580   - 2.356     1,00   84,02         C
ATOM     768   CE1   HIS  A   99     -12.,860    129..427   -0.,566     I,00   92.57         C
ATOM     769   NE2   HIS  A   99     -12..363    130..183   - 1,530     1,00   89..70        N
ATOM     770   N     A.P.G A  100    -18. 465    130.,060   - 4.311     1,00   69,47         N
ATOM     771   CA    ARG  A  100     -19..915    129.,880   - 4.378     1,00   66..99        C
ATOM     772   C     ARG  A  100     -20,282     128..914   -5.,508     1,00   58..86        C
ATOM     773   O     AP.G A  100     -21..242    128,159    -5...398    1.00   58,.20        0
ATOM     774   CB    ARG  A  100     -20.623     131.,235   - 4.541     1,00   60..64        C
ATOM     775   CG    ARG  A  100     -2.1.,514   131. 602   -3.,339     1,00   69..85        C
ATOM     776   CD    AP.G A  100     -22..151    1.3.3.,012 -3..453     1.00   69,.32        C
ATOM     777   NE    ARG  A  100     -21 .129    134.,046   -3..581     1,00   71,02         N
ATOM     778   CZ    ARG  A  100     -2.1.,009   .134. 860  - 4,623     1,00   69..49        C
ATOM     779   NH1   AP.G A  100     -21..869    134.,787   -5.,622     1,00   70..59        N
ATOM     780   NH2   ARG  A  100     -20.033     135.,755   - 4.663     1,00   71,07         N
ATOM     781   N     LEU  A  101     -19.,500    128.938    -6.,582     I,00   58..15        N
ATOM     782   CA    LEU  A  101     -19..615    127 .953   - 7,655     1,00   60..14        C
ATOM     783   C     LEU  A  101     -19. 395    126,519    - 7.177     1,00   59,73         C
ATOM     784   O     LEU  A  101     -20.,186    125..621   - 7,478     I,00   58..19        O
ATOM     785   CB    LEU  A  101     -18.,610    128..233   -8.,756     1,00   60..68        C
ATOM     786   CG    LEU  A  101     -18. 626    129,547    -9. 500     1,00   57,57         C
ATOM     787   CD1   LEU  A  101     -17 .613    129.,440   -10.,613    1,00   62.72         C
ATOM     788   CD2   LEU  A  101     -19,996     129..807   -10.,050    1,00   61.41         C
ATOM     789   N     GLU  A  102     -18.312     126,306    -6..443     1.00   57,10         N
ATOM     790   CA    GLU  A  102     -17 .973    124.,972   -5..989     1,00   60..91        C
ATOM     791   C     GLU  A  102     -18.,786    124 .513   - 4,812     1,00   57.73         C
ATOM     792   O     GLU  A  102     -18.490     12.3.,479  - 4.237     1.00   66,.84        0
ATOM     793   CB    GLU  A  102     -16..493    124.,883   -5..634     1,00   68,.79        C
ATOM     794   CG    GLU  A  102     -15.,628    124 .580   -6.,839     1,00   73..87        C
ATOM     795   CD    GLU  A  102     -15..483    125.,780   - 7,748     1,00   75..09        C
ATOM     796   OE1   GLU  A  102     -16. 069    125,788    -8. 869     1,00   69,33         0
ATOM     797   OE2   GLU  A  102     -14,763     126..711   -7.,329     I,00   73..87        0
ATOM     798   N     GLU  A  103     -19,818     125..255   - 4,457     1,00   54.26         N
ATOM     799   CA    GLU  A  103     -20. 702    124,828    - 3.375     1,00   58,02         C
ATOM     800   C     GLU  A  103     -22.,151    124.,776   -3.,849     1,00   56..67        C
ATOM     801   O     GLU  A  103     -23,038     124 .414   -3.,075     1,00   58..17        0
ATOM     802   CB    GLU  A  103     -20.563     125.,759   - 2.167     1.00   68,.02        C
ATOM     803   CG    GLU  A  103     -19..169    125,737    - 1.548     1,00   71.82         C
ATOM     804   CD    GLU  A  103     -18.,860    126. 939   -0.,646     1,00   79..27        C
ATOM     805   OE1   GLU  A  10.3    -19.731     127,840    -0..505     1.00   79,.00        0
ATOM     806   OE2   GLU  A  103     -17 .726    126.,970   -0..088     1,00   77,83         0
ATOM     807   N     SER  A  104     -22.,366    125. 110   - 5,126     1,00   51.07         N
ATOM     808   CA    SER  A  104     -23,698     125..195   -5.,738     1,00   46..92        C
ATOM     809   C     SER  A  104     -24.645     124.,009   -5..467     1,00   52,70         C
ATOM     810   0     SER  A  104     -25.,862    124..203   -5.,390     I,00   55..19        0
ATOM     811   CB    SER  A  104     -23,545     125..397   - 7,252     1,00   55..22        C
ATOM     812   OG    SER  A  104     -23 .115    124,213    - 7.944     1,00   51,31         0
ATOM     813   O     PHE  A  105     -26.,512    120..845   -.3.,437    I,00   50..19        0
ATOM     814   N     PHE  A  105     -24,094     122..798   -5.,326     1,00   49..74        N
ATOM     815   CA    PHE  A  105     -24 ,869    121,575    -5. 064     1,00   52,12         C
ATOM     816   C     PHE  A  105     -25,485     121.,499   -3.,662     1,00   53..27        C
ATOM     817   CB    PHE  A  105     -23,962     120..349   -5.,269     1,00   49..91        C
ATOM     818   CG    PHE  A  105     -24..702    119,032    -5..411     1.00   50,.94        C
ATOM     819   CD2   PHE  A  105     -24.754     118.,132   - 4.362     1,00   51.06         C
ATOM     820   CD1   PHE  A  105     -25,295     118. 674   -6.,619     1,00   56..73        C
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ATOM	821	CE2	PHE	A	105	-25.417	116.902	-4.510	1.00	57.47	c
ATOM	822	CEl	PHE	A	105	--25,949	117.439	-8,779	1,00	51.91	C
ATOM	823	CZ	PHE	A	105	-26.014	116,556	-5.727	1,00	49,07	c
ATOM	824	O	LEU	A	106	-26.912	123.659	-1.474	1.00	65.82	0
ATOM	825	N	LEU	A	106	-24,827	122.157	-2,716	1,00	60,77	N
ATOM	826	CA	LEU	A	106	-25.170	122,027	-1.303	1,00	62,74	c
ATOM	827	c	LEU	A	106	-26.521	122,604	-0.963	1,00	64,26	c
ATOM	828	CB	LEU	A	106	-24,109	122.694	-0,435	1,00	62,67	c
ATOM	829	CG	LEU	A	106	-22.792	121.940	-0.416	1,00	65.31	c
ATOM	830	CD1	LEU	A	106	-21.755	122,681	0.407	1,00	63,79	c
ATOM	831	CD2	LEU	A	106	-23,026	120.528	0,102	I,00	63.48	c
ATOM	832	O	VAL	A	107	-26.965	123.771	1,816	1,00	70.20	0
ATOM	833	N	VAL	A	107	-27.230	121,886	-0.103	1,00	64,84	N
ATOM	834	CA	VAL	A	107	-28.448	122.393	0.493	1.00	68.01	c
ATOM	835	C	VAL	A	107	-28,085	123.661	1,285	1,00	72.21	c
ATOM	836	CB	VAL	A	107	-29.112	121,309	1.373	1,00	70,23	c
ATOM	837	CGI	VAL	A	107	-29.918	121.911	2.480	1.00	73.78	c
ATOM	838	CG2	VAL	A	107	-29,984	120.395	0,516	1,00	67.15	c
ATOM	839	O	GLU	A	108	-27.037	126,581	3.365	1,00	74,43	0
ATOM	840	N	GLU	A	108	-29.014	124,623	1.306	1,00	73,46	N
ATOM	841	CA.	GLU	A	108	-28,802	125.956	1,880	1,00	74.12	c
ATOM	842	C	GLU	A	108	-28.063	125.927	3.217	1,00	73.51	c
ATOM	843	CB	GLU	A	108	-30.151	126,668	2.039	1,00	72,78	c
ATOM	844	CG	GLU	A	108	-30,089	128.178	2,262	I,00	67.57	c
ATOM	845	CD	GLU	A	108	-31.486	128.795	2.231	1,00	78.65	c
ATOM	846	OE1	GLU	A	108	-32.431	128,025	1.964	1,00	80,16	0
ATOM	847	OE2	GLU	A	108	-31,649	130.022	2,463	I,00	72.05	0
ATOM	848	O	GLU	A	109	-25,558	125.264	5,878	1,00	80.33	0
ATOM	849	N	GLU	A	109	-28.572	125,160	4.178	1,00	71,35	N
ATOM	850	CA	GLU	A	109	-27.905	125.023	5.477	1.00	80.06	c
ATOM	851	C	GLU	A	109	-26,443	124.589	5,347	1,00	77.58	c
ATOM	852	CB	GLU	A	109	-28.649	124,040	6.397	1,00	84,36	c
ATOM	853	CG	GLU	A	109	-29.635	123.099	5.724	1.00	84.38	c
ATOM	854	CD	GLU	A	109	-30,887	123.813	5,229	1,00	84.43	c
ATOM	855	OE1	GLU	A	109	-30.822	124,428	4.141	1,00	80,57	0
ATOM	856	OE2	GLU	A	109	-31.927	123,760	5.922	1,00	88,74	0
ATOM	857	O	ASP	A	110	-22,746	124.085	3,890	1,00	73.82	0
ATOM	858	N	ASP	A	110	-26.182	123.488	4.644	1,00	71.46	N
ATOM	859	CA	ASP	A	110	-24.801	123,010	4.500	1,00	74,13	c
ATOM	860	C	ASP	A	110	-23,968	124.017	3,731	I,00	72.82	c
ATOM	861	CB	ASP	A	110	-24,750	121.656	3,793	1,00	71.03	c
ATOM	862	CG	ASP	A	110	-25.631	120,624	4.452	1,00	76,13	c
ATOM	863	OD1	ASP	A	110	-26.300	120.967	5.451	1.00	83.40	0
ATOM	864	OD2	ASP	A	110	-25,676	119.474	3,962	1,00	68.86	0
ATOM	865	O	LYS	A	111	-24.090	127,433	3.935	1,00	75,71	0
ATOM	866	N	LYS	A	111	-24.639	124.784	2.880	1.00	71.24	N
ATOM	867	CA.	LYS	A	111	-23,979	125.835	2,120	1,00	76.91	c
ATOM	868	C	LYS	A	111	-23.384	126,864	3.089	1,00	78,41	c
ATOM	869	CB	LYS	A	111	-24.964	126,501	1.147	1,00	72,42	c
ATOM	870	CG	LYS	A	111	-24,375	126.833	-0,221	1,00	71.96	c
ATOM	871	CD	LYS	A	111	-25.315	127.727	-1.039	1,00	61.15	c
ATOM	872	CE	LYS	A	111	-26.630	127,033	-1.392	1,00	63,78	c
ATOM	873	NZ	LYS	A	111	-26,488	126.099	-2,558	I,00	65.97	N
ATOM	874	O	LYS	A	112	-22.201	130.217	4.329	1,00	75.76	0
ATOM	875	N	LYS	A	112	-22.078	127,079	2.974	1,00	77,79	N
ATOM	876	CA	LYS	A	112	-21,370	128.017	3,833	I,00	70.05	c
ATOM	877	C	LYS	A	112	-21,736	129.448	3,480	1,00	77.08	c
ATOM	878	CB	LYS	A	112	-19.854	127,825	3.714	1,00	69,70	c
ATOM	879	O	HIS	A	113	-24.077	130.409	1.782	1.00	61.30	0
ATOM	880	N	HIS	A	113	-21,521	129.798	2,215	1,00	76.84	N
ATOM	881	CA	HIS	A	113	-21.810	131,136	1.730	1,00	63,25	c
ATOM	882	c	HIS	A	113	-23.282	131.262	1.418	1.00	60.47	c
ATOM	883	CB	HIS	A	113	-20,975	131.468	0,501	1,00	67.99	c

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ATOM   884  CG   HIS A 113    -19.498 131.382    0.732  1.00 75.70      C
ATOM   885  ND1  HI S A 113   --18,896 130.301    1,343  1,00 79.38      N
ATOM   886  CD2  HIS A 113    -18.498 1.32,241    0.421  1.00 77,23      C
ATOM   887  CE1  HIS A 113    -17.591 130:500    1.402  1.00 82.03      C
ATOM   888  NE2  HI S A 113    -17,323 131.670    0,849  1,00 77.88      N
ATOM   889  O    GLU A 114    -24.867 131,774   -1.702  1.00 68,15      O
ATOM   890  N    GLU A 114    -23.655 132,345    0.759  1,00 66,58      N
ATOM   891  CA.  GLU A 114    -25,067 132.617    0,557  1,00 69.69      C
ATOM   892  C    GLU A 114    -25.586 131,923   -0:715  1,00 68.09      C
ATOM   893  CB   GLU A 114    -25.302 134,125    0.519  1,00 67,10      C
ATOM   894  CG   GLU A 114    -26,737 134.527    0,731  I,00 69.15      C
ATOM   895  CD   GLU A 114    -27.260 135.243   -0:476  1,00 71.51      C
ATOM   896  OE1  GLU A 114    -28.432 135,671   -0.490  1,00 76,52      0
ATOM   897  OE2  GLU A 114    -26.476 135:365   -1,427  1.00 70.05      0
ATOM   898  O    ARG A 115    -27,801 130.181   -3,955  1,00 66.28      0
ATOM   899  N    AP.G A 115    -26.848 131,516   -0.681  1.00 67,25      N
ATOM   900  CA   ARG A 115    -27.377 130:549   -1.628  1,00 63.48      C
ATOM   901  C    ARG A 115    -27,406 130.972   -3,101  1,00 68.22      C
ATOM   902  CB   ARG A 115    -28.793 130,144   -1.186  1.00 62,15      C
ATOM   903  CG   ARG A 115    -29.856 131,178   -1.409  1,00 59,81      C
ATOM   904  CD   ARG A 115    -31,219 130.713   -0,907  1,00 60.38      C
ATOM   905  ME   ARG A 115    -32 .242 131:675   -1:303  1,00 73.62      N
ATOM   906  CZ   ARG A 115    -33.272 131,414   -2.108  1,00 75,13      C
ATOM   907  NH1  ARG A 115    -34,125 132.397   -2,413  I,00 73.02      N
ATOM   908  NH2  ARG A 115    -33.464 130.183   -2:597  1,00 58.34      N
ATOM   909  O    HIS A 116    -24.864 133,594   -4.980  1,00 67,36      0
ATOM   910  N    HIS A 116    -26,992 132.198   -3,411  I,00 67.97      N
ATOM   911  CA   HI S A 116    -27,080 132.693   -4,785  1,00 64.20      C
ATOM   912  C    HIS A 116    -25.684 1.32,794   -5.402  1,00 64,39      C
ATOM   913  CB   HIS A 116    -27.820 134:044   -4,823  1.00 67.12      C
ATOM   914  CG   HI S A 116    -29,226 133.973   -4,304  1,00 66.24      C
ATOM   915  ND1  HIS A 116    -29.556 134,271   -3.000  1.00 69,66      N
ATOM   916  CD2  HIS A 116    -30.384 133:608   -4.908  1,00 66.78      C
ATOM   917  CE1  HI S A 116    -30,858 134.106   -2,827  1,00 70.36      C
ATOM   918  NE2  HIS A 116    -31.382 133,698   -3.969  1.00 63,64      N
ATOM   919  O    PRO A 117    -22.224 133,253   -7.301  1,00 59,93      0
ATOM   920  N    PRO A 117    -25,402 131.948   -6,400  1,00 66.71      N
ATOM   921  CA   PRO A 117    -23.988 131:777   -6:749  1,00 63.94      C
ATOM   922  C    PRO A 117    -23.395 1.32,948   -7.508  1,00 58,84      C
ATOM   923  CB   PRO A 117    -23,979 130.507   -7,627  I,00 55.62      C
ATOM   924  CG   FRO A 117    -25,295 129.862   -7,427  1,00 60.15      C
ATOM   925  CD   PRO A 117    -26.266 130,959   -7.071  1,00 64,81      C
ATOM   926  O    ILE A 118    -21:999 136:293   -8:387  1.00 61.34      0
ATOM   927  N    ILE A 118    -24,148 133.595   -8,382  1,00 59.17      N
ATOM   928  CA   ILE A 118    -23.496 134,606   -9.211  1.00 67,17      C
ATOM   929  C    ILE A 118    -23.160 135:884   -8.444  1.00 64.51      C
ATOM   930  CB   ILE A 118    -24,340 134.969  -10.436  1,00 63.73      C
ATOM   931  CGI  ILE A 118    -24.791 133,690  -11.130  1.00 58,35      C
ATOM   932  CG2  ILE A 118    -23.524 135,829  -11.391  1,00 59,01      C
ATOM   933  CD1  ILE A 118    -25,290 133.899  -12,517  1,00 62.03      C
ATOM   934  O    PHE A 119    -23:604 138:850   -5:156  1,00 74.63      0
ATOM   935  N    PHE A 119    -24.168 136,495   -7.831  1,00 71,86      N
ATOM   936  CA   PHE A 119    -23,995 137.839   -7,278  I,00 69.36      C
ATOM   937  C    PHE A 119    -24:100 137.911   -5:764  1,00 68.58      C
ATOM   938  CB   PHE A 119    -24.999 138.777   -7.912  1,00 63,20      C
ATOM   939  CG   PHE A 119    -24,699 139.090   -9,341  I,00 62.35      C
ATOM   940  CD1  PHE A 119    -23,604 139.865   -9,674  1,00 63.97      C
ATOM   941  CD2  PHE A 119    -25.507 138,610  -10.352  1,00 63,48      C
ATOM   942  CE1  PHE A 119    -23:314 140:156  -10:989  1.00 60.99      C
ATOM   943  CE2  PHE A 119    -25,221 138.892  -11,674  1,00 60.76      C
ATOM   944  CZ   PHE A 119    -24.118 139,668  -11.987  1.00 60,98      C
ATOM   945  O    GLY A 120    -25.830 137:781   -1.816  1.00 76.41      0
ATOM   946  N    GLY A 120    -24,731 136.916   -5,154  1,00 69,37      N
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ATOM	947	CA	GLY	A	120	-24.751	136.831	-3.709	1,00	68.58	c
ATOM	948	C	GLY	A	120	--25,892	137.548	-3,019	1,00	71.94	C
ATOM	949	O	ASN	A	121	-29.155	138,086	-5:288	1,00	68,23	O
ATOM	950	N	ASN	A	121	-26.938	137:893	-3,762	1,00	71.17	N
ATOM	951	CA.	ASM	A	121	-28,163	138.392	-3,152	1,00	68,11	C
ATOM	952	C	ASN	A	121	-29.334	138,125	-4:074	1,00	67,02	C
ATOM	953	CB	ASN	A	121	-28.048	139,886	-2.851	1,00	69,39	c
ATOM	954	CG	ASN	A	121	-27,829	140.713	-4,100	1,00	68,97	c
ATOM	955	OD1	ASN	A	121	-28.787	141,122	-4,767	1,00	68.03	0
ATOM	956	ND2	ASN	A	121	-26.567	140,960	-4.431	1,00	67,50	N
ATOM	957	N	ILE	A	122	-30,527	137,961	-3,509	I,00	65.79	N
ATOM	958	CA	ILE	A	122	-31.699	137.588	-4,298	1,00	61.17	C
ATOM	959	C	ILE	A	122	-32.003	138,566	-5.421	1,00	63,82	C
ATOM	960	O	ILE	A	122	-32.450	138:151	-6,487	1,00	63.34	0
ATOM	961	CB	ILE	A	122	-32,958	137.463	-3,429	1,00	66.47	c
ATOM	962	CGI	ILE	A	122	-32.624	136,820	-2:080	1,00	73,06	c
ATOM	963	CG2	ILE	A	122	-34.019	136:643	-4,149	1,00	60.64	c
ATOM	964	CD1	ILE	A	122	-32,314	137.794	-0,964	1,00	76,88	c
ATOM	965	N	VAL	A	123	-31.745	139,855	-5:184	1,00	64,40	N
ATOM	966	CA	VAL	A	123	-32.168	140,930	-6.097	1,00	65,97	c
ATOM	967	C	VAL	A	123	-31,353	140.971	-7,401	1,00	64,13	C
ATOM	968	O	VAL	A	123	-31.912	141,167	-8:490	1,00	61.74	0
ATOM	969	CB	VAL	A	123	-32.098	142,352	-5.393	1,00	69,18	c
ATOM	970	CGI	VAL	A	123	-31,897	143:466	-6,410	I,00	54.08	c
ATOM	971	CG2	VAL	A	123	-33.340	142,610	-4:543	1,00	52.67	c
ATOM	972	N	ASP	A	124	-30.039	140,812	-7.291	1,00	6.1.,99	N
ATOM	973	CA	ASP	A	124	-29,186	140:778	-8,475	I,00	66.30	C
ATOM	974	C	ASP	A	124	-29,428	139:498	-9,298	1,00	64.89	C
ATOM	975	O	ASP	A	124	-29.532	139,541	-10.528	1,00	62,53	O
ATOM	976	CB	ASP	A	124	-27.712	140:872	-8,069	1,00	69.92	c
ATOM	977	CG	ASP	A	124	-27,391	142,148	-7,311	1,00	71.87	c
ATOM	978	OD1	ASP	A	124	-27.931	143,206	-7:701	1,00	79,12	0
ATOM	979	OD2	ASP	A	124	-26.595	142:096	-6,344	1,00	69.93	0
ATOM	980	N	GLU	A	125	-29,526	138.369	-8,603	1,00	61,95	N
ATOM	981	CA	GLU	A	125	-29.644	137,066	-9:255	1,00	68,95	c
ATOM	982	c	GLU	A	125	-30.878	137,005	-10,154	1,00	66,72	c
ATOM	983	0	GLU	A	125	-30,771	136.665	-11,338	1,00	68,62	0
ATOM	984	CB	GLU	A	125	-29.691	135:939	-8:212	1,00	66.10	c
ATOM	985	CG	GLU	A	125	-29.072	134,622	-8.669	1,00	67,06	c
ATOM	986	CD	GLU	A	125	-27,573	134:572	-8,477	I,00	67.08	c
ATOM	987	OE1	GLU	A	125	-26,998	135.558	-7,977	1,00	64.46	0
ATOM	988	OE2	GLU	A	125	-26.964	133,534	-8.819	1,00	67,73	0
ATOM	989	N	VAL	A	126	-32.036	137:349	-9,592	1,00	65.94	N
ATOM	990	CA	VAL	A	126	-33,301	137.313	-10:327	1,00	66.15	c
ATOM	991	C	VAL	A	126	-33.227	138,239	-11:539	1,00	63,79	c
ATOM	992	O	VAL	A	126	-33.766	137,944	-12:613	1,00	64.71	0
ATOM	993	CB	VAL	A	126	-34,490	137.708	-9,417	1,00	64,41	c
ATOM	994	CGI	VAL	A	126	-35.766	137,882	-10:223	1,00	66,07	c
ATOM	995	CG2	VAL	A	126	-34.693	136,666	-8.322	1,00	63:77	c
ATOM	996	N	ALA	A	127	-32,512	139..342	-11,367	1,00	61,76	N
ATOM	997	CA	ALA	A	127	-32,333	140.301	-12,441	1,00	64.57	C
ATOM	998	c	ALA	A	127	-31.587	139,635	-13.585	1,00	60,44	c
ATOM	999	0	ALA	A	127	-32,010	139:704	-14,746	I,00	54.66	0
ATOM	1000	CB	ALA	A	127	-31:581	141,551	-11:937	1,00	56.79	c
ATOM	1001	N	TYR	A	128	-30.487	138,971	-13.231	1,00	62,32	N
ATOM	1002	CA	TYR	A	128	-29,643	138:276	-14,192	I,00	55.57	C
ATOM	1003	C	TYR	A	128	-30,424	137.253	-15,014	1,00	53.29	C
ATOM	1004	O	TYR	A	128	-30.412	137,288	-16.250	1,00	52,11	O
ATOM	1005	CB	TYR	A	128	-28:480	137:594	-13:475	1,00	63.32	c
ATOM	1006	CG	TYR	A	128	-27,743	136.667	-14,393	1,00	60.55	c
ATOM	1007	CD1	TYR	A	128	-26.808	137,160	-15:293	1,00	64,36	c
ATOM	1008	CD2	TYR	A	128	-28.016	135:302	-14,401	1,00	62.43	c
ATOM	1009	CE1	TYR	A	128	-26,142	136.316	-16,165	1,00	64,75	c

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ATOM  1010  CE2  TYR  A  128   -27.352  134.445  -15.272  1.00  61.26  C
ATOM  1011  CZ   TYR  A  128   --26.419 134.961  -16.147  1.00  60.92  C
ATOM  1012  OH   TYR  A  128   -25.768  1.34.125 -17.016  1.00  59.27  0
ATOM  1013  N    HIS  A  129   -31.100  136.341  -14.329  1.00  54.68  N
ATOM  1014  CA.  HIS  A  129   -31.927  135..343 -15.004  I.00  57.77  C
ATOM  1015  C    HIS  A  129   -33.040  1.35.983 -15.850  1.00  61.42  C
ATOM  1016  O    HIS  A  129   -33.564  135.354  -16.791  1.00  59.08  O
ATOM  1017  CB   HIS  A  129   -.32.562  134..388 -13.995  I.00  55.58  C
ATOM  1018  CG   HIS  A  129   -31.599  133.446  -13.342  1.00  60.77  C
ATOM  1019  ND1  HIS  A  129   -31.012  132.398  -14.017  1.00  57.63  N
ATOM  1020  CD2  HIS  A  129   -31.150  133..369 -12.067  I.00  62.90  C
ATOM  1021  CE1  HIS  A  129   -30.229  131.726  -13.192  1.00  55.84  C
ATOM  1022  NE2  HIS  A  129   -30.294  1.32.292 -12.002  1.00  59.57  N
ATOM  1023  N    GLU  A  130   -33.421  137.218  -15.503  1.00  59.60  N
ATOM  1024  CA   GLU  A  130   -34.421  137.940  -16.289  1.00  58.61  C
ATOM  1025  C    GLU  A  1.30  -33.792  1.38.617 -17.508  1.00  54.13  C
ATOM  1026  O    GLU  A  130   -34.327  138.523  -18.597  1.00  52.95  O
ATOM  1027  CB   GLU  A  130   -.35.159  138.958  -15.428  I.00  63.49  C
ATOM  1028  CG   GLU  A  1.30  -36..340  1.39.582 -16.148  1.00  74.37  C
ATOM  1029  CD   GLU  A  130   -37.520  139.854  -15.225  1.00  87.68  C
ATOM  1030  OE1  GLU  A  130   -.37.579  139.233  -14.130  I.00  81.54  0
ATOM  1031  OE2  GLU  A  130   -38.381  140.692  -15.601  1.00  92.65  0
ATOM  1032  N    LYS  A  131   -32.653  139.284  -17.337  1.00  50.66  N
ATOM  1033  CA   LYS  A  131   -31.886  139.756  -18.497  I.00  51.48  C
ATOM  1034  C    LYS  A  131   -31.298  138.597  -19.341  1.00  59.62  C
ATOM  1035  O    LYS  A  131   -31.286  1.38.672 -20.576  1.00  60.59  O
ATOM  1036  CB   LYS  A  131   -.30.755  140.685  -18.055  I.00  50.85  C
ATOM  1037  N    TYR  A  132   -30.813  137.533  -18.698  1.00  51.95  N
ATOM  1038  CA   TYR  A  1.32  -30.233  1.36.419 -19.477  1.00  59.18  C
ATOM  1039  C    TYR  A  132   -30.833  135.047  -19.156  1.00  55.25  C
ATOM  1040  O    TYR  A  132   -30.292  134.298  -18.353  1.00  54.70  0
ATOM  1041  CB   TYR  A  1.32  -28.725  1.36.355 -19.272  1.00  53.16  C
ATOM  1042  CG   TYR  A  132   -28.002  137.661  -19.485  1.00  57.50  C
ATOM  1043  CD1  TYR  A  132   -27.728  138.137  -20.765  I.00  57.66  C
ATOM  1044  CD2  TYR  A  1.32  -27.567  1.38.410 -18..396  1.00  60.53  C
ATOM  1045  CE1  TYR  A  132   -27.048  139.342  -20.945  1.00  60.58  C
ATOM  1046  CE2  TYR  A  132   -26.890  139.597  -18.561  I.00  57.58  C
ATOM  1047  CZ   TYR  A  132   -26.632  140.064  -19.827  1.00  59.62  C
ATOM  1048  OH   TYR  A  1.32  -25.948  141.257  -19.955  1.00  61.77  0
ATOM  104 9  O    PRO  A  133   -.32.072  131.193  -19.210  I.00  52.84  0
ATOM  1050  N    FRO  A  133   -31.962  134.720  -19.792  1.00  55.37  N
ATOM  1051  CA   PRO  A  1.33  -32.706  1.33.489 -19.520  1.00  50.68  C
ATOM  1052  C    PRO  A  133   -31.855  132.252  -19.787  1.00  52.74  C
ATOM  1053  CB   FRO  A  133   -33.874  133.558  -20.502  1.00  55.81  C
ATOM  1054  CG   PRO  A  1.33  -33.943  1.34.974 -20.960  1.00  57.30  C
ATOM  1055  CD   PRO  A  133   -32.569  135.520  -20.869  1.00  57.80  C
ATOM  1056  O    TH.R A  134   -28.313  133.068  -21.267  I.00  47.88  0
ATOM  1057  N    THR  A  1.34  -30.908  1.32.393 -20.703  1.00  54.97  N
ATOM  1058  CA   THR  A  134   -29.965  131.332  -20.984  1.00  49.94  C
ATOM  1059  C    TH.R A  134   -28.529  131.874  -21.068  I.00  48.48  C
ATOM  1060  CB   THR  A  134   -30.326  130.601  -22.278  1.00  46.62  C
ATOM  1061  OG1  THR  A  134   -29.984  131.414  -23.395  1.00  45.58  0
ATOM  1062  CG2  THR  A  134   -31.800  130.230  -22.317  I.00  45..30  C
ATOM  1063  O    ILE  A  135   -24.898  132.698  -22.516  1.00  49.28  0
ATOM  1064  N    ILE  A  1.35  -27.550  1.30.977 -20.911  1.00  47.86  N
ATOM  1065  CA   ILE  A  135   -26.126  131..324 -20.976  I.00  40.28  C
ATOM  1066  C    ILE  A  135   -25.808  131.885  -22.356  1.00  43.64  C
ATOM  1067  CB   ILE  A  1.35  -25.207  1.30.064 -20.638  1.00  45.11  C
ATOM  1068  CGI  ILE  A  135   -23.700  130.423  -20.557  1.00  42.61  C
ATOM  1069  CG2  ILE  A  135   -25.427  128.951  -21.633  1.00  37.83  C
ATOM  1070  CD1  ILE  A  1.35  -23.294  131.166  -19.277  1.00  42.29  C
ATOM  1071  N    TYR  A  136   -26.562  131.461  -23.363  1.00  44.72  N
ATOM  1072  CA.  TYR  A  136   -26.308  131.931  -24.718  I.00  48.11  C
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ATOM   1073  C    TYR  A  136     -26..698   133.,415   -24,882    1.00   52.78     C
ATOM   1074  0    TYR  A  136     --26,056   134..130   -25,646    1,00   53..93    O
ATOM   1075  CB   TYR  A  1.36    -27.028    131.,045   -25.740    1.00   49,.80    C
ATOM   1076  CG   TYR  A  136     -26..648   129.,578   -25.,618   1.00   50..50    C
ATOM   1077  GDI  TYR  A  136     -25,468    129. 075   -26,189    1,00   52..33    C
ATOM   1078  CD2  TYR  A  1.36    -27.439    128,704    -24..902   1.00   50,.20    C
ATOM   1079  CE1  TYR  A  136     -25..116   127,740    -26.046    1,00   43,.85    C
ATOM   1080  CE2  TYR  A  136     -27,100    127 .370   -24.,763   1,00   46..62    C
ATOM   1081  CZ   TYR  A  136     -25..949   126.,897   -25,335    1,00   47.52     C
ATOM   1082  OH   TYR  A  136     -25..651   125,567    -25.167    1,00   50,.53    0
ATOM   1083  N    HIS  A  137     -27.,718   133..883   -24.,159   I,00   51.94     N
ATOM   1084  CA   HIS  A  137     -28..025   135.,322   -24,151    1,00   53..50    C
ATOM   1085  C    HIS  A  1.37    -26. 790   1.36,104   -23 .696   1,00   52,88     C
ATOM   1086  O    HIS  A  137     -26..331   137.,014   -24,383    1.00   58..19    0
ATOM   1087  CB   HIS  A  137     -29,222    135..639   -23,245    1,00   50..69    C
ATOM   1088  CG   HIS  A  1.37    -30..543   1.35.,204  -23.803    1.00   52,61     C
ATOM   1089  ND1  HIS  A  137     -31..074   133.,954   -23,575    1.00   49..21    N
ATOM   1090  CD2  HIS  A  137     -.31.,450  135. 863   -24.,566   1,00   52.55     C
ATOM   1091  CE1  HIS  A  1.37    -32..241   1.3.3.,851 -24..183   1.00   51,70     C
ATOM   1092  NE2  HIS  A  137     -32..495   134.,998   -24.789    1,00   57,46     N
ATOM   1093  N    LEU  A  138     -26,237    135. 721   -22.,553   1,00   51.45     N
ATOM   1094  CA   LEU  A  138     -24..987   136.,312   -22.,074   1,00   53..47    C
ATOM   1095  C    LEU  A  138     -23..818   136.,163   -23.066    1,00   57,64     C
ATOM   1096  0    LEU  A  138     -23,104    137..120   -2.3.,331  I,00   58..3.3   0
ATOM   1097  CB   LEU  A  138     -24,598    135.,698   -20,735    1,00   50..23    C
ATOM   1098  CG   LEU  A  1.38    -23 .256   1.36,229   -20. 247   1,00   59,10     C
ATOM   1099  CD1  LEU  A  138     -23,373    137..724   -20.,096   I,00   58..07    C
ATOM   1100  CD2  LEU  A  138     -22.,768   135..559   -18.,931   1,00   55..53    C
ATOM   1101  N    A.RG A  1.39    -23 .618   1.34.,963  -23 .602   1,00   56,66     N
ATOM   1102  CA   ARG  A  139     -22.,551   134.,738   -24,566    1.00   57.26     C
ATOM   1103  C    ARG  A  139     -22.,649   135..700   -25,733    1,00   56..81    C
ATOM   1104  O    ARG  A  1.39    -21..699   1.36,416   -26.029    1.00   60,.54    0
ATOM   1105  CB   ARG  A  139     -22..568   133.,289   -25.,092   1.00   56..76    C
ATOM   1106  CG   ARG  A  139     -22.,033   132. 272   -24.,109   1,00   52.51     C
ATOM   1107  CD   ARG  A  1.39    -22...301  1.30.,845  -24..545   1.00   47,37     C
ATOM   1108  NE   ARG  A  139     -21 .635   130.,486   -25.796    1,00   52,52     N
ATOM   1109  CZ   ARG  A  139     -21.,254   129. 248   -26,124    1,00   50..14    C
ATOM   1110  NH1  ARG  A  139     -21.,462   128.,233   -25,297    1,00   40..24    N
ATOM   1111  NH2  AR.G A  1.39    -20. 670   129,022    -27.291    1,00   52,16     N
ATOM   1112  N    LYS  A  140     -23,791    135..691   -26.,412   I,00   60..0.3   N
ATOM   1113  CA   LYS  A  140     -24,028    136..609   -27,528    1,00   61.80     C
ATOM   1114  C    LYS  A  140     -23 .877   1.38.,056  -27.102    1,00   65,26     C
ATOM   1115  O    LYS  A  140     -23,351    138.,879   -27,847    1.00   67.31     0
ATOM   1116  CB   LYS  A  140     -25,417    136..416   -28,115    1,00   57.25     C
ATOM   1117  CG   LYS  A  140     -25..649   1.37,255   -29..349    1.00   6.3,.16   C
ATOM   1118  CD   LYS  A  140     -26.,871   138.,145   -29,176    1.00   68..63    C
ATOM   1119  CE   LYS  A  140     -27,103    139. 027   -.30.,397  1,00   70..73    C
ATOM   1120  NZ   LYS  A  140     -28...336  1.39,871   -30..252   1.00   82,67     N
ATOM   1121  N    LYS  A  141     -24.348    138.,363   -25.900    1,00   59,.49    N
ATOM   1122  CA.  LYS  A  141     -24.,179   139. 695   -25,375    1,00   61.83     C
ATOM   1123  C    LYS  A  141     -22.,700   140.,056   -25,373    1,00   63..90    C
ATOM   1124  O    LYS  A  141     -22.312    141 ,108   -25.868    1,00   67,40     0
ATOM   1125  CB   LYS  A  141     -24.,776   139.796    -2.3.,973  I,00   59..91    C
ATOM   1126  CG   LYS  A  141     -24,768    141 ,193   -23,378    1,00   65..31    C
ATOM   1127  CD   LYS  A  141     -23 .440   14.1.,514  -22.713    1,00   67,19     C
ATOM   1128  CE   LYS  A  141     -23,488    142 .823   -21.,945   I,00   66..00    C
ATOM   1129  NZ   LYS  A  141     -23,481    142..539   -20,479    1,00   72.59     N
ATOM   1130  N    LEU  A  142     -21.870    1.39,179   -24 .825   1,00   62,80     N
ATOM   1131  CA   LEU  A  142     -20.,465   139.,509   -24,628    1.00   57.01     C
ATOM   1132  C    LEU  A  142     -19,682    139..469   -25,926    1,00   57.69     C
ATOM   1133  O    LEU  A  142     -18.654    140.,099   -26.054    1.00   64,67     0
ATOM   1134  CB   LEU  A  142     -19..844   138.,573   -23,603    1.00   61.20     C
ATOM   1135  CG   LEU  A  142     -20.,412   138. 646   -22.,185   1,00   57.22     C
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ATOM   1136  GDI LEU A 142     -19.742 137.634 -21.295  1.00 59.50           c
ATOM   1137  CD2 LEU A 142     --20.282 140.036 -21.595  1.00 64.20           C
ATOM   1138  N   VAL A 143     -20.177 138.737 -26.904  1.00 63.11           N
ATOM   1139  CA  VAL A 143     -19.546 138.724 -28.211  1.00 60.79           c
ATOM   1140  C   VAL A 143     -19.733 140.057 -28.955  1.00 72.93           c
ATOM   1141  O   VAL A 143     -18.765 140.632 -29.480  1.00 71.61           0
ATOM   1142  CB  VAL A 143     -20.106 137.580 -29.064  1.00 62.88           c
ATOM   1143  CGI VAL A 143     -19.725 137.756 -30.531  1.00 62.35           c
ATOM   1144  CG2 VAL A 143     -19.620 136.232 -28.513  1.00 67.08           c
ATOM   1145  N   ASP A 144     -20.974 140.549 -28.977  1.00 66.63           N
ATOM   1146  CA  ASP A 144     -21.352 141.703 -29.795  1.00 70.47           C
ATOM   1147  C   ASP A 144     -21.068 143.098 -29.174  1.00 72.42           c
ATOM   1148  O   ASP A 144     -20.672 144.020 -29.886  1.00 76.62           0
ATOM   1149  CB  ASP A 144     -22.847 141.593 -30.162  1.00 68.60           c
ATOM   1150  CG  ASP A 144     -23.115 140.575 -31.285  1.00 69.92           c
ATOM   1151  OD1 ASP A 144     -22.224 140.373 -32.131  1.00 69.60           0
ATOM   1152  OD2 ASP A 144     -24.220 139.988 -31.332  1.00 62.39           0
ATOM   1153  N   SER A 145     -21.253 143.253 -27.864  1.00 75.46           N
ATOM   1154  CA  SER A 145     -21.234 144.584 -27.228  1.00 69.50           c
ATOM   1155  c   SER A 145     -19.844 145.093 -26.808  1.00 75.27           c
ATOM   1156  0   SER A 145     -18.945 144.308 -26.502  1.00 75.46           0
ATOM   1157  CB  SER A 145     -22.157 144.577 -26.011  1.00 62.41           c
ATOM   1158  OG  SER A 145     -21.471 145.004 -24.847  1.00 74.59           0
ATOM   1159  O   THR A 146     -17.155 147.960 -24.642  1.00 76.34           0
ATOM   1160  N   THR A 146     -19.690 146.418 -26.766  1.00 79.35           N
ATOM   1161  CA  THR A 146     -18.398 147.053 -26.475  1.00 75.38           C
ATOM   1162  C   THR A 146     -18.235 147.528 -25.032  1.00 77.16           c
ATOM   1163  CB  THR A 146     -18.164 148.260 -27.382  1.00 76.28           c
ATOM   1164  OG1 THR A 146     -19.409 148.950 -27.585  1.00 80.84           0
ATOM   1165  CG2 THR A 146     -17.596 147.823 -28.719  1.00 70.96           c
ATOM   1166  O   ASP A 147     -18.472 145.863 -22.117  1.00 81.69           0
ATOM   1167  N   ASP A 147     -19.301 147.439 -24.247  1.00 74.97           N
ATOM   1168  CA  ASP A 147     -19.305 147.964 -22.887  1.00 72.68           c
ATOM   1169  C   ASP A 147     -18.508 147.075 -21.942  1.00 78.80           c
ATOM   1170  CB  ASP A 147     -20.740 148.100 -22.397  1.00 75.16           c
ATOM   1171  CG  ASP A 147     -21.672 148.683 -23.461  1.00 84.72           c
ATOM   1172  OD2 ASP A 147     -22.844 148.990 -23.127  1.00 79.89           0
ATOM   1173  OD1 ASP A 147     -21.238 148.818 -24.633  1.00 85.85           0
ATOM   1174  O   LYS A 148     -18.742 146.513 -18.302  1.00 80.77           0
ATOM   1175  N   LYS A 148     -17.869 147.673 -20.940  1.00 77.24           N
ATOM   1176  CA  LYS A 148     -17.074 146.904 -19.982  1.00 75.59           c
ATOM   1177  C   LYS A 148     -17.956 146.014 -19.108  1.00 78.81           c
ATOM   1178  CB  LYS A 148     -16.244 147.826 -19.087  1.00 76.79           c
ATOM   1179  CG  LYS A 148     -15.503 147.078 -17.992  1.00 77.68           c
ATOM   1180  CD  LYS A 148     -15.053 147.990 -16.862  1.00 79.15           c
ATOM   1181  CE  LYS A 148     -14.539 147.189 -15.659  1.00 73.81           c
ATOM   1182  NZ  LYS A 148     -14.866 147.809 -14.322  1.00 67.01           N
ATOM   1183  O   ALA A 149     -16.909 143.206 -17.102  1.00 67.04           0
ATOM   1184  N   ALA A 149     -17.806 144.698 -19.247  1.00 81.49           N
ATOM   1185  CA. ALA A 149     -18.699 143.755 -18.575  1.00 74.22           C
ATOM   1186  C   ALA A 149     -18.125 143.263 -17.263  1.00 69.19           C
ATOM   1187  CB  ALA A 149     -19.003 142.583 -19.471  1.00 72.17           c
ATOM   1188  N   ASP A 150     -19.025 142.932 -16.334  1.00 66.75           N
ATOM   1189  CA  ASP A 150     -18.687 142.326 -15.051  1.00 66.91           C
ATOM   1190  C   ASP A 150     -17.820 141.089 -15.295  1.00 67.27           c
ATOM   1191  O   ASP A 150     -18.118 140.285 -16.178  1.00 66.43           0
ATOM   1192  CB  ASP A 150     -19.976 141.976 -14.291  1.00 64.74           c
ATOM   1193  CG  ASP A 150     -19.723 141.390 -12.896  1.00 73.24           c
ATOM   1194  OD2 ASP A 150     -20.452 141.780 -11.940  1.00 72.08           0
ATOM   1195  OD1 ASP A 150     -18.819 140.532 -12.749  1.00 69.21           0
ATOM   1196  N   LEU A 151     -16.752 140.935 -14.518  1.00 65.49           N
ATOM   1197  CA  LEU A 151     -15.789 139.867 -14.781  1.00 70.70           c
ATOM   1198  C   LEU A 151     -16.408 138.500 -14.496  1.00 67.99           C
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ATOM	1199	O	LEU	A	151	-16.117	137.526	-15.189	1.00	67.49	O
ATOM	1200	CB	LEU	A	151	-14.512	140.061	-13.954	1.00	69.13	C
ATOM	1201	CG	LEU	A	151	-13.247	139.354	-14.456	1.00	65.24	C
ATOM	1202	GDI	LEU	A	151	-12.894	139.773	-15.872	1.00	62.07	C
ATOM	1203	CD2	LEU	A	151	-12.082	139.622	-13.519	I.00	70.58	C
ATOM	1204	N	AP.G	A	152	-17.258	138.437	-13.475	1.00	66.07	N
ATOM	1205	CA	ARG	A	152	-17.971	137.213	-13.158	1.00	64.29	C
ATOM	1206	C	ARG	A	152	-18.769	136.691	-14.363	I.00	69.69	C
ATOM	1207	O	ARG	A	152	-18.833	135.476	-14.602	1.00	62.89	0
ATOM	1208	CB	ARG	A	152	-18.896	137.432	-11.961	1.00	61.71	C
ATOM	1209	CG	ARG	A	152	-18.156	137.564	-10.631	I.00	69.68	C
ATOM	1210	CD	ARG	A	152	-19.052	138.082	-y.500	1.00	69.20	C
ATOM	1211	NE	ARG	A	152	-19.499	139.450	-9.756	1.00	69.30	N
ATOM	1212	CZ	ARG	A	152	-20.174	140.196	-8.884	1.00	73.64	C
ATOM	1213	NH1	ARG	A	152	-20.482	139.709	-7.685	1.00	67.64	N
ATOM	1214	NH2	ARG	A	152	-20.537	141.435	-9.214	1.00	63.70	N
ATOM	1215	N	LEU	A	153	-19.364	137.601	-15.130	1.00	60.50	N
ATOM	1216	CA.	LEU	A	153	-20.157	137.175	-16.274	I.00	61.41	C
ATOM	1217	C	LEU	A	153	-19.252	136.837	-17.452	1.00	64.84	C
ATOM	1218	O	LEU	A	153	-19.627	136.053	-18.324	1.00	65.01	O
ATOM	1219	CB	LEU	A	153	-21.189	138.246	-16.650	I.00	63.87	C
ATOM	1220	CG	LEU	A	153	-22.211	138.485	-15.529	1.00	65.13	C
ATOM	1221	CD1	LEU	A	153	-23.406	139.351	-15.967	1.00	62.18	C
ATOM	1222	CD2	LEU	A	153	-22.687	137.150	-14.970	I.00	63.83	C
ATOM	1223	N	ILE	A	154	-18.052	137.414	-17.461	1.00	63.75	N
ATOM	1224	CA	ILE	A	154	-17.009	137.024	-18.409	1.00	61.96	C
ATOM	1225	C	ILE	A	154	-16.429	135.648	-18.069	I.00	64.46	C
ATOM	1226	O	ILE	A	154	-16.126	134.847	-18.966	1.00	58.52	0
ATOM	1227	CB	ILE	A	154	-15.858	138.040	-18.441	1.00	62.63	C
ATOM	1228	CGI	ILE	A	154	-16.419	139.450	-18.662	1.00	68.52	C
ATOM	1229	CG2	ILE	A	154	-14.827	137.672	-19.521	1.00	50.49	C
ATOM	1230	CD1	ILE	A	154	-15.457	140.562	-18.304	1.00	67.29	C
ATOM	1231	N	TYR	A	155	-16.263	135.367	-16.779	1.00	58.79	N
ATOM	1232	CA.	TYR	A	155	-15.803	134.053	-16.418	I.00	55.06	C
ATOM	1233	C	TYR	A	155	-16.842	133.015	-16.865	1.00	57.64	C
ATOM	1234	O	TYR	A	155	-16.527	132.136	-17.676	1.00	53.49	O
ATOM	1235	CB	TYR	A	155	-15.525	133.937	-14.920	I.00	59.86	C
ATOM	1236	CG	TYR	A	155	-15.344	132.502	-14.525	1.00	58.68	C
ATOM	1237	GDI	TYR	A	155	-14.166	131.820	-14.811	1.00	57.22	C
ATOM	1238	CD2	TYR	A	155	-16.376	131.802	-13.921	I.00	60.53	C
ATOM	1239	CEl	TYR	A	155	-14.022	130.478	-14.481	1.00	55.47	C
ATOM	1240	CE2	TYR	A	155	-16.237	130.485	-13.584	1.00	52.60	C
ATOM	1241	CZ	TYR	A	155	-15.063	129.825	-13.870	1.00	57.37	C
ATOM	1242	OH	TYR	A	155	-14.960	128.507	-13.527	1.00	52.56	0
ATOM	1243	N	LEU	A	156	-18.081	133.134	-16.373	1.00	58.70	N
ATOM	1244	CA	LEU	A	156	-19.126	132.158	-16.695	1.00	46.46	C
ATOM	1245	C	LEU	A	156	-19.297	131.958	-18.199	I.00	51.24	C
ATOM	1246	O	LEU	A	156	-19.398	130.814	-18.651	1.00	58.40	0
ATOM	1247	CB	LEU	A	156	-20.453	132.535	-16.066	1.00	46.09	C
ATOM	1248	CG	LEU	A	156	-20.430	132.540	-14.528	I.00	54.21	C
ATOM	1249	CD1	LEU	A	156	-21.648	133.226	-13.940	1.00	58.99	C
ATOM	1250	CD2	LEU	A	156	-20.306	131.161	-13.956	1.00	49.70	C
ATOM	1251	N	ALA	A	157	-19.291	133.018	-18.996	I.00	50.11	N
ATOM	1252	CA	ALA	A	157	-19.397	132.797	-20.443	1.00	54.32	C
ATOM	1253	C	ALA	A	157	-18.224	131.982	-21.036	1.00	55.27	C
ATOM	1254	O	ALA	A	157	-18.416	131.209	-21.981	I.00	52.74	0
ATOM	1255	CB	ALA	A	157	-19.522	134.095	-21.167	1.00	51.60	C
ATOM	1256	N	LEU	A	158	-17.018	132.162	-20.500	1.00	53.52	N
ATOM	1257	CA	LEU	A	158	-15.840	131.468	-21.030	1.00	51.64	C
ATOM	1258	C	LEU	A	158	-15.789	130.018	-20.514	1.00	51.46	C
ATOM	1259	O	LEU	A	158	-15.512	129.106	-21.269	1.00	49.92	0
ATOM	1260	CB	LEU	A	158	-14.549	132.211	-20.657	1.00	51.36	C
ATOM	1261	CG	LEU	A	158	-14.322	133.630	-21.183	I.00	44.13	C

ATOM	1262	GDI	LEU	A	158	-13.152	134.247	-20.464	1.00	52.20	C
ATOM	1263	CD2	LEU	A	158	-14.112	133.689	-22.675	1.00	47.11	C
ATOM	1264	N	ALA	A	159	-16.072	129.844	-19.224	1.00	50.47	N
ATOM	1265	CA	ALA	A	159	-16.204	128.547	-18.579	1.00	44.87	C
ATOM	1266	C	ALA	A	159	-17.143	127.610	-19.324	I.00	51.86	C
ATOM	1267	O	ALA	A	159	-16.848	126.413	-19.514	1.00	44.96	0
ATOM	1268	CB	ALA	A	159	-16.694	128.727	-17.155	1.00	46.80	C
ATOM	1269	N	HIS	A	160	-18.289	128.162	-19.713	I.00	43.12	N
ATOM	1270	CA	HIS	A	160	-19.321	127.412	-20.415	1.00	44.61	C
ATOM	1271	C	HIS	A	160	-18.761	126.860	-21.708	1.00	41.47	C
ATOM	1272	0	HIS	A	160	-19.135	125.788	-22.141	I.00	41.11	0
ATOM	1273	CB	HIS	A	160	-20.537	128.307	-20.722	1.00	39.84	C
ATOM	1274	CG	HIS	A	160	-21.711	127.566	-21.265	1.00	34.41	C
ATOM	1275	ND1	HIS	A	160	-21.989	127.506	-22.608	1.00	36.14	N
ATOM	1276	CD2	HIS	A	160	-22.667	126.831	-20.647	1.00	37.98	C
ATOM	1277	CE1	HIS	A	160	-23.057	126.753	-22.800	1.00	42.49	C
ATOM	1278	NE2	HIS	A	160	-23.502	126.350	-21.623	1.00	39.74	N
ATOM	1279	N	MET	A	161	-17.908	127.658	-22.337	I.00	43.78	N
ATOM	1280	CA	MET	A	161	-17.332	127.317	-23.620	1.00	45.25	C
ATOM	1281	C	MET	A	161	-16.209	126.304	-23.411	1.00	47.84	C
ATOM	1282	0	MET	A	161	-16.053	125.361	-24.187	I.00	44.66	0
ATOM	1283	CB	MET	A	161	-16.801	128.564	-24.325	1.00	47.06	C
ATOM	1284	CG	MET	A	161	-17.881	129.511	-24.836	1.00	51.65	C
ATOM	1285	SD	MET	A	161	-17.237	131.171	-25.174	I.00	56.22	S
ATOM	1286	CE	MET	A	161	-18.741	132.013	-25.605	1.00	61.27	C
ATOM	1287	N	ILE	A	162	-15.449	126.500	-22.340	1.00	40.27	N
ATOM	1288	CA	ILE	A	162	-14.329	125.634	-22.083	I.00	52.31	C
ATOM	1289	C	ILE	A	162	-14.837	124.246	-21.701	1.00	46.07	C
ATOM	1290	O	ILE	A	162	-14.340	123.255	-22.182	1.00	42.77	0
ATOM	1291	CB	ILE	A	162	-13.412	126.178	-20.963	1.00	48.29	C
ATOM	1292	CGI	ILE	A	162	-12.700	127.459	-21.396	1.00	48.89	C
ATOM	1293	CG2	ILE	A	162	-12.405	125.147	-20.586	1.00	47.29	C
ATOM	1294	CD1	ILE	A	162	-12.033	127.371	-22.712	1.00	52.36	C
ATOM	1295	N	LYS	A	163	-15.841	124.211	-20.833	I.00	44.86	N
ATOM	1296	CA	LYS	A	163	-16.310	122.984	-20.230	1.00	40.12	C
ATOM	1297	C	LYS	A	163	-17.112	122.173	-21.222	1.00	46.62	C
ATOM	1298	0	LYS	A	163	-17.129	120.938	-21.140	I.00	42.88	0
ATOM	1299	CB	LYS	A	163	-17.148	123.260	-18.984	1.00	36.96	C
ATOM	1300	CG	LYS	A	163	-17.603	122.007	-18.245	1.00	40.81	C
ATOM	1301	CD	LYS	A	163	-18.558	122.346	-17.125	I.00	39.52	C
ATOM	1302	CE	LYS	A	163	-18.560	121.288	-16.024	1.00	37.42	C
ATOM	1303	NZ	LYS	A	163	-19.487	121.660	-14.906	1.00	38.57	N
ATOM	1304	N	PHE	A	164	-17.732	122.860	-22.186	1.00	41.79	N
ATOM	1305	CA	PHE	A	164	-18.472	122.178	-23.245	1.00	40.99	C
ATOM	1306	C	PHE	A	164	-18.000	122.607	-24.638	1.00	46.13	C
ATOM	1307	O	PHE	A	164	-18.696	123.356	-25.342	1.00	47.85	0
ATOM	1308	CB	PHE	A	164	-19.964	122.448	-23.073	I.00	45.20	C
ATOM	1309	CG	PHE	A	164	-20.484	122.105	-21.702	1.00	42.52	C
ATOM	1310	CD1	PHE	A	164	-20.526	120.791	-21.277	1.00	28.69	C
ATOM	1311	CD2	PHE	A	164	-20.943	123.108	-20.844	I.00	34.60	C
ATOM	1312	CE1	PHE	A	164	-21.006	120.485	-20.022	1.00	37.41	C
ATOM	1313	CE2	PHE	A	164	-21.413	122.805	-19.581	1.00	30.69	C
ATOM	1314	CZ	PHE	A	164	-21.460	121.523	-19.165	I.00	34.86	C
ATOM	1315	O	ARG	A	165	-15.758	122.942	-28.415	1.00	44.58	0
ATOM	1316	N	AP.G	A	165	-16.839	122.101	-25.057	1.00	43.89	N
ATOM	1317	CA	ARG	A	165	-16.061	122.790	-26.079	I.00	39.10	C
ATOM	1318	C	ARG	A	165	-16.312	122.356	-27.503	1.00	38.80	C
ATOM	1319	CB	AP.G	A	165	-14.573	122.661	-25.752	1.00	42.79	C
ATOM	1320	CG	ARG	A	165	-14.094	121.213	-25.601	1.00	51.72	C
ATOM	1321	CD	ARG	A	165	-12.628	121.170	-25.219	1.00	52.06	C
ATOM	1322	NE	AP.G	A	165	-12.160	119.813	-25.027	1.00	49.01	N
ATOM	1323	CZ	ARG	A	165	-10.879	119.441	-25.042	1.00	50.35	C
ATOM	1324	NH1	ARG	A	165	-9.916	120.323	-25.260	I.00	52.65	N

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ATOM  1325  NH2  ARG  A  165   -10.569  118.174  -24.859  1.00  46.16  N
ATOM  1326  O    GLY  A  166   -15.317  119.758  -28.997  1.00  45.03  O
ATOM  1327  N    GLY  A  166   -17.153  121.355  -27.717  1.00  40.73  N
ATOM  1328  CA   GLY  A  166   -17.427  120.894  -29.073  1.00  40.92  C
ATOM  1329  C    GLY  A  166   -16.341  119.983  -29.634  I.00  44.56  C
ATOM  1330  O    HIS  A  167   -14.197  119.961  -32.281  1.00  49.73  O
ATOM  1331  N    HIS  A  167   -16.538  119.480  -30.839  1.00  38.69  N
ATOM  1332  CA.  HIS  A  167   -15.715  118.383  -31.262  I.00  47.30  C
ATOM  1333  C    HIS  A  167   -14.455  118.788  -32.031  1.00  48.38  C
ATOM  1334  CB   HIS  A  167   -16.555  117.396  -32.059  1.00  42.00  C
ATOM  1335  CG   HIS  A  167   -16.945  117.864  -33.424  I.00  53.00  C
ATOM  1336  ND1  HIS  A  167   -16.022  118.178  -34.402  1.00  51.37  N
ATOM  1337  CD2  HIS  A  167   -18.166  118.007  -33.996  1.00  47.40  C
ATOM  1338  CE1  HIS  A  167   -16.658  118.516  -35.512  1.00  50.00  C
ATOM  1339  NE2  HIS  A  167   -17.959  118.417  -35.292  1.00  52.73  N
ATOM  1340  O    PHE  A  168   -11.409  116.212  -34.350  1.00  54.57  O
ATOM  1341  N    PHE  A  168   -13.645  117.784  -32.332  1.00  45.25  N
ATOM  1342  CA.  PHE  A  168   -12.357  117.957  -32.998  I.00  46.93  C
ATOM  1343  C    PHE  A  168   -12.292  117.065  -34.236  1.00  48.23  C
ATOM  1344  CB   PHE  A  168   -11.215  117.607  -32.038  1.00  47.04  C
ATOM  1345  CG   PHE  A  168   -11.052  118.573  -30.933  I.00  46.58  C
ATOM  1346  CD2  PHE  A  168   -10.059  119.527  -30.986  1.00  45.56  C
ATOM  1347  CD1  PHE  A  168   -11.931  118.570  -29.851  1.00  48.42  C
ATOM  1348  CE2  PHE  A  168    -9.931  120.456  -29.961  I.00  51.49  C
ATOM  1349  CE1  PHE  A  168   -11.807  119.493  -28.833  1.00  45.33  C
ATOM  1350  CZ   PHE  A  168   -10.801  120.437  -28.888  1.00  49.16  C
ATOM  1351  O    LEU  A  169   -12.681  116.484  -38.582  I.00  54.77  0
ATOM  1352  N    LEU  A  169   -13.244  117.228  -35.136  1.00  43.09  N
ATOM  1353  CA   LEU  A  169   -13.343  116.350  -36.271  1.00  48.70  C
ATOM  1354  C    LEU  A  169   -12.920  117.092  -37.529  1.00  51.47  C
ATOM  1355  CB   LEU  A  169   -14.760  115.794  -36.404  1.00  44.06  C
ATOM  1356  CG   LEU  A  169   -15.208  114.818  -35.304  1.00  50.03  C
ATOM  1357  CD1  LEU  A  169   -16.620  114.342  -35.563  1.00  45.22  C
ATOM  1358  CD2  LEU  A  169   -14.264  113.610  -35.144  I.00  45.57  C
ATOM  1359  O    ILE  A  170   -11.021  120.751  -37.306  1.00  59.00  0
ATOM  1360  N    ILE  A  170   -12.812  118.409  -37.410  1.00  53.31  N
ATOM  1361  CA.  ILE  A  170   -12.363  119.237  -38.515  I.00  54.38  C
ATOM  1362  C    ILE  A  170   -11.061  119.871  -38.150  1.00  58.72  C
ATOM  1363  CB   ILE  A  170   -13.345  120.343  -38.857  1.00  55.42  C
ATOM  1364  CGI  ILE  A  170   -14.681  119.749  -39.282  I.00  53.94  C
ATOM  1365  CG2  ILE  A  170   -12.777  121.209  -39.950  1.00  54.17  C
ATOM  1366  GDI  ILE  A  170   -15.821  120.672  -39.011  1.00  56.20  C
ATOM  1367  O    GLU  A  171    -9.210  121.359  -40.458  1.00  65.13  0
ATOM  1368  N    GLU  A  171    -9.992  119.403  -38.777  1.00  63.37  N
ATOM  1369  CA   GLU  A  171    -8.682  120.001  -38.595  1.00  6.3.31  C
ATOM  1370  C    GLU  A  171    -8.688  121.297  -39.356  1.00  61.88  C
ATOM  1371  CB   GLU  A  171    -7.561  119.070  -39.096  I.00  61.43  C
ATOM  1372  O    GLY  A  172    -9.883  124.293  -38.244  1.00  73.05  0
ATOM  1373  N    GLY  A  172    -8.125  122.345  -38.779  1.00  62.79  N
ATOM  1374  CA.  GLY  A  172    -8.018  123.583  -39.519  I.00  61.56  C
ATOM  1375  C    GLY  A  172    -9.010  124.600  -39.043  1.00  69.00  C
ATOM  1376  O    ASP  A  173   -10.818  126.411  -41.265  1.00  75.57  0
ATOM  1377  N    ASP  A  173    -8.867  125.827  -39.518  I.00  72.97  N
ATOM  1378  CA   ASP  A  173    -9.806  126.876  -39.161  1.00  75.72  C
ATOM  1379  C    ASP  A  173   -10.957  126.885  -40.145  1.00  73.15  C
ATOM  1380  CB   ASP  A  173    -9.108  128.230  -39.140  I.00  78.72  C
ATOM  1381  CG   ASP  A  173    -7.755  128.170  -38.465  1.00  85.85  C
ATOM  1382  OD2  ASP  A  173    -6.832  128.879  -38.926  1.00  94.13  0
ATOM  1383  OD1  ASP  A  173    -7.615  127.405  -37.482  1.00  80.17  0
ATOM  1384  O    LEU  A  174   -13.263  129.853  -39.819  1.00  81.69  0
ATOM  1385  N    LEU  A  174   -12.103  127.402  -39.730  1.00  75.39  N
ATOM  1386  CA   LEU  A  174   -13.172  127.639  -40.682  1.00  76.83  C
ATOM  1387  C    LEU  A  174   -13.376  129.130  -40.803  I.00  78.46  C
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ATOM  1388  CB   LEU  A  174    -14 .463   126..935   -40 ..267   1 ,00  76..67   C
ATOM  1389  CG   LEU  A  174    --14 ,997  127 .119   -38.,845    1 ,00  79..65   C
ATOM  1390  GD1  LEU  A  174    -15..925   128 ,343   -38.. 721   1 ,00  81 ,50   C
ATOM  1391  CD2  LEU  A  174    -15..711   125 ,839   -38.,405    1 ,00  72 .25   C
ATOM  1392  O    ASM  A  175    -16 ,235   130. 774   -42.,326    1 ,00  83.,87   0
ATOM  1393  N    ASN  A  175    -13..659   129 ,597   -42 .012    1 ,00  81 ,52   N
ATOM  1394  CA   ASN  A  175    -13..866   131.,022   -42.. 209   1 ,00  84 ,75   C
ATOM  1395  C    ASM  A  175    -15.,290   131. 394   -41 ,848    1 ,00  82 ,9.1   C
ATOM  1396  CB   ASN  A  175    -13.,550   131.,435   -43 ,646    1 ,00  83..43   C
ATOM  1397  CG   ASN  A  175    -13.. 122  132.,885   -43 .748    1 ,00  85,.48   C
ATOM  1398  OD1  ASN  A  175    -13.,688   133.. 750  -43 ,086    1 ,00  85..69   0
ATOM  1399  ND2  ASN  A  175    -12.,098   133.,153   -44 ,556    1 ,00  85..88   N
ATOM  1400  O    PRO  A  176    -18. 716   133.,534   -41 .868    1 ,00  83 ,25   O
ATOM  1401  N    PRO  A  176    -15.,446   132.,383   -40 ,960    1 ,00  84 .07   N
ATOM  1402  CA   FRO  A  176    -16.,769   132.. 910  -40 ,597    1 ,00  86..28   C
ATOM  1403  C    PRO  A  176    -17 .477   1.33.,582  -41 .786    1 ,00  88,.71   C
ATOM  1404  CB   PRO  A  176    -16.,451   133.,931   -39 ,497    1 ,00  83..46   C
ATOM  1405  CG   PRO  A  176    -15.,143   133. 491   -38.,937    1 ,00  90.,13   C
ATOM  1406  CD   PRO  A  176    -14 ..37 9  1.32.,923  -40 .102    1 ,00  85,.60   C
ATOM  1407  O    ASP  A  177    -19..055   134.,593   -45 ..316   1 ,00  82 ,55   0
ATOM  1408  N    ASP  A  177    -16 ,684   134. 180   -42.,683    1 ,00  88.,45   N
ATOM  1409  CA   ASP  A  177    -17 .177   134.,909   -43 ,862    1 ,00  87 .54   C
ATOM  1410  C    ASP  A  177    -18..094   134.,078   -44 .752    1 ,00  84 ,56   C
ATOM  1411  CB   ASP  A  177    -16.,005   135.. 418  -44 ,717    1 ,00  87 .93   C
ATOM  1412  CG   ASP  A  177    -15..258   136.,575   -44 ,076    1 ,00  91 .02   C
ATOM  1413  OD1  ASP  A  177    -15. 903   137 ,406    -43. 395    1 ,00  94 ,18   0
ATOM  1414  OD2  ASP  A  177    -14 ,022   136 .654   -44 ,267    1 ,00  89..30   0
ATOM  1415  O    ASN  A  178    -19.,801   130.. 294  -44 ,592    1 ,00  72 .37   0
ATOM  1416  N    ASN  A  178    -17 .780   132.,794   -44 .883    1 ,00  83 ,61   N
ATOM  1417  CA   ASN  A  178    -18.,499   131.,925   -45 ,798    1 ,00  79..13   C
ATOM  1418  C    ASN  A  178    -19.,792   131.. 367  -45 ,209    1 ,00  80..53   C
ATOM  1419  CB   ASN  A  178    -17 .576   1.30.,798  -46.. 247   1 ,00  75,.70   C
ATOM  1420  CG   ASN  A  178    -16.,334   131.,324   -46 ,945    1 ,00  80..91   C
ATOM  1421  OD1  ASN  A  178    -16 ,383   132. 352   -47 ,627    1 ,00  84 ,39   0
ATOM  1422  ND2  ASN  A  178    -15.. 215  1.30.,637  -46.. 768   1 ,00  78,.54   N
ATOM  1423  O    SER  A  179    -24 .098   130.,604   -45 .733    1 ,00  87 ,69   O
ATOM  1424  N    SER  A  179    -20.,884   132. 105   -45 ,420    1 ,00  78.,11   N
ATOM  1425  CA   SER  A  179    -22.,181   131.,751   -44 ,852    1 ,00  77 .85   C
ATOM  1426  C    SER  A  179    -23 .227   131.,461   -45. 918    1 ,00  82 ,08   C
ATOM  1427  CB   SER  A  179    -22.,674   132..870   -43 ,939    1 ,00  73..38   C
ATOM  1428  OG   SER  A  179    -22.,516   134..124   -44 ,571    1 ,00  74 .46   O
ATOM  1429  N    ASP  A  180    -23 .142   132.,179   -47 .033    1 ,00  8.1 ,85   N
ATOM  1430  CA   ASP  A  180    -24 ..127   132.,054   -48 ,111    1 ,00  84 .94   C
ATOM  1431  C    ASP  A  180    -23 ,928   130.. 767  -48 ,913    1 ,00  82 .97   C
ATOM  1432  O    ASP  A  180    -23 ..040   1.30.,695  -49 .756    1 ,00  84 ,62   O
ATOM  1433  CB   ASP  A  180    -24 ,038   133.,266   -49 ,047    1 ,00  85..00   C
ATOM  1434  CG   ASP  A  180    -25 ,362   133. 598   -49.,718    1 ,00  85.,68   C
ATOM  1435  OD1  ASP  A  180    -26 .269   1.32.,734  -49 .760    1 ,00  85,.84   0
ATOM  1436  OD2  ASP  A  180    -25 .486   134.,741   -50.. 210   1 ,00  92 ,06   0
ATOM  1437  N    VAL  A  181    -24.,757   129. 759   -48 ,663    1 ,00  82 ,94   N
ATOM  1438  CA   VAL  A  181    -24 ,694   128.,519   -49 ,436    1 ,00  75..45   C
ATOM  1439  C    VAL  A  181    -24 .950   128 ,790   -50.. 922   1 ,00  80,.94   C
ATOM  1440  0    VAL  A  181    -24.,505   128 .039   -51.,785    1 ,00  76..88   0
ATOM  1441  CB   VAL  A  181    -25 ,705   127 ,479   -48 ,915    1 ,00  73..22   C
ATOM  1442  CGI  VAL  A  181    -25. 507   126 ,136   -49. 601    1 ,00  75 ,01   C
ATOM  1443  CG2  VAL  A  181    -25 ,564   127 ..321  -47 ,413    1 ,00  77 .34   C
ATOM  1444  N    ASP  A  182    -25 ,640   129..887   -51.,216    1 ,00  80..36   N
ATOM  1445  CA   ASP  A  182    -25. 963   130.,233   -52. 592    1 ,00  78 ,68   C
ATOM  1446  C    ASP  A  182    -24 ,839   130.,963   -53.,325    1 ,00  79..15   C
ATOM  1447  O    ASP  A  182    -24 ,401   130.. 519  -54.,385    1 ,00  79..83   0
ATOM  1448  CB   ASP  A  182    -27 .228   131.,084   -52.. 628   1 ,00  82 ,51   C
ATOM  1449  CG   ASP  A  182    -28 ,454   130.,319   -52.,185    1 ,00  87 .21   C
ATOM  1450  OD1  ASP  A  182    -28 ,557   129. 115   -52.,506    1 ,00  87 ,25   0
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ATOM    1451  OD2  ASP  A  182     -29..320  130.,925  -51.,515   1.00  93..36          O
ATOM    1452  N    LYS  A  183     --24,380  132..086  -52.,771   1,00  82.24           N
ATOM    1453  CA   LYS  A  183     -23..384  1.32.,924  -53..444  1,00  80,.77          C
ATOM    1454  C    LYS  A  183     -22..075  132.,169  -53.,597   1.00  79..27          C
ATOM    1455  O    LYS  A  183     -2.1.,222  132. 533  -54 ,409   1,00  78.,52          0
ATOM    1456  CB   LYS  A  183     -23..153  1.34.,231  -52..680   1,00  77,52           C
ATOM    1457  N    LEU  A  184     -21 .933  131.,114  -52..802   1,00  79,,22          N
ATOM    1458  CA.  LEU  A  184     -20.,781  130. 240  -52.,872   1,00  78.,03          C
ATOM    1459  C    LEU  A  184     -21..042  129.,110  -53.,842   1,00  79..32          C
ATOM    1460  O    LEU  A  184     -20..159  128,760  -54..625   1,00  79,.59          O
ATOM    1461  CB   LEU  A  184     -20.,434  129..697  -51.,495   I,00  76..94          C
ATOM    1462  CG   LEU  A  184     -19..989  130.,814  -50.,556   1,00  78..14          C
ATOM    1463  GDI  LEU  A  184     -19. 450  130.,234  -49. 266   1,00  76,52           C
ATOM    1464  CD2  LEU  A  184     -18..961  131.,709  -51.,232   1.00  72.26           C
ATOM    1465  N    PHE  A  185     -22.,249  128..546  -53.,801   1,00  78..52          N
ATOM    1466  CA   PHE  A  185     -22..627  127,525  -54..775   1,00  75,.43          C
ATOM    1467  C    PHE  A  185     -22.,478  128.,076  -56,181   1.00  77.06           C
ATOM    1468  0    PHE  A  185     -2.1.,874  127 .443  -57 ,046   1,00  74,18           0
ATOM    1469  CB   PHE  A  185     -24..058  127,045  -54..563   1,00  74,00           C
ATOM    1470  CG   PHE  A  185     -24.522  126.,056  -55..593   1,00  73,.70          C
ATOM    1471  CD1  PHE  A  185     -24.,247  124 .707  -55.,448   1,00  68.,81          C
ATOM    1472  CD2  PHE  A  185     -25,236  126.,473  -56,704    1,00  72.27           C
ATOM    1473  CE1  PHE  A  185     -24.672  123,796   -56.391    1,00  69,.23          C
ATOM    1474  CE2  PHE  A  185     -25,661  125..569  -57.,640   I,00  72.51           C
ATOM    1475  CZ   PHE  A  185     -25,378  124,226   -57.,486   1,00  71.24           C
ATOM    1476  N    ILE  A  186     -23 .028  129,266   -56. 402   1,00  76,29           N
ATOM    1477  CA   ILE  A  186     -22.,947  129..896  -57.,711   I,00  76..61          C
ATOM    1478  C    ILE  A  186     -21.,489  130..217  -58.,032   1,00  79..71          C
ATOM    1479  O    ILE  A  186     -21 .031  130.,009  -59. 170   1,00  77,70           0
ATOM    1480  CB   ILE  A  186     -23,819  131.,164  -57.,785   1.00  80..95          C
ATOM    1481  CGI  ILE  A  186     -25,196  130..825  -58.,364   1,00  78..12          C
ATOM    1482  CG2  ILE  A  186     -23..159  1.32.,228  -58..655   1,00  81,23           C
ATOM    1483  GDI  ILE  A  186     -25,960  129.,751  -57.,620   1.00  76..51          C
ATOM    1484  N    GLN  A  187     -20.,752  130. 681  -57 ,021   1,00  77,28           N
ATOM    1485  CA   GLN  A  187     -19..314  1.30.,902  -57..168   1,00  77,29           C
ATOM    1486  C    GLN  A  187     -18..602  129.,585  -57..474   1,00  75,.80          C
ATOM    1487  0    GLN  A  187     -17 ,559  129. 579  -58.,113   1,00  77,12           0
ATOM    1488  CB   GLN  A  187     -18.,718  131.,548  -55.,915   1,00  77.58           C
ATOM    1489  N    LEU  A  188     -19. 172  128,467   -57. 035   1,00  73,93           N
ATOM    1490  CA   LEU  A  188     -18.,586  127.162   -57.,343   I,00  75..35          C
ATOM    1491  C    LEU  A  188     -18.,884  126..742  -58.,778   1,00  73..83          C
ATOM    1492  O    LEU  A  188     -17 .988  126,304   -59. 509   1,00  75,19           O
ATOM    1493  CB   LEU  A  188     -19.,091  126.,088  -56,377    1.00  68..65          C
ATOM    1494  CG   LEU  A  188     -18.,761  124 .656  -56,813    1,00  70..77          C
ATOM    1495  GD1  LEU  A  188     -17.246  124,422   -56.871    1,00  63,.71          C
ATOM    1496  CD2  LEU  A  188     -19.,440  123.,645  -55,901    1.00  70..89          C
ATOM    1497  N    VAL  A  189     -20.,150  126. 870  -59.,164   1,00  75.,20          N
ATOM    1498  CA   VAL  A  189     -20..607  126,503   -60..498   1,00  74,61           C
ATOM    1499  C    VAL  A  189     -19..922  127,334   -61..579   1,00  74,69           C
ATOM    1500  0    VAL  A  189     -19,556  126. 825  -62.,637   1,00  72,3.1          0
ATOM    1501  CB   VAL  A  189     -22.,119  126.,670  -60.,619   1,00  73..13          C
ATOM    1502  CGI  VAL  A  189     —22.581  126.,288  -62..001   1,00  73,.64          C
ATOM    1503  CG2  VAL  A  189     -22.,803  125..817  -59,593    I,00  77.15           C
ATOM    1504  N    GLN  A  190     -19.,732  128.,616  -61.,305   1,00  77.93           N
ATOM    1505  CA   GLN  A  190     -19. 091  129,491   -62. 272   1,00  80,01           C
ATOM    1506  C    GLN  A  190     -17,611  129..164  -62.,512   I,00  80..58          C
ATOM    1507  O    GLN  A  190     -17,178  129..095  -63.,659   1,00  84.60           0
ATOM    1508  CB   GLN  A  190     -19. 253  130.,941  -61. 839   1,00  82,12           C
ATOM    1509  CG   GLN  A  190     -20,639  131.,483  -62.,145   1.00  84.25           C
ATOM    1510  CD   GLN  A  190     -20,861  132..848  -61.,560   1,00  81.20           C
ATOM    1511  OE1  GLN  A  190     -19.999  1.33.,373  -60..856   1,00  80,.63          0
ATOM    1512  NE2  GLN  A  190     -22..023  133.,434  -61.,838   1.00  89..99          N
ATOM    1513  N    TH.R A  191     -16,835  128. 963  -61.,452   1,00  79.,39          N
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ATOM    1514   CA    THR  A  191       -15.431   128.598  -61.624    1.00  78.77                C
ATOM    1515   C     THR  A  191       -15.288   127.283  -62.384    1.00  80.05                C
ATOM    1516   O     THR  A  191       -14..317  127.070  -63.116    1.00  81.67                0
ATOM    1517   CB    THR  A  191       -14.715   128.449  -60.286    1.00  82.85                C
ATOM    1518   OG1   THR  A  191       -15.253   127..315 -59.584    1.00  85.12                0
ATOM    1519   CG2   THR  A  191       -14.865   129.726  -59.455    1.00  73.87                C
ATOM    1520   N     TYR  A  192       -16.251   126.394  -62.180    1.00  74.66                N
ATOM    1521   CA.   TYR  A  192       -16.327   125.170  -62.955    1.00  75.29                C
ATOM    1522   C     TYR  A  192       -16.518   125.504  -64.433    1.00  80.55                C
ATOM    1523   O     TYR  A  192       -15.746   125.057  -65.292    1.00  81.37                0
ATOM    1524   CB    TYR  A  192       -17.468   124..300 -62.452    1.00  73..34                C
ATOM    1525   CG    TYR  A  192       -17.623   122.996  -63.180    1.00  70.83                C
ATOM    1526   GDI   TYR  A  192       -18.503   122.873  -64.243    1.00  75.96                C
ATOM    1527   CD2   TYR  A  192       -16.899   121.880  -62.795    1.00  74.30                C
ATOM    1528   CEl   TYR  A  192       -18.651   121.672  -64.906    1.00  75.01                C
ATOM    152 9  CE2   TYR  A  192       -17.040   120.675  -63.449    1.00  70.88                C
ATOM    1530   CZ    TYR  A  192       -17.918   120.579  -64.503    1.00  72.15                C
ATOM    1531   OH    TYR  A  192       -18.064   119..382 -65.154    1.00  71.57                0
ATOM    1532   N     ASN  A  193       -17.545   126.303  -64.714    1.00  78.56                N
ATOM    1533   CA    ASN  A  193       -17.845   126.737  -66.073    1.00  79.43                C
ATOM    1534   C     ASM  A  193       -16.688   127.519  -66.686    1.00  76.55                C
ATOM    1535   O     ASN  A  193       -16.453   127.446  -67.883    1.00  81.05                0
ATOM    1536   CB    ASN  A  193       -19.131   127.578  -66.102    1.00  76.65                C
ATOM    1537   CG    ASN  A  193       -20.380   126.746  -65.866    1.00  77.66                C
ATOM    1538   OD1   ASN  A  193       -20.358   125.521  -66.001    1.00  80.84                0
ATOM    1539   ND2   ASN  A  193       -21.478   127.408  -65.518    1.00  76.39                N
ATOM    1540   N     GLN  A  194       -15.955   128.252  -65.864    1.00  73.84                N
ATOM    1541   CA    GLN  A  194       -14.780   128.955  -66.351    1.00  78.71                C
ATOM    1542   C     GLN  A  194       -13.739   127.946  -66.842    1.00  84.17                C
ATOM    1543   O     GLN  A  194       -12.950   128.230  -67.748    1.00  85.83                0
ATOM    1544   CB    GLN  A  194       -14.191   129.851  -65.257    1.00  81.16                C
ATOM    1545   CG    GLN  A  194       -12.915   1.30.561 -65.664    1.00  81.73                C
ATOM    1546   CD    GLN  A  194       -13.080   131.327  -66.962    1.00  88.51                C
ATOM    1547   OE1   GLN  A  194       -12.354   131.097  -67.933    1.00  85.22                0
ATOM    1548   NE2   GLN  A  194       -14.047   1.32.241 -66.988    1.00  90.21                N
ATOM    1549   N     LEU  A  195       -13.751   126.759  -66.249    1.00  78.40                N
ATOM    1550   CA.   LEU  A  195       -12.774   125.745  -66.587    1.00  78.29                C
ATOM    1551   C     LEU  A  195       -13.246   124.914  -67.753    1.00  78.20                C
ATOM    1552   O     LEU  A  195       -12.442   124.361  -68.498    1.00  79.04                O
ATOM    1553   CB    LEU  A  195       -12.500   124.849  -65.386    1.00  80.42                C
ATOM    1554   CG    LEU  A  195       -11.122   124.992  -64.765    1.00  74.33                C
ATOM    1555   GDI   LEU  A  195       -11.201   124.563  -63..329   1.00  71.85                C
ATOM    1556   CD2   LEU  A  195       -10.138   124.135  -65.535    1.00  77.57                C
ATOM    1557   N     PHE  A  196       -14.558   124.828  -67.913    1.00  78.62                N
ATOM    1558   CA    PHE  A  196       -15.131   123.968  -68.937    1.00  80.22                C
ATOM    1559   C     PHE  A  196       -16.212   124.696  -69.736    1.00  82.91                C
ATOM    1560   0     PHE  A  196       -17.402   124.583  -69.443    1.00  82.51                0
ATOM    1561   CB    PHE  A  196       -15.684   122.687  -68.293    1.00  82.66                C
ATOM    1562   CG    PHE  A  196       -14.676   121.963  -67.426    1.00  79.65                C
ATOM    1563   CD1   PHE  A  196       -13.797   121.046  -67.977    1.00  76.50                C
ATOM    1564   CD2   PHE  A  196       -14.600   122.216  -66.064    1.00  81.56                C
ATOM    1565   CEl   PHE  A  196       -12.867   120.392  -67.184    1.00  79.24                C
ATOM    1566   CE2   PHE  A  196       -13.669   121.569  -65.269    1.00  77.44                C
ATOM    1567   CZ    PHE  A  196       -12.805   120.656  -65.831    1.00  78.15                C
ATOM    1568   O     GLU  A  197       -18.750   125.428  -72.626    1.00  89.00                0
ATOM    1569   N     GLU  A  197       -15.777   125.454  -70.739    1.00  83.48                N
ATOM    1570   CA    GLU  A  197       -16.683   126.157  -71.635    1.00  80.82                C
ATOM    1571   C     GLU  A  197       -17.563   125.179  -72.422    1.00  87.62                C
ATOM    1572   CB    GLU  A  197       -15.895   127.049  -72.597    1.00  74.74                C
ATOM    157 3  O     GLU  A  198       -19.953   122.348  -73.664    1.00  89.14                0
ATOM    1574   N     GLU  A  198       -16.983   124.059  -72.844    1.00  85.00                N
ATOM    1575   CA    GLU  A  198       -17.676   123.105  -73.707    1.00  85.35                C
ATOM    157 6  C     GLU  A  198       -18.896   122.459  -73.050    1.00  87.95                C
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ATOM   1577  CB   GLU  A  198   -16.706  122.013  -74.166  1.00  88.67   C
ATOM   1578  O    ASM  A  199   --20,036  121.658  -68,729  1,00  80.89   O
ATOM   1579  N    ASN  A  199   -18.751  122,022  -71.807  1,00  90,94   N
ATOM   1580  CA   ASN  A  199   -19.864  121.395  -71.097  1.00  91.06   C
ATOM   1581  C    ASM  A  199   -20,243  122.156  -69,834  1,00  87,11   C
ATOM   1582  CB   ASN  A  199   -19.519  119,953  -70.728  1,00  89,40   C
ATOM   1583  CG   ASN  A  199   -19.092  119,143  -71.916  1,00  92,91   C
ATOM   1584  OD1  ASN  A  199   -19,886  118.395  -72,486  1,00101,03   0
ATOM   1585  ND2  ASN  A  199   -17.831  119.287  -72.310  1,00  92.78   N
ATOM   1586  O    PRO  A  200   -22.509  122,412  -68.022  1,00  84,54   O
ATOM   1587  N    PRO  A  200   -20,819  123..358  -69,991  I,00  88.09   N
ATOM   1588  CA   PRO  A  200   -21.097  124.193  -68.818  1,00  86.83   C
ATOM   1589  C    PRO  A  200   -22.020  123,525  -67.804  1,00  85,44   C
ATOM   1590  CB   PRO  A  200   -21,773  125.434  -69.419  1.00  79.32   C
ATOM   1591  CG   FRO  A  200   -21,361  125.442  -70,846  1,00  81.57   C
ATOM   1592  CD   PRO  A  200   -21.271  124,003  -71.236  1,00  83,74   C
ATOM   1593  N    ILE  A  201   -22,241  124.202  -66.687  1.00  82.57   N
ATOM   1594  CA.  ILE  A  201   -23,285  123.786  -65,772  1,00  81,15   C
ATOM   1595  C    ILE  A  201   -24.151  125,000  -65.487  1,00  79,98   C
ATOM   1596  O    ILE  A  201   -23.646  126,082  -65.177  1,00  77,98   O
ATOM   1597  CB   ILE  A  201   -22,719  123.178  -64,478  1,00  80,54   C
ATOM   1598  CGI  ILE  A  201   -22.145  121.789  -64.773  1,00  84.66   C
ATOM   1599  CG2  ILE  A  201   -23.799  123,073  -63.424  1,00  80,04   C
ATOM   1600  CD1  ILE  A  201   -21,809  120.958  -63,538  I,00  76.90   C
ATOM   1601  N    ASN  A  202   -25.458  124.820  -65.645  1,00  82.67   N
ATOM   1602  CA   ASN  A  202   -26.408  125,902  -65.466  1,00  76,09   C
ATOM   1603  C    ASN  A  202   -27,225  125.667  -64,189  I,00  79.39   C
ATOM   1604  O    ASN  A  202   -27,945  124.673  -64,050  1,00  82.28   0
ATOM   1605  CB   ASN  A  202   -27.278  126,043  -66.732  1,00  83,28   C
ATOM   1606  CG   ASN  A  202   -28.754  125.762  -66.492  1.00  85.31   C
ATOM   1607  OD1  ASN  A  202   -29,478  126.590  -65.927  1,00  71.63   0
ATOM   1608  ND2  ASK  A  202   -29.211  124,595  -66.946  1,00  87,73   N
ATOM   1609  N    ALA  A  203   -27.070  126.581  -63..237  1.00  79.24   N
ATOM   1610  CA.  ALA  A  203   -27,642  126.405  -61,911  1,00  80,92   C
ATOM   1611  C    ALA  A  203   -28.828  127,318  -61.658  1,00  81,11   C
ATOM   1612  O    ALA  A  203   -29.160  127,598  -60.505  1,00  83,17   O
ATOM   1613  CB   ALA  A  203   -26,579  126.639  -60,859  1,00  84,27   C
ATOM   1614  O    SER  A  204   -31.926  128.904  -60.677  1,00  84.71   0
ATOM   1615  N    SER  A  204   -29.453  127,778  -62.738  1,00  84,54   N
ATOM   1616  CA   SER  A  204   -.30,583  128.705  -62,669  I,00  80.14   C
ATOM   1617  C    SER  A  204   -31,648  128.238  -61,683  1,00  82.39   C
ATOM   1618  CB   SER  A  204   -31.198  128,881  -64.064  1,00  77,52   C
ATOM   1619  OG   SER  A  204   -32,321  129.746  -64.053  1.00  75.40   0
ATOM   1620  O    GLY  A  205   -33,578  126.700  -58,795  1,00  89.28   0
ATOM   1621  N    GLY  A  205   -32,225  127,078  -61.967  1,00  82,38   N
ATOM   1622  CA   GLY  A  205   -33..310  126.562  -61.156  1.00  89.16   C
ATOM   1623  C    GLY  A  205   -32,940  126.216  -59,727  1,00  88,07   C
ATOM   1624  O    VAL  A  206   -30.764  126,569  -56.956  1,00  82,22   O
ATOM   1625  N    VAL  A  206   -31.899  125,400  -59.566  1,00  88,85   N
ATOM   1626  CA.  VAL  A  206   -.31,584  124.737  -58,297  1,00  89,21   C
ATOM   1627  C    VAL  A  206   -31.565  125.633  -57.064  1,00  88.62   C
ATOM   1628  CB   VAL  A  206   -30.216  124,023  -58.359  1,00  87,03   C
ATOM   1629  CGI  VAL  A  206   -.30,323  122.726  -59,125  I,00  88.74   C
ATOM   1630  CG2  VAL  A  206   -29.178  124.919  -58.987  1,00  88.82   C
ATOM   1631  N    ASP  A  207   -32.470  125,326  -56.140  1,00  88,10   N
ATOM   1632  CA   ASP  A  207   -.32 ,422  125.879  -54,798  I,00  87.94   C
ATOM   1633  C    ASP  A  207   -31,373  125.107  -53,989  1,00  84.54   C
ATOM   1634  O    ASP  A  207   -31.698  124,190  -53.237  1,00  81,57   O
ATOM   1635  CB   ASP  A  207   -33..797  125.805  -54.131  1.00  84.84   C
ATOM   1636  CG   ASP  A  207   -33,901  126.694  -52 ,913  1,00  85.80   C
ATOM   1637  OD1  ASP  A  207   -32,859  126,947  -52 .266  1,00  86,46   0
ATOM   1638  OD2  ASP  A  207   -35.025  127.138  -52 ,592  1.00  93.25   0
ATOM   1639  N    ALA  A  208   -.30,112  125.488  -54,161  1,00  83,47   N
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ATOM	1640	CA	ALA	A	208	-29.001	124.818	-53.499	1.00	82.85	C
ATOM	1641	C	ALA	A	208	--29.102	124.889	-51.973	1.00	82.86	C
ATOM	1642	O	ALA	A	208	-29.066	123.853	-51.304	1.00	80.94	0
ATOM	1643	CB	ALA	A	208	-27.676	125.411	-53.968	1.00	77.52	C
ATOM	1644	N	LYS	A	209	-29.226	126.100	-51.431	I.00	80.66	N
ATOM	1645	CA	LYS	A	209	-29.310	126.277	-49.982	1.00	82.60	C
ATOM	1646	C	LYS	A	209	-30.387	125.387	-49.380	1.00	80.99	C
ATOM	1647	0	LYS	A	209	-30.190	124.796	-48.325	I.00	80.67	0
ATOM	1648	CB	LYS	A	209	-29.581	127.737	-49.619	1.00	85.12	C
ATOM	1649	CG	LYS	A	209	-30.063	127.917	-48.191	1.00	85.05	C
ATOM	1650	CD	LYS	A	209	-29.902	129.353	-47.691	I.00	90.83	C
ATOM	1651	CE	LYS	A	209	-28.543	129.565	-47.021	1.00	93.41	C
ATOM	1652	NZ	LYS	A	209	-28.538	130.754	-46.119	1.00	93.43	N
ATOM	1653	N	ALA	A	210	-31.520	125.276	-50.063	1.00	80.58	N
ATOM	1654	CA	ALA	A	210	-32.567	124.373	-49.609	1.00	82.10	C
ATOM	1655	C	ALA	A	210	-32.127	122.919	-49.736	1.00	81.76	C
ATOM	1656	O	ALA	A	210	-32.301	122.133	-48.809	1.00	79.41	0
ATOM	1657	CB	ALA	A	210	-33.839	124.597	-50.383	I.00	78.21	C
ATOM	1658	N	ILE	A	211	-31.562	122.571	-50.890	1.00	80.20	N
ATOM	1659	CA	ILE	A	211	-31.165	121.196	-51.170	1.00	78.02	C
ATOM	1660	C	ILE	A	211	-29.986	120.757	-50.295	I.00	80.52	C
ATOM	1661	O	ILE	A	211	-29.992	119.662	-49.720	1.00	78.25	0
ATOM	1662	CB	ILE	A	211	-30.797	121.019	-52.651	1.00	73.71	C
ATOM	1663	CGI	ILE	A	211	-32.053	120.998	-53.508	I.00	76.38	C
ATOM	1664	CG2	ILE	A	211	-30.047	119.721	-52.875	1.00	80.04	C
ATOM	1665	GDI	ILE	A	211	-31.760	120.850	-54.974	1.00	79.69	C
ATOM	1666	N	LEU	A	212	-28.984	121.621	-50.183	I.00	76.79	N
ATOM	1667	CA	LEU	A	212	-27.757	121.262	-49.487	1.00	79.85	C
ATOM	1668	C	LEU	A	212	-27.896	121.323	-47.965	1.00	81.11	C
ATOM	1669	O	LEU	A	212	-27.183	120.612	-47.254	1.00	79.56	0
ATOM	1670	CB	LEU	A	212	-26.602	122.163	-49.942	1.00	75.88	C
ATOM	1671	CG	LEU	A	212	-26.186	122.010	-51.403	1.00	70.50	C
ATOM	1672	GDI	LEU	A	212	-25.075	122.978	-51.765	1.00	62.35	C
ATOM	1673	CD2	LEU	A	212	-25.779	120.586	-51.680	I.00	64.68	C
ATOM	1674	N	SER	A	213	-28.799	122.159	-47.458	1.00	76.91	N
ATOM	1675	CA	SER	A	213	-28.953	122.267	-46.013	1.00	79.25	C
ATOM	1676	C	SER	A	213	-30.143	121.472	-45.493	I.00	81.46	C
ATOM	1677	O	SER	A	213	-30.533	121.608	-44.331	1.00	84.46	0
ATOM	1678	CB	SER	A	213	-29.070	123.727	-45.593	1.00	84.05	C
ATOM	1679	OG	SER	A	213	-27.783	124.306	-45.499	I.00	86.20	0
ATOM	1680	N	ALA	A	214	-30.698	120.631	-46.357	1.00	78.64	N
ATOM	1681	CA	ALA	A	214	-31.746	119.698	-45.969	1.00	78.65	C
ATOM	1682	C	ALA	A	214	-31.311	118.833	-44.779	1.00	82.43	C
ATOM	1683	O	ALA	A	214	-30.116	118.589	-44.578	1.00	84.08	0
ATOM	1684	CB	ALA	A	214	-32.124	118.826	-47.151	1.00	75.30	C
ATOM	1685	O	ARG	A	215	-31.252	115.279	-42.436	1.00	91.86	0
ATOM	1686	N	ARG	A	215	-32.279	118.377	-43.988	I.00	81.29	N
ATOM	1687	CA	ARG	A	215	-31.972	117.541	-42.831	1.00	85.42	C
ATOM	1688	C	ARG	A	215	-31.644	116.106	-43.259	1.00	87.35	C
ATOM	1689	CB	ARG	A	215	-33.134	117.549	-41.834	I.00	81.84	C
ATOM	1690	O	LEU	A	216	-29.128	115.083	-44.732	1.00	74.73	0
ATOM	1691	N	LEU	A	216	-31.789	115.820	-44.550	1.00	85.13	N
ATOM	1692	CA	LEU	A	216	-31.451	114.505	-45.086	I.00	84.13	C
ATOM	1693	C	LEU	A	216	-29.950	114.229	-45.090	1.00	80.71	C
ATOM	1694	CB	LEU	A	216	-31.985	114.338	-46.517	1.00	84.14	C
ATOM	1695	CG	LEU	A	216	-33.492	114.351	-46.756	I.00	77.46	C
ATOM	1696	CD1	LEU	A	216	-33.919	115.739	-47.161	1.00	79.56	C
ATOM	1697	CD2	LEU	A	216	-33.882	113.325	-47.810	1.00	80.61	C
ATOM	1698	N	SER	A	217	-29.615	113.016	-45.521	1.00	86.34	N
ATOM	1699	CA	SER	A	217	-28.239	112.527	-45.553	1.00	81.82	C
ATOM	1700	C	SER	A	217	-27.367	113.333	-46.501	1.00	81.12	C
ATOM	1701	O	SER	A	217	-27.868	114.027	-47.393	1.00	82.43	O
ATOM	1702	CB	SER	A	217	-28.222	111.050	-45.963	I.00	84.25	C

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ATOM   1703  OG   SER  A  217    -26..939  110.,650  -46..421  1.00  87.65     O
ATOM   1704  N    LYS  A  218    --26,059  113..244  -46,300   1,00  77.06     N
ATOM   1705  CA   LYS  A  218    -25..119  113.,774  -47 .274  1.00  81,92     C
ATOM   1706  C    LYS  A  218    -25..389  113.,121  -48..633  1.00  84.54     C
ATOM   1707  O    LYS  A  218    -25,588   113. 816  -49.,638  1,00  81 ,37     0
ATOM   1708  CB   LYS  A  218    -23..669  113.,527  -46..842  1.00  77,35     C
ATOM   1709  CG   LYS  A  218    -23..213  114 ,303   -45..617  1,00  71,24     C
ATOM   1710  CD   LYS  A  218    -21.,770  113. 942   -45,277   1,00  70..50     C
ATOM   1711  CE   LYS  A  218    -21..361  114 ,455   -43,902   1,00  64.92     C
ATOM   1712  NZ   LYS  A  218    -21 .516  115.. 927  -43..823  1,00  67,13     N
ATOM   1713  N    SER  A  219    -25,411   111 .788   -48.,647  1,00  82.19     N
ATOM   1714  CA   SER  A  219    -25..673  111 .031   -49,867   1,00  82.36     C
ATOM   1715  C    SER  A  219    -27.021   111 ,388   -50. 483  1,00  81,54     C
ATOM   1716  O    SER  A  219    -27..146  111 ,482   -51.,704  1.00  83..78     0
ATOM   1717  CB   SER  A  219    -25,622   109..530  -49,588   1,00  82.42     C
ATOM   1718  OG   SER  A  219    -24..498  109.,198  -48..804  1.00  84,67     0
ATOM   1719  N    ARG  A  220    -28..036  111 ,571   -49..646  1,00  82.96     N
ATOM   1720  CA.  ARG  A  220    -29.,337  111.991   -50.,151  1.00  83.,99     C
ATOM   1721  C    ARG  A  220    -29..254  113.,413  -50..719  1.00  82,30     C
ATOM   1722  O    ARG  A  220    -29..769  113.,686  -51..799  1,00  81,38     O
ATOM   1723  CB   ARG  A  220    -.30.,398  111.909   -49.,057  1,00  82,13     C
ATOM   1724  N    ARG  A  221    -28..588  114 ,314   -50.,006  1,00  81.11     N
ATOM   1725  CA   ARG  A  221    -28..453  115.,686  -50..485  1,00  81,44     C
ATOM   1726  C    ARG  A  221    -27.,626  115.806   -51.,776  1,00  83..68     C
ATOM   1727  O    ARG  A  221    -27..936  116..634  -52.,635  1,00  83..21     O
ATOM   1728  CB   ARG  A  221    -27.849   116,564   -49. 401  1,00  76,60     C
ATOM   1729  CG   ARG  A  221    -28.,855  116..989  -48.,373  1,00  78..81     C
ATOM   1730  CD   ARG  A  221    -28,181   117 .688   -47,218   1,00  76..10     C
ATOM   1731  NE   ARG  A  221    -27..344  116,773   -46. 454  1,00  75,39     N
ATOM   1732  CZ   ARG  A  221    -26..652  117 ,128   -45,382   1.00  75..44     C
ATOM   1733  NH1  ARG  A  221    -26,701   118..381  -44,943   1,00  84.08     N
ATOM   1734  NH2  ARG  A  221    -25..914  116.,234  -44 .749   1.00  70,.85     N
ATOM   1735  N    LEU  A  222    -26..576  114 ,997   -51..906  1.00  80..65     N
ATOM   1736  CA.  LEU  A  222    -25,828   114. 911   -53.,161  1,00  79.,88     C
ATOM   1737  C    LEU  A  222    -26..767  114,451    -54..266  1.00  80,.83     C
ATOM   1738  O    LEU  A  222    -26..766  114 ,999   -55..376  1,00  78,.38     O
ATOM   1739  CB   LEU  A  222    -24.,637  113. 952   -53.,031  1,00  77,97     C
ATOM   1740  CG   LEU  A  222    -23..801  113.,591  -54 ,260   1,00  73..22     C
ATOM   1741  CD2  LEU  A  222    -22.750   112.,567  -53. 882  1,00  75,68     C
ATOM   1742  CD1  LEU  A  222    -23,148   114 .807   -54.,890  1,00  72.95     C
ATOM   1743  N    GLU  A  223    -27,582   113..451  -53.,944  1,00  81.65     N
ATOM   1744  CA   GLU  A  223    -28. 576  112.,941  -54. 879  1,00  83,29     C
ATOM   1745  C    GLU  A  223    -29..554  114 ,036   -55,267   1.00  84.28     C
ATOM   1746  O    GLU  A  223    -29.777   114 .287   -56,452   1,00  84.22     0
ATOM   1747  CB   GLU  A  223    -29...331  111,753   -54..283  1.00  83,.05     C
ATOM   1748  CG   GLU  A  223    -30..504  111 ,293   -55..136  1.00  85..68     C
ATOM   1749  CD   GLU  A  223    -.30.,092  110. 900   -56.,546  1,00  90.,18     C
ATOM   1750  OE1  GLU  A  223    -30..068  111,788    -57..434  1.00  85,.40     0
ATOM   1751  OE2  GLU  A  223    -29..800  109.,699  -56..766  1,00  89,.56     0
ATOM   1752  N    ASM  A  224    -.30.,119  114. 688   -54 ,254   1,00  83.,89     N
ATOM   1753  CA   ASN  A  224    -31..074  115.,770  -54,451   1,00  81.31     C
ATOM   1754  C    ASN  A  224    -30..610  116.,783  -55..484  1,00  81,56     C
ATOM   1755  0    ASM  A  224    -31.,369  117 .165   -56,375   1,00  82.45     0
ATOM   1756  CB   ASN  A  224    -31..344  116..490  -53.,130  1,00  81.02     C
ATOM   1757  CG   ASN  A  224    -32. 076  115.,623  -52. 126  1,00  84,57     C
ATOM   1758  OD1  ASN  A  224    -.32.,576  114 .552   -52.,466  1,00  85..57     0
ATOM   1759  ND2  ASN  A  224    -32.,154  116..091  -50.,880  1,00  82.89     N
ATOM   1760  N    LEU  A  225    -29. .349  117 ,189   -55. 375  1,00  79,96     N
ATOM   1761  CA   LEU  A  225    -28..843  118.,327  -56,136   1.00  83..13     C
ATOM   1762  C    LEU  A  225    -28..484  118..042  -57.,607  1,00  84.46     C
ATOM   1763  O    LEU  A  225    -28..904  118.,787  -58..495  1.00  85,.85     O
ATOM   1764  CB   LEU  A  225    -27..622  118.,927  -55..433  1.00  74.57     C
ATOM   1765  CG   LEU  A  225    -27,163   120. 220   -56.,109  1,00  73.,32     C
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ATOM    1766  GDI  LEU  A  225    -27..027  121..322  -55..087  1.00  73..04       C
ATOM    1767  CD2  LEU  A  225    --25,864  120..039  -56,882   1,00  69..09       C
ATOM    1768  N    ILE  A  226    -27.693   117,006   -57..880  1.00  78,.57       N
ATOM    1769  CA   ILE  A  226    -27..277  116..791  -59,258   1.00  83..02       C
ATOM    1770  C    ILE  A  226    -28,493   116..323  -60..058  1,00  90..28       C
ATOM    1771  O    ILE  A  226    -28..563  116,524   -61..273  1.00  90,.82       O
ATOM    1772  CB   ILE  A  226    -26..092  115.,769  -59..406  1,00  84,20        C
ATOM    1773  CGI  ILE  A  226    -26,533   114..343  -59.,095  1,00  82.14        C
ATOM    1774  CG2  ILE  A  226    -24..887  116.,179  -58..573  1,00  75..56       C
ATOM    1775  CD1  ILE  A  226    -26..531  113.,454  -60..304  1,00  89,.26       C
ATOM    1776  N    ALA  A  227    -29.,471  115.737   -59,371   I,00  89..35       N
ATOM    1777  CA   ALA  A  227    -30..680  115..278  -60..041  1,00  87.18        C
ATOM    1778  C    ALA  A  227    -31. 627  116,446   -60. .303  1,00  90,22        C
ATOM    1779  O    ALA  A  227    -32..764  116..256  -60..726  1.00  95..75       0
ATOM    1780  CB   ALA  A  227    -31.,366  114 .201  -59,231   1,00  87.93        C
ATOM    1781  N    GLN  A  228    -31..157  117,659   -60..048  1.00  88,.90       N
ATOM    1782  CA   GLN  A  228    -31..855  118..846  -60.,513  1.00  88..86       C
ATOM    1783  C    GLN  A  228    -30.,982  119. 492  -61.,585  1,00  89..86       C
ATOM    1784  O    GLN  A  228    -31..157  120,654   -61..950  1.00  92,81        O
ATOM    1785  CB   GLN  A  228    -32..152  119.,809  -59..359  1,00  86,.55       C
ATOM    1786  CG   GLN  A  228    -33.,222  120. 840  -59.,686  1,00  93..67       C
ATOM    1787  CD   GLN  A  228    -33..760  121.,554  -58..455  1,00100..57       C
ATOM    1788  OE1  GLN  A  228    -33..793  120,988   -57..363  1,00101,.91       0
ATOM    1789  NE2  GLN  A  228    -34.,198  122..802  -58.,631  I,00  93..95       N
ATOM    1790  N    LEU  A  229    -30.,041  118..709  -62..099  1,00  89..77       N
ATOM    1791  CA   LEU  A  229    -29. 143  119,172   -63. 149  1,00  88,66        C
ATOM    1792  C    LEU  A  229    -29.,136  118.230   -64.,351  I,00  92.50        C
ATOM    1793  O    LEU  A  229    -28,830   117.039   -64.,219  1,00  91.13        O
ATOM    1794  CB   LEU  A  229    -27.722   119,326   -62. 614  1,00  84,27        C
ATOM    1795  CG   LEU  A  229    -27,437   120..504  -61.,692  1.00  85..39       C
ATOM    1796  CD1  LEU  A  229    -26,006   120..408  -61.,179  1,00  80..87       C
ATOM    1797  CD2  LEU  A  229    -27.668   121.,812  -62..430  1.00  84,96        C
ATOM    1798  O    PRO  A  230    -27..160  117.730   -67..251  1.00  88..40       0
ATOM    1799  N    PRO  A  230    -29.,469  118. 775  -65.,532  1,00  90..87       N
ATOM    1800  CA   PRO  A  230    -29..495  118.,093  -66..827  1.00  89,.69       C
ATOM    1801  C    PRO  A  230    -28..273  117,214   -67..107  1,00  90,.82       C
ATOM    1802  CB   PRO  A  230    -29.,550  119. 255  -67.,817  1,00  91..30       C
ATOM    1803  CG   PRO  A  230    -30..300  120.,307  -67..092  1,00  96..99       C
ATOM    1804  CD   PRO  A  230    -29. 892  120,182   -65. 650  1,00  94,81        C
ATOM    1805  O    GLY  A  231    -25,148   114.475   -67.,490  I,00  84.87        0
ATOM    1806  N    GLY  A  231    -28,494   115..901  -67.,173  1,00  88..56       N
ATOM    1807  CA   GLY  A  231    -27.494   114,952   -67. 640  1,00  92,58        C
ATOM    1808  C    GLY  A  231    -26,144   114.962   -66,943   1.00  91.24        C
ATOM    1809  O    GLU  A  232    -25,930   113..970  -63.,419  1,00  86..45       0
ATOM    1810  N    GLU  A  232    -26..115  115.,526  -65..739  1.00  91,66        N
ATOM    1811  CA   GLU  A  232    -24..914  115..551  -64..914  1.00  86..62       C
ATOM    1812  C    GLU  A  232    -24.,903  114..327  -64.,001  1,00  84.03        C
ATOM    1813  CB   GLU  A  232    -24..854  116,846   -64..097  1.00  82,70        C
ATOM    1814  CG   GLU  A  232    -23..628  116.,981  -63..226  1,00  81,75        C
ATOM    1815  CD   GLU  A  232    -22.,340  117.116   -64.,024  1,00  81..30       C
ATOM    1816  OE1  GLU  A  232    -22..382  117,707   -65..120  1,00  81.28        0
ATOM    1817  OE2  GLU  A  232    -21 .287  116.,635  -63..546  1,00  75,.77       0
ATOM    1818  O    LYS  A  233    -22.,369  113.671   -61.,440  I,00  78..3.3      0
ATOM    1819  N    LYS  A  233    -23..745  113..679  -63..888  1,00  82.85        N
ATOM    1820  CA   LYS  A  233    -23 .630  112.,455  -63. 098  1,00  76,30        C
ATOM    1821  C    LYS  A  233    -23,122   112.719   -61.,677  I,00  79.94        C
ATOM    1822  CB   LYS  A  233    -22.,713  Ill .460  -63.,808  1,00  82.90        C
ATOM    1823  O    LYS  A  234    -20. 892  112.,289  -58. 472  1,00  79,27        0
ATOM    1824  N    LYS  A  234    -23,543   Ill ,871  -60.,736  1.00  83..36       N
ATOM    1825  CA   LYS  A  234    -23,112   Ill .976  -59,342   1.00  81.53        C
ATOM    1826  C    LYS  A  234    -21..634  111,605   -59..177  1.00  78,.84       C
ATOM    1827  CB   LYS  A  234    -23..984  Ill .094  -58..450  1.00  84.44        C
ATOM    1828  O    ASN  A  235    -17,757   110. 969  -60.,779  1,00  74.94        0
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ATOM   1829  N   ASN A 235     -21.209 110.531 -59.836  1.00 75.99           N
ATOM   1830  CA  ASM A 235     -19.799 110.150 -59.840  1.00 77.54           C
ATOM   1831  C   ASN A 235     -18.973 111.094 -60.704  1.00 75.14           C
ATOM   1832  CB  ASN A 235     -19.625 108.709 -60.330  1.00 71.41           C
ATOM   1833  O   GLY A 236     -18.303 114.095 -60.259  I.00 76.38           0
ATOM   1834  N   GLY A 236     -19.645 112.043 -61.351  1.00 76.90           N
ATOM   1835  CA  GLY A 236     -18.999 112.995 -62.245  1.00 72.27           C
ATOM   1836  C   GLY A 236     -18.172 114.004 -61.478  I.00 74.88           C
ATOM   1837  N   LEU A 237     -17.329 114.765 -62.178  1.00 72.21           N
ATOM   1838  CA  LEU A 237     -16.399 115.679 -61.514  1.00 68.94           C
ATOM   1839  C   LEU A 237     -17.110 116.705 -60.645  I.00 68.40           C
ATOM   1840  O   LEU A 237     -16.660 116.982 -59.537  1.00 75.57           0
ATOM   1841  CB  LEU A 237     -15.503 116.403 -62.522  1.00 66.48           C
ATOM   1842  CG  LEU A 237     -14.729 117.599 -61.943  1.00 66.09           C
ATOM   1843  CD1 LEU A 237     -13.740 117.181 -60.850  1.00 62.94           C
ATOM   1844  CD2 LEU A 237     -14.027 118.408 -63.027  1.00 66.42           C
ATOM   1845  N   PHE A 238     -18.221 117.258 -61.121  1.00 66.26           N
ATOM   1846  CA. PHE A 238     -18.952 118.234 -60.318  I.00 69.71           C
ATOM   1847  C   PHE A 238     -19.718 117.548 -59.185  1.00 72.26           C
ATOM   1848  O   PHE A 238     -19.854 118.102 -58.090  1.00 71.32           O
ATOM   1849  CB  PHE A 238     -19.916 119.050 -61.179  I.00 71.65           C
ATOM   1850  CG  PHE A 238     -20.500 120.238 -60.463  1.00 70.98           C
ATOM   1851  CD1 PHE A 238     -19.826 121.450 -60.443  1.00 67.72           C
ATOM   1852  CD2 PHE A 238     -21.712 120.142 -59.800  I.00 68.19           C
ATOM   1853  CE1 PHE A 238     -20.353 122.543 -59.782  1.00 64.01           C
ATOM   1854  CE2 PHE A 238     -22.239 121.236 -59.135  1.00 66.05           C
ATOM   1855  CZ  PHE A 238     -21.559 122.433 -59.130  I.00 65.45           C
ATOM   1856  N   GLY A 239     -20.224 116.347 -59.461  1.00 71.56           N
ATOM   1857  CA  GLY A 239     -20.871 115.547 -58.442  1.00 71.28           C
ATOM   1858  C   GLY A 239     -19.928 115.347 -57.275  1.00 72.58           C
ATOM   1859  O   GLY A 239     -20.323 115.523 -56.120  1.00 73.32           0
ATOM   1860  N   ASN A 240     -18.671 115.026 -57.587  1.00 67.48           N
ATOM   1861  CA  ASN A 240     -17.646 114.797 -56.572  1.00 70.85           C
ATOM   1862  C   ASN A 240     -17.212 116.053 -55.856  I.00 69.79           C
ATOM   1863  O   ASK A 240     -16.824 116.007 -54.693  1.00 69.04           0
ATOM   1864  CB  ASN A 240     -16.422 114.128 -57.186  1.00 71.00           C
ATOM   1865  CG  ASN A 240     -16.667 112.680 -57.500  I.00 74.60           C
ATOM   1866  OD1 ASN A 240     -17.633 112.091 -57.008  1.00 79.24           0
ATOM   1867  ND2 ASN A 240     -15.800 112.089 -58.320  1.00 72.32           N
ATOM   1868  N   LEU A 241     -17.272 117.179 -56.548  I.00 72.14           N
ATOM   1869  CA  LEU A 241     -16.954 118.438 -55.909  1.00 68.98           C
ATOM   1870  C   LEU A 241     -18.061 118.829 -54.923  1.00 74.03           C
ATOM   1871  O   LEU A 241     -17.810 119.564 -53.963  1.00 76.72           0
ATOM   1872  CB  LEU A 241     -16.731 119.522 -56.957  1.00 69.31           C
ATOM   1873  CG  LEU A 241     -15.467 119.344 -57.797  1.00 60.07           C
ATOM   1874  CD1 LEU A 241     -15.447 120.336 -58.940  1.00 62.87           C
ATOM   1875  CD2 LEU A 241     -14.233 119.507 -56.947  I.00 62.15           C
ATOM   1876  N   ILE A 242     -19.278 118.329 -55.143  1.00 74.33           N
ATOM   1877  CA  ILE A 242     -20.372 118.584 -54.200  1.00 73.38           C
ATOM   1878  C   ILE A 242     -20.248 117.671 -52.973  I.00 68.57           C
ATOM   1879  O   ILE A 242     -20.350 118.139 -51.832  1.00 67.29           0
ATOM   1880  CB  ILE A 242     -21.759 118.397 -54.854  1.00 70.99           C
ATOM   1881  CGI ILE A 242     -22.002 119.464 -55.921  I.00 68.59           C
ATOM   1882  CG2 ILE A 242     -22.856 118.470 -53.806  1.00 67.60           C
ATOM   1883  GDI ILE A 242     -22.200 120.870 -55.365  1.00 71.32           C
ATOM   1884  N   ALA A 243     -20.015 116.381 -53.215  I.00 67.98           N
ATOM   1885  CA  ALA A 243     -19.719 115.417 -52.150  1.00 68.57           C
ATOM   1886  C   ALA A 243     -18.627 115.933 -51.210  1.00 68.23           C
ATOM   1887  O   ALA A 243     -18.778 115.920 -49.987  1.00 67.17           0
ATOM   1888  CB  ALA A 243     -19.304 114.081 -52.746  1.00 68.81           C
ATOM   1889  N   LEU A 244     -17.534 116.402 -51.794  1.00 67.52           N
ATOM   1890  CA  LEU A 244     -16.454 117.007 -51.027  1.00 69.49           C
ATOM   1891  C   LEU A 244     -16.967 118.160 -50.156  I.00 65.96           C
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ATOM	1892	O	LEU	A	244	-16.696	118.212	-48.958	1.00	61.47	O
ATOM	1893	CB	LEU	A	244	-15.349	117.496	-51.966	1.00	67.65	C
ATOM	1894	CG	LEU	A	244	-14.104	118.038	-51.280	1.00	66.20	C
ATOM	1895	GDI	LEU	A	244	-13.522	116.948	-50.405	1.00	70.54	C
ATOM	1896	CD2	LEU	A	244	-13.079	118.527	-52 .291	1.00	63.22	C
ATOM	1897	N	SER	A	245	-17.716	119.077	-50.766	1.00	70.35	N
ATOM	1898	CA	SER	A	245	-18.330	120.180	-50.040	1.00	60.76	C
ATOM	1899	C	SER	A	245	-19.295	119.667	-48.988	1.00	61.32	C
ATOM	1900	O	SER	A	245	-19.518	120.319	-47.979	1.00	59.94	O
ATOM	1901	CB	SER	A	245	-19.063	121.106	-50.996	1.00	67.97	C
ATOM	1902	OG	SER	A	245	-18.179	121.579	-51.985	1.00	71.45	0
ATOM	1903	N	LEU	A	246	-19.862	118.487	-49.223	1.00	61.68	N
ATOM	1904	CA	LEU	*A*	246	-20.810	117.904	-48.280	1.00	61.64	C
ATOM	1905	C	LEU	A	246	-20.156	117.228	-47.066	1.00	62.87	C
ATOM	1906	O	LEU	A	246	-20.815	116.955	-46.067	1.00	58.34	0
ATOM	1907	CB	LEU	A	246	-21.715	116.903	-49.002	1.00	64.77	C
ATOM	1908	CG	LEU	A	246	-22.898	117.548	-49.732	1.00	62.60	C
ATOM	1909	CD1	LEU	A	246	-23.859	116.504	-50.253	1.00	70.43	C
ATOM	1910	CD2	LEU	A	246	-23.599	118.511	-48.793	1.00	58.03	C
ATOM	1911	O	GLY	A	247	-17.656	114.075	-45.370	1.00	68.00	0
ATOM	1912	N	GLY	A	247	-18.861	116.960	-47.146	1.00	67.12	N
ATOM	1913	CA	GLY	A	247	-18.179	116.310	-46.044	1.00	65.25	C
ATOM	1914	C	GLY	A	247	-18.004	114.824	-46.285	1.00	65.31	C
ATOM	1915	0	LEU	A	248	-15.749	113.767	-48.345	1.00	68.73	0
ATOM	1916	N	LEU	A	248	-18.252	114.397	-47.519	1.00	67.93	N
ATOM	1917	CA	LEU	*A*	248	-17.988	113.016	-47.931	1.00	69.08	C
ATOM	1918	C	LEU	A	248	-16.542	112.834	-48.396	1.00	68.58	C
ATOM	1919	CB	LEU	A	248	-18.952	112.606	-49.041	1.00	68.43	C
ATOM	1920	CG	LEU	*A*	248	-20.404	112.465	-48.591	1.00	72.82	C
ATOM	1921	CD1	LEU	A	248	-21.356	112.367	-49.781	1.00	74.87	C
ATOM	1922	CD2	LEU	A	248	-20.519	111.241	-47.706	1.00	71.87	C
ATOM	1923	O	THR	A	249	-14.956	109.601	-50.958	1.00	81.34	0
ATOM	1924	N	THR	A	249	-16.195	111.626	-48.833	1.00	68.88	N
ATOM	1925	CA.	THR	A	249	-14.848	111.383	-49.339	1.00	74.38	C
ATOM	1926	C	THR	A	249	-14.933	110.821	-50.763	1.00	78.27	C
ATOM	1927	CB	THR	A	249	-14.019	110.407	-48.418	1.00	70.84	C
ATOM	1928	OG1	THR	A	249	-14.083	110.830	-47.050	1.00	66.85	0
ATOM	1929	CG2	THR	A	249	-12.555	110.379	-48.827	1.00	61.76	C
ATOM	1930	O	PRO	*A*	250	-12.647	111.330	-53.146	1.00	75.05	0
ATOM	1931	N	PRO	A	250	-15.001	111.721	-51.762	1.00	74.24	N
ATOM	1932	CA	FRO	A	250	-15.032	111.377	-53.192	1.00	72.56	C
ATOM	1933	C	PRO	*A*	250	-13.663	110.951	-53.728	1.00	74.27	C
ATOM	1934	CB	PRO	A	250	-15.486	112.684	-53.852	1.00	73.79	C
ATOM	1935	CG	FRO	A	250	-14.994	113.756	-52 .929	1.00	71.28	C
ATOM	1936	CD	PRO	A	250	-15.095	113.178	-51.540	1.00	70.99	C
ATOM	1937	O	ASN	A	251	-12.948	109.844	-57.812	1.00	72.80	0
ATOM	1938	N	ASM	A	251	-13.638	110.176	-54.812	1.00	78.51	N
ATOM	1939	CA	ASN	A	251	-12.376	109.814	-55.466	1.00	75.87	C
ATOM	1940	C	ASN	A	251	-12.303	110.358	-56.895	1.00	73.13	C
ATOM	1941	CB	ASN	A	251	-12.174	108.294	-55.475	1.00	74.02	C
ATOM	1942	CG	ASN	A	251	-10.710	107.890	-55.709	1.00	74.52	C
ATOM	1943	OD1	ASN	A	251	-9.806	108.728	-55.742	1.00	72.67	0
ATOM	1944	ND2	ASN	A	251	-10.478	106.594	-55.845	1.00	76.84	N
ATOM	1945	O	PHE	A	252	-10.129	111.750	-60.420	1.00	73.38	0
ATOM	1946	N	PHE	*A*	252	-11.491	111.394	-57.069	1.00	69.05	N
ATOM	1947	CA	PHE	A	252	-11.330	112.052	-58.353	1.00	73.09	C
ATOM	1948	C	PHE	A	252	-10.453	111.255	-59.342	1.00	74.43	C
ATOM	1949	CB	PHE	*A*	252	-10.726	113.445	-58.148	1.00	73.10	C
ATOM	1950	CG	PHE	A	252	-11.510	114.334	-57.210	1.00	72.88	C
ATOM	1951	CD2	PHE	A	252	-12.309	115.344	-57.703	1.00	72.64	C
ATOM	1952	CD1	PHE	A	252	-11.408	114.185	-55.831	1.00	73.64	C
ATOM	1953	CE2	PHE	A	252	-13.015	116.174	-56.844	1.00	74.34	C
ATOM	1954	CE1	PHE	A	252	-12.111	115.008	-54.972	1.00	68.59	C

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ATOM    1955  CZ   PHE  A  252    -12.911  116.004  -55.478  1.00  72.07           C
ATOM    1956  O    LYS  A  253     -9.151  109.225  -62.211  1.00  75.97           O
ATOM    1957  N    LYS  A  253    -10.064  110.035  -58.977  1.00  73.20           N
ATOM    1958  CA   LYS  A  253    --9.165  109.250  -59.815  1.00  75.78           C
ATOM    1959  C    LYS  A  253     -9.789  108.996  -61.182  1.00  75.08           C
ATOM    1960  CB   LYS  A  253     -8.802  107.927  -59.142  1.00  77.43           C
ATOM    1961  O    SER  A  254   --11.499  109.798  -64.358  1.00  77.60           0
ATOM    1962  N    SER  A  254    -11.035  108.539  -61.194  1.00  69.22           N
ATOM    1963  CA   SER  A  254   --11.759  108.375  -62.453  1.00  71.00           C
ATOM    1964  C    SER  A  254    -11.894  109.701  -63.199  1.00  73.78           C
ATOM    1965  CB   SER  A  254    -13.143  107.776  -62.211  1.00  70.70           C
ATOM    1966  OG   SER  A  254    -13.707  107.304  -63.424  1.00  61.79           0
ATOM    1967  O    ASN  A  255    -11.683  113.429  -64.821  1.00  76.29           0
ATOM    1968  N    ASN  A  255    -12.425  110.722  -62.523  1.00  73.47           N
ATOM    1969  CA   ASM  A  255    -12.662  112.036  -63.135  1.00  73.95           C
ATOM    1970  C    ASN  A  255    -11.492  112.594  -63.933  1.00  74.91           C
ATOM    1971  CB   ASN  A  255    -13.030  113.078  -62.076  1.00  70.03           C
ATOM    1972  CG   ASN  A  255    -14.347  112.798  -61.402  1.00  69.74           C
ATOM    1973  OD1  ASN  A  255    -14.616  113.312  -60..314 1.00  70.01           0
ATOM    1974  ND2  ASN  A  255    -15.173  111.977  -62.031  1.00  67.57           N
ATOM    1975  O    PHE  A  256     -7.163  111.805  -65.402  1.00  83.16           O
ATOM    1976  N    PHE  A  256    -10.286  112.153  -63.601  1.00  72.49           N
ATOM    1977  CA   PHE  A  256     -9.082  112.657  -64.246  1.00  74.77           C
ATOM    1978  C    PHE  A  256     -8.298  111.566  -64.981  1.00  80.57           C
ATOM    1979  CB   PHE  A  256     -8.165  113.324  -63.218  1.00  71.39           C
ATOM    1980  CG   PHE  A  256     -8.740  114.553  -62.594  1.00  75.06           C
ATOM    1981  CD1  PHE  A  256     -8.854  115.725  -63.318  1.00  77.16           C
ATOM    1982  CD2  PHE  A  256     -9.144  114.550  -61.273  1.00  77.07           C
ATOM    1983  CE1  PHE  A  256     -9.380  116.865  -62.741  1.00  75.86           C
ATOM    1984  CE2  PHE  A  256     -9.670  115.689  -60.693  1.00  72.83           c
ATOM    1985  CZ   PHE  A  256     -9.788  116.843  -61.432  1.00  76.48           C
ATOM    1986  0    ASP  A  257     -5.967  108.430  -65.709  1.00  87.39           0
ATOM    1987  N    ASP  A  257     -8.899  110.384  -65.134  1.00  78.90           N
ATOM    1988  CA.  ASP  A  257     -8.234  109.217  -65.737  1.00  84.17           C
ATOM    1989  C    ASP  A  257     -6.904  108.890  -65.053  1.00  85.94           C
ATOM    1990  CB   ASP  A  257     -7.966  109.421  -67.244  1.00  90.48           C
ATOM    1991  CG   ASP  A  257     -9.072  110.205  -67.960  1.00  86.78           C
ATOM    1992  OD1  ASP  A  257    -10.084  109.590  -68.363  1.00  85.85           0
ATOM    1993  OD2  ASP  A  257     -8.907  111.432  -68.154  1.00  82.92           0
ATOM    1994  O    LEU  A  258     -6.295  106.620  -62.772  1.00  87..37           0
ATOM    1995  N    LEU  A  258     -6.810  109.135  -63.747  1.00  86.75           N
ATOM    1996  CA   LEU  A  258     -5.560  108.892  -63.023  1.00  85.50           C
ATOM    1997  c    LEU  A  258     -5.337  107.396  -62.812  1.00  86.76           c
ATOM    1998  CB   LEU  A  258     -5.554  109.627  -61.674  1.00  79.48           C
ATOM    1999  CG   LEU  A  258     -5.636  111.161  -61.692  1.00  79.44           C
ATOM    2000  CD1  LEU  A  258     -5.056  111.791  -60.421  1.00  74.23           c
ATOM    2001  CD2  LEU  A  258     -4.963  111.744  -62.918  1.00  77.36           C
ATOM    2002  O    ALA  A  259     -4.468  104.251  -60.561  1.00  86.24           0
ATOM    2003  N    ALA  A  259     -4.075  106.994  -62.686  1.00  83.00           N
ATOM    2004  CA.  ALA  A  259     -3.748  105.594  -62.414  1.00  86.05           C
ATOM    2005  C    ALA  A  259     -3.871  105.263  -60.932  1.00  85.16           C
ATOM    2006  CB   ALA  A  259     -2.352  105.269  -62.901  1.00  86.53           C
ATOM    2007  O    GLU  A  260     -4.963  107.713  -58.676  1.00  81.87           0
ATOM    2008  N    GLU  A  260     -3.297  106.118  -60.089  1.00  83.66           N
ATOM    2009  CA   GLU  A  260     -3.376  105.933  -58.642  1.00  84.74           C
ATOM    2010  C    GLU  A  260     -4.515  106.747  -58.062  1.00  81.17           C
ATOM    2011  CB   GLU  A  260     -2.058  106.321  -57.966  1.00  83.87           C
ATOM    2012  O    ASP  A  261     -4.648  108.932  -55.658  1.00  78.89           0
ATOM    2013  N    ASP  A  261     -4.973  106.363  -56.873  1.00  82.37           N
ATOM    2014  CA   ASP  A  261     -6.079  107.055  -56.205  1.00  75.74           C
ATOM    2015  C    ASP  A  261     -5.801  108.513  -55.823  1.00  78.50           C
ATOM    2016  CB   ASP  A  261     -6.489  106.301  -54.946  1.00  73.20           C
ATOM    2017  CG   ASP  A  261     -7.582  105.309  -55.207  1.00  78.37           C
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ATOM	2018	OD1	ASP	A	261	-8.131	105.329	-56.325	1.00	78.78	O
ATOM	2019	OD2	ASP	A	261	-7.900	104.521	-54.296	1.00	84.12	O
ATOM	2020	O	ALA	A	262	-8.926	111.788	-55.002	1.00	73.93	O
ATOM	2021	N	ALA	A	262	-6.884	109.273	-55.678	1.00	71.01	N
ATOM	2022	CA	ALA	A	262	-6.810	110.671	-55.293	1.00	70.30	C
ATOM	2023	C	ALA	A	262	-8.060	111.055	-54.507	1.00	76.86	C
ATOM	2024	CB	ALA	A	262	-6.654	111.555	-56.515	1.00	70.31	C
ATOM	2025	O	LYS	A	263	-7.979	112.249	-51.097	1.00	72.33	0
ATOM	2026	N	LYS	A	263	-8.157	110.545	-53.284	1.00	75.89	N
ATOM	2027	CA	LYS	A	263	-9.327	110.787	-52.453	1.00	72.74	C
ATOM	2028	C	LYS	A	263	-9.092	112.004	-51.573	1.00	72.87	C
ATOM	2029	CB	LYS	A	263	-9.652	109.551	-51.619	1.00	71.00	C
ATOM	2030	CG	LYS	A	263	-9.769	108.283	-52.454	1.00	68.03	C
ATOM	2031	CD	LYS	A	263	-9.995	107.079	-51.576	1.00	63.53	C
ATOM	2032	CE	LYS	A	263	-10.259	105.847	-52.407	1.00	73.23	C
ATOM	2033	NZ	LYS	A	263	-10.482	104.653	-51.543	1.00	75.47	N
ATOM	2034	O	LEU	A	264	-12.308	114.047	-49.980	1.00	76.52	0
ATOM	2035	N	LEU	A	264	-10.144	112.778	-51.375	1.00	68.29	N
ATOM	2036	CA	LEU	A	264	-10.009	114.067	-50.720	1.00	72.51	C
ATOM	2037	C	LEU	A	264	-11.135	114.285	-49.689	1.00	74.38	C
ATOM	2038	CB	LEU	A	264	-9.999	115.180	-51.780	1.00	73.53	C
ATOM	2039	CG	LEU	A	264	-8.726	115.983	-52.074	1.00	72.95	C
ATOM	2040	CD1	LEU	A	264	-7.500	115.100	-52.198	1.00	73.81	C
ATOM	2041	CD2	LEU	A	264	-8.904	116.828	-53.335	1.00	65.73	C
ATOM	2042	O	GLN	A	265	-10.306	116.238	-45.934	1.00	70.38	0
ATOM	2043	N	GLN	A	265	-10.772	114.720	-48.483	1.00	72.33	N
ATOM	2044	CA	GLN	A	265	-11.740	114.996	-47.420	1.00	65.92	C
ATOM	2045	C	GLN	A	265	-11.308	116.257	-46.652	1.00	67.52	C
ATOM	2046	CB	GLN	A	265	-11.866	113.792	-46.476	1.00	61.76	C
ATOM	2047	CG	GLN	A	265	-12.923	113.965	-45.382	1.00	68.74	C
ATOM	2048	CD	GLN	A	265	-12.802	112.938	-44.249	1.00	75.23	C
ATOM	2049	OE1	GLN	A	265	-12.033	111.976	-44.331	1.00	72.10	0
ATOM	2050	NE2	GLN	A	265	-13.563	113.149	-43.185	1.00	73.47	N
ATOM	2051	O	LEU	A	266	-10.586	119.408	-44.217	1.00	60.76	O
ATOM	2052	N	LEU	A	266	-12.059	117.347	-46.804	1.00	69.27	N
ATOM	2053	CA	LEU	A	266	-11.676	118.653	-46.235	1.00	68.37	C
ATOM	2054	C	LEU	A	266	-11.419	118.648	-44.710	1.00	64.56	C
ATOM	2055	CB	LEU	A	266	-12.744	119.702	-46.572	1.00	63.50	C
ATOM	2056	CG	LEU	A	266	-12.996	120.074	-48.039	1.00	62.94	C
ATOM	2057	CD1	LEU	A	266	-14.445	120.384	-48.228	1.00	65.14	C
ATOM	2058	CD2	LEU	A	266	-12.184	121.272	-48.470	1.00	66.42	C
ATOM	2059	O	SER	A	267	-9.964	117.369	-41.131	1.00	68.75	0
ATOM	2060	N	SER	A	267	-12.111	117.782	-43.974	1.00	68.41	N
ATOM	2061	CA	SER	A	267	-11.900	117.662	-42.526	1.00	70.04	C
ATOM	2062	C	SER	A	267	-10.554	117.019	-42.153	1.00	68.90	C
ATOM	2063	CB	SER	A	267	-13.037	116.852	-41.884	1.00	66.51	C
ATOM	2064	OG	SER	A	267	-13.014	115.500	-42.326	1.00	69.85	0
ATOM	2065	O	LYS	A	268	-7.533	117.174	-43.374	1.00	71.61	0
ATOM	2066	N	LYS	A	268	-10.082	116.077	-42.969	1.00	66.29	N
ATOM	2067	CA	LYS	A	268	-8.875	115.316	-42.644	1.00	68.52	C
ATOM	2068	C	LYS	A	268	-7.664	116.256	-42.573	1.00	69.18	C
ATOM	2069	CB	LYS	A	268	-8.658	114.200	-43.676	1.00	68.68	C
ATOM	2070	CG	LYS	A	268	-8.036	112.913	-43.148	1.00	72.58	C
ATOM	2071	CD	LYS	A	268	-7.225	112.238	-44.254	1.00	76.79	C
ATOM	2072	CE	LYS	A	268	-6.533	110.969	-43.795	1.00	71.11	C
ATOM	2073	NZ	LYS	A	268	-7.482	109.817	-43.778	1.00	75.44	N
ATOM	2074	O	ASP	A	269	-3.774	117.878	-42.515	1.00	72.55	0
ATOM	2075	N	ASP	A	269	-6.788	116.035	-41.600	1.00	73.21	N
ATOM	2076	CA	ASP	A	269	-5.664	116.946	-41.345	1.00	76.26	C
ATOM	2077	C	ASP	A	269	-4.591	116.953	-42.447	1.00	77.31	C
ATOM	2078	CB	ASP	A	269	-5.013	116.617	-39.990	1.00	76.67	C
ATOM	2079	CG	ASP	A	269	-4.396	115.219	-39.937	1.00	82.13	C
ATOM	2080	OD2	ASP	A	269	-3.688	114.936	-38.940	1.00	85.20	0

ATOM	2081	OD1	ASP	A	269	-4.612	114.404	-40.868	1.00	78.83	O
ATOM	2082	O	THR	A	270	-3.949	115.834	-46.838	1.00	83.45	O
ATOM	2083	N	THR	A	270	-4.607	115.928	-43.301	1.00	73.55	N
ATOM	2084	CA	THR	A	270	-3.708	115.843	-44.449	1.00	73.77	C
ATOM	2085	C	THR	A	270	-4.365	116.275	-45.764	1.00	79.01	C
ATOM	2086	CB	THR	A	270	-3.189	114.415	-44.656	1.00	73.78	C
ATOM	2087	OG1	THR	A	270	-4.302	113.528	-44.834	1.00	75.34	O
ATOM	2088	CG2	THR	A	270	-2.341	113.959	-43.473	1.00	75.07	C
ATOM	2089	N	TYR	A	271	-5.386	117.121	-45.693	1.00	70.44	N
ATOM	2090	CA	TYR	A	271	-6.104	117.501	-46.898	1.00	74.23	C
ATOM	2091	C	TYR	A	271	-5.314	118.456	-47.779	1.00	77.95	C
ATOM	2092	O	TYR	A	271	-5.318	118.329	-49.004	1.00	77.87	0
ATOM	2093	CB	TYR	A	271	-7.441	118.148	-46.565	1.00	69.51	C
ATOM	2094	CG	TYR	A	271	-8.061	118.805	-47.775	1.00	67.68	C
ATOM	2095	CD1	TYR	A	271	-8.642	118.041	-48.774	1.00	66.87	C
ATOM	2096	CD2	TYR	A	271	-8.041	120.193	-47.931	1.00	68.73	C
ATOM	2097	CE1	TYR	A	271	-9.206	118.633	-49.890	1.00	70.32	C
ATOM	2098	CE2	TYR	A	271	-8.594	120.796	-49.043	1.00	66.64	C
ATOM	2099	CZ	TYR	A	271	-9.180	120.011	-50.023	1.00	71.33	C
ATOM	2100	OH	TYR	A	271	-9.743	120.595	-51.142	1.00	72.54	0
ATOM	2101	N	ASP	A	272	-4.680	119.441	-47.157	1.00	77.62	N
ATOM	2102	CA	ASP	A	272	-3.895	120.407	-47.903	1.00	75.84	C
ATOM	2103	C	ASP	A	272	-2.770	119.694	-48.664	1.00	84.15	C
ATOM	2104	0	ASP	A	272	-2.405	120.095	-49.771	1.00	83.60	0
ATOM	2105	CB	ASP	A	272	-3.342	121.477	-46.965	1.00	71.71	C
ATOM	2106	CG	ASP	A	272	-4.379	122.538	-46.624	1.00	84.92	C
ATOM	2107	OD2	ASP	A	272	-4.220	123.222	-45.589	1.00	89.34	0
ATOM	2108	OD1	ASP	A	272	-5.351	122.697	-47.397	1.00	81.98	0
ATOM	2109	N	ASP	A	273	-2.252	118.619	-48.074	1.00	78.15	N
ATOM	2110	CA	ASP	A	273	-1.204	117.828	-48.697	1.00	81.39	C
ATOM	2111	C	ASP	A	273	-1.751	117.036	-49.880	1.00	82.46	C
ATOM	2112	O	ASP	A	273	-1.297	117.217	-51.007	1.00	84.50	0
ATOM	2113	CB	ASP	A	273	-0.561	116.870	-47.678	1.00	88.35	C
ATOM	2114	CG	ASP	A	273	0.571	117.518	-46.874	1.00	93.63	C
ATOM	2115	OD1	ASP	A	273	0.530	118.749	-46.640	1.00	87.26	0
ATOM	2116	OD2	ASP	A	273	1.502	116.781	-46.461	1.00	91.84	0
ATOM	2117	N	ASP	A	274	-2.715	116.155	-49.621	1.00	82.15	N
ATOM	2118	CA	ASP	A	274	-3.262	115.272	-50.656	1.00	82.17	C
ATOM	2119	C	ASP	A	274	-3.839	116.019	-51.845	1.00	79.62	C
ATOM	2120	O	ASP	A	274	-3.887	115.488	-52.954	1.00	80.43	0
ATOM	2121	CB	ASP	A	274	-4.339	114.375	-50.067	1.00	79.84	C
ATOM	2122	CG	ASP	A	274	-3.786	113.415	-49.071	1.00	81.89	C
ATOM	2123	OD2	ASP	A	274	-4.521	113.024	-48.138	1.00	81.64	0
ATOM	2124	OD1	ASP	A	274	-2.602	113.055	-49.228	1.00	89.85	0
ATOM	2125	N	LEU	A	275	-4.292	117.243	-51.595	1.00	77.66	N
ATOM	2126	CA	LEU	A	275	-4.796	118.111	-52.649	1.00	81.14	C
ATOM	2127	C	LEU	A	275	-3.627	118.624	-53.484	1.00	82.07	C
ATOM	2128	O	LEU	A	275	-3.654	118.554	-54.717	1.00	81.40	0
ATOM	2129	CB	LEU	A	275	-5.597	119.283	-52.071	1.00	72.84	C
ATOM	2130	CG	LEU	A	275	-5.875	120.408	-53.069	1.00	73.76	C
ATOM	2131	CD1	LEU	A	275	-6.771	119.910	-54.182	1.00	72.92	C
ATOM	2132	CD2	LEU	A	275	-6.468	121.631	-52.391	1.00	67.37	C
ATOM	2133	N	ASP	A	276	-2.599	119.132	-52.807	1.00	81.26	N
ATOM	2134	CA	ASP	A	276	-1.388	119.596	-53.481	1.00	80.08	C
ATOM	2135	C	ASP	A	276	-0.679	118.419	-54.154	1.00	81.80	C
ATOM	2136	O	ASP	A	276	0.099	118.596	-55.087	1.00	80.32	0
ATOM	2137	CB	ASP	A	276	-0.454	120.290	-52.494	1.00	82.63	C
ATOM	2138	CG	ASP	A	276	0.783	120.847	-53.159	1.00	87.28	C
ATOM	2139	OD1	ASP	A	276	0.665	121.389	-54.279	1.00	90.53	0
ATOM	2140	OD2	ASP	A	276	1.875	120.736	-52.564	1.00	81.84	0
ATOM	2141	N	ASN	A	277	-0.965	117.218	-53.657	1.00	80.45	N
ATOM	2142	CA	ASN	A	277	-0.543	115.974	-54.272	1.00	75.76	C
ATOM	2143	C	ASM	A	277	-1.315	115.711	-55.567	1.00	80.71	C

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ATOM    2144   O    ASN  A  277      --0..744  115..283  -56..573   1.00  81.65          O
ATOM    2145   CB   ASM  A  277      -0.,744   114 .824  --53.,280  1,00  80..58          C
ATOM    2146   CG   ASN  A  277      -0..267   113.,491  -53..812   1,00  77,73           C
ATOM    2147   OD1  ASN  A  277      --0..948  112.,848  -54 .611   1.00  73..77          O
ATOM    2148   ND2  ASN  A  277       0„901    113. 052  -53.,345   1,00  86.,42          N
ATOM    2149   N    LEU  A  278      -2 .619   115.,966  -55..536   1,00  80,.24          N
ATOM    2150   CA   LEU  A  278      --3..457  115.,820  -56..719   1,00  77,50           C
ATOM    2151   C    LEU  A  278      -3.,142   116.876   -57 ,765   1,00  72,75           C
ATOM    2152   O    LEU  A  278      -2..939   116.,560  -58.,925   1,00  69..90          O
ATOM    2153   CB   LEU  A  278      -4 .933   115.,909  -56..346   1,00  76,58           C
ATOM    2154   CG   LEU  A  278      -5.,873   115.963   -57.,550   I,00  75..10          C
ATOM    2155   CD1  LEU  A  278      -5..902   114 .612  -58.,246   1,00  66..25          C
ATOM    2156   CD2  LEU  A  278      -7.269    116,418   -57. 142   1,00  69,37           C
ATOM    2157   N    LEU  A  279      --3..120  118.,134  -57..331   1.00  76..22          N
ATOM    2158   CA   LEU  A  279      -2.,908   119..280  -58.,215   1,00  75..17          C
ATOM    2159   C    LEU  A  279      -1 .513   119.,288  -58..820   1,00  76,.00          C
ATOM    2160   O    LEU  A  279      --1 .269  119.,953  -59..828   1.00  75..20          O
ATOM    2161   CB   LEU  A  279      -3.,139   120. 596  -57 ,470   1,00  74,60           C
ATOM    2162   CG   LEU  A  279      -4 .562   120,951   -57..049   1,00  74,12           C
ATOM    2163   CD1  LEU  A  279      -4 .575   122.,300  -56..358   1,00  75,.92          C
ATOM    2164   CD2  LEU  A  279      -5„486    120. 968  -58.,240   1,00  70.,.30         C
ATOM    2165   N    ALA  A  280      -0..594   118.,571  -58.,188   1,00  74 .06          N
ATOM    2166   CA   ALA  A  280       0..708   118.,346  -58..784   1,00  75,.47          C
ATOM    2167   C    ALA  A  280       0„520    117.510   -60.,040   I,00  76..36          C
ATOM    2168   O    ALA  A  280       1 .169   117 .753  -61.,050   1,00  71 .45          O
ATOM    2169   CB   ALA  A  280       1 .644   117 ,651  -57. 814   1,00  73,54           C
ATOM    2170   N    GLN  A  281      -0,,396   116.549   -59,967   I,00  71 .67          N
ATOM    2171   CA   GLN  A  281      -0.,630   115..623  -61.,059   1,00  71 .44          C
ATOM    2172   C    GLN  A  281      -1 .659   116,110   -62. 080   1,00  72,26           C
ATOM    2173   O    GLN  A  281      --1 .378  116.,145  -63.,275   1.00  70..91          0
ATOM    2174   CB   GLN  A  281      -1,062    114 .267  -60.,506   1,00  71 .72          C
ATOM    2175   CG   GLN  A  281       0..086   113.,320  -60..281   1,00  74,93           C
ATOM    2176   CD   GLN  A  281      --0..154  Ill ,970  -60..931   1.00  86..76          C
ATOM    2177   OE1  GLN  A  281      -.1 .217   111.365   -60.,751   1,00  86.,52          0
ATOM    2178   NE2  GLN  A  281       0..827   I1l,494   -61..707   1,00  80,.70          N
ATOM    2179   N    ILE  A  282      -2 .855   116.,471  -61..634   1,00  77,63           N
ATOM    2180   CA.  ILE  A  282      -3.,868   116.896   -62.,592   1,00  72,54           C
ATOM    2181   C    ILE  A  282      -3..529   118.,266  -63.,138   1,00  70..21          C
ATOM    2182   O    ILE  A  282      -3.605    118.,478  -64. .339   1,00  75,95           O
ATOM    2183   CB   ILE  A  282      -5.,282   116.902   -61.,992   I,00  71 .70          C
ATOM    2184   CGI  ILE  A  282      -5.,351   117 .741  -60.,722   1,00  72 .11          C
ATOM    2185   CG2  ILE  A  282      -5. 698   115.,497  -61. 689   1,00  74,90           C
ATOM    2186   CD1  ILE  A  282      --6.,733  118.,187  -60.,392   1.00  71 .77          C
ATOM    2187   N    GLY  A  283      -3.,126   119..186  -62.,269   1,00  72 .68          N
ATOM    2188   C    GLY  A  283      -3..202   121.,631  -61..756   1,00  80,.01          C
ATOM    2189   CA   GLY  A  283      -2 .774   120.,525  -62..702   1.00  72 .13          C
ATOM    2190   O    GLY  A  283      -4„301    121 .617  -61.,190   1,00  78.,0.1          0
ATOM    2191   N    ASP  A  284      -2 .326   122.,618  -61..613   1,00  80,.06          N
ATOM    2192   CA   ASP  A  284      -2 .575   123,780   -60..776   1,00  74,91           C
ATOM    2193   C    ASP  A  284      -3.,603   124 .713  -61.,383   1,00  76.,75          C
ATOM    2194   O    ASP  A  284      -3.,747   125.,850  -60.,948   1,00  77 .52          0
ATOM    2195   CB   ASP  A  284      --1 .279  124.,543  -60..559   1,00  78,.89          C
ATOM    2196   CG   ASP  A  284      -1„242    125..257  -59,245    I,00  88..48          C
ATOM    2197   OD2  ASP  A  284      -0.,726   124..665  -58.,268   1,00  92 .72          0
ATOM    2198   OD1  ASP  A  284      -1 .717   126,412   -59. 194   1,00  91,29           0
ATOM    2199   N    GLN  A  285      -4„300    124..242  -62.,407   I,00  76..94          N
ATOM    2200   CA   GLN  A  285      -5.,345   125..027  -63.,040   1,00  72 .27          C
ATOM    2201   C    GLN  A  285      -6. 652   124,791   -62. .300   1,00  76,50           C
ATOM    2202   O    GLN  A  285      --7,581   125,591   -62..387   1.00  80..25          0
ATOM    2203   CB   GLN  A  285      -5.,486   124 .662  -64.,519   1,00  72 .03          C
ATOM    2204   CG   GLN  A  285      -6..030   123,267   -64..765   1,00  74,39           C
ATOM    2205   CD   GLN  A  285      --5..753  122.,741  -66..172   1.00  75..96          C
ATOM    2206   OE1  GLN  A  285      -5„175    121.665   -66.,340   1,00  76.,06          0
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ATOM   2207  NE2 GLN A 285     -6.178 123.488 -67.182 1.00 73.58    N
ATOM   2208  N   TYR A 286     -6.703 123.685 -61.560 1.00 77.12    N
ATOM   2209  CA  TYR A 286     -7.867 123.320 -60.754 1.00 78.54    C
ATOM   2210  C   TYR A 286     -7.766 123.791 -59.301 1.00 76.97    C
ATOM   2211  O   TYR A 286     -8.519 123.334 -58.441 1.00 73.79    0
ATOM   2212  CB  TYR A 286     -8.056 121.806 -60.770 1.00 74.68    C
ATOM   2213  CG  TYR A 286     -8.177 121.234 -62.149 1.00 78.77    C
ATOM   2214  CD1 TYR A 286     -9.392 121.263 -62.823 1.00 81.65    C
ATOM   2215  CD2 TYR A 286     -7.079 120.663 -62.788 1.00 78.39    C
ATOM   2216  CE1 TYR A 286     -9.514 120.735 -64.099 1.00 84.07    C
ATOM   2217  CE2 TYR A 286     -7.186 120.137 -64.060 1.00 74.50    C
ATOM   2218  CZ  TYR A 286     -8.406 120.174 -64.714 1.00 81.43    C
ATOM   2219  OH  TYR A 286     -8.534 119.648 -65.982 1.00 82.10    0
ATOM   2220  N   ALA A 287     -6.819 124.684 -59.032 1.00 79.95    N
ATOM   2221  CA  ALA A 287     -6.589 125.176 -57.679 1.00 80.65    C
ATOM   2222  C   ALA A 287     -7.809 125.926 -57.163 1.00 78.73    C
ATOM   2223  O   ALA A 287     -8.355 125.605 -56.110 1.00 80.49    0
ATOM   2224  CB  ALA A 287     -5.364 126.071 -57.640 1.00 78.10    C
ATOM   2225  N   ASP A 288     -8.247 126.917 -57.924 1.00 76.25    N
ATOM   2226  CA  ASP A 288     -9.369 127.736 -57.508 1.00 75.90    C
ATOM   2227  C   ASP A 288    -10.698 126.977 -57.582 1.00 77.99    C
ATOM   2228  O   ASP A 288    -11.733 127.476 -57.118 1.00 73.27    0
ATOM   2229  CB  ASP A 288     -9.418 129.009 -58.348 1.00 70.09    C
ATOM   2230  CG  ASP A 288     -8.372 130.029 -57.912 1.00 79.78    C
ATOM   2231  OD1 ASP A 288     -7.964 130.014 -56.726 1.00 68.74    0
ATOM   2232  OD2 ASP A 288     -7.958 130.849 -58.758 1.00 86.74    0
ATOM   2233  N   LEU A 289    -10.668 125.765 -58.137 1.00 74.30    N
ATOM   2234  CA  LEU A 289    -11.871 124.943 -58.205 1.00 71.19    C
ATOM   2235  C   LEU A 289    -12.086 124.216 -56.893 1.00 69.60    C
ATOM   2236  O   LEU A 289    -13.223 124.026 -56.464 1.00 69.36    0
ATOM   2237  CB  LEU A 289    -11.801 123.936 -59.351 1.00 68.49    C
ATOM   2238  CG  LEU A 289    -13.133 123.221 -59.588 1.00 67.95    C
ATOM   2239  CD2 LEU A 289    -13.054 122.339 -60.811 1.00 70.67    C
ATOM   2240  CD1 LEU A 289    -14.240 124.236 -59.739 1.00 68.06    C
ATOM   2241  N   PHE A 290    -10.995 123.810 -56.252 1.00 68.89    N
ATOM   2242  CA  PHE A 290    -11.107 123.160 -54.952 1.00 69.56    C
ATOM   2243  C   PHE A 290    -11.280 124.196 -53.843 1.00 73.98    C
ATOM   2244  O   PHE A 290    -11.941 123.931 -52.837 1.00 73.78    0
ATOM   2245  CB  PHE A 290     -9.901 122.274 -54.693 1.00 68.36    C
ATOM   2246  CG  PHE A 290     -9.924 121.005 -55.478 1.00 67.56    C
ATOM   2247  CD1 PHE A 290    -10.605 119.902 -55.006 1.00 63.68    C
ATOM   2248  CD2 PHE A 290     -9.284 120.920 -56.702 1.00 68.00    C
ATOM   2249  CE1 PHE A 290    -10.631 118.732 -55.735 1.00 64.24    C
ATOM   2250  CE2 PHE A 290     -9.305 119.756 -57.430 1.00 62.50    C
ATOM   2251  CZ  PHE A 290     -9.977 118.663 -56.950 1.00 62.84    C
ATOM   2252  N   LEU A 291    -10.695 125.375 -54.042 1.00 69.53    N
ATOM   2253  CA. LEU A 291    -10.943 126.510 -53.166 1.00 72.27    C
ATOM   2254  C   LEU A 291    -12.445 126.833 -53.136 1.00 75.76    C
ATOM   2255  O   LEU A 291    -13.017 127.025 -52.070 1.00 77.78    0
ATOM   2256  CB  LEU A 291    -10.145 127.729 -53.626 1.00 74.96    C
ATOM   2257  CG  LEU A 291    -10.019 128.922 -52.674 1.00 79.02    C
ATOM   2258  CD2 LEU A 291    -10.339 130.257 -53.373 1.00 75.90    C
ATOM   2259  CD1 LEU A 291     -8.632 128.956 -52.040 1.00 82.61    C
ATOM   2260  N   ALA A 292    -13.083 126.877 -54.304 1.00 73.84    N
ATOM   2261  CA  ALA A 292    -14.522 127.119 -54.371 1.00 68.28    C
ATOM   2262  C   ALA A 292    -15.307 125.977 -53.735 1.00 68.67    C
ATOM   2263  O   ALA A 292    -16.347 126.197 -53.124 1.00 68.89    0
ATOM   2264  CB  ALA A 292    -14.962 127.327 -55.811 1.00 71.09    C
ATOM   2265  N   ALA A 293    -14.806 124.754 -53.867 1.00 70.26    N
ATOM   2266  CA  ALA A 293    -15.417 123.640 -53.164 1.00 70.95    C
ATOM   2267  C   ALA A 293    -15.180 123.767 -51.660 1.00 71.61    C
ATOM   2268  O   ALA A 293    -16.060 123.440 -50.862 1.00 71.13    0
ATOM   2269  CB  ALA A 293    -14.882 122.327 -53.675 1.00 69.57    C
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ATOM	2270	N	LYS	A	294	-13.994	124.248	-51.284	1.00	70.41	N
ATOM	2271	CA	LYS	A	294	-13.644	124.453	-49.876	1.00	70.71	C
ATOM	2272	C	LYS	A	294	-14.613	125.420	-49.213	1.00	69.41	C
ATOM	2273	O	LYS	A	294	-15.210	125.114	-48.187	1.00	73.35	0
ATOM	2274	CB	LYS	A	294	-12.208	124.971	-49.734	1.00	67.52	c
ATOM	2275	N	ASN	A	295	-14.775	126.584	-49.822	1.00	70.61	N
ATOM	2276	CA	ASN	A	295	-15.664	127.607	-49.294	1.00	77.26	c
ATOM	2277	C	ASM	A	295	-17.089	127.109	-49.122	1.00	77.99	C
ATOM	2278	O	ASN	A	295	-17.730	127.407	-48.114	1.00	78.76	O
ATOM	2279	CB	ASN	A	295	-15.667	128.844	-50.198	1.00	71.68	c
ATOM	2280	CG	ASN	A	295	-14.311	129.499	-50.290	1.00	75.43	c
ATOM	2281	OD1	ASN	A	295	-13.510	129.447	-49.352	1.00	74.07	0
ATOM	2282	ND2	ASN	A	295	-14.034	130.113	-51.434	1.00	75.98	N
ATOM	2283	N	LEU	A	296	-17.589	126.362	-50.106	1.00	76.49	N
ATOM	2284	CA	LEU	A	296	-18.981	125.928	-50.063	1.00	71.69	C
ATOM	2285	C	LEU	A	296	-19.209	125.068	-48.826	1.00	68.25	c
ATOM	2286	O	LEU	A	296	-20.222	125.218	-48.161	1.00	65.68	0
ATOM	2287	CB	LEU	A	296	-19.373	125.175	-51.338	1.00	69.39	c
ATOM	2288	CG	LEU	A	296	-20.842	124.735	-51.426	1.00	71.16	c
ATOM	2289	CD1	LEU	A	296	-21.791	125.924	-51.335	1.00	69.00	c
ATOM	2290	CD2	LEU	A	296	-21.093	123.941	-52.699	1.00	67.44	c
ATOM	2291	N	SER	A	297	-18.248	124.206	-48.491	1.00	71.35	N
ATOM	2292	CA	SER	A	297	-18.393	123.323	-47.329	1.00	70.81	c
ATOM	2293	C	SER	A	297	-18.371	124.117	-46.024	1.00	70.52	C
ATOM	2294	O	SER	A	297	-19.013	123.728	-45.049	1.00	68.72	O
ATOM	2295	CB	SER	A	297	-17.302	122.249	-47.310	1.00	67.58	C
ATOM	2296	OG	SER	A	297	-16.021	122.790	-47.051	1.00	69.27	0
ATOM	2297	N	ASP	A	298	-17.624	125.221	-46.019	1.00	68.07	N
ATOM	2298	CA	ASP	A	298	-17.642	126.169	-44.907	1.00	70.04	C
ATOM	2299	c	ASP	A	298	-19.072	126.698	-44.685	1.00	74.39	c
ATOM	2300	O	ASP	A	298	-19.539	126.816	-43.544	1.00	70.16	0
ATOM	2301	CB	ASP	A	298	-16.680	127.343	-45.167	1.00	73.81	c
ATOM	2302	CG	ASP	A	298	-15.245	127.087	-44.671	1.00	79.77	c
ATOM	2303	OD1	ASP	A	298	-14.820	125.911	-44.558	1.00	77.89	0
ATOM	2304	OD2	ASP	A	298	-14.535	128.086	-44.400	1.00	78.28	0
ATOM	2305	N	ALA	A	299	-19.765	127.007	-45.782	1.00	71.60	N
ATOM	2306	CA.	ALA	A	299	-21.126	127.533	-45.710	1.00	72.73	C
ATOM	2307	C	ALA	A	299	-22.152	126.437	-45.446	1.00	71.62	C
ATOM	2308	O	ALA	A	299	-23.148	126.672	-44.765	1.00	72.02	O
ATOM	2309	CB	ALA	A	299	-21.479	128.281	-46.986	1.00	74.84	c
ATOM	2310	N	ILE	A	300	-21.916	125.244	-45.982	1.00	67.71	N
ATOM	2311	CA	ILE	A	300	-22.827	124.137	-45.753	1.00	65.23	C
ATOM	2312	c	ILE	A	300	-22.804	123.791	-44.276	1.00	69.82	c
ATOM	2313	O	ILE	A	300	-23.839	123.504	-43.676	1.00	72.83	0
ATOM	2314	CB	ILE	A	300	-22.462	122.899	-46.601	1.00	66.25	c
ATOM	2315	CGI	ILE	A	300	-22.659	123.189	-48.094	1.00	66.93	c
ATOM	2316	CG2	ILE	A	300	-23.301	121.697	-46.204	1.00	61.04	c
ATOM	2317	CD1	ILE	A	300	-22.207	122.052	-49.015	1.00	66.82	c
ATOM	2318	N	LEU	A	301	-21.622	123.863	-43.678	1.00	72.67	N
ATOM	2319	CA.	LEU	A	301	-21.453	123.447	-42.293	1.00	72.27	C
ATOM	2320	C	LEU	A	301	-22.177	124.378	-41.326	1.00	73.10	C
ATOM	2321	O	LEU	A	301	-22.910	123.926	-40.452	1.00	76.47	O
ATOM	2322	CB	LEU	A	301	-19.969	123.380	-41.930	1.00	74.11	c
ATOM	2323	CG	LEU	A	301	-19.638	122.407	-40.797	1.00	70.01	c
ATOM	2324	GDI	LEU	A	301	-19.398	121.008	-41.360	1.00	73.40	c
ATOM	2325	CD2	LEU	A	301	-18.450	122.885	-39.990	1.00	67.92	c
ATOM	2326	N	LEU	A	302	-21.958	125.675	-41.480	1.00	69.46	N
ATOM	2327	CA	LEU	A	302	-22.604	126.653	-40.619	1.00	78.82	C
ATOM	2328	c	LEU	A	302	-24.126	126.551	-40.691	1.00	83.62	c
ATOM	2329	O	LEU	A	302	-24.796	126.439	-39.668	1.00	87.64	0
ATOM	2330	CB	LEU	A	302	-22.169	128.072	-40.989	1.00	76.93	c
ATOM	2331	CG	LEU	A	302	-21.017	128.709	-40.213	1.00	75.69	c
ATOM	2332	CD1	LEU	A	302	-19.726	127.927	-40.387	1.00	77.42	c

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ATOM   2333  CD2  LEU  A  302    -20.826  130.148  -40.663   1.00  81.28    c
ATOM   2334  N    SER  A  303    --24,654 126.571  -41,910   1,00  84.39    N
ATOM   2335  CA   SER  A  303    -26.088  126,684  -42.161   1,00  80,24    c
ATOM   2336  c    SER  A  303    -26.896  125.617  -41.442   1.00  82.43    c
ATOM   2337  0    SER  A  303    -28,003  125.876  -40,965   1,00  84,25    0
ATOM   2338  CB   SER  A  303    -26..355  126,618  -43.665   1,00  79,04    c
ATOM   2339  OG   SER  A  303    -27.746  126,627  -43.941   1,00  96,85    0
ATOM   2340  N    ASP  A  304    -26,323  124.423  -41,365   1,00  82,33    N
ATOM   2341  C    ASP  A  304    --26.940 123.388  -39.197   1,00  83.67    c
ATOM   2342  CA   ASP  A  304    -26.962  123,280  -40.723   1,00  84,94    c
ATOM   2343  O    ASP  A  304    -27,868  122.955  -.38,512   I,00  84.79    0
ATOM   2344  CB   ASP  A  304    -26.264  121.988  -41.161   1,00  84.03    c
ATOM   2345  CG   ASP  A  304    -27.224  120,826  -41.326   1,00  94,92    c
ATOM   2346  OD1  ASP  A  304    -28.316  120.854  -40.707   1.00  97.71    0
ATOM   2347  OD2  ASP  A  304    -26,877  119.878  -42,075   1,00  98.12    0
ATOM   2348  N    ILE  A  305    -25.868  123,975  -38.677   1,00  84,34    N
ATOM   2349  c    ILE  A  305    -26.049  125.224  -36.598   1.00  85.60    c
ATOM   2350  CA.  ILE  A  305    -25,561  123.930  -37,245   1,00  85,02    C
ATOM   2351  O    ILE  A  305    -26.135  125,346  -35..371   1,00  86,49    O
ATOM   2352  CB   ILE  A  305    -24.022  123,665  -37.025   1,00  81,83    c
ATOM   2353  CGI  ILE  A  305    -23,761  122.157  -36,887   1,00  73,86    c
ATOM   2354  CG2  ILE  A  305    -23.441  124.398  -35.820   1,00  73.99    c
ATOM   2355  CD1  ILE  A  305    -24.315  121,316  -38.029   1,00  68,29    c
ATOM   2356  O    LEU  A  306    -26,871  128.192  -.39,291   I,00  87.21    0
ATOM   2357  N    LEU  A  306    -26.434  126.167  -37.451   1,00  83.54    N
ATOM   2358  CA   LEU  A  306    -26.920  127,458  -37.008   1,00  80,17    c
ATOM   2359  C    LEU  A  306    -27,405  128.293  -.38,189   I,00  86.70    c
ATOM   2360  CB   LEU  A  306    -25,826  128.206  -36,239   1,00  77.44    c
ATOM   2361  CG   LEU  A  306    -24.382  128,185  -36.749   1,00  79,87    c
ATOM   2362  CD2  LEU  A  306    -23.431  128.506  -35.619   1.00  74.99    c
ATOM   2363  CD1  LEU  A  306    -24,153  129.140  -37,918   1,00  82.69    c
ATOM   2364  O    AP.G A  307    -29.059  131,594  -37.194   1,00  87,18    0
ATOM   2365  N    ARG  A  307    -28.428  129.111  -37.959   1.00  85.51    N
ATOM   2366  CA.  ARG  A  307    -28,900  130.027  -38,984   1,00  89,40    c
ATOM   2367  C    AP.G A  307    -29.457  131,266  -38.312   1,00  88,26    c
ATOM   2368  CB   ARG  A  307    -29.953  129,363  -39.878   1,00  95,36    c
ATOM   2369  O    LYS  A  314    -19,749  135.915  -33,734   1,00  72,88    0
ATOM   2370  N    LYS  A  314    -22.292  137.906  -35.360   1,00  67.51    N
ATOM   2371  CA   LYS  A  314    -20.940  137,721  -34.841   1,00  68,30    c
ATOM   2372  C    LYS  A  314    -20,821  136.535  -.33,859   I,00  75.94    c
ATOM   2373  CB   LYS  A  314    -20,460  139.002  -34,167   1,00  69.88    c
ATOM   2374  O    ALA  A  315    -24.226  134,040  -32.201   1,00  60,16    0
ATOM   2375  N    ALA  A  315    -21.922  136.225  -33.172   1.00  75.54    N
ATOM   2376  CA   ALA  A  315    -22,041  135.015  -32 ,341   1,00  63.14    c
ATOM   2377  C    ALA  A  315    -23.182  134,137  -32 .843   1,00  61,I9    c
ATOM   2378  CB   ALA  A  315    -22.269  135.375  -30.885   1.00  56.95    c
ATOM   2379  N    PRO  A  316    -22,974  133.479  -33,990   1,00  63,69    N
ATOM   2380  CA   PRO  A  316    -23.989  1.32,725 -34.743   1,00  63,21    C
ATOM   2381  c    PRO  A  316    -24.688  131,600  -33.957   1,00  66,16    c
ATOM   2382  0    PRO  A  316    -25,905  131.440  -34,090   1,00  69,01    0
ATOM   2383  CB   PRO  A  316    -23.189  132.132  -35.905   1,00  69.56    c
ATOM   2384  CG   PRO  A  316    -21.962  132,957  -35.997   1,00  69,08    c
ATOM   2385  CD   PRO  A  316    -21,644  133.382  -.34,611   I,00  66.19    c
ATOM   2386  N    LEU  A  317    -23.936  130.831  -33.171   1,00  62.71    N
ATOM   2387  CA   LEU  A  317    -24.505  129,720  -32.405   1,00  60,38    C
ATOM   2388  C    LEU  A  317    -25,397  130.222  -31,293   I,00  60.62    C
ATOM   2389  O    LEU  A  317    -26,550  129.806  -31,173   1,00  55.04    0
ATOM   2390  CB   LEU  A  317    -23.407  128,848  -31.796   1,00  59,29    c
ATOM   2391  CG   LEU  A  317    -23.930  127.698  -30.937   1.00  57.81    c
ATOM   2392  CD1  LEU  A  317    -24,424  126.567  -31,824   1,00  55.29    c
ATOM   2393  CD2  LEU  A  317    -22.867  127,196  -29.967   1,00  53,80    c
ATOM   2394  N    SER  A  318    -24.832  131.100  -30.464   1.00  59.04    N
ATOM   2395  CA.  SER  A  318    -25,556  131.669  -29,349   1,00  55,54    C
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ATOM   2396  C    SER  A  318    -26..812  132..386  -29..828  1,00  57.81   C
ATOM   2397  O    SER  A  318    --27,846  132..316  -29,173   1,00  53..42   O
ATOM   2398  CB   SER  A  318    -24..666  1.32.,620  -28.566  1.00  55,.64   C
ATOM   2399  OG   SER  A  318    -23..720  131.,880  -27,835   1,00  58..34   0
ATOM   2400  N    ALA  A  319    -26,720  133. 046  -.30.,981  1,00  53..45   N
ATOM   2401  CA   ALA  A  319    -27.880  1.3.3.,696  -31..560  1.00  57,22   C
ATOM   2402  C    ALA  A  319    -28..895  132.,649  -32..003  1,00  55,.71   C
ATOM   2403  0    ALA  A  319    -30.,098  132. 797  -.3.1 ,794  1,00  60.,92   0
ATOM   2404  CB   ALA  A  319    -27..474  134.,582  -32.,713  1,00  56..53   C
ATOM   2405  N    SER  A  320    -28..406  131.,579  -32.. 608  1,00  60,.92   N
ATOM   2406  CA   SER  A  320    -29.,271  130.. 482  -.32.,998  I,00  59..27   C
ATOM   2407  C    SER  A  320    -29..972  129.,877  -31.,781  1,00  57.40   C
ATOM   2408  O    SER  A  320    -31. 147  129,537  -31. 834  1,00  58,70   O
ATOM   2409  CB   SER  A  320    -28..465  129.,429  -33.,741  1,00  63..24   C
ATOM   2410  OG   SER  A  320    -29,249  128.. 276  -33.,996  1,00  76..85   0
ATOM   2411  N    MET  A  321    -29.. 252  129,771  -30.. 673  1.00  57,.15   N
ATOM   2412  CA   MET  A  321    -29,824  129.,225  -29,452  1,00  54.45   C
ATOM   2413  C    MET  A  321    -30.,809  130. 220  -28,862  1,00  56..07   C
ATOM   2414  O    MET  A  321    -31.. 793  129,835  -28.,232  1.00  57,64   0
ATOM   2415  CB   MET  A  321    -28.726  128,885  -28.438  1,00  56,.04   C
ATOM   2416  CG   MET  A  321    -27,847  127 .702  -28,840  1,00  48..2.3   C
ATOM   2417  SD   MET  A  321    -28,774  126.,185  -28,727  1,00  56..87   S
ATOM   2418  CE   MET  A  321    -27.630  124.,977  -29.388  1,00  55,.95   C
ATOM   2419  N    ILE  A  322    -30.,549  131.. 506  -29.,068  I,00  56..26   N
ATOM   2420  CA   ILE  A  322    -31.,479  132.,519  -28,602  1,00  54.62   C
ATOM   2421  C    ILE  A  322    -32. 772  1.32.,485  -29. 424  1,00  54,60   C
ATOM   2422  O    ILE  A  322    -33.,875  132.. 502  -28.,867  I,00  56..65   0
ATOM   2423  CB   ILE  A  322    -30.,871  133.. 906  -28,655  1,00  53..12   C
ATOM   2424  CGI  ILE  A  322    -29. 825  1.34.,034  -27.569  1,00  49,34   C
ATOM   2425  CG2  ILE  A  322    -31.,953  134.,970  -28,411  1,00  51.29   C
ATOM   2426  CD1  ILE  A  322    -28,977  135.. 269  -27,711  1,00  53..81   C
ATOM   2427  N    LYS  A  323    -32.. 635  1.32.,420  -30.. 739  1.00  52,.18   N
ATOM   2428  CA   LYS  A  323    -33.,805  132.,337  -31.,594  1,00  54.95   C
ATOM   2429  C    LYS  A  323    -34.,691  131. 197  -.3.1 ,118  1,00  57.55   C
ATOM   2430  O    LYS  A  323    -35.. 880  131.,383  -30.. 907  1.00  59,.84   0
ATOM   2431  CB   LYS  A  323    -33.408  132.,138  -33.056  1,00  54,90   C
ATOM   2432  N    ARG  A  324    -34.,077  130. 036  -.30.,897  1,00  60..44   N
ATOM   2433  CA   ARG  A  324    -34.,759  128.,820  -30.,449  1,00  54.80   C
ATOM   2434  C    ARG  A  324    -35. 495  128,970  -29. 118  1,00  53,39   C
ATOM   2435  O    ARG  A  324    -36,574  128.425  -28.,921  I,00  55..83   0
ATOM   2436  CB   ARG  A  324    -33.,738  127.686  -30.,342  1,00  58..31   C
ATOM   2437  CG   ARG  A  324    -34. 173  126,527  -29. 493  1,00  55,01   C
ATOM   2438  CD   ARG  A  324    -33.,121  125,449  -29,499  1,00  55..87   C
ATOM   2439  NE   ARG  A  324    -32.,803  125.. 003  -30.,846  1,00  55..38   N
ATOM   2440  CZ   ARG  A  324    -32.. 004  12.3.,973  -31.. 122  1.00  66,.60   C
ATOM   2441  NH1  ARG  A  324    -31.,436  123.,272  -30..143  1,00  58..13   N
ATOM   2442  NH2  ARG  A  324    -31,775  123. 639  -.32.,386  1,00  69..90   N
ATOM   2443  N    TYR  A  325    -34.. 899  129,708  -28.202  1.00  52,06   N
ATOM   2444  CA   TYR  A  325    -35.. 535  129.,981  -26.932  1,00  58,.17   C
ATOM   2445  C    TYR  A  325    -36,766  130. 902  -27,117  1,00  60..13   C
ATOM   2446  O    TYR  A  325    -37.,809  130.,702  -26,467  1,00  53..25   0
ATOM   2447  CB   TYR  A  325    -34.. 513  130.,593  -25.970  1,00  54,34   C
ATOM   2448  CG   TYR  A  325    -35.,108  131.. 172  -24.,716  I,00  56..44   C
ATOM   2449  CD1  TYR  A  325    -35.,269  130..397  -23,581  1,00  56..00   C
ATOM   2450  CD2  TYR  A  325    -35. 507  1.32.,506  -24 .665  1,00  62,46   C
ATOM   2451  CE1  TYR  A  325    -35.,809  130.. 927  -22.,422  I,00  59..10   C
ATOM   2452  CE2  TYR  A  325    -36,054  133.. 049  -23,516  1,00  64.85   C
ATOM   2453  CZ   TYR  A  325    -36. 203  1.32.,254  -22.395  1,00  66,33   C
ATOM   2454  OH   TYR  A  325    -36,746  132.,794  -21.,248  1,00  70..14   0
ATOM   2455  N    ASP  A  326    -36,628  131.. 895  -28,001  1,00  59..86   N
ATOM   2456  CA   ASP  A  326    -37.. 731  1.32.,806  -28..359  1.00  60,.19   C
ATOM   2457  C    ASP  A  326    -38.,895  132.,047  -28..987  1,00  61.70   C
ATOM   2458  O    ASP  A  326    -40.,041  132. 162  -28,541  1,00  57.96   0
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ATOM  2459  CB   ASP  A  326   -37..262   133..890   -29..333   1,00  50..58   C
ATOM  2460  CG   ASP  A  326   --36,349   134..902   -28,688    1,00  51.03    C
ATOM  2461  OD1  ASP  A  326   -36..443   1.35.,081  -27.461    1.00  54,84    0
ATOM  2462  OD2  ASP  A  326   -35..541   135.,532   -29..408   1,00  52.65    0
ATOM  2463  N    GLU  A  327   -38,,593   131. 271   -30.,024   1,00  57.18    N
ATOM  2464  CA   GLU  A  327   -39..613   1.30.,472  -30. .699   1.00  6.3,.04   C
ATOM  2465  C    GLU  A  327   -40..283   129.,479   -29..761   1,00  63,.61   C
ATOM  2466  0    GLU  A  327   -41,495    129. 261   -29.,850   1,00  67.00    0
ATOM  2467  CB   GLU  A  327   -39..017   129.,731   -31.,890   1,00  56..85   C
ATOM  2468  CG   GLU  A  327   -38..327   130.,660   -32..838   1,00  61,40    C
ATOM  2469  CD   GLU  A  327   -38.,235   130..098   -.34.,224  I,00  66..07   C
ATOM  2470  OE1  GLU  A  327   -38..896   129..065   -34.,479   1,00  66..09   0
ATOM  2471  OE2  GLU  A  327   -37. 505   130.,696   -35. 051   1,00  65,42    0
ATOM  2472  N    HIS  A  328   -39,501    128.,875   -28,870    1,00  60..06   N
ATOM  2473  CA   HIS  A  328   -40,065    127.977    -27,868    1,00  62.05    C
ATOM  2474  C    HIS  A  328   -41 .078   128,785    -27.056    1.00  58,.42   C
ATOM  2475  O    HIS  A  328   -42..139   128.,288   -26..712   1,00  58..96   0
ATOM  2476  CB   HIS  A  328   -38.,959   127 .356   -26,984    1,00  57.18    C
ATOM  2477  CG   HIS  A  328   -39..463   126,498    -25..856   1.00  55,.16   C
ATOM  2478  ND1  HIS  A  328   -38..987   125,228    -25..621   1,00  60,.92   N
ATOM  2479  CD2  HIS  A  328   -40.,366   126. 741   -24.,875   1,00  55..18   C
ATOM  2480  CE1  HIS  A  328   -39,588    124,716    -24,561    1,00  54.20    C
ATOM  2481  NE2  HIS  A  328   -40..430   125,614    -24.089    1,00  56,.54   N
ATOM  2482  N    HIS  A  329   -40.,768   130..044   -26.,784   I,00  57,87    N
ATOM  2483  CA   HIS  A  329   -41 ,709   130..868   -26,045    1,00  64.59    C
ATOM  2484  C    HIS  A  329   -42 .983   131.,218   -26. 832   1,00  62,79    C
ATOM  2485  O    HIS  A  329   -44 ,082   131..056   -26.,310   I,00  57,22    0
ATOM  2486  CB   HIS  A  329   -41 ,065   132..160   -25,582    1,00  61.07    C
ATOM  2487  CG   HIS  A  329   -42 .025   133.,068   -24 .880   1,00  67,93    C
ATOM  2488  ND1  HIS  A  329   -42,657    134.,119   -25,510    1,00  63..64   N
ATOM  2489  CD2  HIS  A  329   -42.,486   133..058   -23,607    1,00  65..85   C
ATOM  2490  CE1  HIS  A  329   -43..447   1.34.,733  -24..649   1.00  61,37    C
ATOM  2491  NE2  HIS  A  329   -43..362   134.,109   -23..487   1,00  68..54   N
ATOM  2492  N    GLN  A  330   -42.,826   131. 705   -28,064    1,00  62.85    N
ATOM  2493  CA   GLN  A  330   -43..969   131.,974   -28..930   1.00  6.3,.07   C
ATOM  2494  C    GLN  A  330   -44.870    130.,770   -28..942   1,00  68,.41   C
ATOM  2495  O    GLN  A  330   -46,037    130. 838   -28,555    1,00  70..23   0
ATOM  2496  CB   GLN  A  330   -43,549    132.,265   -30.,369   1,00  67.42    C
ATOM  2497  CG   GLN  A  330   -42 .665   133.,467   -30. 567   1,00  69,62    C
ATOM  2498  CD   GLN  A  330   -41 ,883   133. ..385  -31.,867   I,00  74.50    C
ATOM  2499  OE1  GLN  A  330   -42.,014   132..415   -32.,634   1,00  73..84   0
ATOM  2500  NE2  GLN  A  330   -41.052    134.,397   -32. 119   1,00  70,16    N
ATOM  2501  N    ASP  A  331   -44,291    129.,658   -29..377   1,00  65..68   N
ATOM  2502  CA   ASP  A  331   -45,036    128..437   -29,627    1,00  66..33   C
ATOM  2503  C    ASP  A  331   -45..632   127,841    -28..360   1.00  65,.68   C
ATOM  2504  O    ASP  A  331   -46..586   127 ,087   -28..439   1,00  65..38   O
ATOM  2505  CB   ASP  A  331   -44 ,135   127 .419   -30.,324   1,00  61.45    C
ATOM  2506  CG   ASP  A  331   -43..710   127,873    -31. .712  1.00  70,.46   C
ATOM  2507  OD1  ASP  A  331   -43..759   129.,095   -32..005   1,00  73,.88   O
ATOM  2508  OD2  ASP  A  331   -43,330    127 .003   -32.,517   1,00  68..92   O
ATOM  2509  N    LEU  A  332   -45,075    128.,170   -27,196    1,00  66..64   N
ATOM  2510  CA   LEU  A  332   -45..666   127,708    -25..944   1,00  63,.05   C
ATOM  2511  C    LEU  A  332   -46.,876   128..590   -25,678    I,00  64.36    C
ATOM  2512  O    LEU  A  332   -47,945    128..097   -25,340    1,00  65..04   0
ATOM  2513  CB   LEU  A  332   -44 .669   127,756    -24 .775   1,00  55,74    C
ATOM  2514  CG   LEU  A  332   -45,121    127..222   -2.3.,397  I,00  59..30   C
ATOM  2515  CD1  LEU  A  332   -45,591    125..775   -23,461    1,00  53..39   C
ATOM  2516  CD2  LEU  A  332   -44 .046   127,375    -22.317    1,00  49,14    C
ATOM  2517  N    THR  A  333   -46,692    129.,896   -25..848   1,00  61.67    N
ATOM  2518  CA   THR  A  333   -47,762    130..875   -25,641    1,00  63..81   C
ATOM  2519  C    THR  A  333   -48..998   1.30.,551  -26.483    1.00  68,.10   C
ATOM  2520  O    THR  A  333   -50..096   130.,406   -25..947   1,00  71.80    0
ATOM  2521  CB   THR  A  333   -47,291    132. 298   -25,971    1,00  61,39    C
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ATOM  2522  OG1  THR  A  333   -46.327  132.718  -25.000  1.00  57.81   O
ATOM  2523  CG2  THR  A  333   --48,481 133.285  -25,977  1,00  61.31   C
ATOM  2524  N    LEU  A  3.34  -48.804  130,422  -27.793  1.00  64,21   N
ATOM  2525  CA   LEU  A  334   -49,870  130:006  -28:696  1.00  69.99   C
ATOM  2526  C    LEU  A  334   -50.512  128.709  -28,230  1,00  72,35   C
ATOM  2527  O    LEU  A  3.34  -51.733  128,554  -28:291  1.00  77,26   0
ATOM  2528  CB   LEU  A  334   -49.345  129,825  -30.128  1,00  67,01   C
ATOM  2529  CG   LEU  A  334   -50.434  129.373  -31,107  1,00  71,46   C
ATOM  2530  GDI  LEU  A  334   -51.467  130.493  -31:242  1,00  67.67   C
ATOM  2531  CD2  LEU  A  334   -49.889  128,955  -32 .469  1,00  62,07   C
ATOM  2532  N    LEU  A  335   -49,676  127.789  -27,757  1,00  75.07   N
ATOM  2533  CA   LEU  A  335   -50.095  126.431  -27.408  1,00  73.85   C
ATOM  2534  C    LEU  A  335   -50.969  126,384  -26.159  1,00  72,32   C
ATOM  2535  O    LEU  A  335   -51.872  125:559  -26.062  1.00  71.19   0
ATOM  2536  CB   LEU  A  335   -48,863  125.543  -27,211  1,00  73.72   C
ATOM  2537  CG   LEU  A  3.35  -48.993  124,026  -27.208  1.00  77,58   C
ATOM  2538  CD1  LEU  A  335   -49.237  123:520  -25:805  1.00  74.79   C
ATOM  2539  CD2  LEU  A  335   -50.102  123.594  -28,151  1,00  78,11   C
ATOM  2540  O    LYS  A  3.36  -53.908  127,344  -23:907  1.00  77,83   0
ATOM  2541  N    LYS  A  336   -50.689  127,248  -25.192  1,00  68,82   N
ATOM  2542  CA.  LYS  A  336   -51,507  127.268  -23,998  1,00  72,59   C
ATOM  2543  C    LYS  A  336   -52 .881 127.787  -24:419  1,00  77.37   C
ATOM  2544  CB   LYS  A  336   -50.863  128,120  ~22.895  1,00  70.30   C
ATOM  2545  CG   LYS  A  336   -49,953  127.323  -21,941  1,00  68.73   C
ATOM  2546  CD   LYS  A  336   -48.942  128:218  -21:239  1,00  64.22   C
ATOM  2547  CE   LYS  A  336   -48.167  127,483  -20.163  1,00  58,47   C
ATOM  2548  NZ   LYS  A  336   -47,266  128:421  -19,410  1,00  60.89   N
ATOM  2549  O    ALA  A  337   -56,172  128:093  -26,111  1,00  82.21   0
ATOM  2550  N    ALA  A  337   -52.885  128,680  -25.404  1,00  75,11   N
ATOM  2551  CA   ALA  A  337   -54:115  129:293  -25:894  1.00  79.74   C
ATOM  2552  C    ALA  A  337   -55,037  128.274  -26,554  1,00  80.12   C
ATOM  2553  CB   ALA  A  3.37  -53.798  130,424  -26:868  1.00  73,66   C
ATOM  2554  O    LEU  A  338   -57.136  125:187  -27:656  1,00  79.17   0
ATOM  2555  N    LEU  A  338   -54,555  127.613  -27,605  1,00  77,70   N
ATOM  2556  CA   LEU  A  3.38  -55..379  126,658  -28:.349  1,00  76,72   C
ATOM  2557  C    LEU  A  338   -56.023  125,643  -27.410  1,00  79,07   C
ATOM  2558  CB   LEU  A  338   -54,562  125.934  -29,428  1,00  74,21   C
ATOM  2559  CG   LEU  A  338   -53:791  126:823  -30:411  1,00  77.85   C
ATOM  2560  GDI  LEU  A  338   -53.342  126,047  -31.630  1,00  80,16   C
ATOM  2561  CD2  LEU  A  338   -54,600  128:024  -.30,829  1,00  76.74   C
ATOM  2562  O    VAL  A  339   -57,954  124.535  -24,137  1,00  74.97   0
ATOM  2563  N    VAL  A  339   -55.338  125,314  -26.319  1,00  78,17   N
ATOM  2564  CA   VAL  A  339   -55.887  124:390  -25.335  1.00  78.68   C
ATOM  2565  C    VAL  A  339   -56,907  125.091  -24,457  1,00  74.87   C
ATOM  2566  CB   VAL  A  3.39  -54.777  123,768  -24:451  1.00  80,05   C
ATOM  2567  CGI  VAL  A  339   -55.360  123:146  -23:163  1.00  72.40   C
ATOM  2568  CG2  VAL  A  339   -53,981  122.745  -25,258  1,00  73,59   C
ATOM  2569  O    AP.G A  340   -59.881  127,397  -23:431  1,00  75,10   0
ATOM  2570  N    ARG  A  340   -56.601  126,317  -24.066  1,00  72,02   N
ATOM  2571  CA.  ARG  A  340   -57,515  127.055  -23,222  1,00  78,68   C
ATOM  2572  C    ARG  A  340   -58:793  127.389  -23:996  1,00  79.22   C
ATOM  2573  CB   ARG  A  340   -56.845  128,315  ~22.686  1,00  74,00   C
ATOM  2574  CG   ARG  A  340   -55,991  128:062  -21,458  1,00  73.92   C
ATOM  2575  CD   ARG  A  340   -56:375  129:027  -20:354  1,00  79.49   C
ATOM  2576  NE   ARG  A  340   -55.596  128,868  -19.126  1,00  80,14   N
ATOM  2577  CZ   ARG  A  340   -55,761  127.879  -18,254  1,00  76.12   C
ATOM  2578  NH1  ARG  A  340   -56,660  126.932  -18,488  1,00  74.03   N
ATOM  2579  NH2  ARG  A  340   -55.019  127,833  -17.154  1,00  70,19   N
ATOM  2580  O    GLN  A  341   -61:761  126:814  -26.756  1.00  89.98   0
ATOM  2581  N    GLN  A  341   -58,645  127.624  -25,298  1,00  80.10   N
ATOM  2582  CA   GLN  A  341   -59:756  127,974  -26:171  1.00  76,02   C
ATOM  2583  C    GLN  A  341   -60..540  126:756  -26.653  1.00  79.23   C
ATOM  2584  CB   GLN  A  341   -59,253  128.762  -27,385  1,00  75,86   C
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ATOM	2585	O	GLN	A	342	-61..599	122..558	-26..700	1,00	83..65	O
ATOM	2586	N	GLN	A	342	--59,857	125..658	-26,958	1,00	74.55	N
ATOM	2587	CA	GLN	A	342	-60..542	124,517	-27.547	1.00	70,.98	C
ATOM	2588	C	GLN	A	342	-60..624	123..297	-26..645	1,00	79..54	C
ATOM	2589	CB	GLN	A	342	-59.,871	124 .110	-28,851	1,00	71.13	C
ATOM	2590	CG	GLN	A	342	-59..584	125,247	-29..811	1.00	69,.39	C
ATOM	2591	CD	GLN	A	342	-58..972	124.,748	-31..106	1,00	78,.38	C
ATOM	2592	OE1	GLN	A	342	-59.,113	123. 578	-31.,463	1,00	80..68	0
ATOM	2593	NE2	GLN	A	342	-58..287	125.,629	-31.,814	1,00	79..87	N
ATOM	2594	O	LEU	A	343	-58..408	121.,111	-23..097	1,00	81,99	O
ATOM	2595	N	LEU	A	343	-59,605	123..062	-25,825	1,00	82.95	N
ATOM	2596	CA	LEU	A	343	-59..538	121..799	-25..087	1,00	81.17	C
ATOM	2597	C	LEU	A	343	-59. 216	121.,897	-23 .593	1,00	8.1 ,26	C
ATOM	2598	CB	LEU	A	343	-58..502	120..886	-25,747	1,00	74.32	C
ATOM	2599	CG	LEU	A	343	-59,001	119..608	-26,424	1,00	86..01	C
ATOM	2600	CD1	LEU	A	343	-60..524	119.,470	-26...315	1.00	94,03	C
ATOM	2601	CD2	LEU	A	343	-58..554	119..533	-27..879	1,00	79..35	C
ATOM	2602	O	PRO	A	344	-59.,215	121 .640	-19,497	1,00	79..00	0
ATOM	2603	N	PP.0	A	344	-59..874	122.,817	-22..855	1.00	82,10	N
ATOM	2604	CA	PRO	A	344	-59..502	123,019	-21 .444	1,00	81,14	C
ATOM	2605	C	PRO	A	344	-59.,704	121 .753	-20.,623	1,00	80..04	C
ATOM	2606	CB	PRO	A	344	-60..449	124,135	-20..976	1,00	81.02	C
ATOM	2607	CG	PRO	A	344	-60..968	124.,755	—22.229	1,00	79,.73	C
ATOM	2608	CD	PRO	A	344	-61.,034	123..642	-2.3.,228	1,00	78..47	C
ATOM	2609	N	GLU	A	345	-60..412	120..796	-21.,211	1,00	79..24	N
ATOM	2610	CA	GLU	A	345	-60. 541	119,463	-20. 643	1,00	84,45	C
ATOM	2611	C	GLU	A	345	-59,177	118..777	-20.,488	1,00	82.95	C
ATOM	2612	O	GLU	A	345	-59,079	117 .693	-19.,907	1,00	87.55	0
ATOM	2613	CB	GLU	A	345	-61. 460	118.,604	-21 .522	1,00	84,24	C
ATOM	2614	N	LYS	A	346	-58..122	119..398	-21.,004	1,00	81.61	N
ATOM	2615	CA	LYS	A	346	-56,819	118..736	-21.,037	1,00	80..28	C
ATOM	2616	C	LYS	A	346	-55..675	119.,520	-20..372	1.00	76,.15	C
ATOM	2617	O	LYS	A	346	-54.638	118..938	-20..061	1,00	75..94	0
ATOM	2618	CB	LYS	A	346	-56.,453	118. 417	-22.,489	1,00	70..62	C
ATOM	2619	N	TYR	A	347	-55..873	120,817	-20..130	1.00	76,.01	N
ATOM	2620	CA	TYR	A	347	-54..803	121.,696	-19..633	1,00	74,44	C
ATOM	2621	C	TYR	A	347	-54 ,071	121 .201	-18.,364	1,00	73..61	C
ATOM	2622	O	TYR	A	347	-52..850	121.,279	-18..313	1,00	76..22	O
ATOM	2623	CB	TYR	A	347	-55. 356	12.3.,115	-19. 388	1,00	70,55	C
ATOM	2624	CG	TYR	A	347	-54.,306	124..214	-19.,217	1,00	69..11	C
ATOM	2625	CD1	TYR	A	347	-53.,639	124 .391	-18.,006	1,00	66..87	C
ATOM	2626	CD2	TYR	A	347	-54. 005	125.,092	-20. 259	1,00	68,99	C
ATOM	2627	CE1	TYR	A	347	-52..689	125..396	-17 ,841	1,00	62.28	C
ATOM	2628	CE2	TYR	A	347	-53.,047	126..098	-20,102	1,00	63..47	C
ATOM	2629	CZ	TYR	A	347	-52...395	126,239	-18..892	1.00	6.3,.42	C
ATOM	2630	OH	TYR	A	347	-51..446	127 ,224	-18..724	1,00	69..38	0
ATOM	2631	N	LYS	A	348	-54 ,775	120. 702	-17 ,348	1,00	73..12	N
ATOM	2632	CA	LYS	A	348	-54..086	120,337	-16..098	1.00	72,77	C
ATOM	2633	C	LYS	A	348	-53..130	119.,171	-16..309	1,00	78,.00	C
ATOM	2634	0	LYS	A	348	-52.,063	119. 107	-15.,697	1,00	77.41	0
ATOM	2635	CB	LYS	A	348	-55..077	119..980	-14 .987	1,00	71 .74	C
ATOM	2636	N	GLU	A	349	-53..519	118.,237	-17 .167	1,00	75,.53	N
ATOM	2637	CA	GLU	A	349	-52.,657	117 .099	-17,452	1,00	77.67	C
ATOM	2638	C	GLU	A	349	-51..409	117 ,629	-18..132	1,00	74.83	C
ATOM	2639	O	GLU	A	349	-50. 321	117 ,591	-17 .560	1,00	75,01	O
ATOM	2640	CB	GLU	A	349	-53.,370	116..068	-18.,335	1,00	76..54	C
ATOM	2641	CG	GLU	A	349	-52.,725	114 .686	-18.,351	1,00	82.49	C
ATOM	2642	CD	GLU	A	349	-53. 572	113.,650	-19. 094	1,00	89,55	C
ATOM	2643	OE1	GLU	A	349	-54.708	113..992	-19.,497	1,00	87.73	0
ATOM	2644	OE2	GLU	A	349	-53.,103	112..499	-19,272	1,00	87.56	0
ATOM	2645	N	ILE	A	350	-51..617	118.,180	-19...327	1.00	70,.85	N
ATOM	2646	CA	ILE	A	350	-50..586	118..722	-20..208	1,00	65..08	C
ATOM	2647	C	ILE	A	350	-49.,551	119. 645	-19,560	1,00	68..47	C

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ATOM   2648  O    ILE A 350    -48..377 119..605 -19..926  1.00 71.04     O
ATOM   2649  CB   ILE A 350    -51.,240 119..497 -21.,366  1,00 66..46    C
ATOM   2650  CGI  ILE A 350    -52..157 118.,585 -22..179  1,00 66,.96    C
ATOM   2651  CG2  ILE A 350    -50..203 120.097  -22..270  1.00 66..56    C
ATOM   2652  GDI  ILE A 350    -52.,768 119. 261 -23,384   1,00 67.92     C
ATOM   2653  N    PHE A 351    -49..948 120,460  -18.590   1,00 68,.37    N
ATOM   2654  CA   PHE A 351    -49..015 121.,457 -18..066  1,00 66,.81    C
ATOM   2655  C    PHE A 351    -48,655  121.327  -16,590   1,00 66.,37    C
ATOM   2656  O    PHE A 351    -47.813  122..080 -16..085  1,00 64.73     O
ATOM   2657  CB   PHE A 351    -49..574 122.,842 -18..341  1,00 65,.62    C
ATOM   2658  CG   PHE A 351    -49.,696 123..141 -19,795   I,00 68..65    C
ATOM   2659  CD1  PHE A 351    -48..561 123..387 -20.557   1,00 65..40    C
ATOM   2660  CD2  PHE A 351    -50. 935 123,150  -20. 410  1,00 65,50     C
ATOM   2661  CE1  PHE A 351    -48..665 123.. 657 -21.. 908 1.00 66..73    C
ATOM   2662  CE2  PHE A 351    -51.,051 123..418 -21.,752  1,00 64.69     C
ATOM   2663  CZ   PHE A 351    -49..916 123,669  -22..507  1,00 67,67     C
ATOM   2664  N    PHE A 352    -49..256 120.353  -15..913  1.00 69..25    N
ATOM   2665  CA.  PHE A 352    -49.,021 120. 159 -14,479   1,00 70.,06    C
ATOM   2666  C    PHE A 352    -48..613 118.,737 -14.098   1,00 65,.14    C
ATOM   2667  O    PHE A 352    -47.922  118.,530 -13..096  1,00 64,26     O
ATOM   2668  CB   PHE A 352    -50.,276 120. 531 -13.,690  1,00 67,01     C
ATOM   2669  CG   PHE A 352    -50..440 121.. 999 -13.. 462 1,00 65..80    C
ATOM   2670  CD2  PHE A 352    -49..910 122.,593 -12..329  1,00 64,67     C
ATOM   2671  CDI  PHE A 352    -51.,140 122..778 -14,369   I,00 66..45    C
ATOM   2672  CE2  PHE A 352    -50.. 061 123..940 -12.. 107 1,00 72.29     C
ATOM   2673  CE1  PHE A 352    -51. 299 124,123  -14 .159   1,00 64,86     C
ATOM   2674  CZ   PHE A 352    -50.,759 124..711 -13.,025  I,00 73..23    C
ATOM   2675  N    ASP A 353    -49,080  117.768  -14,884   1,00 65..01    N
ATOM   2676  CA   ASP A 353    -48. 899 116,364  -14 .562   1,00 67,97     C
ATOM   2677  C    ASP A 353    -47.537  115.. 890 -15.. 063 1.00 69..50    C
ATOM   2678  O    ASP A 353    -47,342  115..650 -16,256   1,00 66..30    0
ATOM   2679  CB   ASP A 353    -50..023 115.,505 -15.159   1,00 65,.25    C
ATOM   2680  CG   ASP A 353    -50..140 114.140  -14 .475   1.00 76..77    C
ATOM   2681  OD1  ASP A 353    -49.,944 114.076  -13.,239  1,00 77,59     0
ATOM   2682  OD2  ASP A 353    -50..421 113.,131 -15.163   1,00 78,.63    0
ATOM   2683  O    GLN A 354    -44.216  113.,420 -15..425  1,00 74,03     0
ATOM   2684  N    GLN A 354    -46,599  115. 768 -14 ,134   1,00 67,57     N
ATOM   2685  CA   GLN A 354    -45.258  115.. 323 -14.466   1,00 73..32    C
ATOM   2686  C    GLN A 354    -45. 193 113.,848 -14 .831   1,00 71,75     C
ATOM   2687  CB   GLN A 354    -44 ,310 115.598  -13.,308  I,00 69..09    C
ATOM   2688  CG   GLN A 354    -44,199  117 .056  -12.,972  1,00 71.53     C
ATOM   2689  CD   GLN A 354    -43. 185 117 ,299  -11.886   1,00 76,32     C
ATOM   2690  OE1  GLN A 354    -42..413 116.. 400 -11 .540   1.00 63..72    0
ATOM   2691  NE2  GLN A 354    -43,183  118..517 -11,325   1,00 75..88    N
ATOM   2692  O    SER A 355    -46..536 110.,197 -16.641   1,00 74,09     0
ATOM   2693  N    SER A 355    -46..221 113.. 076 -14 .486   1.00 71.16     N
ATOM   2694  CA.  SER A 355    -46,218  111.640  -14 ,760   1,00 63.,85    C
ATOM   2695  C    SER A 355    -46..606 111,339  -16.197   1,00 68,.16    C
ATOM   2696  CB   SER A 355    -47.166  110.,913 -13..814  1,00 70,.82    C
ATOM   2697  OG   SER A 355    -48,514  111.250  -14 ,088   1,00 74,96     0
ATOM   2698  O    LYS A 356    -45.832  113.. 797 -18.. 869 1,00 61.81     0
ATOM   2699  N    LYS A 356    -47.025  112.,367 -16..920  1,00 67,46     N
ATOM   2700  CA   LYS A 356    -47 ,505 112.190  -18.,281  I,00 68..53    C
ATOM   2701  C    LYS A 356    -46.549  112..874 -19.. 244 1,00 65..65    C
ATOM   2702  CB   LYS A 356    -48. 932 112.,744 -18. 432  1,00 69,91     C
ATOM   2703  O    ASM A 357    -45,635  114.254  -23,369   I,00 65..49    0
ATOM   2704  N    ASM A 357    -46,543  112.. 427 -20,492   1,00 67.41     N
ATOM   2705  CA   ASN A 357    -45. 515 112.,865 -21.429   1,00 64,88     C
ATOM   2706  C    ASN A 357    -45.873  114.140  -22.. 166 1.00 67.33     C
ATOM   2707  CB   ASM A 357    -45,209  Ill .755  -22.,431  1,00 65..90    C
ATOM   2708  CG   ASN A 357    -44 .433 110.,609 -21..807  1,00 62,73     C
ATOM   2709  OD1  ASN A 357    -43..979 110.. 701 -20..663  1.00 59..72    0
ATOM   2710  ND2  ASN A 357    -44 ,266 109.530  -22.,559  1,00 65.,07    N
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ATOM    2711  O    GLY  A  358      -44.638  116.,961  -21.,113   1.00  67.96          O
ATOM    2712  N    GLY  A  358      --46„436  115..097  -21.,430   1,00  66..67         N
ATOM    2713  CA   GLY  A  358      -46..765  116,404   -21..972   1.00  64,.30         C
ATOM    2714  c    GLY  A  358      -45..688  117 ,385  -21.,577   1.00  64.13          c
ATOM    2715  O    TYR  A  359      -43,248   119. 758  -19,801    1,00  64.42          0
ATOM    2716  N    TYR  A  359      -45.947   118.,682  -21..747   1.00  62,.55         N
ATOM    2717  CA   TYR  A  359      -44.962   119.,713  -21 .455   1,00  56,.59         c
ATOM    2718  C    TYR  A  359      -44 ,432  119. 556  -20.,047   1,00  61 .9.3         c
ATOM    2719  CB   TYR  A  359      -45,563   121.,109  -21.,638   1,00  60..85         c
ATOM    2720  CG   TYR  A  359      -44.541   122.,222  -21 .627   1,00  58,.42          c
ATOM    2721  CDI  TYR  A  359      -43,698   122..430  -22.,720   I,00  55..18          c
ATOM    2722  CD2  TYR  A  359      -44,410   123.,061  -20,528    1,00  57.39          c
ATOM    2723  CE1  TYR  A  359      -42 .750  123,453   -22.718    1,00  53,.25         c
ATOM    2724  CE2  TYR  A  359      -43,466   124.,079  -20,515    1.00  59..00          c
ATOM    2725  CZ   TYR  A  359      -42.,636  124 .268  -21.,613   1,00  57.68          c
ATOM    2726  OH   TYR  A  359      -41 .696  125,273   -21..597   1.00  56,.23          0
ATOM    2727  O    ALA  A  360      -42,876   118.,100  -16.,959   1.00  63..50          0
ATOM    2728  N    ALA  A  360      -45,313   119. 170  -19,129    1,00  66.,0.1         N
ATOM    2729  CA   ALA  A  360      -44 .943  118.,997  -17.729    1.00  60,.66          c
ATOM    2730  c    ALA  A  360      -43.907   117 ,903  -17 .589   1,00  63,.50          c
ATOM    2731  CB   ALA  A  360      -46,158   118. 677  -16,892    1,00  55..45          c
ATOM    2732  O    GLY  A  361      -40,914   115.,523  -18.,533   1,00  63..87          0
ATOM    2733  N    GLY  A  361      -44.197   116.,744  -18..168   1,00  61,88          N
ATOM    2734  CA   GLY  A  361      -43,277   115.625   -18.,120   I,00  64.39          C
ATOM    2735  C    GLY  A  361      -42.,016  115.,949  -18.,891   1,00  64.83          c
ATOM    2736  O    TYR  A  362      -38. 926  117 ,958  -20. 186   1,00  6.1. ,53         0
ATOM    2737  N    TYR  A  362      -42.,203  116.719   -19,958    I,00  63..84          N
ATOM    2738  CA   TYR  A  362      -41 ,131  117 .216  -20,806    1,00  63..14          C
ATOM    2739  C    TYR  A  362      -40. 134  118.,078  -20. 021   1,00  6.3 ,34          C
ATOM    2740  CB   TYR  A  362      -41 ,750  118.,010  -21.,950   1.00  61 .76          c
ATOM    2741  CG   TYR  A  362      -40,803   118..544  -22.,978   1,00  59..70          c
ATOM    2742  CD1  TYR  A  362      -39.848   117,720   -23.565    1.00  64,33           c
ATOM    2743  CD2  TYR  A  362      -40,877   119.,866  -23,389    1.00  56..43          c
ATOM    2744  CE1  TYR  A  362      -38.,981  118. 202  -24.,529   1,00  58..47          c
ATOM    2745  CE2  TYR  A  362      -40.020   120,367   -24...355   1.00  59,.09          c
ATOM    2746  CZ   TYR  A  362      -39.071   119.,525  -24.922    1,00  60,.47          c
ATOM    2747  OH   TYR  A  362      -38.,203  119. 994  -25,885    1,00  58..85          0
ATOM    2748  O    1LE  A  363      -38.,197  119.,587  -16.,723   1,00  58..58          0
ATOM    2749  N    ILE  A  363      -40. 646  118.,926  -19. 141   1,00  6.3 ,49          N
ATOM    2750  CA   ILE  A  363      -39,815   119.902   -18.,447   I,00  60..13          c
ATOM    2751  C    ILE  A  363      -39,355   119..429  -17,081    1,00  54.13          c
ATOM    2752  CB   ILE  A  363      -40. 576  121 ,250  -18. 281   1,00  57,63          c
ATOM    2753  CGI  ILE  A  363      -40,872   121.,853  -19.,649   1.00  56..20          c
ATOM    2754  CG2  ILE  A  363      -39,795   122..230  -17,422    1,00  51.42          c
ATOM    2755  CD1  ILE  A  363      -39.652   122.,213  -20..418    1.00  57,87          c
ATOM    2756  O    ASP  A  364      -39,478   116.,573  -13..629   1.00  62.67          0
ATOM    2757  N    ASP  A  364      -40.,271  118. 872  -16,304    1,00  59..61          N
ATOM    2758  CA   ASP  A  364      -39.997   118.,543  -14.908    1.00  59,.99          c
ATOM    2759  c    ASP  A  364      -39.931   117 ,039  -14 .679   1,00  63,.76          c
ATOM    2760  CB   ASP  A  364      -41 ,071  119. 161  -14 ,003   1,00  66..55          c
ATOM    2761  CG   ASP  A  364      -41,116   120.,687  -14 ,094   1,00  71.01          c
ATOM    2762  OD1  ASP  A  364      -40.038   121.,312  -14 .012   1,00  71,18          0
ATOM    2763  OD2  ASP  A  364      -42.,225  121..255  -14,246    I,00  70..89          0
ATOM    2764  O    GLY  A  365      -38.,247  114 ,877  -16.,572   1,00  68..73          0
ATOM    2765  N    GLY  A  365      -40. 393  116,280   -15. 665   1,00  59,76           N
ATOM    2766  CA   GLY  A  365      -40.,407  114.844   -15.,545   I,00  66..14          c
ATOM    2767  C    GLY  A  365      -39,258   114 .226  -16,305    1,00  66..10          c
ATOM    2768  O    GLY  A  366      -37. 528  113.,213  -19. 468   1,00  77,66           0
ATOM    2769  N    GLY  A  366      -39,407   112.,959  -16.,649   1.00  64.37           N
ATOM    2770  CA   GLY  A  366      -38.,398  112..311  -17,452    1,00  72.83           c
ATOM    2771  C    GLY  A  366      -38..514  112.,789  -18.881    1.00  72,.16          c
ATOM    2772  O    ALA  A  367      -38.,537  114 ,453  -21..635   1.00  63..38          0
ATOM    2773  N    ALA  A  367      -39,746   112.780   -19,387    1,00  66..61          N
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ATOM	2774	CA	ALA	A	367	-40,066	112.769	-20,819	1.00	70.90	C
ATOM	2775	C	ALA	A	367	--38,999	113.313	-21,768	1,00	64.42	C
ATOM	2776	CB	ALA	A	367	-41..387	113,523	-21:059	1,00	65,57	C
ATOM	2777	N	SER	A	368	-38..631	112:490	-22:739	1.00	55,94	N
ATOM	2778	CA.	SER	A	368	-37,730	112.936	-23,792	1,00	61,36	C
ATOM	2779	C	SER	A	368	-38.490	113,749	-24:824	1,00	62,87	C
ATOM	2780	O	SER	A	368	-39:717	113,777	-24.827	1,00	62,44	O
ATOM	2781	CB	SER	A	368	-37,050	111.749	-24,472	1,00	59,76	C
ATOM	2782	OG	SER	A	368	-37.930	Ill:101	-25:364	1,00	61.31	0
ATOM	2783	N	GLN	A	369	-37.761	114,414	-25.708	1,00	59,63	N
ATOM	2784	CA	GLN	A	369	-38,404	115.186	-26,754	1,00	57.28	C
ATOM	2785	C	GLN	A	369	-39.274	114.288	-27:616	1,00	64.74	C
ATOM	2786	O	GLN	A	369	-40..341	114,698	-28.079	1,00	63,06	O
ATOM	2787	CB	GLN	A	369	-37.375	115:894	-27:616	1.00	53,86	C
ATOM	2788	CG	GLN	A	369	-37,950	116.514	-28,849	1,00	56.62	C
ATOM	2789	CD	GLN	A	369	-36.886	117,090	-29:733	1,00	58,17	C
ATOM	2790	OE1	GLN	A	369	-36,138	117:982	-29.318	1.00	59.98	0
ATOM	2791	NE2	GLN	A	369	-36,780	116.570	-.30,954	1,00	54.50	N
ATOM	2792	N	GLU	A	370	-38.819	113,057	-27,827	1,00	65,56	N
ATOM	2793	CA	GLU	A	370	-39.561	112,143	-28,666	1,00	62,98	C
ATOM	2794	C	GLU	A	370	-40,853	111.725	-27,983	1,00	64.55	C
ATOM	2795	O	GLU	A	370	-41.888	Ill:633	-28:631	1,00	68.73	O
ATOM	2796	CB	GLU	A	370	-38.734	110,909	-29.019	1,00	68,06	C
ATOM	2797	CG	GLU	A	370	-39,385	110.050	-.30,095	1,00	64.93	C
ATOM	2798	CD	GLU	A	370	-38.554	108.836	-30:485	1,00	82.49	C
ATOM	2799	OE1	GLU	A	370	-37.771	108,337	-29.645	1,00	87,66	0
ATOM	2800	OE2	GLU	A	370	-38,694	108..376	-31,639	1,00	87,88	0
ATOM	2801	N	GLU	A	371	-40,796	Ill:474	-26,682	1,00	61.10	N
ATOM	2802	CA	GLU	A	371	-41.976	111,032	-25.949	1,00	63,03	C
ATOM	2803	C	GLU	A	371	-43.025	112:153	-25.868	1.00	66.33	C
ATOM	2804	O	GLU	A	371	-44,235	Ill.923	-25,934	1,00	65.36	0
ATOM	2805	CB	GLU	A	371	-41.575	110,552	-24:554	1,00	63,50	C
ATOM	2806	CG	GLU	A	371	-40.571	109:401	-24,604	1.00	66.07	C
ATOM	2807	CD	GLU	A	371	-40,222	108.841	-23,239	1,00	68.14	C
ATOM	2808	OE1	GLU	A	371	-40.140	107,605	-23:121	1,00	72,14	0
ATOM	2809	OE2	GLU	A	371	-40.011	109,625	—22.291	1,00	73.51	0
ATOM	2810	N	PHE	A	372	-42,530	113.371	-25,739	1,00	63.62	N
ATOM	2811	CA	PHE	A	372	-43:360	114.550	-25:743	1,00	64,83	C
ATOM	2812	C	PHE	A	372	-44.047	114,703	-27.097	1,00	67,85	C
ATOM	2813	O	PHE	A	372	-45,260	114.890	-27,171	1,00	68.88	0
ATOM	2814	CB	PHE	A	372	-42,504	115:774	-25,405	1,00	62.59	C
ATOM	2815	CG	PHE	A	372	-43.205	117,077	-25.569	1,00	63,24	C
ATOM	2816	CD1	PHE	A	372	-44:316	117:388	-24,800	1.00	63.79	C
ATOM	2817	CD2	PHE	A	372	-42,734	118.010	-26,463	1,00	63.87	C
ATOM	2818	CE1	PHE	A	372	-44.954	118,596	-24:935	1,00	61,69	C
ATOM	2819	CE2	PHE	A	372	-43.368	119:226	-26.603	1.00	64,95	C
ATOM	2820	CZ	PHE	A	372	-44,483	119.518	-25,836	1,00	64.09	C
ATOM	2821	N	TYR	A	373	-43.271	114,598	-28:167	1,00	65,72	N
ATOM	2822	CA	TYR	A	373	-43.805	114,775	-29.501	1,00	62,96	C
ATOM	2823	C	TYR	A	373	-44,895	113.765	-29,826	1,00	70.77	C
ATOM	2824	O	TYR	A	373	-45:905	114:136	-30:434	1,00	70.16	0
ATOM	2825	CB	TYR	A	373	-42.704	114,677	-30.541	1,00	60,48	C
ATOM	2826	CG	TYR	A	373	-41,871	115:927	-.30,692	1,00	65.84	C
ATOM	2827	CD1	TYR	A	373	-42:180	117:099	-30:009	1,00	58.80	C
ATOM	2828	CD2	TYR	A	373	-40.774	115,934	-31.538	1,00	63,36	C
ATOM	2829	CE1	TYR	A	373	-41,399	118:234	-.30,165	1,00	58.91	C
ATOM	2830	CE2	TYR	A	373	-40,007	117.053	-31,705	1,00	60.62	C
ATOM	2831	CZ	TYR	A	373	-40..309	118,195	-31.021	1,00	62,11	C
ATOM	2832	OH	TYR	A	373	-39.497	119:288	-31.221	1.00	63.67	0
ATOM	2833	N	LYS	A	374	-44,704	112.502	-29,432	1,00	69.49	N
ATOM	2834	CA	LYS	A	374	-45.678	Ill,451	-29:761	1,00	70,38	C
ATOM	2835	C	LYS	A	374	-46.973	Ill:636	-28.962	1.00	78.94	C
ATOM	2836	O	LYS	A	374	-48,072	111..339	-29,454	1,00	77,15	0

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ATOM    2837  CB   LYS  A  374     -45..108   110..052   -29..510   1.00   58..86          c
ATOM    2838  N    PHE  A  375     --46,831   112..131   -27,735    1,00   72.05           N
ATOM    2839  CA   PHE  A  375     -47.967    112.,386   -26..864   1,00   72,29           c
ATOM    2840  c    PHE  A  375     -48..796   113.,580   -27..316   1.00   73..36          c
ATOM    2841  0    PHE  A  375     -50.,023    113. 518   -27,386    1,00   76..93          0
ATOM    2842  CB   PHE  A  375     -47.473    112.,615   -25..439   1,00   70,.65          c
ATOM    2843  CG   PHE  A  375     -48..512   113.,165   -24.511    1,00   69,.70          c
ATOM    2844  GDI  PHE  A  375     -48,718    114.539    -24.,397   1,00   73..69          c
ATOM    2845  CD2  PHE  A  375     -49..256   112.,318   -23,717    1,00   70..13          c
ATOM    2846  CE1  PHE  A  375     -49..670   115.,054   -23..519   1,00   74,23           c
ATOM    2847  CE2  PHE  A  375     -50.,205    112.827    -22.,833   I,00   76..25          c
ATOM    2848  CZ   PHE  A  375     -50..409   114.197    -22.,735   1,00   71.77           c
ATOM    2849  N    ILE  A  376     -48. 118   114,681    -27.594    1,00   72,91           N
ATOM    2850  CA   ILE  A  376     -48..807   115.,926   -27,861    1.00   75..93          c
ATOM    2851  C    ILE  A  376     -49,276    116..003   -29,310    1,00   75..54          c
ATOM    2852  O    ILE  A  376     -50..070   116,868    -29..666   1,00   78,.07          0
ATOM    2853  CB   ILE  A  376     -47,910    117,140    -27..545   1.00   74.95           c
ATOM    2854  CGI  ILE  A  376     -48,772    118. 342   -27,141    1,00   70..75          c
ATOM    2855  CG2  ILE  A  376     -46..992   117,469    -28..740   1,00   70,.92          c
ATOM    2856  CD1  ILE  A  376     -48..953   119.,342   -28..232   1,00   67,98           c
ATOM    2857  N    LYS  A  377     -48,786    115. 096   -30.,144   1,00   75..72          N
ATOM    2858  CA   LYS  A  377     -49,142    115.,115   -31.,562   1,00   79..33          c
ATOM    2859  c    LYS  A  377     -50..657   114,995    -31..792   1,00   83,.47          c
ATOM    2860  0    LYS  A  377     -51.,235    115.860    -.32.,457   I,00   81.26           0
ATOM    2861  CB   LYS  A  377     -48,403    114.013    -32.,332   1,00   77.08           c
ATOM    2862  N    PP.0 A  378     -51. 308   113.,947   -31. 238   1,00   81,44           N
ATOM    2863  CA   PRO  A  378     -52.,738    113.802    -31.,549   I,00   79.03           c
ATOM    2864  C    FRO  A  378     -53.,586    114.964    -31.,018   1,00   81.84           c
ATOM    2865  O    PRO  A  378     -54. 623   115.,291   -31. 606   1,00   80,56           0
ATOM    2866  CB   PRO  A  378     -53.,114    112.,484   -30.,858   1.00   82.38           c
ATOM    2867  CG   FRO  A  378     -51.,810    Ill.770    -30.,635   1,00   83..55          c
ATOM    2868  CD   PRO  A  378     -50..842   112.,864   -30...353   1,00   75,.93          c
ATOM    2869  N    ILE  A  379     -53..139   115.,568   -29..919   1.00   78..43          N
ATOM    2870  CA.  ILE  A  379     -53.,780    116.752    -29.,357   1,00   75..35          c
ATOM    2871  C    ILE  A  379     -53..768   117,869    -30...389  1,00   80,.85          c
ATOM    2872  O    ILE  A  379     -54..777   118.,533   -30..626   1,00   81,62           0
ATOM    2873  CB   ILE  A  379     -53.,069    117.230    -28,071    1,00   69..81          c
ATOM    2874  CGI  ILE  A  379     -53.,529    116.,424   -26,855    1,00   71.23           c
ATOM    2875  CG2  ILE  A  379     -53. 307   118.,700   -27.838    1,00   72,38           c
ATOM    2876  CD1  ILE  A  379     -53.,012    114.986    -26.,815   I,00   72.73           c
ATOM    2877  N    LEU  A  380     -52.,607    118..058   -31.,005   1,00   83..58          N
ATOM    2878  CA   LEU  A  380     -52. 427   119,046    -32. 058   1,00   81,01           c
ATOM    2879  c    LEU  A  380     -53.,454    118.,857   -33.,171   1.00   81.34           c
ATOM    2880  O    LEU  A  380     -54.,184    119..787   -33.,514   1,00   83..32          0
ATOM    2881  CB   LEU  A  380     -51..003   118.,963   -32..623   1,00   78,.43          c
ATOM    2882  CG   LEU  A  380     -50..170   120,245    -32..549   1.00   78..97          c
ATOM    2883  CD1  LEU  A  380     -50.,288    120. 860   -31,168    1,00   76..86          c
ATOM    2884  CD2  LEU  A  380     -48..710   119,981    -32..887   1,00   73,.84          c
ATOM    2885  O    GLU  A  381     -56..618   117,992    -35..443   1,00   78,.74          0
ATOM    2886  N    GLU  A  381     -53.,519    117.641    -33.,707   1,00   80..18          N
ATOM    2887  CA   GLU  A  381     -54.,370    117,323    -34.,856   1,00   84.30           c
ATOM    2888  c    GLU  A  381     -55..881   117,503    -34..584   1,00   84,31           c
ATOM    2889  CE   GLU  A  381     -54.,077    115.888    -.35.,322  I,00   80..01          c
ATOM    2890  CG   GLU  A  381     -52.,640    115..680   -35.,835   1,00   78..62          c
ATOM    2891  CD   GLU  A  381     -52. 234   114,202    -35. 933   1,00   78,36           c
ATOM    2892  OE1  GLU  A  381     -52.,635    113.402    -.35.,063  I,00   76..07          0
ATOM    2893  OE2  GLU  A  381     -51.,510    113..840   -36,883    1,00   79..82          0
ATOM    2894  O    LYS  A  382     -59. 372   118.,980   -33. 095   1,00   91,96           0
ATOM    2895  N    LYS  A  382     -56,324    117,118    -33.,387   1.00   86..27          N
ATOM    2896  CA   LYS  A  382     -57.,728    117.226    -32.,991   1,00   80..75          c
ATOM    2897  C    LYS  A  382     -58..187   118.,683   -32..976   1,00   86,.68          c
ATOM    2898  CB   LYS  A  382     -57..946   116.,592   -31..613   1.00   76..43          c
ATOM    2899  O    MET  A  383     -56.,711    120. 939   -35.,082   1,00   79..33          0
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ATOM 2900 N   MET A 383 -57.231  119.587 -32.,822 1.00 85.70 N
ATOM 2901 CA  MET A 383 --57,501 121.005 -32 ,827 1,00 79.91 C
ATOM 2902 C   MET A 383 -57.168  121,619 -34.169  1.00 80,46 C
ATOM 2903 CB  MET A 383 -56,691  121,698 -31.,746 1.00 81.12 C
ATOM 2904 CG  MET A 383 -56,825  121.074 -.30,394 1,00 77,97 C
ATOM 2905 SD  MET A 383 -55.841  122,005 -29.216  1.00 84,.32 S
ATOM 2906 CE  MET A 383 -54.200  121,700 -29.882  1.00 81,18 C
ATOM 2907 O   ASP A 384 -56,509  125.363 -.33,813 1.00 89.43 0
ATOM 2908 N   ASP A 384 -57.404  122.920 -34,269  1.00 82.81 N
ATOM 2909 CA  ASP A 384 -57.063  123,695 -35.451  1.00 86,75 C
ATOM 2910 C   ASP A 384 -56,394  124.985 -.34,985 1.00 89.25 C
ATOM 2911 CB  ASP A 384 -58.307  123.986 -36,300  1.00 92..31 C
ATOM 2912 CG  ASP A 384 -59.518  124,327 -35.453  1.00 94,30 C
ATOM 2913 OD2 ASP A 384 -60..401 125,074 -35,930  1.00 98.36 0
ATOM 2914 OD1 ASP A 384 -59,578  123.847 -34,299  1.00 94.88 0
ATOM 2915 N   GLY A 385 -55.697  125,660 -35.893  1.00 85,61 N
ATOM 2916 CA  GLY A 385 -54.824  126,749 -35.506  1.00 81.70 C
ATOM 2917 C   GLY A 385 -53,479  126.157 -.35,135 1.00 83.35 C
ATOM 2918 O   GLY A 385 -52 .531  126,868 -34.809  1.00 84,82 0
ATOM 2919 N   THR A 386 -53.412  124,831 -35.185  1.00 79,85 N
ATOM 2920 CA. TH.R A 386 -52 ,180 124.092 -.34,965 1.00 81.88 C
ATOM 2921 C   THR A 386 -51.500  123,876 -36,310  1.00 81.60 C
ATOM 2922 O   THR A 386 -50.897  122,832 -36.565  1.00 77,04 O
ATOM 2923 CB  THR A 386 -52 ,447  122.737 -.34,290 1.00 81.18 C
ATOM 2924 OG1 THR A 386 -52 .969  121.811 -35,254  1.00 77.41 0
ATOM 2925 CG2 THR A 386 -53.443  122,897 -33.162  1.00 80,83 C
ATOM 2926 N   GLU A 387 -51,628  124.875 -.37,175 1.00 84.74 N
ATOM 2927 CA  GLU A 387 -51,120  124.801 -38,535  1.00 82.57 C
ATOM 2928 C   GLU A 387 -49.606  124,716 -38.533  1.00 82,36 C
ATOM 2929 O   GLU A 387 -49.023  123,673 -38.,848 1.00 82.47 O
ATOM 2930 CB  GLU A 387 -51,582  126.019 -39,339  1.00 84.47 C
ATOM 2931 N   GLU A 388 -48.978  125,823 -38.156  1.00 77,76 N
ATOM 2932 CA  GLU A 388 -47.533  125,929 -38.,173 1.00 76.42 C
ATOM 2933 C   GLU A 388 -46,902  125.009 -.37,125 1.00 79.86 C
ATOM 2934 O   GLU A 388 -45.755  124,579 -37.282  1.00 75,.32 0
ATOM 2935 CB  GLU A 388 -47.105  127,379 -37.949  1.00 72,09 C
ATOM 2936 N   LEU A 389 -47,660  124.705 -.36,070 1.00 79.07 N
ATOM 2937 CA  LEU A 389 -47.198  123,820 -35,001  1.00 72.88 C
ATOM 2938 C   LEU A 389 -46.882  122,433 -35.527  1.00 76,50 C
ATOM 2939 O   LEU A 389 -45,792  121.903 -.35,303 1.00 78.71 0
ATOM 2940 CB  LEU A 389 -48,246  123.714 -33,893  1.00 73.85 C
ATOM 2941 CG  LEU A 389 -47.990  124,507 -32.610  1.00 68,35 C
ATOM 2942 CD1 LEU A 389 -47,878  126,002 -32.,879 1.00 65.04 C
ATOM 2943 CD2 LEU A 389 -49,085  124.227 -31,606  1.00 70.25 C
ATOM 2944 N   LEU A 390 -47.845  121,841 -36.219  1.00 78,90 N
ATOM 2945 CA  LEU A 390 -47.676  120,501 -36,768  1.00 77,38 C
ATOM 2946 C   LEU A 390 -46,502  120.419 -.37,742 1,00 77.28 C
ATOM 2947 O   LEU A 390 -45.772  119,435 -37.739  1,00 79,44 O
ATOM 2948 CB  LEU A 390 -48.954  120,051 -37.463  1,00 79,10 C
ATOM 2949 CG  LEU A 390 -48,909  118.642 -.38,049 1,00 77.06 C
ATOM 2950 CD1 LEU A 390 -49,872  117,726 -37,301  1,00 74.51 C
ATOM 2951 CD2 LEU A 390 -49.187  118,652 -39.562  1,00 75,67 C
ATOM 2952 N   VAL A 391 -46,325  121.446 -.38,575 1,00 76.44 N
ATOM 2953 CA  VAL A 391 -45,181  121.519 -39,484  1,00 74.55 C
ATOM 2954 C   VAL A 391 -43.876  121,428 -38.708  1,00 78,28 C
ATOM 2955 O   VAL A 391 -43,021  120.573 -.38,982 1,00 77.43 0
ATOM 2956 CB  VAL A 391 -45,173  122.828 -40,296  1,00 81.41 C
ATOM 2957 CGI VAL A 391 -43.810  123,039 -40.969  1,00 80,40 C
ATOM 2958 CG2 VAL A 391 -46,306  122,832 -41,320  1.00 80.97 C
ATOM 2959 N   LYS A 392 -43,749  122.328 -37,736  1,00 77.14 N
ATOM 2960 CA  LYS A 392 -42.638  122,355 -36.793  1.00 74,38 C
ATOM 2961 C   LYS A 392 -42.378  121,017 -36,090  1.00 71.78 C
ATOM 2962 0   LYS A 392 -41,231  120.607 -.35,980 1,00 76.53 0
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ATOM	2963	CB	LYS	A	392	-42.876	123.448	-35.745	1.00	69.56	C
ATOM	2964	CG	LYS	A	392	--42,606	124.842	-36,255	1,00	70.74	C
ATOM	2965	CD	LYS	A	392	-42.431	125,804	-35.107	1.00	70,45	C
ATOM	2966	CE	LYS	A	392	-42.291	127.231	-35.588	1.00	62.71	C
ATOM	2967	NZ	LYS	A	392	-41,960	128.121	-34,448	1,00	72.21	N
ATOM	2968	N	LEU	A	393	-43.426	120,340	-35.623	1.00	69,96	N
ATOM	2969	CA	LEU	A	393	-43.257	119,078	-34.900	1,00	67,43	C
ATOM	2970	C	LEU	A	393	-42,742	117.967	-35,815	1,00	72.00	C
ATOM	2971	O	LEU	A	393	-42.076	117.025	-35.368	1,00	76.88	0
ATOM	2972	CE	LEU	A	393	-44.571	118,652	-34.253	1,00	64,77	C
ATOM	2973	CG	LEU	A	393	-44,531	117.466	-33,294	1,00	61.86	C
ATOM	2974	CD1	LEU	A	393	-45.574	117.653	-32,224	1,00	63.38	C
ATOM	2975	CD2	LEU	*A*	393	-44.757	116,142	-34.008	1,00	61,69	C
ATOM	2976	N	ASN	A	394	-43.038	118.085	-37.099	1.00	73.02	N
ATOM	2977	CA	ASM	A	394	-42,626	117.077	-38,059	1,00	75.44	C
ATOM	2978	C	ASN	A	394	-41.197	117,297	-38.560	1.00	73,51	C
ATOM	2979	O	ASN	A	394	-40,513	116.348	-38.943	1,00	71.18	0
ATOM	2980	CB	ASN	A	394	-43,604	117.049	-39,232	1,00	81.55	C
ATOM	2981	CG	ASN	A	394	-44.076	115,650	-39.552	1.00	84,58	C
ATOM	2982	OD1	ASN	A	394	-44.837	115,049	-38.783	1,00	85,53	0
ATOM	2983	ND2	ASN	A	394	-43,623	115.117	-40,687	1,00	78.09	N
ATOM	2984	N	ARG	A	395	-40.751	118.550	-38.554	1,00	71.90	N
ATOM	2985	CA	ARG	A	395	-39.353	118,853	-38.827	1,00	72,67	C
ATOM	2986	C	ARG	A	395	-38,556	118.807	-37,518	1,00	73.43	C
ATOM	2987	O	ARG	A	395	-37.455	119.345	-37.444	1,00	70.20	0
ATOM	2988	CB	ARG	*A*	395	-39.209	120,220	-39.502	1,00	57,66	C
ATOM	2989	N	GLU	A	396	-39,125	118.143	-36,507	1,00	71.98	N
ATOM	2990	CA	GLU	A	396	-38,619	118.144	-35,130	1,00	70.09	C
ATOM	2991	C	GLU	*A*	396	-38.053	119,503	-34.701	1,00	69,05	C
ATOM	2992	O	GLU	A	396	-36,886	119.621	-34.335	1.00	68.40	0
ATOM	2993	CB	GLU	A	396	-37,564	117.058	-34,954	1,00	68.79	C
ATOM	2994	CG	GLU	A	396	-38.123	115,645	-35.018	1.00	71,06	C
ATOM	2995	CD	GLU	A	396	-37.051	114.601	-35.303	1,00	80.42	C
ATOM	2996	OE1	GLU	A	396	-36,081	114.904	-36,040	1,00	74.84	0
ATOM	2997	OE2	GLU	A	396	-37.181	113,471	-34.784	1.00	86,65	0
ATOM	2998	O	ASP	A	397	-39.293	123,838	-33.387	1,00	65,61	0
ATOM	2999	N	ASP	A	397	-38,901	120.526	-34,736	1,00	72.22	N
ATOM	3000	CA	ASP	A	397	-38.468	121.903	-34.521	1,00	69.71	C
ATOM	3001	C	ASP	*A*	397	-39.287	122,612	-33.457	1,00	67,74	C
ATOM	3002	CB	ASP	A	397	-38,557	122.679	-35,827	1,00	72.54	C
ATOM	3003	CG	ASP	A	397	-37,231	123.241	-36,253	1,00	79.64	C
ATOM	3004	OD1	ASP	*A*	397	-36.572	123,877	-35.400	1.00	78,00	0
ATOM	3005	OD2	ASP	A	397	-36,845	123.041	-37.432	1.00	82.34	0
ATOM	3006	O	LEU	A	398	-40,650	121.279	-29,695	1,00	67.59	0
ATOM	3007	N	LEU	A	398	-39.957	121,835	-32.616	1.00	66,87	N
ATOM	3008	CA	LEU	A	398	-41.022	122.369	-31.782	1.00	62.07	C
ATOM	3009	C	LEU	A	398	-40,748	122..347	-30,287	1,00	58.16	C
ATOM	3010	CB	LEU	A	398	-42..308	121,593	-32.055	1,00	66,98	C
ATOM	3011	CG	LEU	A	398	-43.483	121,930	-31.148	1,00	60,90	C
ATOM	3012	CD2	LEU	A	398	-44,552	120.874	-31,262	1,00	54.96	C
ATOM	3013	CD1	LEU	A	398	-44.001	123.315	-31.474	1,00	57.66	C
ATOM	3014	O	LEU	A	399	-39.076	122,338	-26.854	1,00	53,96	0
ATOM	3015	N	LEU	A	399	-40,683	123.536	-29,690	1,00	57.79	N
ATOM	3016	CA	LEU	A	399	-40.470	123.721	-28.260	1,00	55.58	C
ATOM	3017	C	LEU	*A*	399	-39.142	123,087	-27.825	1,00	58,74	C
ATOM	3018	CB	LEU	A	399	-41,646	123.138	-27,463	1,00	54.95	C
ATOM	3019	CG	LEU	A	399	-43,053	123.749	-27,619	1,00	60.03	C
ATOM	3020	GDI	LEU	*A*	399	-44.084	122,894	-26.885	1,00	53,93	C
ATOM	3021	*CD2*	LEU	A	399	-43.122	125.215	-27.139	1.00	51.21	C
ATOM	3022	O	ARG	A	400	-36,072	124.639	-26,977	1,00	50.51	0
ATOM	3023	N	ARG	A	400	-38.080	123,398	-28.555	1.00	58,40	N
ATOM	3024	CA	ARG	A	400	-36,803	122.759	-28.305	1.00	51.87	C
ATOM	3025	C	ARG	A	400	-36,032	123.410	-27,170	1,00	52.55	C

ATOM	3026	CB	ARG	A	400	-35.958	122.738	-29.578	1.00	51.48	C
ATOM	3027	CG	ARG	A	400	--36.289	121.544	-30.444	1.00	56.91	C
ATOM	3028	CD	ARG	A	400	-35.427	121.468	-31.679	1.00	65.23	C
ATOM	3029	NE	ARG	A	400	-34.084	120.958	-31.416	1.00	63.00	N
ATOM	3030	CZ	ARG	A	400	-33.816	119.692	-31.105	1.00	62.07	C
ATOM	3031	NH1	ARG	A	400	-34.805	118.823	-30.997	1.00	70.18	N
ATOM	3032	NH2	ARG	A	400	-32.569	119.294	-30.893	1.00	52.49	N
ATOM	3033	O	LYS	A	401	-32.865	122.927	-27.223	1.00	49.41	O
ATOM	3034	N	LYS	A	401	-35.357	122.559	-26.396	1.00	49.23	N
ATOM	3035	CA	LYS	A	401	-34.418	123.014	-25.390	1.00	44.19	C
ATOM	3036	C	LYS	A	401	-33.078	123.298	-26.065	1.00	49.52	C
ATOM	3037	CB	LYS	A	401	-34.267	121.985	-24.291	1.00	46.17	C
ATOM	3038	CG	LYS	A	401	-35.524	121.217	-23.994	1.00	51.17	C
ATOM	3039	CD	LYS	A	401	-35.338	120.409	-22.743	1.00	48.77	C
ATOM	3040	CE	LYS	A	401	-36.445	119.402	-22.528	1.00	55.43	C
ATOM	3041	NZ	LYS	A	401	-36.218	118.679	-21.241	1.00	57.56	N
ATOM	3042	O	GLN	A	402	-29.052	123.075	-26.727	1.00	39.33	O
ATOM	3043	N	GLN	A	402	-32.178	123.978	-25.365	1.00	47.99	N
ATOM	3044	CA	GLN	A	402	-30.933	124.368	-26.007	1.00	45.77	C
ATOM	3045	C	GLN	A	402	-29.884	123.257	-25.852	1.00	46.32	C
ATOM	3046	CB	GLN	A	402	-30.416	125.679	-25.448	1.00	41.98	C
ATOM	3047	CG	GLN	A	402	-31.169	126.920	-25.932	1.00	50.68	C
ATOM	3048	CD	GLN	A	402	-32.599	127.017	-25.391	1.00	48.33	C
ATOM	3049	OE1	GLN	A	402	-32.814	127.082	-24.184	1.00	48.65	0
ATOM	3050	NE2	GLN	A	402	-33.573	127.008	-26.291	1.00	47.79	N
ATOM	3051	O	ARG	A	403	-30.591	119.530	-24.057	1.00	42.55	O
ATOM	3052	N	ARG	A	403	-29.969	122.534	-24.734	1.00	46.69	N
ATOM	3053	CA	ARG	A	403	-29.132	121.386	-24.414	1.00	44.26	C
ATOM	3054	C	ARG	A	403	-29.770	120.059	-24.795	1.00	41.57	C
ATOM	3055	CB	ARG	A	403	-28.827	121.396	-22.929	1.00	46.80	C
ATOM	3056	CG	ARG	A	403	-28.051	122.605	-22.550	1.00	42.56	C
ATOM	3057	CD	ARG	A	403	-26.687	122.541	-23.176	1.00	45.85	C
ATOM	3058	NE	ARG	A	403	-25.746	122.917	-22.152	1.00	52.37	N
ATOM	3059	CZ	ARG	A	403	-24.792	122.149	-21.648	1.00	48.77	C
ATOM	3060	NH1	ARG	A	403	-24.057	122.651	-20.675	1.00	54.15	N
ATOM	3061	NH2	ARG	A	403	-24.577	120.914	-22.073	1.00	43.06	N
ATOM	3062	N	TH.R	A	404	-29.405	119.538	-25.959	1.00	42.47	N
ATOM	3063	CA	THR	A	404	-30.014	118.309	-26.449	1.00	44.21	C
ATOM	3064	C	THR	A	404	-29.025	117.454	-27.183	1.00	42.56	C
ATOM	3065	O	THR	A	404	-27.946	117.916	-27.547	1.00	44.30	O
ATOM	3066	CB	THR	A	404	-31.204	118.548	-27.427	1.00	46.00	C
ATOM	3067	OG1	THR	A	404	-30.824	119.471	-28.452	1.00	41.84	O
ATOM	3068	CG2	THR	A	404	-32.413	119.051	-26.683	1.00	52.96	C
ATOM	3069	N	FHE	A	405	-29.471	116.230	-27.450	1.00	46.30	N
ATOM	3070	CA	PHE	A	405	-28.669	115.107	-27.951	1.00	45.99	C
ATOM	3071	C	PHE	A	405	-27.993	115.337	-29.299	1.00	49.85	C
ATOM	3072	0	PHE	A	405	-27.184	114.514	-29.723	1.00	55.82	0
ATOM	3073	CB	PHE	A	405	-29.561	113.860	-28.062	1.00	49.00	C
ATOM	3074	CG	PHE	A	405	-30.787	114.066	-28.927	1.00	55.41	C
ATOM	3075	CD2	PHE	A	405	-30.813	113.609	-30.235	1.00	55.60	C
ATOM	3076	CD1	PHE	A	405	-31.913	114.744	-28.433	1.00	58.05	C
ATOM	3077	CE2	PHE	A	405	-31.938	113.817	-31.032	1.00	59.07	C
ATOM	3078	CE1	PHE	A	405	-33.033	114.959	-29.222	1.00	48.41	C
ATOM	3079	CZ	PHE	A	405	-33.048	114.500	-30.514	1.00	59.91	C
ATOM	3080	N	ASP	A	406	-28.323	116.426	-29.987	1.00	46.36	N
ATOM	3081	CA	ASP	A	406	-27.780	116.621	-31.322	1.00	46.34	C
ATOM	3082	C	ASP	A	406	-26.879	117.822	-31.375	1.00	43.21	C
ATOM	3083	O	ASP	A	406	-26.408	118.195	-32.437	1.00	47.00	0
ATOM	3084	CB	ASP	A	406	-28.891	116.732	-32.378	1.00	46.60	C
ATOM	3085	CG	ASP	A	406	-29.824	117.905	-32.141	1.00	52.37	C
ATOM	3086	OD1	ASP	A	406	-30.106	118.223	-30.967	1.00	54.81	0
ATOM	3087	OD2	ASP	A	406	-30.284	118.505	-33.137	1.00	58.67	0
ATOM	3088	N	ASM	A	407	-26.587	118.410	-30.226	1.00	43.33	N

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ATOM  3089  CA   ASN  A 407   -25.534  119.414  -30.187   1.00  41.80   C
ATOM  3090  C    ASM  A 407   --24.145 118.823  -30.569   1.00  43.81   C
ATOM  3091  O    ASN  A 407   -23.191  119.559  -30.781   1.00  43.03   O
ATOM  3092  CB   ASN  A 407   -25.471  120.046  -28.815   1.00  41.91   C
ATOM  3093  CG   ASM  A 407   -26.665  120.980  -28.524   I.00  51.70   C
ATOM  3094  OD1  ASN  A 407   -27.443  121.329  -29.417   1.00  52.98   0
ATOM  3095  ND2  ASK  A 407   -26.789  121.401  -27.265   1.00  42.13   N
ATOM  3096  N    GLY  A 408   -24.071  117.494  -30.685   I.00  41.01   N
ATOM  3097  CA   GLY  A 408   -22.842  116.782  -30.980   1.00  43.70   C
ATOM  3098  C    GLY  A 408   —22.143  117.193  -32 .255   1.00  50.34   C
ATOM  3099  0    GLY  A 408   -20.932  116.975  -32 .421   I.00  46.00   0
ATOM  3100  N    SER  A 409   -22.905  117.818  -33.148   1.00  51.64   M
ATOM  3101  CA   SER  A 409   -22.415  118.168  -34.472   1.00  49.18   C
ATOM  3102  C    SER  A 409   -21.628  119.466  -34.447   1.00  50.83   C
ATOM  3103  0    SER  A 409   -21.004  119.831  -35.437   1.00  59.46   0
ATOM  3104  CB   SER  A 409   -23.585  118.274  -35.453   1.00  45.92   C
ATOM  3105  OG   SER  A 409   -24.369  119.407  -35.154   1.00  57.17   0
ATOM  3106  O    ILE  A 410   -18.993  120.741  -32 .098   I.00  49.76   0
ATOM  3107  N    ILE  A 410   -21.637  120.152  -33.310   1.00  44.08   N
ATOM  3108  CA   ILE  A 410   -20.994  121.456  -33.219   1.00  45.49   C
ATOM  3109  C    ILE  A 410   -19.475  121.317  -33.089   I.00  51.14   C
ATOM  3110  CB   ILE  A 410   -21.537  122.263  -32 .006   1.00  41.60   C
ATOM  3111  CGI  ILE  A 410   -23.044  122.454  -32 .097   1.00  50.48   C
ATOM  3112  CG2  ILE  A 410   -20.860  123.589  -31.885   I.00  40.91   C
ATOM  3113  CD1  ILE  A 410   -23.598  123.296  -30.954   1.00  47.79   C
ATOM  3114  N    PRO  A 411   -18.710  121.858  -34.063   1.00  55.86   N
ATOM  3115  CA   PRO  A 411   -17.239  121.817  -33.984   I.00  54.02   C
ATOM  3116  C    FRO  A 411   -16.715  122.780  -32 .923   1.00  51.89   C
ATOM  3117  O    PRO  A 411   -17.420  123.728  -32.533   1.00  52.91   O
ATOM  3118  CB   PRO  A 411   -16.779  122.266  -35.381   1.00  50.24   C
ATOM  3119  CG   FRO  A 411   -18.026  122.477  -36.181   1.00  52.81   C
ATOM  3120  CD   PRO  A 411   -19.157  122.645  -35.217   1.00  49.02   C
ATOM  3121  N    HI S A 412   -15.490  122.552  -32 .471   1.00  48.91   N
ATOM  3122  CA.  HI S A 412   -14.936  123.328  -31.370   I.00  50.27   C
ATOM  3123  C    HIS  A 412   -14.528  124.708  -31.840   1.00  53.88   C
ATOM  3124  O    HIS  A 412   -14.484  125.644  -31.048   1.00  51.37   O
ATOM  3125  CB   HI S A 412   -13.739  122.617  -30.731   I.00  48.21   C
ATOM  3126  CG   HIS  A 412   -12.492  122.651  -31.564   1.00  55.27   C
ATOM  3127  ND1  HIS  A 412   -12.252  121.755  -32.585   1.00  47.75   N
ATOM  3128  CD2  HIS  A 412   -11.410  123.468  -31.517   I.00  53.91   C
ATOM  3129  CEl  HI S A 412   -11.090  122.036  -33.146   1.00  49.28   C
ATOM  3130  NE2  HIS  A 412   -10.553  123.063  -32.511   1.00  48.81   N
ATOM  3131  N    GLN  A 413   -14.224  124.826  -33.129   1.00  52.60   N
ATOM  3132  CA   GLN  A 413   -13.940  126.129  -33.728   1.00  52.42   C
ATOM  3133  C    GLN  A 413   -15.045  127.173  -33.422   1.00  57.78   C
ATOM  3134  O    GLN  A 413   -14.759  128.333  -33.085   1.00  56.28   0
ATOM  3135  CB   GLN  A 413   -13.765  125.985  -35.241   I.00  56.64   C
ATOM  3136  CG   GLN  A 413   -12.446  125.360  -35.673   1.00  59.77   C
ATOM  3137  CD   GLN  A 413   -12.520  123.855  -35.775   1.00  56.11   C
ATOM  3138  OE1  GLN  A 413   -13.412  123.233  -35.216   I.00  59.90   0
ATOM  3139  ME2  GLN  A 413   -11.586  123.265  -36.495   1.00  56.83   M
ATOM  3140  N    ILE  A 414   -16.301  126.756  -33.519   1.00  50.91   N
ATOM  3141  CA   ILE  A 414   -17.417  127.666  -33.282   I.00  51.72   C
ATOM  3142  C    ILE  A 414   -17.427  128.272  -31.862   1.00  53.36   C
ATOM  3143  O    ILE  A 414   -17.462  129.493  -31.717   1.00  57.45   O
ATOM  3144  CB   ILE  A 414   -18.718  126.966  -33.555   I.00  49.56   C
ATOM  3145  CGI  ILE  A 414   -18.986  126.988  -35.052   1.00  52.93   C
ATOM  3146  CG2  ILE  A 414   -19.833  127.614  -32.804   1.00  55.91   C
ATOM  3147  CD1  ILE  A 414   -20.257  126.265  -35.436   1.00  62.45   C
ATOM  3148  N    HI S A 415   -17.359  127.442  -30.821   1.00  55.44   M
ATOM  3149  CA   HIS  A 415   -17.199  127.957  -29.460   1.00  51.05   C
ATOM  3150  C    HIS  A 415   -15.932  128.797  -29.389   1.00  57.13   C
ATOM  3151  O    HI S A 415   -15.837  129.718  -28.581   I.00  59.51   0
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ATOM	3152	CB	HIS	A	415	-17.112	126.833	-28.412	1.00	50.11	c
ATOM	3153	CG	HI S	A	415	-18.320	125.954	-28.346	1.00	50.29	C
ATOM	3154	ND1	HIS	A	415	-19.545	126.397	-27.889	1.00	48.47	N
ATOM	3155	CD2	HIS	A	415	-18.485	124.650	-28.665	1.00	41.98	c
ATOM	3156	CE1	HI S	A	415	-20.413	125.403	-27.937	I.00	44.64	C
ATOM	3157	NE2	HIS	A	415	-19.798	124.336	-28.414	1.00	47.68	N
ATOM	3158	N	LEU	A	416	-14.951	128.459	-30.224	1.00	55.29	N
ATOM	3159	CA.	LEU	A	416	-13.660	129.138	-30.193	I.00	58.69	C
ATOM	3160	C	LEU	A	416	-13.800	130.561	-30.720	1.00	58.67	C
ATOM	3161	O	LEU	A	416	-13.284	131.501	-30.121	1.00	61.69	O
ATOM	3162	CB	LEU	A	416	-12.621	128.368	-31.008	I.00	56.71	C
ATOM	3163	CG	LEU	A	416	-11.241	128.995	-31.128	1.00	54.89	c
ATOM	3164	GDI	LEU	A	416	-10.637	129.181	-29.754	1.00	52.36	c
ATOM	3165	CD2	LEU	A	416	-10.356	128.105	-32 .000	1.00	61.77	c
ATOM	3166	N	GLY	A	417	-14.492	130.702	-31.842	1.00	53.67	N
ATOM	3167	CA	GLY	A	417	-14.832	1.32.008	-32 .372	1.00	54.97	C
ATOM	3168	c	GLY	A	417	-15.418	132.895	-31.292	1.00	60.53	c
ATOM	3169	0	GLY	A	417	-14.875	133.969	-31.018	I.00	63.41	0
ATOM	3170	N	GLU	A	418	-16.493	1.32.424	-30.653	1.00	60.59	N
ATOM	3171	CA	GLU	A	418	-17.162	133.169	-29.585	1.00	55.35	c
ATOM	3172	C	GLU	A	418	-16.215	133.488	-28.433	I.00	59.51	c
ATOM	3173	O	GLU	A	418	-16.248	134.595	-27.894	1.00	65.40	0
ATOM	3174	CB	GLU	A	418	-18.409	132.408	-29.062	1.00	55.80	c
ATOM	3175	CG	GLU	A	418	-19.583	132.273	-.30.087	I.00	58.24	c
ATOM	3176	CD	GLU	A	418	-20.981	132.011	-29.455	1.00	59.19	c
ATOM	3177	OE1	GLU	A	418	-21.110	132.014	-28.212	1.00	55.93	0
ATOM	3178	OE2	GLU	A	418	-21.963	131.803	-.30.212	I.00	57.23	0
ATOM	3179	N	LEU	A	419	-15.367	132.536	-28.051	1.00	61.01	N
ATOM	3180	CA	LEU	A	419	-14.453	132.748	-26.920	1.00	60.25	c
ATOM	3181	c	LEU	A	419	-13.453	133.844	-27.241	1.00	67.71	c
ATOM	3182	O	LEU	A	419	-13.156	134.728	-26.415	1.00	63.50	0
ATOM	3183	CB	LEU	A	419	-13.718	131.474	-26.585	1.00	51.05	c
ATOM	3184	CG	LEU	A	419	-12.662	131.498	-25.481	1.00	59.15	c
ATOM	3185	CD1	LEU	A	419	-13.061	130.661	-24.258	I.00	48.83	c
ATOM	3186	CD2	LEU	A	419	-11..346	131.002	-26.059	1.00	64.55	c
ATOM	3187	N	HIS	A	420	-12.944	133.759	-28.464	1.00	64.54	N
ATOM	3188	CA.	HI S	A	420	-12.017	134.727	-29.021	I.00	64.70	C
ATOM	3189	C	HI S	A	420	-12.582	136.147	-28.951	1.00	72.51	c
ATOM	3190	O	HIS	A	420	-12.011	137.035	-28.285	1.00	72.35	0
ATOM	3191	CB	HIS	A	420	-11.708	134..337	-.30.465	I.00	63.93	c
ATOM	3192	CG	HI S	A	420	-10.734	135.240	-31.142	1.00	65.89	c
ATOM	3193	ND1	HIS	A	420	-9.448	135.423	-30.683	1.00	65.18	N
ATOM	3194	CD2	HIS	A	420	-10.854	136.003	-32 .255	1.00	62.02	c
ATOM	3195	CEl	HI S	A	420	-8.816	136.262	-31.483	1.00	69.65	c
ATOM	3196	NE2	HIS	A	420	-9.648	136.628	-32 .444	1.00	74.25	N
ATOM	3197	N	ALA	A	421	-13.713	136.336	-29.636	1.00	70.22	N
ATOM	3198	CA.	ALA	A	421	-14.450	137.594	-29.632	I.00	65.36	C
ATOM	3199	C	ALA	A	421	-14.604	138.179	-28.236	1.00	66.36	C
ATOM	3200	O	ALA	A	421	-14.219	139.317	-28.009	1.00	76.97	O
ATOM	3201	CB	ALA	A	421	-15.810	137.398	-30.268	I.00	66.89	C
ATOM	3202	N	ILE	A	422	-15.161	137.417	-27.304	1.00	66.27	N
ATOM	3203	CA	ILE	A	422	-15.380	137.942	-25.961	1.00	68.30	c
ATOM	3204	C	ILE	A	422	-14.067	138.418	-25.389	I.00	69.75	c
ATOM	3205	O	ILE	A	422	-14.004	139.455	-24.732	1.00	73.27	0
ATOM	3206	CB	ILE	A	422	-16.000	136.905	-25.003	1.00	59.63	c
ATOM	3207	CGI	ILE	A	422	-17.411	136.546	-25.456	I.00	61.40	c
ATOM	3208	CG2	ILE	A	422	-16.038	137.435	-23.573	1.00	52.83	c
ATOM	3209	GDI	ILE	A	422	-18.087	135.541	-24.554	1.00	62.54	c
ATOM	3210	N	LEU	A	423	-13.002	137.679	-25.666	1.00	72.33	N
ATOM	3211	CA	LEU	A	423	-11.717	138.028	-25.074	1.00	76.05	C
ATOM	3212	C	LEU	A	423	-11.200	139.334	-25.661	1.00	79.38	C
ATOM	3213	O	LEU	A	423	-10.669	140.176	-24.931	1.00	75.82	0
ATOM	3214	CB	LEU	A	423	-10.704	136.908	-25.262	I.00	70.55	c

ATOM	3215	CG	LEU	A	423	-10.702	135.937	-24.085	1.00	70.07	C
ATOM	3216	GDI	LEU	A	423	-9.705	134.825	-24.311	1.00	68.93	C
ATOM	3217	CD2	LEU	A	423	-10..395	1.36.682	-22.803	1.00	68.22	C
ATOM	3218	N	ARG	A	424	-11.379	139.500	-26.972	1.00	76.39	N
ATOM	3219	CA.	ARG	A	424	-1.1.055	140.757	-27.645	1.00	79.93	C
ATOM	3220	C	ARG	A	424	-11.790	14.1.948	-27.002	1.00	80.66	C
ATOM	3221	O	ARG	A	424	-11.153	142.819	-26.402	1.00	81.63	O
ATOM	3222	CB	ARG	A	424	-1.1.389	140.666	-29.144	1.00	72.95	C
ATOM	3223	N	ARG	A	425	-13.121	141.957	-27.117	1.00	81.00	N
ATOM	3224	CA	ARG	A	425	-13.981	143.002	-26.547	1.00	77.55	C
ATOM	3225	C	ARG	A	425	-13.512	143.509	-25.189	1.00	82.66	C
ATOM	3226	O	ARG	A	425	-13.487	144.714	-24.940	1.00	89.83	O
ATOM	3227	CB	ARG	A	425	-15.420	142.499	-26.392	1.00	74.08	C
ATOM	3228	CG	ARG	A	425	-16.092	142.033	-27.661	1.00	74.68	C
ATOM	3229	CD	ARG	A	425	-15.902	143.038	-28.763	1.00	78.82	C
ATOM	3230	NE	ARG	A	425	-17.124	143.242	-29.524	1.00	75.68	N
ATOM	3231	CZ	ARG	A	425	-17.195	143.979	-30.627	1.00	79.54	C
ATOM	3232	NH1	ARG	A	425	-16.106	144.576	-3.1.097	1.00	79.47	N
ATOM	3233	NH2	ARG	A	425	-18.354	144.115	-31.263	1.00	73.73	N
ATOM	3234	N	GLN	A	426	-13.143	142.590	-24.309	1.00	77.98	N
ATOM	3235	C	GLN	A	426	-1.1.390	142.941	-22.606	1.00	82.59	C
ATOM	3236	CA	GLN	A	426	-12.876	142.962	-22.931	1.00	79.97	C
ATOM	3237	O	GLN	A	426	-10.996	143.092	-21.445	1.00	82.52	O
ATOM	3238	CB	GLN	A	426	-13.666	142.043	-21.991	1.00	76.48	C
ATOM	3239	CG	GLN	A	426	-14.854	142.734	-21.284	1.00	84.12	C
ATOM	3240	CD	GLN	A	426	-15.966	143.235	-22.228	1.00	77.26	C
ATOM	3241	OE1	GLN	A	426	-15.790	143..342	-23.434	1.00	76.47	0
ATOM	3242	NE2	GLN	A	426	-17.115	143.535	-21.661	1.00	72.07	N
ATOM	3243	O	GLU	A	427	-7.710	144.273	-22.220	1.00	89.17	O
ATOM	3244	N	GLU	A	427	-10.565	142.780	-23.640	1.00	81.53	N
ATOM	3245	CA	GLU	A	427	-9.117	142.788	-23.455	1.00	82.55	C
ATOM	3246	C	GLU	A	427	-8.657	144.161	-22.988	1.00	87.23	C
ATOM	3247	CB	GLU	A	427	-8.391	142.398	-24.746	1.00	81.85	C
ATOM	3248	O	ASP	A	428	-8.541	147.435	-20.888	1.00	84.77	0
ATOM	3249	N	ASP	A	428	-9..342	145.205	-23.447	1.00	92.31	N
ATOM	3250	CA	ASP	A	428	-8.985	146.576	-23.084	1.00	89.98	C
ATOM	3251	C	ASP	A	428	-9.370	146.936	-2.1.646	1.00	86.4.1	C
ATOM	3252	CB	ASP	A	428	y.626	147.562	-24.057	1.00	90.09	C
ATOM	3253	CG	ASP	A	428	-8.870	147.654	-25.371	1.00102.14		C
ATOM	3254	OD2	ASP	A	428	-8.890	148.747	-25.985	1.00.107.45		0
ATOM	3255	OD1	ASP	A	428	-8.255	146.641	-25.785	1.00	99.99	0
ATOM	3256	N	PHE	A	429	-10.616	146.678	-21.270	1.00	82.95	N
ATOM	3257	CA	PHE	A	429	-11.085	147.049	-19.946	1.00	78.13	C
ATOM	3258	C	PHE	A	429	-10.477	146.156	-18.871	1.00	78.68	C
ATOM	3259	O	PHE	A	429	-10.493	146.491	-17.686	1.00	77.25	O
ATOM	3260	CB	PHE	A	429	-12.607	146.985	-19.890	1.00	77.92	C
ATOM	3261	CG	PHE	A	429	-13.272	147.467	-2.1.138	1.00	78.86	C
ATOM	3262	CD1	PHE	A	429	-13..333	148.817	-21.428	1.00	80.89	C
ATOM	3263	CD2	PHE	A	429	-13.834	146.573	-22.026	1.00	80.93	C
ATOM	3264	CE1	PHE	A	429	-13.943	149.268	-22.576	1.00	78.86	C
ATOM	3265	CE2	PHE	A	429	-14.453	147.018	-23.179	1.00	82.30	C
ATOM	3266	CZ	PHE	A	429	-14.502	148.366	-23.457	1.00	83.31	C
ATOM	3267	N	TYR	A	430	-9.940	145.014	-19.278	1.00	83.99	N
ATOM	3268	CA	TYR	A	430	y.362	144.088	-18.313	1.00	78.33	C
ATOM	3269	C	TYR	A	430	-7.940	143.754	-18.676	1.00	82.49	C
ATOM	3270	O	TYR	A	430	-7.667	143..343	-19.799	1.00	79.84	0
ATOM	3271	CB	TYR	A	430	-10.200	142.820	-18.212	1.00	75.62	C
ATOM	3272	CG	TYR	A	430	-11.501	143.055	-17.494	1.00	72.55	C
ATOM	3273	CD1	TYR	A	430	-11.544	143.092	-16.104	1.00	68.46	C
ATOM	3274	CD2	TYR	A	430	-12.679	143.272	-18.200	1.00	69.13	C
ATOM	3275	CE1	TYR	A	430	-12.721	143.320	-15.435	1.00	65.45	C
ATOM	3276	CE2	TYR	A	430	-13.866	143.511	-17.537	1.00	69.78	C
ATOM	3277	CZ	TYR	A	430	-13.879	143.527	-16.155	1.00	66.88	C

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ATOM   3278  OH   TYR  A  430    -15..050  143..756  -15..479  1.00  71.04    O
ATOM   3279  N    FRO  A  431    -7,026    143..922  -17 ,708  1,00  87.02    M
ATOM   3280  CA   PRO  A  431    -5..589   143,814   -17 .967  1,00  84,92    C
ATOM   3281  C    PRO  A  431    --5..205  142..438  -18.,500  1.00  82.43    C
ATOM   3282  O    PRO  A  431    -4,983    142 .265  -19.,702  1,00  81,89    0
ATOM   3283  CB   PRO  A  431    -4.964    144 ,062  -16..587  1,00  82,17    C
ATOM   3284  CG   PRO  A  431    --6..029  143.,696  -15..615  1,00  79,.37    C
ATOM   3285  CD   PRO  A  431    -7,323    144 .056  -16,268   1,00  81,03    C
ATOM   3286  O    PHE  A  432    -4.617    138..562  -19.,585  1,00  83..88    0
ATOM   3287  N    PHE  A  432    --5..168  141 ,475  -17 .587  1,00  83,.19    M
ATOM   3288  CA   PHE  A  432    -4,614    140.154   -17 .816  1,00  82.36    C
ATOM   3289  C    PHE  A  432    -5..259   139..410  -18.,977  1,00  80..79    C
ATOM   3290  CB   PHE  A  432    -4.725    139,328   -16. 533  1,00  81,15    C
ATOM   3291  CG   PHE  A  432    --6..119  138..912  -16.,200  1.00  79..49    C
ATOM   3292  CD2  PHE  A  432    ...g,468   137..572  -16.,194  1,00  79..74    C
ATOM   3293  CD1  PHE  A  4.32   -7.080    1.39,851  -15..885  1,00  78,.76    C
ATOM   3294  CE2  PHE  A  432    --7.760   137..179  -15.,884  1.00  80..58    C
ATOM   3295  CE1  PHE  A  432    -8.,374   139. 475  -15.,568  1,00  78.,84    C
ATOM   3296  CZ   PHE  A  4.32   -8..720   1.38.,134 -15..570  1,00  77,97    C
ATOM   3297  N    LEU  A  433    --6..512  139.,718  -19..289  1,00  77,96    M
ATOM   3298  CA.  LEU  A  433    -7,148    139. 144  -20.,475  1,00  78.,63    C
ATOM   3299  C    LEU  A  433    -6.322    139..277  -21.,770  1,00  81.69    C
ATOM   3300  O    LEU  A  433    --6..258  138.,337  ~22.555   1,00  84,40    0
ATOM   3301  CB   LEU  A  433    -8.,527   139.771   -20.,704  1,00  81.47    C
ATOM   3302  CG   LEU  A  433    -9.754    139..085  -20,095   1,00  81.09    C
ATOM   3303  GDI  LEU  A  433    -9. 785   139,277   -18. 602  1,00  78,12    C
ATOM   3304  CD2  LEU  A  433    -11 ,048   139.596   -20.,727  1,00  79.00    C
ATOM   3305  N    LYS  A  434    -5.,700   140..431  -22.,004  1,00  86..36    M
ATOM   3306  CA   LYS  A  434    -4.984    140.,659  -23 .264  1,00  83,95    C
ATOM   3307  C    LYS  A  434    -3..751   139.,793  -23,328   1.00  78..82    C
ATOM   3308  O    LYS  A  434    -3.,363   139..320  -24,394   1,00  79..93    0
ATOM   3309  CB   LYS  A  4.34   -4.590    142.,130  -23..426  1,00  86,.69    C
ATOM   3310  N    ASP  A  435    -3..136   139.,595  -22..170  1.00  79..16    M
ATOM   3311  CA.  ASP  A  435    -1,965    138. 740  -22.,064  1,00  82,82    C
ATOM   3312  C    ASP  A  4.35   -2..341   1.37,269  -22..233  1,00  85,.04    C
ATOM   3313  O    ASP  A  435    -1.657    136.,523  ~22 .930  1,00  85,.92    O
ATOM   3314  CB   ASP  A  435    -1,265    138. 950  -20.,718  1,00  85.,65    C
ATOM   3315  K    ASN  A  436    -3..444   136.,871  -21.,605  1,00  84.08    K
ATOM   3316  CA   ASN  A  436    -3.839    135.,471  -21 .522  1,00  76,50    C
ATOM   3317  C    ASM  A  436    -4,601    134..935  -22.,720  1,00  75..42    C
ATOM   3318  O    ASM  A  436    -4,976    133..764  -22.,728  1,00  76..39    0
ATOM   3319  CB   A.SM A  436    -4.690    135.,256  -20. 274  1,00  75,79    C
ATOM   3320  CG   ASM  A  436    -3..918   135.,501  -19.,001  1.00  78..92    C
ATOM   3321  OD1  ASM  A  436    -3.,108   134..676  -18.,587  1,00  77.53    0
ATOM   3322  KD2  ASN  A  4.36   -4.161    1.36,641  -18..373  1,00  82,.73    K
ATOM   3323  N    ARG  A  437    -4.834    135.,781  -23,719   1.00  74.86    M
ATOM   3324  CA.  ARG  A  437    -5,736    135. 427  -24.,811  1,00  74,78    C
ATOM   3325  C    ARG  A  4.37   -5...308  1.34.,121 -25.472   1,00  69,.46    C
ATOM   3326  O    ARG  A  437    -6..124   133.,219  -25..643  1,00  71,89    0
ATOM   3327  CB   ARG  A  437    -5,821    136. 556  -25,851   1,00  70.,14    C
ATOM   3328  K    GLU  A  438    -4.033    134.,005  -25,820   1,00  67.79    K
ATOM   3329  CA   GLU  A  438    -3..557   132.,786  -26..461  1,00  70,.83    C
ATOM   3330  C    GLU  A  438    -3.,589   131..627  -25,463   1,00  71.10    C
ATOM   3331  O    GLU  A  438    -3..770   130..466  -25,839   1,00  67.12    0
ATOM   3332  CB   GLU  A  438    -2.144    132.,975  -27.022   1,00  69,88    C
ATOM   3333  N    LYS  A  439    -3.,432   131..966  -24.,186  1,00  70..41    M
ATOM   3334  CA   LYS  A  439    -3.327    130..977  -23,125   1,00  66..22    C
ATOM   3335  C    LYS  A  439    -4.673    130.,316  -22.900   1,00  69,85    C
ATOM   3336  O    LYS  A  439    -4.780    129.,081  -22.,829  1.00  64.84    0
ATOM   3337  CB   LYS  A  439    -2.,839   131..635  -21.,835  1,00  67.58    C
ATOM   3338  CG   LYS  A  4.39   -2.062    1.30.,740 -20..899  1,00  68,.05    C
ATOM   3339  CD   LYS  A  439    -1.860    131.,415  -19.,555  1.00  73..27    C
ATOM   3340  CE   LYS  A  439    -1,075    130. 546  -18.,586  1,00  74,69    C
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ATOM   3341  NZ   LYS A 439     -1.051  131.151  -17.215  1.00 82.44      N
ATOM   3342  N    ILE A 440     -5.697  131.160  -22.784  1.00 66.75      N
ATOM   3343  CA   ILE A 440     -7.045  130.705  -22.517  1.00 62.55      C
ATOM   3344  C    ILE A 440     -7.577  129.951  -23.728  1.00 60.06      C
ATOM   3345  O    ILE A 440     -8.241  128.935  -23.590  I.00 62.95      0
ATOM   3346  CB   ILE A 440     -7.961  131.886  -22.150  1.00 63.87      C
ATOM   3347  CGI  ILE A 440     -7.848  132.182  -20.652  1.00 63.69      C
ATOM   3348  CG2  ILE A 440     -9.400  131.592  -22.516  I.00 55.89      C
ATOM   3349  CD1  ILE A 440     -8.231  133.605  -20.285  1.00 65.88      C
ATOM   3350  N    GLU A 441     -7.261  130.434  -24.916  1.00 58.67      N
ATOM   3351  CA   GLU A 441     -7.651  129.739  -26.124  I.00 58.80      C
ATOM   3352  C    GLU A 441     -7.015  128.336  -26.205  1.00 62.92      C
ATOM   3353  O    GLU A 441     -7.654  127.390  -26.661  1.00 60.09      O
ATOM   3354  CB   GLU A 441     -7.274  130.562  -27.353  1.00 63.83      C
ATOM   3355  N    LYS A 442     -5.772  128.193  -25.748  1.00 63.98      N
ATOM   3356  CA   LYS A 442     -5.091  126.896  -25.837  1.00 62.70      C
ATOM   3357  C    LYS A 442     -5.814  125.854  -24.983  1.00 60.76      C
ATOM   3358  O    LYS A 442     -6.028  124.716  -25.431  I.00 56.62      0
ATOM   3359  CB   LYS A 442     -3.622  127.011  -25.418  1.00 60.09      C
ATOM   3360  CG   LYS A 442     -2.833  125.719  -25.578  1.00 61.88      C
ATOM   3361  CD   LYS A 442     -2.923  125.201  -26.991  I.00 61.53      C
ATOM   3362  CE   LYS A 442     -1.604  124.625  -27.475  1.00 65.76      C
ATOM   3363  NZ   LYS A 442     -0.596  125.679  -27.819  1.00 73.09      N
ATOM   3364  N    ILE A 443     -6.190  126.265  -23.767  I.00 61.65      N
ATOM   3365  CA   ILE A 443     -7.018  125.467  -22.860  1.00 57.82      C
ATOM   3366  C    ILE A 443     -8.238  124.907  -23.579  1.00 64.09      C
ATOM   3367  O    ILE A 443     -8.564  123.729  -23.452  I.00 64.95      0
ATOM   3368  CB   ILE A 443     -7.518  126.279  -21.665  1.00 59.82      C
ATOM   3369  CGI  ILE A 443     -6.356  126.740  -20.790  1.00 63.06      C
ATOM   3370  CG2  ILE A 443     -8.515  125.466  -20.837  1.00 55.69      C
ATOM   3371  CD1  ILE A 443     -6.810  127.503  -19.545  1.00 63.20      C
ATOM   3372  N    LEU A 444     -8.925  125.742  -24.344  1.00 61.78      N
ATOM   3373  CA   LEU A 444    -10.040  125.209  -25.098  1.00 58.82      C
ATOM   3374  C    LEU A 444     -9.500  124.223  -26.137  I.00 61.18      C
ATOM   3375  O    LEU A 444     -9.978  123.090  -26.233  1.00 62.70      0
ATOM   3376  CB   LEU A 444    -10.862  126.328  -25.760  1.00 54.54      C
ATOM   3377  CG   LEU A 444    -12.164  125.911  -26.462  I.00 56.88      C
ATOM   3378  CD1  LEU A 444    -13.409  126.601  -25.898  1.00 51.58      C
ATOM   3379  CD2  LEU A 444    -12.069  126.151  -27.958  1.00 56.95      C
ATOM   3380  N    THR A 445     -8.478  124.629  -26.880  I.00 56.92      N
ATOM   3381  CA   THR A 445     -8.085  123.881  -28.062  1.00 56.77      C
ATOM   3382  C    THR A 445     -7.217  122.641  -27.821  1.00 61.11      C
ATOM   3383  O    THR A 445     -7.133  121.793  -28.696  1.00 52.46      0
ATOM   3384  CB   THR A 445     -7.320  124.764  -29.041  1.00 58.64      C
ATOM   3385  OG1  THR A 445     -6.253  125.415  -28.343  1.00 61.60      0
ATOM   3386  CG2  THR A 445     -8.249  125.795  -29.664  1.00 56.51      C
ATOM   3387  N    PHE A 446     -6.564  122.525  -26.669  I.00 61.72      N
ATOM   3388  CA   PHE A 446     -5.538  121.489  -26.569  1.00 57.56      C
ATOM   3389  C    PHE A 446     -6.112  120.096  -26.450  1.00 57.92      C
ATOM   3390  0    PHE A 446     -6.834  119.768  -25.514  I.00 60.31      0
ATOM   3391  CB   PHE A 446     -4.587  121.729  -25.395  1.00 61.74      C
ATOM   3392  CG   PHE A 446     -3.698  120.537  -25.098  1.00 64.15      C
ATOM   3393  CDI  PHE A 446     -2.804  120.067  -26.057  I.00 64.54      C
ATOM   3394  CD2  PHE A 446     -3.785  119.862  -23.880  1.00 57.60      C
ATOM   3395  CE1  PHE A 446     -2.003  118.960  -25.798  1.00 58.67      C
ATOM   3396  CE2  PHE A 446     -2.991  118.757  -23.624  I.00 57.96      C
ATOM   3397  CZ   PHE A 446     -2.095  118.313  -24.578  1.00 57.43      C
ATOM   3398  O    ARG A 447     -4.229  116.888  -28.328  1.00 56.56      0
ATOM   3399  N    ARG A 447     -5.739  119.253  -27.392  1.00 56.27      N
ATOM   3400  CA   ARG A 447     -9.166  117.879  -27.334  1.00 51.82      C
ATOM   3401  C    ARG A 447     -4.976  116.938  -27.346  1.00 52.70      C
ATOM   3402  CB   ARG A 447     -7.091  117.586  -28.493  1.00 50.56      C
ATOM   3403  CG   ARG A 447     -7.502  116.181  -28.534  I.00 48.23      C
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ATOM   3404  CD   ARG  A  447    --8..148  115..905  -29..835   1.00  46..40   C
ATOM   3405  NE   ARG  A  447    -8.,493   114 .498  --29,904   1,00  53..98   N
ATOM   3406  CZ   ARG  A  447    -9.034    113.,938  -30..972   1,00  55,.04   C
ATOM   3407  NHl  ARG  A  447    --9..303  114 ,696  -32..025   1.00  58..53   N
ATOM   3408  NH2  ARG  A  447    -9.,314   112.640   -30..983   1,00  56..29   N
ATOM   3409  O    ILE  A  448    -4.851    113.,602  -27..393   1,00  47,64    O
ATOM   3410  N    ILE  A  448    -4.790    116.,232  -26..233   1,00  52,.13   N
ATOM   3411  CA.  ILE  A  448    -3.,745   115. 217  -26,072   1,00  46..77   C
ATOM   3412  C    ILE  A  448    -3..813   114 ,221  -27,207   1,00  48..53   C
ATOM   3413  CB   ILE  A  448    --3..908  114 ,410  -24.767   1,00  46,.96   C
ATOM   3414  CGI  ILE  A  448    -3.,869   115.292   -23,537   I,00  49.02    C
ATOM   3415  CG2  ILE  A  448    -2..828   113..358  -24,653   1,00  56..69   C
ATOM   3416  GDI  ILE  A  448    -3.999    114 ,491  -22.233   1,00  44,89    C
ATOM   3417  O    PRO  A  449    -2.554    Ill ,286  -27,602   1.00  52.42    0
ATOM   3418  N    FRO  A  449    -2.,712   114 .046  -27,957   1,00  51.67    N
ATOM   3419  CA   PRO  A  449    -2.788    113.,152  -29..111   1,00  51,98    C
ATOM   3420  C    PRO  A  449    -2.979    Ill ,687  -28.687   1.00  49..03   C
ATOM   3421  CB   PRO  A  449    -.1 ,437   113. 363  -29.,807   1,00  56..08   C
ATOM   3422  CG   PRO  A  449    -0..868   114 ,621  -29..180   1,00  51,82    C
ATOM   3423  CD   PRO  A  449    --1 .351  114 ,577  -27.786    1,00  50,.67   C
ATOM   3424  O    TYR  A  450    -2.,600   107 .682  -28,397   1,00  55..65   0
ATOM   3425  N    TYR  A  450    -3..645   110.,913  -29,530   1,00  46..85   N
ATOM   3426  CA   TYR  A  450    --3..897  109.,508  -29..244   1,00  52,67    C
ATOM   3427  C    TYR  A  450    -2,,608   108..674  -29.,114   I,00  52.49    C
ATOM   3428  CB   TYR  A  450    -4.802    108..905  -30.,330   1,00  49..09   C
ATOM   3429  CG   TYR  A  450    -4.141    108.,753  -31. 670   1,00  50,06    C
ATOM   3430  CD1  TYR  A  450    -3.,360   107..637  -31.,950   I,00  55..73   C
ATOM   3431  CD2  TYR  A  450    -4„297     109.. 714  -32.,666   1,00  54.01    C
ATOM   3432  CE1  TYR  A  450    -2.738    107 ,474  -33. 163   1,00  52,07    C
ATOM   3433  CE2  TYR  A  450    --3.,683  109.,562  -33..903   1.00  59..78   C
ATOM   3434  CZ   TYR  A  450    -2.,895   108..421  -34.,136   1,00  63..14   C
ATOM   3435  OH   TYR  A  450    -2.268    108.,201  -35...341   1,00  62,02    0
ATOM   3436  O    TYR  A  451     1.698    108.,081  -28.487    1.00  62.07    0
ATOM   3437  N    TYR  A  451    -.1 ,537   109.072   -29.,806   1,00  51.28    N
ATOM   3438  CA   TYR  A  451    -0..281   108.,305  -29..819   1,00  52,59    C
ATOM   3439  C    TYR  A  451     0..618   108.,659  -28.647    1,00  56,.91   C
ATOM   3440  CB   TYR  A  451     0„491     108. 525  -31,114    1,00  51.85    C
ATOM   3441  CG   TYR  A  451     0,900    109.,964  -31.,350   1,00  54.10    C
ATOM   3442  CD2  TYR  A  451     0.261    110.,739  -32. 314   1,00  57,27    C
ATOM   3443  CD1  TYR  A  451     1„934     110.540   -.30.,624   I,00  50..38   C
ATOM   3444  CE2  TYR  A  451     0„631     112..057  -32.,531   1,00  58..72   C
ATOM   3445  CE1  TYR  A  451     2.304    111,843   -30. 825   1,00  60,72    C
ATOM   3446  CZ   TYR  A  451     1.652    112.,602  -31.,780   1.00  60..80   C
ATOM   3447  OH   TYR  A  451     2,044    113..907  -31.,968   1,00  62.73    0
ATOM   3448  O    VAL  A  452    -1.272    109.,157  -25.553    1,00  57,50    0
ATOM   3449  N    VAL  A  452     0..185   109.,635  -27.856    1.00  52.95    N
ATOM   3450  CA.  VAL  A  452     0„775     109.893   -26,550    1,00  52.79    C
ATOM   3451  C    VAL  A  452    -0..039   109.,139  -25.506    1,00  55,.49   C
ATOM   3452  CB   VAL  A  452     0.787    111 ,401  -26.223    1,00  46,.95   C
ATOM   3453  CGI  VAL  A  452     1„235     111.647   -24.,806   1,00  49..41   C
ATOM   3454  CG2  VAL  A  452     1,669    112.,137  -27,193    1,00  48..65   C
ATOM   3455  O    GLY  A  453    --1 .265  109.,993  -23.151    1,00  46,.23   0
ATOM   3456  N    GLY  A  453     0„601     108..470  -24.,556   I,00  55..43   N
ATOM   3457  CA   GLY  A  453    -0.,205   107 .845  -23,518    1,00  62.69    C
ATOM   3458  C    GLY  A  453    -1.137    108.,827  -22.780    1,00  54,89    C
ATOM   3459  O    PRO  A  454     0„323     109.147   -20.,272   I,00  53..85   0
ATOM   3460  N    FRO  A  454    -1,789    108..346  -21.,717   1,00  44.49    N
ATOM   3461  CA   PRO  A  454    -2.040    109.,264  -20. 616   1,00  47,96    C
ATOM   3462  C    PRO  A  454    --0.,716  109.,785  -20,082    1.00  56..00   C
ATOM   3463  CB   FRO  A  454    -2.,733   108..392  -19,575    1,00  51.52    C
ATOM   3464  CG   PRO  A  454    -2..384   107 ,006  -19.954    1,00  45,.73   C
ATOM   3465  CD   PRO  A  454    -2.321    107 ,008  -21..434   1.00  44.77    C
ATOM   3466  O    LEU  A  455     0„939     111.901   -16,731    1,00  58..40   0
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ATOM   3467   N    LEU  A  455    --0.752  110.930  -19.414   1.00  57.93      N
ATOM   3468   CA   LEU  A  455     0,466  Ill.635  --19,044   1,00  56.49      C
ATOM   3469   C    LEU  A  455     0.948  I11,150   -17.697   1.00  54,49      C
ATOM   3470   CB   LEU  A  455     0.208  113.144   -19,012   1.00  56.18      C
ATOM   3471   CG   LEU  A  455    -0,618  113.722   -20,152   1,00  47.30      C
ATOM   3472   GD1  LEU  A  455    -0.762  115,203   -19.949   1.00  57,27      C
ATOM   3473   CD2  LEU  A  455    --0.002  113,441   -21.527   1,00  51,85      C
ATOM   3474   O    ALA  A  456     3,972  109.650   -16,723   1,00  65.53      0
ATOM   3475   N    ALA  A  456     1.355  109,886   -17.631   1,00  61.29      M
ATOM   3476   CA   ALA  A  456     1.632  109,241   -16.347   1,00  61,48      C
ATOM   3477   C    ALA  A  456     3,081  109.390   -15,909   1,00  69.34      C
ATOM   3478   CB   ALA  A  456     1.266  107.774   -16.398   1,00  51.56      C
ATOM   3479   O    A.P.G A  457     5.474  107,610   -12.451   1,00  67,91      0
ATOM   3480   N    ARG  A  457     3.279  109.216   -14,604   1.00  71.34      N
ATOM   3481   CA   ARG  A  457     4,573  109.313   -13,938   1,00  74.03      C
ATOM   3482   C    ARG  A  457     5.016  107,880   -13.558   1.00  71,44      C
ATOM   3483   CB   ARG  A  457     4.454  110.248   ~12.720   1,00  69.46      C
ATOM   3484   CG   ARG  A  457     5,706  110.443   -11,852   1,00  79.69      C
ATOM   3485   CD   ARG  A  457     6.643  I11,578   -12.312   1.00  80,92      C
ATOM   3486   NE   ARG  A  457     6.381  112,886   -11.701   1,00  79,06      N
ATOM   3487   CZ   ARG  A  457     6,386  113.147   -10,391   1,00  82.15      C
ATOM   3488   NH1  ARG  A  457     6.148  114.383    -9.959   1.00  73.50      M
ATOM   3489   NH2  ARG  A  457     6.625  112,186    -9.505   1,00  86,83      N
ATOM   3490   O    GLY  A  458     4,864  103.789   -12,685   1,00  69.19      O
ATOM   3491   N    GLY  A  458     4.832  106,953   -14.490   1,00  66.05      M
ATOM   3492   CA   GLY  A  458     5.191  105,570   -14.257   1,00  73,75      C
ATOM   3493   C    GLY  A  458     4,383  104.795   -13,224   1,00  71.42      C
ATOM   3494   O    ASM  A  459     0,082  103.475   -12,262   1,00  55,12      O
ATOM   3495   N    ASN  A  459     3.161  105,240   -12.945   1,00  66,54      N
ATOM   3496   CA   ASN  A  459     2.264  104,467   ~12,081   1.00  61.55      C
ATOM   3497   C    ASM  A  459     1,066  103.931   -12,847   1,00  54.95      C
ATOM   3498   CB   ASN  A  459     1.794  105,301   -10.891   1.00  64,99      C
ATOM   3499   CG   ASN  A  459     2.947  105.782   -10.024   1,00  72.10      C
ATOM   3500   OD1  ASM  A  459     3,965  106.254   -10,531   1,00  73.68      0
ATOM   3501   ND2  ASN  A  459     2.797  105,651    -8.713   1.00  71,64      N
ATOM   3502   O    SER  A  460     1.396  102,390   -16.558   1,00  60,37      0
ATOM   3503   N    SER  A  460     1,153  103.957   -14,164   1,00  48.14      M
ATOM   3504   CA   SER  A  460     0.026  103,490   -14.943   1,00  54.94      C
ATOM   3505   C    SER  A  460     0.428  102,309   -15.797   1,00  56,96      C
ATOM   3506   CB   SER  A  460    -0,551  104.623   -15,813   1,00  53.01      C
ATOM   3507   OG   SER  A  460    -1,407  104.115   -16,816   1,00  51.82      0
ATOM   3508   O    ARG  A  461    -0.103   99,328   -18.739   1,00  57,07      0
ATOM   3509   N    ARG  A  461   --0.325  101.215   -15,681   1.00  53.04      N
ATOM   3510   CA   ARG  A  461    -0,021  100.027   -16,454   1,00  51.75      C
ATOM   3511   C    ARG  A  461    -0.396  100,200   -17.917   1.00  58,06      C
ATOM   3512   CB   ARG  A  461   --0.724   98,809   -15.862   1,00  54.89      C
ATOM   3513   CG   ARG  A  461    -2,170   98.627   -16,242   1,00  55.94      C
ATOM   3514   CD   ARG  A  461    -2.692   97,333   -15.611   1.00  46,98      C
ATOM   3515   NE   ARG  A  461    -4.017   96,981   -16.098   1,00  52,88      N
ATOM   3516   CZ   ARG  A  461    -4,232   96.416   -17,282   1,00  60.10      C
ATOM   3517   NH1  ARG  A  461    -3.198   96,149   -18,073   1,00  61.45      M
ATOM   3518   NH2  ARG  A  461   --5.469   96,112   -17.678   1,00  56,03      N
ATOM   3519   O    PHE  A  462    -0,651  102.758   -21,541   1,00  60.73      O
ATOM   352 0  N    FHE  A  462    -1.030  101.332   -18.241   1,00  56.41      M
ATOM   352 1  CA   PHE  A  462    -1.469  101,602   -19.612   1,00  53,02      C
ATOM   3522   C    PHE  A  462    -0,577  102.626   -20,315   1,00  56.83      C
ATOM   352 3  CB   FHE  A  462    -2,934  102.105   -19,646   1,00  52.16      C
ATOM   352 4  CG   PHE  A  462    -3.906  101,273   -18.827   1,00  46,77      C
ATOM   352 5  CD1  PHE  A  462    -4,476  100,114   -19,353   1.00  41.28      C
ATOM   352 6  CD2  FHE  A  462    -4,240  101.656   -17,537   1,00  37.40      C
ATOM   352 7  CE1  PHE  A  462    -5.369   99,357   -18.597   1.00  41,25      C
ATOM   352 8  CE2  PHE  A  462   --5.116  100.906   -16.777   1.00  39.67      C
ATOM   3529   CZ   PHE  A  462    -5,683   99.755   -17,307   1,00  40.87      C
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ATOM   3530  O    ALA A 463     2.768 102.930 -20.729  1.00 64.76      O
ATOM   3531  N    ALA A 463     0.259 103.352 -19.562  1.00 57.23      N
ATOM   3532  CA   ALA A 463     1.023 104.484 -20.138  1.00 55.94      C
ATOM   3533  C    ALA A 463     2.288 104.050 -20.896  1.00 58.28      C
ATOM   3534  CB   ALA A 463     1.385 105.468 -19.055  1.00 51.61      C
ATOM   3535  O    TRP A 464     5.839 105.760 -23.545  1.00 59.88      0
ATOM   3536  N    TRP A 464     2.820 104.933 -21.735  1.00 56.58      N
ATOM   3537  CA   TRP A 464     3.999 104.604 -22.527  1.00 55.37      C
ATOM   3538  C    TRP A 464     4.755 105.843 -22.944  1.00 59.30      C
ATOM   3539  CB   TRP A 464     3.613 103.825 -23.775  1.00 62.16      C
ATOM   3540  CG   TRP A 464     2.838 104.640 -24.799  1.00 56.15      C
ATOM   3541  CD1  TRP A 464     3.346 105.508 -25.726  1.00 58.46      C
ATOM   3542  CD2  TRP A 464     1.434 104.602 -25.017  1.00 56.06      C
ATOM   3543  NE1  TRP A 464     2.335 106.030 -26.501  1.00 58.15      N
ATOM   3544  CE2  TRP A 464     1.148 105.489 -26.081  1.00 61.25      C
ATOM   3545  CE3  TRP A 464     0.381 103.913 -24.409  1.00 54.54      C
ATOM   3546  CZ2  TRP A 464    -0.148 105.704 -26.541  1.00 55.33      C
ATOM   3547  CZ3  TRP A 464    -0.895 104.121 -24.870  1.00 51.34      C
ATOM   3548  CH2  TRP A 464    -1.152 105.008 -25.924  1.00 54.56      C
ATOM   3549  O    MET A 465     6.201 107.984 -21.068  1.00 56.56      0
ATOM   3550  N    MET A 465     4.145 106.989 -22.665  1.00 52.53      N
ATOM   3551  CA   MET A 465     4.739 108.285 -22.946  1.00 57.18      C
ATOM   3552  C    MET A 465     6.062 108.455 -22.196  1.00 59.55      C
ATOM   3553  CB   MET A 465     3.743 109.401 -22.563  1.00 62.92      C
ATOM   3554  CG   MET A 465     4.254 110.833 -22.710  1.00 59.25      C
ATOM   3555  SD   MET A 465     4.731 111.593 -21.146  1.00 69.16      S
ATOM   3556  CE   MET A 465     4.275 110.327 -19.947  1.00 61.69      C
ATOM   3557  O    THR A 466     8.206 111.807 -23.018  1.00 67.92      0
ATOM   3558  N    THR A 466     7.035 109.110 -22.828  1.00 61.95      N
ATOM   3559  CA   THR A 466     8.240 109.543 -22.108  1.00 68.06      C
ATOM   3560  C    THR A 466     8.361 111.081 -22.025  1.00 65.98      C
ATOM   3561  CB   THR A 466     9.535 108.962 -22.744  1.00 65.32      C
ATOM   3562  OG1  THR A 466     9.457 109.059 -24.170  1.00 69.07      0
ATOM   3563  CG2  THR A 466     9.726 107.497 -22.350  1.00 59.31      C
ATOM   3564  O    ARG A 467    11.175 112.729 -20.660  1.00 74.64      0
ATOM   3565  N    ARG A 467     8.631 111.548 -20.812  1.00 70.20      N
ATOM   3566  CA   ARG A 467     8.805 112.958 -20.482  1.00 65.03      C
ATOM   3567  C    ARG A 467    10.206 113.465 -20.823  1.00 75.06      C
ATOM   3568  CB   ARG A 467     8.549 113.137 -18.989  1.00 69.67      C
ATOM   3569  CG   ARG A 467     7.678 114.321 -18.601  1.00 77.83      C
ATOM   3570  CD   ARG A 467     7.184 114.185 -17.154  1.00 74.81      C
ATOM   3571  NE   ARG A 467     6.290 113.041 -17.021  1.00 78.33      N
ATOM   3572  CZ   ARG A 467     4.993 113.129 -16.735  1.00 77.75      C
ATOM   3573  NH1  ARG A 467     4.252 112.026 -16.651  1.00 71.62      N
ATOM   3574  NH2  ARG A 467     4.439 114.317 -16.520  1.00 73.86      N
ATOM   3575  O    LYS A 468    13.335 116.312 -20.019  1.00 86.42      0
ATOM   3576  N    LYS A 468    10.325 114.719 -21.269  1.00 81.27      N
ATOM   3577  CA   LYS A 468    11.642 115.365 -21.437  1.00 79.35      C
ATOM   3578  C    LYS A 468    12.156 115.993 -20.138  1.00 80.10      C
ATOM   3579  CB   LYS A 468    11.600 116.452 -22.517  1.00 71.91      C
ATOM   3580  CG   LYS A 468    11.431 115.938 -23.931  1.00 73.63      C
ATOM   3581  CD   LYS A 468    10.605 116.905 -24.779  1.00 69.64      C
ATOM   3582  CE   LYS A 468    11.439 117.992 -25.427  1.00 66.51      C
ATOM   3583  NZ   LYS A 468    10.626 118.774 -26.418  1.00 74.03      N
ATOM   3584  O    SER A 469    10.067 115.367 -16.961  1.00 85.37      0
ATOM   3585  N    SER A 469    11.269 116.186 -19.173  1.00 76.96      N
ATOM   3586  CA   SER A 469    11.646 116.842 -17.932  1.00 81.10      C
ATOM   3587  C    SER A 469    10.860 116.279 -16.780  1.00 86.13      C
ATOM   3588  CB   SER A 469    11.408 118.338 -18.027  1.00 77.79      C
ATOM   3589  OG   SER A 469    11.146 118.691 -19.370  1.00 85.27      0
ATOM   3590  O    GLU A 470     9.225 117.958 -12.926  1.00100.09      0
ATOM   3591  N    GLU A 470    11.075 116.822 -15.591  1.00 88.97      N
ATOM   3592  CA   GLU A 470    10.257 116.433 -14.459  1.00 91.12      C
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ATOM    3593   C    GLU  A  470      9 ..385  117 .611  -14 .093   1 .00  90..99         C
ATOM    3594   CB   GLU  A  470     11 ,111  115. 982  --13.,274   1 ,00  97 .08         C
ATOM    3595   CG   GLU  A  470     10 .319  115.,239  -12 .203   1 ,00  98,.07         C
ATOM    3596   CD   GLU  A  470     11 .038  114 .014  -11 .678   1 .00104..50         C
ATOM    3597   OE1  GLU  A  470     12,,216  114 .142  -11 ,261   1 ,00105.,08         0
ATOM    3598   OE2  GLU  A  470     10 .416  112.,925  -11 .686   1 ,00102,.56         0
ATOM    3599   O    GLU  A  471      6 ..261  118.,316  -16. 256   1 ,00  81 ,34         0
ATOM    3600   N    GLU  A  471      8 ,828  118. 251  -15 ,106   1 ,00  85.,82         N
ATOM    3601   CA   GLU  A  471      7 .920  119. 341  -14 .836   1 ,00  87 .24         C
ATOM    3602   C    GLU  A  471      6 ..493  118.,954  -15. 224   1 ,00  85,.73         C
ATOM    3603   CB   GLU  A  471      8 ,368  120. 610  -15.,558   I ,00  82 .80         C
ATOM    3604   CG   GLU  A  471      8 ..932  121. 661  -14 .618   1 ,00  87 .61         C
ATOM    3605   CD   GLU  A  471.     8 .510  123 ,066  -15. 001   1 ,00  93 ,53         C
ATOM    3606   OE1  GLU  A  471      7 .540  123. 206  -15. 782   1 .00  90..19         0
ATOM    3607   OE2  GLU  A  471      9 ,150  124 .031  -14 ,525   1 ,00  91 .64         0
ATOM    3608   O    THR  A  472      3 ..843  120 ,743  -16 .256   1 ,00  70,.64         0
ATOM    3609   N    THR  A  472      5 .555  119. 327  -14 .360   1 .00  79..45         N
ATOM    3610   CA.  THR  A  472      4 ,139  119. 076  -14 ,561   1 ,00  71 ,48         C
ATOM    3611   C    THR  A  472      3 ..669  119 ,571  -15 .924   1 ,00  69,.57         C
ATOM    3612   CB   THR  A  472      3 ..326  119.,747  -13. 451   1 ,00  72 ,16         C
ATOM    3613   OG1  THR  A  472      3 ,563  119. 056  -12.,218   1 ,00  73.,66         0
ATOM    3614   CG2  THR  A  472      1 .862  119. 714  -13. 764   1 ,00  67 .93         C
ATOM    3615   O    ILE  A  473      0 ..462  119.,502  -17 .264   1 ,00  62 ,14         0
ATOM    3616   N    ILE  A  473      3 ,093  118 .658  -16 ,709   I ,00  65..65         N
ATOM    3617   CA   ILE  A  473      2 .641  118. 947  -18. 072   1 ,00  67 .21         C
ATOM    3618   C    ILE  A  473      1 .350  119 ,760  -18. 063   1 ,00  60 ,71         C
ATOM    3619   CB   ILE  A  473      2 ,398  117 .653  -18.,882   I ,00  67 ,39         C
ATOM    3620   CGI  ILE  A  473      3 ,610  116. 717  -18.,805   1 ,00  72 .20         C
ATOM    3621   CG2  ILE  A  473      2 .043  117 ,989  -20. 325   1 ,00  65 ,91         C
ATOM    3622   CD1  ILE  A  473      3 .361  115. 323  -19. 368   1 .00  67 .49         C
ATOM    3623   O    THR  A  474      0 ,457  121 .558  -21.,324   1 ,00  62 .29         0
ATOM    3624   N    THR  A  474      1 .254  120 ,752  -18 .939   1 ,00  60,.64         N
ATOM    3625   CA   THR  A  474      0 .093  121. 634  -18. 966   1 .00  61 .46         C
ATOM    3626   C    THR  A  474     -0.,298  121 .898  -20.,418   1 ,00  62 ,38         C
ATOM    3627   CB   THR  A  474      0 ..362  122.,979  -18 .238   1 ,00  61 ,06         C
ATOM    3628   OG1  THR  A  474      1 .317  123 ,745  -18. 978   1 ,00  63,.25         0
ATOM    3629   CG2  THR  A  474      0 ,809  122 .765  -16 ,787   1 ,00  55.,94         C
ATOM    3630   O    FRO  A  475     -0. 631  123. 484  -23 .981   1 ,00  67 .40         0
ATOM    3631   N    PRO  A  475     -1 .474  122.,513  -20. 651   1 ,00  64 ,78         N
ATOM    3632   CA   PRO  A  475     -1 ,819  122. 717  -22.,061   I ,00  63..53         C
ATOM    3633   C    FRO  A  475     -0.,825  123. 621  -22.,772   1 ,00  60..94         C
ATOM    3634   CB   PRO  A  475     -3 .204  123 ,376  -21 .993   1 ,00  63 ,14         C
ATOM    3635   CG   PRO  A  475     --3. 710  123. 065  -20 .641   1 .00  59..81         C
ATOM    3636   CD   FRO  A  475     -2.,539  122. 998  -19 ,752   1 ,00  56..84         C
ATOM    3637   O    TRP  A  476      2 .774  125 ,018  -23 .846   1 ,00  64 ,86         0
ATOM    3638   N    TRP  A  476     --0. 190  124. 515  -22. 019   1 .00  59..69         N
ATOM    3639   CA.  TRP  A  476      0 ,773  125. 462  -22.,590   1 ,00  68.,42         C
ATOM    3640   C    TRP  A  476      2 .166  124 ,850  -22. 793   1 ,00  63,.22         C
ATOM    3641   CB   TRP  A  476      0 ..862  126.,706  -21 .703   1 ,00  61 ,19         C
ATOM    3642   CG   TRP  A  476     -0.,456  127 .051  -21.,168   1 ,00  61 ,15         C
ATOM    3643   CD1  TRP  A  476     -1 .516  127 .559  -21. 866   1 ,00  64 .17         C
ATOM    3644   CD2  TRP  A  476     --0..906  126.,873  -19. 828   1 ,00  64 ,10         C
ATOM    3645   NE1  TRP  A  476     -2.,591  127 .721  -21.,036   I ,00  62 .66         N
ATOM    3646   CE2  TRP  A  476     -2. 243  127 .312  -19. 776   1 ,00  63..85         C
ATOM    3647   CE3  TRP  A  476     -0. 304  126 ,396  -18. 662   1 ,00  66 ,95         C
ATOM    3648   CZ2  TRP  A  476     -2.,990  127 .288  -18.,606   I ,00  66..77         C
ATOM    3649   CZ3  TRP  A  476     -1 ,043  126. 371  -17 ,498   1 ,00  67 .89         C
ATOM    3650   CH2  TRP  A  476     -2 .377  126 ,814  -17 .478   1 ,00  70 ,00         C
ATOM    3651   O    ASN  A  477      5 .142  121. 577  -22. 371   1 .00  72 .99         0
ATOM    3652   N    ASM  A  477      2 ,674  124 .138  -21.,797   1 ,00  61 .52         N
ATOM    3653   CA   ASN  A  477      4 .025  123 ,616  -21. 926   1 ,00  68,.82         C
ATOM    3654   C    ASN  A  477      4 .102  122. 202  -22. 498   1 .00  69..12         C
ATOM    3655   CB   ASN  A  477      4 ,740  123. 651  -20.,569   1 ,00  66.,10         C
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ATOM  3656  CG   ASN A 477    4.211  122.618  -19.594  1.00  69.07  C
ATOM  3657  OD1  ASM A 477    3,522  121.671  --19,975 1,00  70.50  O
ATOM  3658  ND2  ASN A 477    4.539  122,794  -18.319  1.00  68,61  N
ATOM  3659  O    PHE A 478    4.861  118:937  -23.917  1.00  69.23  0
ATOM  3660  N    PHE A 478    3,015  121.696  -23,087  1,00  66.78  N
ATOM  3661  CA   PHE A 478    2.944  120,276  -23.440  1.00  66,39  C
ATOM  3662  C    PHE A 478    4.125  119,839  -24.304  1,00  70,44  C
ATOM  3663  CB   PHE A 478    1,631  119.940  -24,153  1,00  60.98  C
ATOM  3664  CG   PHE A 478    1.528  118.491  -24.609  1,00  62.08  C
ATOM  3665  CD1  PHE A 478    1.220  117,479  -23.707  1,00  61,13  C
ATOM  3666  CD2  PHE A 478    1,713  118.150  -25,947  1,00  55.26  C
ATOM  3667  CE1  PHE A 478    1.112  116.150  -24.131  1,00  61.84  C
ATOM  3668  CE2  PHE A 478    1.609  116,827  -26.375  1,00  60,87  C
ATOM  3669  CZ   PHE A 478    1.314  115.826  -25.469  1.00  59.60  C
ATOM  3670  O    GLU A 479    7,683  119.477  -26,053  1,00  69.95  0
ATOM  3671  N    GLU A 479    4.316  120.487  -25.452  1.00  67,49  N
ATOM  3672  CA   GLU A 479    5.379  120.114  -26.373  1,00  65.11  C
ATOM  3673  C    GLU A 479    6,763  120.233  -25,727  1,00  73.62  C
ATOM  3674  CB   GLU A 479    5.312  120,975  -27.622  1,00  63,81  C
ATOM  3675  CG   GLU A 479    5.357  120,201  -28.911  1,00  70,92  C
ATOM  3676  CD   GLU A 479    4,796  120.997  -30,081  1,00  83.38  C
ATOM  3677  OE1  GLU A 479    5.145  122,196  -30,206  1,00  81.63  0
ATOM  3678  OE2  GLU A 479    3.996  120,430  -30.868  1,00  81,53  0
ATOM  3679  O    GLU A 480    9,512  119.492  -23,297  1,00  83.03  0
ATOM  3680  N    GLU A 480    6.907  121.177  -24.805  1.00  70.97  N
ATOM  3681  CA   GLU A 480    8.158  121,312  -24.071  1,00  72,48  C
ATOM  3682  C    GLU A 480    8,440  120.085  -23,202  1,00  76.01  C
ATOM  3683  CB   GLU A 480    8,143  122.566  -23,196  1,00  72.68  C
ATOM  3684  O    VAL A 481    8.279  116,281  -21.568  1,00  76,40  0
ATOM  3685  N    VAL A 481    7.494  119.691  -22,358  1.00  71.87  N
ATOM  3686  CA   VAL A 481    7,775  118.628  -21,399  1,00  73.01  C
ATOM  3687  C    VAL A 481    7.645  117,236  -22.023  1,00  74,41  C
ATOM  3688  CB   VAL A 481    6.857  118.736  -20.158  1,00  74.21  C
ATOM  3689  CGI  VAL A 481    7,330  117.800  -19,061  1,00  70,31  C
ATOM  3690  CG2  VAL A 481    6.838  120,172  -19.632  1.00  72,34  C
ATOM  3691  O    VAL A 482    7.361  116,198  -25.934  1,00  68,45  0
ATOM  3692  N    VAL A 482    6,857  117.118  -23,086  1,00  74.49  N
ATOM  3693  CA   VAL A 482    6.601  115.803  -23.664  1,00  73.05  C
ATOM  3694  C    VAL A 482    7.441  115,521  -24.900  1,00  69,25  C
ATOM  3695  CB   VAL A 482    5,093  115.603  -24,017  1,00  67.19  C
ATOM  3696  CGI  VAL A 482    4,899  114.378  -24,938  1,00  61.41  C
ATOM  3697  CG2  VAL A 482    4.284  115,441  -22.745  1,00  61,98  C
ATOM  3698  N    ASP A 483    8.251  114.488  -24,769  1.00  69.17  N
ATOM  3699  CA   ASP A 483    8,946  113.942  -25,900  1,00  68.97  C
ATOM  3700  C    ASP A 483    7.915  113,237  -26.738  1.00  70,71  C
ATOM  3701  O    ASP A 483    7.570  112.080  -26.469  1.00  67.84  O
ATOM  3702  CB   ASP A 483   10,040  112.981  -25.462  1,00  69.17  C
ATOM  3703  CG   ASP A 483   10.809  112,386  -26.642  1,00  69,93  C
ATOM  3704  OD1  ASP A 483   10.492  112,669  -27.827  1,00  65,48  0
ATOM  3705  OD2  ASP A 483   11,741  111.615  -26,363  1,00  73,47  0
ATOM  3706  N    LYS A 484    7.415  113.940  -27.745  1,00  67.20  N
ATOM  3707  CA   LYS A 484    6.414  113,366  -28.616  1,00  65,80  C
ATOM  3708  C    LYS A 484    6,995  112.156  -29.303  1,00  68.37  C
ATOM  3709  O    LYS A 484    6.355  Ill.105  -29.376  1,00  70.08  0
ATOM  3710  CB   LYS A 484    5.932  114,375  -29.653  1,00  73,38  C
ATOM  3711  CG   LYS A 484    4,958  115.412  -29,136  1,00  68.17  C
ATOM  3712  CD   LYS A 484    4,283  116.063  -30,331  1,00  66.35  C
ATOM  3713  CF.  LYS A 484    3.523  117,289  -29.954  1,00  69,55  C
ATOM  3714  NZ   LYS A 484    3.021  117.974  -31.188  1.00  84.62  N
ATOM  3715  N    GLY A 485    8,228  112.312  -29,774  1,00  71.42  N
ATOM  3716  CA   GLY A 485    8.897  I11,303  -30.567  1.00  65,02  C
ATOM  3717  C    GLY A 485    8.919  109.930  -29.941  1.00  66.57  C
ATOM  3718  O    GLY A 485    8,335  108.985  -30,462  1,00  68.05  0
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ATOM    3719  N    ALA  A  486      9 ..598  109.. 829  -28 ..808   1 .00  67 .80          N
ATOM    3720  CA   ALA  A  486      9 „755  108..563  --28 ,107   1 ,00  70..92          C
ATOM    3721  C    ALA  A  486      8 ..416  108.,047  -27 .604   1 ,00  66,.32          C
ATOM    3722  O    ALA  A  486      8 ..264  106.. 870  -27 ..256   1 .00  60..23          0
ATOM    3723  CB   ALA  A  486     10,,731  108. 720  -26 ,942   1 ,00  66.,61          C
ATOM    3724  N    SER  A  487      7 .454  108.,957  -27 .546   1 ,00  67 ,51          N
ATOM    3725  CA   SER  A  487      6 ..110  108.,616  -27 .155   1 ,00  59,.69          C
ATOM    3726  C    SER  A  487      5 „427  107 .970  -28 ,352   1 ,00  59.,59          C
ATOM    3727  O    SER  A  487      4 .923  106.. 853  --28 .246   1 ,00  59..32          O
ATOM    3728  CB   SER  A  487      5 ..372  109.,860  -26 ..657   1 ,00  62 ,81          C
ATOM    3729  OG   SER  A  487      6 „046  110 .415  -25 ,529   I ,00  64 .89          0
ATOM    3730  N    ALA  A  488      5 ..449  108..645  -29 .497   1 ,00  52 .22          N
ATOM    3731  CA   ALA  A  488      4 .888  108.,062  -30. 710   1 ,00  55 ,95          C
ATOM    3732  C    ALA  A  488      5 ..622  106.. 787  -31.. 108   1 .00  65..93          C
ATOM    3733  O    ALA  A  488      5 „007  105..843  -31.,608   1 ,00  67 .90          0
ATOM    3734  CB   ALA  A  488      4 .924  109.,054  -31..858   1 ,00  56,.28          C
ATOM    3735  N    GLN  A  489      6 ..936  106.. 746  -30..901   1 .00  67 .85          N
ATOM    3736  CA.  GLN  A  489      7 „668  105. 587  -31 ,373   1 ,00  65.,39          C
ATOM    3737  C    GLN  A  489      7 .22 6  104.,400  -30..555   1 ,00  62 ,58          C
ATOM    3738  O    GLN  A  489      6 ..787  103.,400  -31..129   1 ,00  64 ,87          O
ATOM    3739  CB   GLN  A  489      9 „181  105. 779  -31 ,301   1 ,00  69.,97          C
ATOM    3740  CG   GLN  A  489      9 .912  105.. 071  -32.. 440   1 ,00  74 .89          C
ATOM    3741  CD   GLN  A  489     11 .330  104.,658  -32..076   1 ,00  85,.40          C
ATOM    3742  OE1  GLN  A  489     12.,296  105..282  -.32.,515   I ,00  89..38          0
ATOM    3743  NE2  GLN  A  489     11 .462  103..600  -31.. 274   1 ,00  75..40          N
ATOM    3744  N    SER  A  490      7 .287  104.,523  -29. 225   1 ,00  60 ,13          N
ATOM    3745  CA   SER  A  490      6 ,897  103..411  -28.,356   I ,00  59..51          C
ATOM    3746  C    SER  A  490      5 ,442  103..026  -28 ,585   1 ,00  60..81          C
ATOM    3747  O    SER  A  490      5 .074  101.,886  -28. 352   1 ,00  60 ,86          O
ATOM    3748  CB   SER  A  490      7 .,115  103.. 730  -26 .872   1 .00  54 .86          C
ATOM    3749  OG   SER  A  490      7 ,890  104 .891  -26 ,686   1 ,00  60..33          0
ATOM    3750  N    PHE  A  491      4 .629  103.,982  -29.. 040   1 ,00  62 ,58          N
ATOM    3751  CA   PHE  A  491      3 ..225  103.. 729  -29 .368   1 .00  60..81          C
ATOM    3752  C    PHE  A  491      3 ,11 6  102. 536  -30.,311   1 ,00  58.,49          C
ATOM    3753  O    PHE  A  491      2 .544  101.,523  -29.. 943   1 ,00  61 ,16          O
ATOM    3754  CB   PHE  A  491      2 .570  104.,982  -29 ..976   1 ,00  56,.55          C
ATOM    3755  CG   PHE  A  491      1 ,149  104 .778  -30.,459   1 ,00  55.,76          C
ATOM    3756  CD2  PHE  A  491      0 .820  104.. 986  -31.. 790   1 ,00  54 .37          C
ATOM    3757  GDI  PHE  A  491      0 .134  104.,415  -29. 579   1 ,00  55 ,51          C
ATOM    3758  CE2  PHE  A  491     -0.,487  104..816  -.32.,244   I ,00  52 .93          C
ATOM    3759  CE1  PHE  A  491     -1 ,176  104 .242  -30.,027   1 ,00  47 .98          C
ATOM    3760  CZ   PHE  A  491     -1 .481  104.,453  -31. 356   1 ,00  49 ,78          C
ATOM    3761  N    ILE  A  492      3 .687  102.. 641  -31..505   1 .00  60..79          N
ATOM    3762  CA   ILE  A  492      3 ,630  101..540  -32.,466   1 ,00  62 .77          C
ATOM    3763  C    ILE  A  492      4 .522  100.,343  -32.. 088   1 ,00  61 ,94          C
ATOM    3764  O    ILE  A  492      4 .160   99.. 192  -32.. 330   1 .00  65..27          0
ATOM    3765  CB   ILE  A  492      4 ,009  102. 024  -33.,876   1 ,00  63.,12          C
ATOM    3766  CGI  ILE  A  492      3 ..113  103.,206  -34.. 285   1 ,00  66,.02          C
ATOM    3767  CG2  ILE  A  492      3 ..923  100.,890  -34.. 891   1 ,00  60,.24          C
ATOM    3768  CD1  ILE  A  492      1 ,974  102. 876  -35.,261   1 ,00  62 ,04          C
ATOM    3769  N    GLU  A  493      5 .676  100.. 597  -31.. 481   1 ,00  65..60          N
ATOM    3770  CA   GLU  A  493      6 ..644   99.,514  -31.. 251   1 ,00  60,.98          C
ATOM    3771  C    GLU  A  493      6 ,189   98..583  -.30.,127   I ,00  64 .65          C
ATOM    3772  O    GLU  A  493      6 . 653   97..436  -30.. 032   1 ,00  60..25          0
ATOM    3773  CB   GLU  A  493      8 .037  100.,089  -30. 941   1 ,00  62 ,42          C
ATOM    3774  CG   GLU  A  493      8 ,352  100..238  -29.,444   I ,00  66..44          C
ATOM    3775  CD   GLU  A  493      9 ,442  101..280  -29 ,146   1 ,00  73..91          C
ATOM    3776  OE1  GLU  A  493      9 .552  101.,695  -27 .969   1 ,00  71 ,29          0
ATOM    3777  OE2  GLU  A  493     10.. 183  101.. 682  -30.. 078   1 .00  80..44          0
ATOM    3778  N    ARG  A  494      5 ,27 6   99..069  -29 ,282   1 ,00  62 .07          N
ATOM    3779  CA   AP.G A  494      4 .795   98.,278  -28 .148   1 ,00  60,.78          C
ATOM    3780  C    ARG  A  494      3 ..723   97.. 293  -28 .594   1 .00  57 .29          C
ATOM    3781  0    ARG  A  494      3 ,277   96. 443  -27 ,81 9   1 ,00  58.,04          0
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ATOM   3782  CB   ARG  A  494      4 .245   99.,178  -27,039   1,00  64.07       C
ATOM   3783  CG   ARG  A  494      2 ,968   99..960  --27,412   1,00  61.21       C
ATOM   3784  CD   ARG  A  494      2 .522  100.,871  -26.276   1,00  59,.11       C
ATOM   3785  NE   ARG  A  494      1 .523  100.,192  -25,454   1,00  66..96       N
ATOM   3786  CZ   ARG  A  494      1 ,610  .100. 0.11  -24,,143   1,00  58.,94       C
ATOM   3787  NH1  ARG  A  494      0 ..646   99.,361  -23.505   1,00  58,.78       N
ATOM   3788  NH2  ARG  A  494      2 .655  100.,473  -23.471   1,00  60,.67       N
ATOM   3789  N    MET  A  495      .3,,317   97. 404  -29,,851   1,00  54,9.3       N
ATOM   3790  CA   MET  A  495      2 ..266   96.,538  -30.,367   1,00  56..54       C
ATOM   3791  C    MET  A  495      2 .724   95.,644  -31..538   1,00  50,.19       C
ATOM   3792  0    MET  A  495      2 ,115   94.. 605  -31.,798   1,00  45..69       0
ATOM   3793  CB   MET  A  495      1 .051   97.,377  -30.,820   1,00  49..56       C
ATOM   3794  CG   MET  A  495      0 .537   98.,421  -29. 805   1,00  53,35       C
ATOM   3795  SD   MET  A  495      --0..985   99.,288  -30.,339   1,00  49..44       S
ATOM   3796  CE   MET  A  495      -0.,443  100.. 405  -31.,617   1,00  48..15       C
ATOM   3797  O    THR  A  496      5 ..226    9.3.,607  -32.. 228   1,00  51,60       O
ATOM   3798  N    THR  A  496      3 ..743   96.,060  -32.,276   1,00  47.01       N
ATOM   3799  CA.  THR  A  496      4 ,102   95. 315  -3.3,,495   1,00  53.,09       C
ATOM   3800  C    THR  A  496      4 .584    9.3.,887  -33.. 228   1,00  47,29       C
ATOM   3801  CB   THR  A  496      5 .172   96.,029  -34.. 307   1,00  52,24       C
ATOM   3802  OG1  THR  A  496      5 ,944   96. 870  -3.3,,443   1,00  63.,0.3       0
ATOM   3803  CG2  THR  A  496      4 .516   96.,876  -35.,355   1,00  54.55       C
ATOM   3804  O    ASN  A  497      6 ..872   92.,317  -34.. 532   1,00  49,.05       0
ATOM   3805  N    ASN  A  497      4 ,230   92.. 975  -.34.,120   1,00  46..94       N
ATOM   3806  CA   ASN  A  497      4 .662   91.,590  -33.,984   1,00  51.99       C
ATOM   3807  C    ASN  A  497      6 .165   91,,471  -33. 979   1,00  50,80       C
ATOM   3808  CB   ASN  A  497      4 ,102   90.. 726  -.35.,104   1,00  45..5.3       C
ATOM   3809  CG   ASN  A  497      2 ,869   89.. 967  -34.,694   1,00  48..23       C
ATOM   38.10 OD.1  ASN  A  497      2 .660   89,,675  -33. 510   1,00  50,70       0
ATOM   3811  ND2  ASN  A  497      2 .046   89.,622  -35,674   1,00  42.34       N
ATOM   3812  O    FHE  A  498      6 ,842   88.. 019  -34.,489   1,00  51.98       0
ATOM   3813  N    PKE  A  498      6 ..634   90.,438  -33.. 296   1,00  5.3,.33       N
ATOM   3814  CA   PHE  A  498      7 .975   89.,915  -33.,499   1,00  57.27       C
ATOM   3815  C    FHE  A  498      7 ,885   88. 692  -34,,428   1,00  56.,25       C
ATOM   3816  CB   PKE  A  498      8 ..630   89.,528  -32.. 161   1,00  59,.96       C
ATOM   3817  CG   PHE  A  498      9 ..273   90.,673  -31.. 435   1,00  57,57       C
ATOM   3818  CD1  PHE  A  498     10,,541   91. 097  -3.1,,776   1,00  56.,00       C
ATOM   3819  CD2  PHE  A  498      8 ..610   91.,323  -30.,398   1,00  65..21       C
ATOM   3820  CE.1  PHE  A  498     11 .140   92,,155  -31. 112   1,00  53,97       C
ATOM   .3821  CE2  PHE  A  498      9 ,203   92.. .377  -29.,725   1,00  61.09       C
ATOM   3822  CZ   FHE  A  498     10.,469   92.. 793  -30.,087   1,00  60..32       C
ATOM   3823  O    ASP  A  499      9 .885   85,,747  -34. 284   1,00  54,20       0
ATOM   3824  N    ASP  A  499      8 ,982   88.,428  -35,144   1,00  61.44       N
ATOM   3825  CA   ASP  A  499      9 ,167   87.236  -35.,991   1,00  53..58       C
ATOM   3826  C    ASP  A  499      9 .075   85.,957  -35.. 168   1,00  49,.43       C
ATOM   3827  CB   ASP  A  499     10.,536   87.,328  -36,677   1,00  59..17       C
ATOM   3828  CG   ASP  A  499     10,,692   86. 390  -37,,878   1,00  59.,67       C
ATOM   3829  OD1  ASP  A  499     10..029   85.,327  -37.. 961   1,00  59,.77       0
ATOM   3830  OD2  ASP  A  499     11 .516   86.,742  -38.. 747   1,00  57,91       0
ATOM   3831  O    LYS  A  500      9 ,477   82. 051  -34,,132   1,00  62,36       0
ATOM   3832  N    LYS  A  500      8 ,086   85.,116  -35.,442   1,00  51.09       N
ATOM   3833  CA   LYS  A  500      7 .956   83.,826  -34.. 754   1,00  55,.78       C
ATOM   .3834  C    LYS  A  500      9 ,169   82.. 894  -.34.,978   1,00  58..74       C
ATOM   3835  CB   LYS  A  500      6 ,674   83.,097  -35.,197   1,00  57.88       C
ATOM   38.36  CG   LYS  A  500      5 .380    8.3,,688  -34. 663   1,00  65,42       C
ATOM   .3837  CD   LYS  A  500      4 ,141   82.. 928  -.35.,150   1,00  63..97       C
ATOM   3838  CE   LYS  A  500      2 ,858   83.. 742  -34.,891   1,00  67.40       C
ATOM   38.39  NZ   LYS  A  500      1 .614    8.3,,017  -35. 291   1,00  6.3,99       N
ATOM   3840  O    ASN  A  501     13.,134   82.,008  -35,182   1,00  61.90       O
ATOM   3841  N    ASN  A  501      9 ,851   83.. 030  -36,111   1,00  58..37       N
ATOM   3842  CA   ASN  A  501     11.056   82.,235  -36.354   1,00  58,.92       C
ATOM   3843  C    ASN  A  501     12..255   82.,774  -35,578   1,00  61.64       C
ATOM   3844  CB   ASN  A  501     11 ,396   82. 188  -37,,848   1,00  59.,9.3       C
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ATOM    3845  CG   ASN  A  501     10.273  81.595  -38.695  1.00  62.25           C
ATOM    3846  OD1  ASM  A  501      9.539  82.322  -39.379  1.00  65.51           O
ATOM    3847  ND2  ASN  A  501     10.138  80.272  -38.656  1.00  57.46           N
ATOM    3848  O    LEU  A  502     12.756  86.912  -33.808  1.00  63.09           O
ATOM    3849  N    LEU  A  502     12.291  84.094  -35.381  1.00  59.94           N
ATOM    3850  CA   LEU  A  502     13.351  84.750  -34.622  1.00  53.18           C
ATOM    3851  C    LEU  A  502     12.758  85.700  -33.597  1.00  60.33           C
ATOM    3852  CB   LEU  A  502     14.282  85.509  -35.551  1.00  54.02           C
ATOM    3853  CG   LEU  A  502     15.256  84.623  -36.322  1.00  58.21           C
ATOM    3854  CD1  LEU  A  502     15.740  85.325  -37.571  1.00  56.93           C
ATOM    3855  CD2  LEU  A  502     16.431  84.262  -35.438  1.00  59.13           C
ATOM    3856  O    FRO  A  503     11.284  87.794  -30.104  1.00  59.90           0
ATOM    3857  N    PRO  A  503     12.250  85.150  -32.481  1.00  61.09           N
ATOM    3858  CA   PRO  A  503     11.415  85.869  -31.507  1.00  56.78           C
ATOM    3859  C    FRO  A  503     12.004  87.137  -30.858  1.00  62.91           C
ATOM    3860  CB   PRO  A  503     11.142  84.805  -30.430  1.00  59.54           C
ATOM    3861  CG   PRO  A  503     12.062  83.646  -30.735  1.00  65.34           C
ATOM    3862  CD   PRO  A  503     12.293  83.706  -32.199  1.00  61.54           C
ATOM    3863  O    ASN  A  504     14.388  90.879  -31.477  1.00  64.90           0
ATOM    3864  N    ASK  A  504     13.259  87.481  -31.129  1.00  65.34           N
ATOM    3865  CA.  ASN  A  504     13.824  88.719  -30.601  1.00  61.57           C
ATOM    3866  C    ASN  A  504     13.938  89.752  -31.692  1.00  63.71           C
ATOM    3867  CB   ASN  A  504     15.185  88.473  -29.964  1.00  64.30           C
ATOM    3868  CG   ASN  A  504     15.064  87.904  -28.557  1.00  76.80           C
ATOM    3869  OD1  ASN  A  504     14.084  88.168  -27.849  1.00  75.75           0
ATOM    3870  ND2  ASN  A  504     16.060  87.123  -28.143  1.00  77.42           N
ATOM    3871  O    GLU  A  505     11.313  90.068  -34.695  1.00  56.52           O
ATOM    3872  N    GLU  A  505     13.505  89.358  -32.875  1.00  61.47           N
ATOM    3873  CA   GLU  A  505     13.604  90.223  -34.027  1.00  61.35           C
ATOM    3874  C    GLU  A  505     12.255  90.797  -34.409  1.00  53.38           C
ATOM    3875  CB   GLU  A  505     14.211  89.454  -35.194  1.00  60.18           C
ATOM    3876  CG   GLU  A  505     15.545  88.879  -34.853  1.00  61.76           C
ATOM    3877  CD   GLU  A  505     16.581  89.964  -34.653  1.00  63.78           C
ATOM    3878  OE1  GLU  A  505     16.511  90.987  -35.358  1.00  67.18           0
ATOM    3879  OE2  GLU  A  505     17.469  89.792  -33.795  1.00  72.08           0
ATOM    3880  O    LYS  A  506     11.575  92.122  -37.081  1.00  62.69           0
ATOM    3881  N    LYS  A  506     12.175  92.117  -34.396  1.00  57.87           N
ATOM    3882  CA   LYS  A  506     10.980  92.823  -34.843  1.00  55.35           C
ATOM    3883  C    LYS  A  506     10.690  92.499  -36.296  1.00  60.15           C
ATOM    3884  CB   LYS  A  506     11.144  94.329  -34.664  1.00  53.93           C
ATOM    3885  CG   LYS  A  506      9.849  95.065  -34.587  1.00  66.14           C
ATOM    3886  CD   LYS  A  506      9.026  94.566  -33.416  1.00  64.50           C
ATOM    3887  CE   LYS  A  506      9.350  95.331  -32.157  1.00  62.67           C
ATOM    3888  NZ   LYS  A  506      8.264  95.136  -31.170  1.00  63.01           N
ATOM    3889  O    VAL  A  507      9.335  94.674  -38.377  1.00  61.39           0
ATOM    3890  N    VAL  A  507      9.425  92.631  -36.642  1.00  54.45           N
ATOM    3891  CA.  VAL  A  507      8.943  92.348  -37.970  1.00  45.21           C
ATOM    3892  C    VAL  A  507      9.231  93.545  -38.870  1.00  48.41           C
ATOM    3893  CB   VAL  A  507      7.451  92.001  -37.899  1.00  48.11           C
ATOM    3894  CGI  VAL  A  507      6.639  92.870  -38.812  1.00  56.11           C
ATOM    3895  CG2  VAL  A  507      7.244  90.522  -38.171  1.00  54.62           C
ATOM    3896  O    LEU  A  508      7.247  94.553  -41.379  1.00  54.78           0
ATOM    3897  N    LEU  A  508      9.410  93.299  -40.169  1.00  49.63           N
ATOM    3898  CA   LEU  A  508      9.628  94.363  -41.155  1.00  55.30           C
ATOM    3899  C    LEU  A  508      8.328  95.118  -41.500  1.00  55.23           C
ATOM    3900  CB   LEU  A  508     10.247  93.772  -42.427  1.00  46.27           C
ATOM    3901  CG   LEU  A  508     11.784  93.707  -42.441  1.00  56.04           C
ATOM    3902  GD1  LEU  A  508     12.329  92.718  -43.473  1.00  47.87           C
ATOM    3903  CD2  LEU  A  508     12.363  95.100  -42.690  1.00  54.54           C
ATOM    3904  O    FRO  A  509      7.500  95.711  -44.435  1.00  61.75           0
ATOM    3905  N    PRO  A  509      8.428  96.400  -41.912  1.00  52.83           N
ATOM    3906  CA   PRO  A  509      7.230  97.047  -42.476  1.00  55.08           C
ATOM    3907  C    PRO  A  509      6.702  96.273  -43.680  1.00  56.39           C
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ATOM  3908  CB   PRO A 509    7.730  98.437 -42.888  1.00 50.64   C
ATOM  3909  CG   FRO A 509    8.825  98.726 -41.935  1.00 52.65   C
ATOM  3910  CD   PRO A 509    9.507  97.373 -41.669  1.00 52.42   C
ATOM  3911  O    LYS A 510    5.253  95.301 -47.281  1.00 60.45   0
ATOM  3912  N    LYS A 510    5.386  96.229 -43.846  I.00 52.47   N
ATOM  3913  CA   LYS A 510    4.766  95.509 -44.946  1.00 52.31   C
ATOM  3914  C    LYS A 510    5.228  96.031 -46.293  1.00 54.73   C
ATOM  3915  CB   LYS A 510    3.247  95.599 -44.851  I.00 50.91   C
ATOM  3916  CG   LYS A 510    2.509  94.715 -45.842  1.00 48.16   C
ATOM  3917  CD   LYS A 510    2.975  93.268 -45.765  1.00 56.71   C
ATOM  3918  CE   LYS A 510    1.886  92.285 -46.178  I.00 56.48   C
ATOM  3919  ¥iZ  LYS A 510    1.739  91.233 -45.109  1.00 59.70   N
ATOM  3920  N    HIS A 511    5.619  97.293 -46.328  1.00 57.36   N
ATOM  3921  CA   HIS A 511    5.991  97.934 -47.582  1.00 59.92   C
ATOM  3922  C    HIS A 511    7.499  98.128 -47.718  1.00 57.13   C
ATOM  3923  O    HIS A 511    7.964  98.874 -48.569  1.00 60.08   O
ATOM  3924  CB   HIS A 511    5.260  99.272 -47.699  1.00 61.39   C
ATOM  3925  CG   HIS A 511    3.773  99.128 -47.732  I.00 60.31   C
ATOM  3926  ND1  HIS A 511    3.066  98.980 -48.906  1.00 54.83   N
ATOM  3927  CD2  HIS A 511    2.862  99.073 -46.733  1.00 58.53   C
ATOM  3928  CE1  HIS A 511    1.783  98.845 -48.631  I.00 54.28   C
ATOM  3929  ME2  HIS A 511    1.631  98.903 -47.320  1.00 59.67   N
ATOM  3930  N    SER A 512    8.251  97.463 -46.853  1.00 59.32   N
ATOM  3931  CA   SER A 512    9.703  97.357 -46.987  I.00 61.19   C
ATOM  3932  C    SER A 512   10.146  96.847 -48.369  1.00 60.57   C
ATOM  3933  O    SER A 512    9.620  95.848 -48.857  1.00 59.82   O
ATOM  3934  CB   SER A 512   10.239  96.421 -45.911  I.00 59.81   C
ATOM  3935  OG   SER A 512   11.300  95.644 -46.426  1.00 57.34   0
ATOM  3936  O    LEU A 513   11.885  94.881 -51.131  1.00 64.01   0
ATOM  3937  N    LEU A 513   11.103  97.539 -48.987  1.00 64.39   N
ATOM  3938  CA   LEU A 513   11.701  97.111 -50.257  1.00 64.26   C
ATOM  3939  C    LEU A 513   12.149  95.656 -50.209  1.00 64.22   C
ATOM  3940  CB   LEU A 513   12.911  97.974 -50.609  1.00 67.34   C
ATOM  3941  CG   LEU A 513   12.745  99.422 -51.065  I.00 72.16   C
ATOM  3942  CD2  LEU A 513   12.341 100.331 -49.888  1.00 76.51   C
ATOM  3943  CD1  LEU A 513   11.760  99.508 -52.225  1.00 70.96   C
ATOM  3944  N    LEU A 514   12.834  95.306 -49.123  I.00 62.15   N
ATOM  3945  CA   LEU A 514   13.320  93.951 -48.914  1.00 64.61   C
ATOM  3946  C    LEU A 514   12.189  92.941 -48.848  1.00 63.47   C
ATOM  3947  O    LEU A 514   12.315  91.827 -49.347  I.00 63.36   0
ATOM  3948  CB   LEU A 514   14.138  93.866 -47.629  1.00 63.23   C
ATOM  3949  CG   LEU A 514   15.658  93.909 -47.784  1.00 73.76   C
ATOM  3950  CD1  LEU A 514   16.331  93.261 -46.570  1.00 67.58   C
ATOM  3951  CD2  LEU A 514   16.094  93.243 -49.084  1.00 65.07   C
ATOM  3952  N    TYR A 515   11.094  93.339 -48.210  1.00 65.26   N
ATOM  3953  CA   TYR A 515    9.953  92.460 -48.018  1.00 60.05   C
ATOM  3954  C    TYR A 515    9.329  92.107 -49.368  I.00 53.35   C
ATOM  3955  O    TYR A 515    9.018  90.956 -49.619  1.00 56.27   O
ATOM  3956  CB   TYR A 515    8.911  93.109 -47.072  1.00 55.84   C
ATOM  3957  CG   TYR A 515    7.988  92.093 -46.418  I.00 50.58   C
ATOM  3958  CD2  TYR A 515    6.697  91.872 -46.893  1.00 49.40   C
ATOM  3959  CD1  TYR A 515    8.432  91.319 -45.357  1.00 52.77   C
ATOM  3960  CE2  TYR A 515    5.869  90.924 -46.304  I.00 46.68   C
ATOM  3961  CE1  TYR A 515    7.622  90.372 -44.768  1.00 50.48   C
ATOM  3962  CZ   TYR A 515    6.341  90.180 -45.240  1.00 52.04   C
ATOM  3963  OH   TYR A 515    5.545  89.233 -44.632  I.00 52.82   0
ATOM  3964  N    GLU A 516    9.169  93.090 -50.245  1.00 55.86   N
ATOM  3965  CA   GLU A 516    8.541  92.844 -51.543  1.00 58.96   C
ATOM  3966  C    GLU A 516    9.436  91.956 -52.423  1.00 59.33   C
ATOM  3967  O    GLU A 516    8.952  91.005 -53.060  1.00 56.33   0
ATOM  3968  CB   GLU A 516    8.217  94.173 -52.239  1.00 60.31   C
ATOM  3969  CG   GLU A 516    7.725  95.255 -51.276  1.00 62.31   C
ATOM  3970  CD   GLU A 516    6.444  95.963 -51.733  I.00 71.11   C
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ATOM   3971  OE1  GLU  A  516     6.533   97.106  -52.227   1.00  66.92     O
ATOM   3972  OE2  GLU  A  516     5.344   95.387  --51.576  1.00  74.76     O
ATOM   3973  N    TYR  A  517    10.734   92.262  -52.437   1.00  53.40     N
ATOM   3974  CA   TYR  A  517    11.728   91.402  -53.081   1.00  57.16     C
ATOM   3975  C    TYR  A  517    11.578   89.942  -52.634   1.00  58.68     C
ATOM   3976  O    TYR  A  517    11.584   89.018  -53.465   1.00  56.67     O
ATOM   3977  CB   TYR  A  517    13.146   91.903  -52.784   1.00  56.84     C
ATOM   3978  CG   TYR  A  517    13.593   93.031  -53.679   1.00  51.89     C
ATOM   3979  GDI  TYR  A  517    13.327   93.000  -55.045   1.00  56.06     C
ATOM   3980  CD2  TYR  A  517    14.263   94.135  -53.160   1.00  52.87     C
ATOM   3981  CE1  TYR  A  517    13.723   94.031  -55.876   1.00  60.10     C
ATOM   3982  CE2  TYR  A  517    14.671   95.173  -53.977   1.00  54.42     C
ATOM   3983  CZ   TYR  A  517    14.391   95.117  -55.339   1.00  66.42     C
ATOM   3984  OH   TYR  A  517    14.777   96.144  -56.169   1.00  72.22     0
ATOM   3985  N    FHE  A  518    11.423   89.746  -51.325   1.00  55.00     N
ATOM   3986  CA   PHE  A  518    11.213   88.412  -50.752   1.00  58.96     C
ATOM   3987  C    PHE  A  518     9.980   87.733  -51.349   1.00  62.56     C
ATOM   3988  O    PHE  A  518    10.077   86.640  -51.944   1.00  60.63     0
ATOM   3989  CB   PHE  A  518    11.075   88.494  -49.219   1.00  53.82     C
ATOM   3990  CG   PHE  A  518    10.724   87.190  -48.572   1.00  57.91     C
ATOM   3991  CD1  PHE  A  518     9.423   86.915  -48.195   1.00  60.64     C
ATOM   3992  CD2  PHE  A  518    11.696   86.220  -48.361   1.00  62.54     C
ATOM   3993  CE1  PHE  A  518     9.090   85.689  -47.604   1.00  61.10     C
ATOM   3994  CE2  PHE  A  518    11.379   84.990  -47.763   1.00  62.32     C
ATOM   3995  CZ   PHE  A  518    10.071   84.728  -47.388   1.00  63.03     C
ATOM   3996  N    THR  A  519     8.826   88.387  -51.187   1.00  56.91     N
ATOM   3997  CA   THR  A  519     7.554   87.835  -51.651   1.00  55.41     C
ATOM   3998  C    THR  A  519     7.571   87.585  -53.155   1.00  52.31     C
ATOM   3999  O    THR  A  519     6.966   86.629  -53.621   1.00  55.62     0
ATOM   4000  CB   THR  A  519     6.332   88.764  -51.315   1.00  55.44     C
ATOM   4001  OG1  THR  A  519     6.449   90.005  -52.022   1.00  53.30     0
ATOM   4002  CG2  THR  A  519     6.223   89.042  -49.816   1.00  46.11     C
ATOM   4003  N    VAL  A  520     8.244   88.438  -53.921   1.00  53.48     N
ATOM   4004  CA.  VAL  A  520     8.264   88.231  -55.369   1.00  56.34     C
ATOM   4005  C    VAL  A  520     9.129   87.012  -55.745   1.00  57.98     C
ATOM   4006  O    VAL  A  520     8.665   86.118  -56.469   1.00  51.97     0
ATOM   4007  CB   VAL  A  520     8.746   89.480  -56.133   1.00  59.55     C
ATOM   4008  CGI  VAL  A  520     9.268   89.093  -57.509   1.00  56.23     C
ATOM   4009  CG2  VAL  A  520     7.601   90.503  -56.278   1.00  54.25     C
ATOM   4010  N    TYR  A  521    10.357   86.946  -55.230   1.00  56.76     N
ATOM   4011  CA   TYR  A  521    11.219   85.803  -55.561   1.00  61.30     C
ATOM   4012  C    TYR  A  521    10.642   84.509  -55.024   1.00  55.57     C
ATOM   4013  O    TYR  A  521    10.853   83.441  -55.606   1.00  60.67     0
ATOM   4014  CB   TYR  A  521    12.651   85.987  -55.041   1.00  52.44     C
ATOM   4015  CG   TYR  A  521    13.472   86.909  -55.906   1.00  54.71     C
ATOM   4016  CD1  TYR  A  521    13.947   86.497  -57.170   1.00  52.88     C
ATOM   4017  CD2  TYR  A  521    13.767   88.195  -55.477   1.00  53.64     C
ATOM   4018  CE1  TYR  A  521    14.701   87.352  -57.967   1.00  45.91     C
ATOM   4019  CE2  TYR  A  521    14.520   89.052  -56.261   1.00  55.35     C
ATOM   4020  CZ   TYR  A  521    14.986   88.631  -57.493   1.00  52.37     C
ATOM   4021  OH   TYR  A  521    15.717   89.526  -58.234   1.00  55.75     0
ATOM   4022  N    ASN  A  522     9.897   84.595  -53.930   1.00  52.18     N
ATOM   4023  CA   ASM  A  522     9.363   83.376  -53.339   1.00  58.40     C
ATOM   4024  C    ASN  A  522     8.311   82.738  -54.237   1.00  59.71     C
ATOM   4025  O    ASN  A  522     8.162   81.507  -54.278   1.00  52.86     0
ATOM   4026  CB   ASN  A  522     8.770   83.648  -51.965   1.00  57.16     C
ATOM   4027  CG   ASN  A  522     8.707   82.403  -51.140   1.00  59.15     C
ATOM   4028  OD1  ASN  A  522     9.346   81.392  -51.484   1.00  54.10     0
ATOM   4029  ND2  ASN  A  522     7.949   82.447  -50.046   1.00  56.25     N
ATOM   4030  N    GLU  A  523     7.585   83.603  -54.947   1.00  59.70     N
ATOM   4031  CA   GLU  A  523     6.584   83.178  -55.910   1.00  59.50     C
ATOM   4032  C    GLU  A  523     7.276   82.815  -57.227   1.00  52.27     C
ATOM   4033  O    GLU  A  523     6.942   81.820  -57.860   1.00  48.29     0
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ATOM	4034	CB	GLU	A	523	5.526	84.285	-56,121	1.00	58.47	C
ATOM	4035	CG	GLU	A	523	4,197	83.784	--56,712	1,00	59.48	C
ATOM	4036	CD	GLU	A	523	3.182	84,898	-56:960	1.00	64,53	C
ATOM	4037	OE1	GLU	A	523	3.481	86:070	-56.646	1.00	65.89	0
ATOM	4038	OE2	GLU	A	523	2,086	84.595	-57,479	1,00	65.80	0
ATOM	4039	N	LEU	A	524	8.241	83,643	-57,619	1.00	55,50	N
ATOM	4040	CA	LEU	A	524	9.014	83,434	-58.838	1,00	58,01	C
ATOM	4041	C	LEU	A	524	9,771	82.101	-58,865	1,00	55,01	C
ATOM	4042	O	LEU	A	524	9.800	81.448	-59:893	1,00	54.59	0
ATOM	4043	CE	LEU	A	524	10.006	84,573	-59.043	1,00	56,99	C
ATOM	4044	CG	LEU	A	524	10,220	84.958	-60,504	1,00	57,14	C
ATOM	4045	CD1	LEU	A	524	8:882	85.230	-61:175	1,00	53.87	C
ATOM	4046	CD2	LEU	A	524	11.136	86,157	-60.619	1,00	60,84	C
ATOM	4047	N	THR	A	525	10:350	81:683	-57:742	1.00	57.98	N
ATOM	4048	CA	THR	A	525	11,168	80.466	-57,738	1,00	54.22	C
ATOM	4049	C	THR	A	525	10:.318	79,209	-57:859	1.00	56,55	C
ATOM	4050	O	THR	A	525	10:847	78:099	-57:949	1.00	60.84	0
ATOM	4051	CB	THR	A	525	12,050	80..359	-56,466	1,00	58.10	C
ATOM	4052	OG1	THR	A	525	13..303	79,746	-56:800	1.00	66,15	0
ATOM	4053	CG2	THR	A	525	11.364	79,538	-55.367	1,00	57,18	C
ATOM	4054	N	LYS	A	526	8,998	79.360	-57,885	1,00	55.03	N
ATOM	4055	CA	LYS	A	526	8:166	78:175	-58:017	1,00	55.89	C
ATOM	4056	C	LYS	A	526	7.310	78,159	-59.288	1,00	56,65	C
ATOM	4057	0	LYS	A	526	6,469	77.269	-59,461	1,00	61.79	0
ATOM	4058	CB	LYS	A	526	7:288	78.003	-56:780	1,00	55.41	C
ATOM	4059	CG	LYS	A	526	8.010	77,361	-55.612	1,00	56,19	C
ATOM	4060	CD	LYS	A	526	8,653	76.016	-55,995	1,00	59.07	C
ATOM	4061	CE	LYS	A	526	9,396	75.381	-54,806	1,00	61.05	C
ATOM	4062	NZ	LYS	A	526	10.209	74,157	-55.124	1,00	58,67	N
ATOM	4063	N	VAL	A	527	7.548	79:093	-60..205	1.00	51.55	N
ATOM	4064	CA	VAL	A	527	6,850	79.006	-61,487	1,00	61.84	C
ATOM	4065	C	VAL	A	527	7.585	78,068	-62:465	1.00	65.99	C
ATOM	4066	O	VAL	A	527	8.782	77:766	-62.310	1.00	64.37	0
ATOM	4067	CB	VAL	A	527	6,612	80.420	-62,128	1,00	64.85	C
ATOM	4068	CG2	VAL	A	527	7..376	80,601	-63:426	1.00	64,63	C
ATOM	4069	CGI	VAL	A	527	6.911	81,543	-61.132	1,00	57,94	C
ATOM	4070	O	LYS	A	528	6,034	77.940	-65,992	1,00	72.32	0
ATOM	4071	N	LYS	A	528	6:833	77,561	-63:435	1,00	64.29	N
ATOM	4072	CA	LYS	A	528	7.375	76,676	-64.449	1,00	70,50	C
ATOM	4073	C	LYS	A	528	6,968	77.156	-65.,836	1,00	71.04	C
ATOM	4074	CB	LYS	A	528	6,911	75.232	-64,217	1,00	69.38	C
ATOM	4075	CG	LYS	A	528	7.140	74,749	-62.794	1,00	68,83	C
ATOM	4076	CD	LYS	A	528	7.026	73:244	-62.656	1.00	75.66	C
ATOM	4077	CE	LYS	A	528	7,245	72.806	-61,206	1,00	79.66	C
ATOM	4078	NZ	LYS	A	528	6.265	73,443	-60:247	1.00	8.3,17	N
ATOM	4079	O	TYR	A	529	8.564	75:035	-68..864	1.00	72.69	0
ATOM	4080	N	TYR	A	529	7,692	76.695	-66,842	1,00	68.16	N
ATOM	4081	CA	TYR	A	529	7..387	77,036	-68:214	1.00	68,40	C
ATOM	4082	C	TYR	A	529	7.707	75,877	-69.148	1,00	74,74	C
ATOM	4083	CB	TYR	A	529	8,157	78.277	-68,645	1,00	69.15	C
ATOM	4084	CG	TYR	A	529	9:644	78:075	-68:655	1,00	74.86	C
ATOM	4085	CD2	TYR	A	529	10.317	77,790	-69.829	1,00	77,46	C
ATOM	4086	CD1	TYR	A	529	10,379	78.156	-67,481	1,00	74.52	C
ATOM	4087	CE2	TYR	A	529	11:695	77.605	-69:833	1,00	78.55	C
ATOM	4088	CE1	TYR	A	529	11.748	77,973	-67.469	1,00	73,64	C
ATOM	4089	CZ	TYR	A	529	12,403	77.697	-68,649	1,00	78.54	C
ATOM	4090	OH	TYR	A	529	13,767	77.519	-68,645	1,00	74.82	0
ATOM	4091	O	VAL	A	530	6.285	76,354	-72.943	1,00	83,98	0
ATOM	4092	N	VAL	A	530	6:977	75:827	-70.252	1.00	75.68	N
ATOM	4093	CA	VAL	A	530	7,264	74.899	-71,325	1,00	79.50	C
ATOM	4094	C	VAL	A	530	7.278	75,704	-72:611	1.00	82,26	C
ATOM	4095	CB	VAL	A	530	6.223	73:763	-71:412	1.00	80.28	C
ATOM	4096	CGI	VAL	A	530	6,415	72.975	-72,679	1,00	83.27	C

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ATOM   4097  CG2  VAL A 530     6.313  72.847 -70.199  1.00 76.16           C
ATOM   4098  O    THR A 531     8.417  73.959 -75.248  1.00 88.41           0
ATOM   4099  N    THR A 531     8.415  75.705 -73.303  1.00 80.28           N
ATOM   4100  CA   THR A 531     8.496  76.269 -74.648  1.00 83.62           C
ATOM   4101  C    THR A 531     8.455  75.119 -75.651  1.00 82.45           C
ATOM   4102  CB   THR A 531     9.767  77.119 -74.862  1.00 88.00           C
ATOM   4103  OG1  THR A 531    10.897  76.261 -75.071  1.00 90.06           O
ATOM   4104  CG2  THR A 531    10.015  78.049 -73.669  1.00 81.90           C
ATOM   4105  O    GLU A 532     8.474  72.072 -78.107  1.00 88.07           O
ATOM   4106  N    GLU A 532     8.474  75.440 -76.944  1.00 88.04           N
ATOM   4107  CA   GLU A 532     8.220  74.461 -78.009  1.00 84.77           C
ATOM   4108  C    GLU A 532     9.017  73.163 -77.892  1.00 87.09           C
ATOM   4109  CB   GLU A 532     8.496  75.090 -79.376  1.00 80.41           C
ATOM   4110  O    GLY A 533    12.889  71.601 -75.964  1.00 86.50           0
ATOM   4111  N    GLY A 533    10.296  73.271 -77.543  1.00 84.61           N
ATOM   4112  CA   GLY A 533    11.165  72.106 -77.545  1.00 90.79           C
ATOM   4113  C    GLY A 533    11.679  71.683 -76.184  1.00 90.65           C
ATOM   4114  0    MET A 534    11.474  68.818 -73.083  1.00 96.72           0
ATOM   4115  N    MET A 534    10.760  71.406 -75.266  1.00 91.79           N
ATOM   4116  CA   MET A 534    11.149  71.037 -73.915  1.00 89.28           C
ATOM   4117  C    MET A 534    10.683  69.628 -73.577  1.00 91.48           C
ATOM   4118  CB   MET A 534    10.603  72.053 -72.903  1.00 87.85           C
ATOM   4119  CG   MET A 534    11.054  73.488 -73.192  1.00 85.55           C
ATOM   4120  SD   MET A 534    11.484  74.489 -71.738  1.00 83.87           S
ATOM   4121  CE   MET A 534    12.504  75.741 -72.523  1.00 77.15           C
ATOM   4122  O    ARG A 535     8.076  66.711 -71.708  1.00 97.17           0
ATOM   4123  N    ARG A 535     9.407  69.349 -73.848  1.00 90.92           N
ATOM   4124  CA   ARG A 535     8.774  68.047 -73.581  1.00 92.61           C
ATOM   4125  C    ARG A 535     8.577  67.768 -72.088  1.00 91.69           C
ATOM   4126  CB   ARG A 535     9.578  66.905 -74.217  1.00 86.90           C
ATOM   4127  O    LYS A 536     9.632  70.883 -69.757  1.00 85.35           0
ATOM   4128  N    LYS A 536     8.958  68.728 -71.253  1.00 92.29           N
ATOM   4129  CA   LYS A 536     8.853  68.609 -69.802  1.00 89.81           C
ATOM   4130  C    LYS A 536     8.962  70.011 -69.194  1.00 88.03           C
ATOM   4131  CB   LYS A 536     9.938  67.677 -69.251  1.00 84.56           C
ATOM   4132  O    PRO A 537     9.980  71.122 -65.882  1.00 78.54           0
ATOM   4133  N    PRO A 537     8.286  70.243 -68.056  1.00 87.33           N
ATOM   4134  CA   PRO A 537     8.233  71.592 -67.463  1.00 83.67           C
ATOM   4135  C    PRO A 537     9.477  71.953 -66.638  1.00 77.38           C
ATOM   4136  CB   PRO A 537     6.985  71.525 -66.579  1.00 83.79           C
ATOM   4137  CG   FRO A 537     6.912  70.079 -66.163  1.00 88.55           C
ATOM   4138  CD   PRO A 537     7.459  69.270 -67.316  1.00 83.56           C
ATOM   4139  O    ALA A 538    10.275  75.729 -65.507  1.00 69.16           0
ATOM   4140  N    ALA A 538     9.954  73.188 -66.781  1.00 72.17           N
ATOM   4141  CA   ALA A 538    11.208  73.615 -66.159  1.00 71.31           C
ATOM   4142  C    ALA A 538    11.050  74.814 -65.222  1.00 72.32           C
ATOM   4143  CB   ALA A 538    12.237  73.945 -67.242  1.00 72.91           C
ATOM   4144  O    PHE A 539    13.702  76.799 -64.513  1.00 70.99           0
ATOM   4145  N    PHE A 539    11.798  74.806 -64.116  1.00 63.62           N
ATOM   4146  CA.  PHE A 539    11.881  75.963 -63.233  1.00 60.26           C
ATOM   4147  C    PHE A 539    12.686  77.067 -63.885  1.00 63.53           C
ATOM   4148  CB   PHE A 539    12.536  75.617 -61.897  1.00 56.44           C
ATOM   4149  CG   PHE A 539    11.647  74.880 -60.936  1.00 60.16           C
ATOM   4150  CD2  PHE A 539    12.045  73.656 -60.404  1.00 64.58           C
ATOM   4151  GDI  PHE A 539    10.441  75.419 -60.522  1.00 61.82           C
ATOM   4152  CE2  PHE A 539    11.237  72.974 -59.507  1.00 64.60           C
ATOM   4153  CEl  PHE A 539     9.631  74.744 -59.632  1.00 59.36           C
ATOM   4154  CZ   PHE A 539    10.029  73.523 -59.121  1.00 67.30           C
ATOM   4155  O    LEU A 540    14.517  78.867 -62.296  1.00 63.99           0
ATOM   4156  N    LEU A 540    12.233  78.304 -63.725  1.00 57.90           N
ATOM   4157  CA   LEU A 540    13.031  79.464 -64.086  1.00 59.60           C
ATOM   4158  C    LEU A 540    14.378  79.430 -63.386  1.00 62.97           C
ATOM   4159  CB   LEU A 540    12.319  80.764 -63.719  1.00 57.20           C
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ATOM   4160  CG  LEU A 540      10.856  80.986 -64.075  1.00 62.11           c
ATOM   4161  GDI LEU A 540      10.413  82.379 --63.603  1.00 53.79           C
ATOM   4162  CD2 LEU A 540      10.653  80.840 -65.557  1.00 60.08           c
ATOM   4163  O   SER A 541      16.507  82.407 -63.308  1.00 63.82           0
ATOM   4164  N   SER A 541      15.364  80.064 -64.001  I.00 65.40           N
ATOM   4165  CA  SER A 541      16.730  80.032 -63.489  1.00 67.52           c
ATOM   4166  c   SER A 541      17.175  81.412 -63.030  1.00 68.02           c
ATOM   4167  CB  SER A 541      17.670  79.513 -64.562  I.00 61.30           c
ATOM   4168  OG  SER A 541      17.574  80.329 -65.716  1.00 62.95           0
ATOM   4169  N   GLY A 542      18.318  81.463 -62.352  1.00 65.56           N
ATOM   4170  CA  GLY A 542      18.825  82.691 -61.760  I.00 61.76           C
ATOM   4171  C   GLY A 542      18.887  83.867 -62.716  1.00 64.32           C
ATOM   4172  O   GLY A 542      18.513  84.986 -62.368  1.00 63.39           O
ATOM   4173  N   GLU A 543      19.369  83.616 -63.927  1.00 66.83           N
ATOM   4174  CA  GLU A 543      19.390  84.652 -64.944  1.00 67.74           C
ATOM   4175  C   GLU A 543      17.941  85.009 -65.298  1.00 68.58           C
ATOM   4176  O   GLU A 543      17.595  86.188 -65.426  1.00 58.96           O
ATOM   4177  CB  GLU A 543      20.165  84.196 -66.188  I.00 63.54           C
ATOM   4178  N   GLN A 544      17.103  83.978 -65.426  1.00 65.36           N
ATOM   4179  CA  GLN A 544      15.710  84.168 -65.825  1.00 69.12           c
ATOM   4180  C   GLN A 544      14.938  84.965 -64.765  I.00 67.02           C
ATOM   4181  O   GLN A 544      14.240  85.930 -65.098  1.00 67.86           O
ATOM   4182  CB  GLN A 544      15.041  82.817 -66.100  1.00 66.71           c
ATOM   4183  CG  GLN A 544      15.481  82.183 -67.422  I.00 65.66           c
ATOM   4184  CD  GLN A 544      14.893  80.795 -67.654  1.00 65.18           c
ATOM   4185  OE1 GLN A 544      14.775  79.988 -66.730  1.00 68.32           0
ATOM   4186  NE2 GLN A 544      14.524  80.514 -68.894  I.00 68.50           N
ATOM   4187  N   LYS A 545      15.090  84.573 -63.502  1.00 60.63           N
ATOM   4188  CA  LYS A 545      14.529  85.312 -62.385  1.00 61.54           C
ATOM   4189  c   LYS A 545      15.004  86.760 -62.391  1.00 64.21           c
ATOM   4190  O   LYS A 545      14.182  87.682 -62.381  1.00 64.26           0
ATOM   4191  CB  LYS A 545      14.882  84.644 -61.054  1.00 58.04           c
ATOM   4192  N   LYS A 546      16.318  86.964 -62.449  1.00 60.22           N
ATOM   4193  CA. LYS A 546      16.891  88.317 -62.349  I.00 62.74           C
ATOM   4194  C   LYS A 546      16.458  89.237 -63.476  1.00 66.65           C
ATOM   4195  O   LYS A 546      16.455  90.445 -63.309  1.00 69.63           O
ATOM   4196  CB  LYS A 546      18.416  88.264 -62.323  I.00 67.73           C
ATOM   4197  N   ALA A 547      16.109  88.657 -64.622  1.00 66.15           N
ATOM   4198  CA  ALA A 547      15.704  89.433 -65.783  1.00 67.02           C
ATOM   4199  C   ALA A 547      14.253  89.828 -65.655  I.00 70.78           C
ATOM   4200  O   ALA A 547      13.892  90.989 -65.850  1.00 70.30           O
ATOM   4201  CB  ALA A 547      15.916  88.653 -67.055  1.00 61.67           c
ATOM   4202  N   ILE A 548      13.423  88.841 -65.339  1.00 70.17           N
ATOM   4203  CA  ILE A 548      12.002  89.069 -65.178  1.00 67.24           C
ATOM   4204  C   ILE A 548      11.777  90.199 -64.190  1.00 66.42           C
ATOM   4205  O   ILE A 548      11.052  91.138 -64.472  1.00 70.64           O
ATOM   4206  CB  ILE A 548      11.285  87.802 -64.712  I.00 67.32           C
ATOM   4207  CGI ILE A 548      11.065  86.865 -65.903  1.00 62.93           C
ATOM   4208  CG2 ILE A 548       9.955  88.155 -64.086  1.00 63.23           c
ATOM   4209  CD1 ILE A 548      10.976  85.424 -65.519  I.00 63.87           c
ATOM   4210  N   VAL A 549      12.446  90.123 -63.052  1.00 65.51           N
ATOM   4211  CA  VAL A 549      12.374  91.171 -62.049  1.00 67.59           c
ATOM   4212  C   VAL A 549      12.900  92.516 -62.579  I.00 72.46           c
ATOM   4213  O   VAL A 549      12.270  93.559 -62.379  1.00 71.86           0
ATOM   4214  CB  VAL A 549      13.161  90.770 -60.776  1.00 61.14           c
ATOM   4215  CGI VAL A 549      13.371  91.971 -59.875  I.00 58.14           c
ATOM   4216  CG2 VAL A 549      12.450  89.630 -60.040  1.00 54.06           c
ATOM   4217  N   ASP A 550      14.046  92.485 -63.257  1.00 74.72           N
ATOM   4218  CA  ASP A 550      14.667  93.694 -63.807  1.00 71.90           c
ATOM   4219  C   ASP A 550      13.828  94.334 -64.899  1.00 71.19           C
ATOM   4220  O   ASP A 550      13.865  95.553 -65.081  1.00 74.87           O
ATOM   4221  CB  ASP A 550      16.060  93.383 -64.362  1.00 69.53           c
ATOM   4222  CG  ASP A 550      17.132  93.413 -63.291  I.00 72.83           c
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ATOM	4223	OD1	ASP	A	550	16.769	93.547	-62.104	1.00	76.08	O
ATOM	4224	OD2	ASP	A	550	18.329	93.304	-63.630	1.00	69.40	O
ATOM	4225	N	LEU	A	551	13.074	93.507	-65.620	1.00	73.73	N
ATOM	4226	CA	LEU	A	551	12.359	93.947	-66.824	1.00	77.34	C
ATOM	4227	C	LEU	A	551	10.828	94.064	-66.640	1.00	76.01	C
ATOM	4228	O	LEU	A	551	10.200	94.926	-67.250	1.00	80.14	O
ATOM	4229	CB	LEU	A	551	12.687	92.998	-67.996	1.00	70.73	C
ATOM	4230	CG	LEU	A	551	14.193	92.919	-68.293	1.00	76.66	C
ATOM	4231	CD1	LEU	A	551	14.550	91.863	-69.355	1.00	66.45	C
ATOM	4232	CD2	LEU	A	551	14.740	94.298	-68.670	1.00	74.24	C
ATOM	4233	N	LEU	A	552	10.234	93.217	-65.801	1.00	71.30	N
ATOM	4234	CA	LEU	A	552	8.790	93.249	-65.600	1.00	67.91	C
ATOM	4235	C	LEU	A	552	8.385	93.872	-64.254	1.00	73.36	C
ATOM	4236	O	LEU	A	552	7.690	94.882	-64.227	1.00	75.74	0
ATOM	4237	CB	LEU	A	552	8.203	91.841	-65.729	1.00	69.35	C
ATOM	4238	CG	LEU	A	552	8.365	91.212	-67.119	1.00	70.69	C
ATOM	4239	CD1	LEU	A	552	7.471	89.995	-67.311	1.00	69.51	C
ATOM	4240	CD2	LEU	A	552	8.089	92.250	-68.182	1.00	69.43	C
ATOM	4241	N	PHE	A	553	8.814	93.300	-63.137	1.00	66.99	N
ATOM	4242	CA	PHE	A	553	8.331	93.797	-61.851	1.00	69.47	C
ATOM	4243	C	PHE	A	553	8.861	95.185	-61.458	1.00	77.12	C
ATOM	4244	O	PHE	A	553	8.371	95.779	-60.492	1.00	76.81	0
ATOM	4245	CB	PHE	A	553	8.658	92.806	-60.743	1.00	63.13	C
ATOM	4246	CG	PHE	A	553	7.881	91.531	-60.825	1.00	68.20	C
ATOM	4247	CD1	PHE	A	553	8.331	90.475	-61.612	1.00	62.33	C
ATOM	4248	CD2	PHE	A	553	6.709	91.376	-60.110	1.00	61.29	C
ATOM	4249	CE1	PHE	A	553	7.621	89.303	-61.694	1.00	56.32	C
ATOM	4250	CE2	PHE	A	553	5.997	90.188	-60.179	1.00	63.33	C
ATOM	4251	CZ	PHE	A	553	6.457	89.152	-60.977	1.00	60.72	C
ATOM	4252	N	LYS	A	554	9.842	95.699	-62.198	1.00	77.56	N
ATOM	4253	CA	LYS	A	554	10.434	97.005	-61.887	1.00	81.45	C
ATOM	4254	C	LYS	A	554	10.030	98.083	-62.893	1.00	82.35	C
ATOM	4255	O	LYS	A	554	10.492	99.229	-62.814	1.00	80.95	0
ATOM	4256	CB	LYS	A	554	11.965	96.917	-61.829	1.00	78.18	C
ATOM	4257	CG	LYS	A	554	12.540	96.631	-60.457	1.00	76.75	C
ATOM	4258	CD	LYS	A	554	14.044	96.849	-60.459	1.00	79.34	C
ATOM	4259	CE	LYS	A	554	14.734	96.003	-59.400	1.00	75.14	C
ATOM	4260	NZ	LYS	A	554	16.175	96.333	-59.292	1.00	76.30	N
ATOM	4261	N	THR	A	555	9.177	97.704	-63.839	1.00	82.35	N
ATOM	4262	CA	THR	A	555	8.639	98.647	-64.815	1.00	81.12	C
ATOM	4263	C	THR	A	555	7.105	98.572	-64.905	1.00	84.91	C
ATOM	4264	O	THR	A	555	6.498	99.291	-65.699	1.00	91.98	O
ATOM	4265	CB	THR	A	555	9.251	98.429	-66.227	1.00	84.05	C
ATOM	4266	OG1	THR	A	555	9.101	97.059	-66.627	1.00	82.03	0
ATOM	4267	CG2	THR	A	555	10.730	98.810	-66.245	1.00	79.14	C
ATOM	4268	N	ASN	A	556	6.480	97.701	-64.109	1.00	85.04	N
ATOM	4269	CA	ASN	A	556	5.054	97.850	-63.820	1.00	83.24	C
ATOM	4270	C	ASN	A	556	4.643	97.262	-62.474	1.00	80.28	C
ATOM	4271	O	ASN	A	556	5.095	96.184	-62.081	1.00	78.06	O
ATOM	4272	CB	ASN	A	556	4.188	97.251	-64.932	1.00	82.92	C
ATOM	4273	CG	ASN	A	556	2.977	98.142	-65.258	1.00	87.41	C
ATOM	4274	OD1	ASN	A	556	3.116	99.178	-65.919	1.00	86.77	0
ATOM	4275	ND2	ASN	A	556	1.798	97.757	-64.768	1.00	77.77	N
ATOM	4276	O	ARG	A	557	2.690	95.750	-59.194	1.00	78.29	0
ATOM	4277	N	ARG	A	557	3.763	97.996	-61.792	1.00	80.24	N
ATOM	4278	CA	ARG	A	557	3.328	97.693	-60.435	1.00	76.72	C
ATOM	4279	C	ARG	A	557	2.695	96.327	-60.281	1.00	78.01	C
ATOM	4280	CB	ARG	A	557	2.340	98.745	-59.966	1.00	77.49	C
ATOM	4281	CG	ARG	A	557	2.964	100.079	-59.742	1.00	73.91	C
ATOM	4282	CD	ARG	A	557	1.917	101.078	-59.302	1.00	67.94	C
ATOM	4283	NE	ARG	A	557	2.563	102.350	-59.040	1.00	68.62	N
ATOM	4284	CZ	ARG	A	557	3.079	102.682	-57.867	1.00	69.26	C
ATOM	4285	NH1	ARG	A	557	2.978	101.836	-56.849	1.00	69.19	N

ATOM	4286	NH2	ARG	A	557	3.681	103,858	-57,712	1,00	70.68	N
ATOM	4287	O	LYS	A	558	2,786	94.508	-63,506	1,00	67.10	O
ATOM	4288	N	LYS	A	558	2.122	95,821	-61:360	1,00	77,31	N
ATOM	4289	CA	LYS	A	558	1.709	94,437	-61.373	1,00	70.87	C
ATOM	4290	C	LYS	A	558	2,241	93.816	-62,648	1,00	72,55	C
ATOM	4291	CB	LYS	A	558	0.194	94,304	-61:260	1,00	74,12	C
ATOM	4292	CG	LYS	A	558	-0.361	94,751	-59.904	1,00	78,94	C
ATOM	4293	O	VAL	A	559	1,640	89.648	-63,264	1,00	68,55	0
ATOM	4294	N	VAL	A	559	2.117	92,498	-62,739	1,00	74.02	N
ATOM	4295	CA	VAL	A	559	2.669	91,736	-63.843	1,00	65,95	C
ATOM	4296	C	VAL	A	559	1,757	90:547	-64,104	1,00	70.48	C
ATOM	4297	CB	VAL	A	559	4.115	91,245	-63,535	1,00	71.24	C
ATOM	4298	CGI	VAL	A	559	4.537	90,108	-64.480	1,00	68,38	C
ATOM	4299	CG2	VAL	A	559	5.112	92,395	-63,598	1,00	64.83	C
ATOM	4300	O	THR	A	560	2,289	88.478	-66,554	1,00	74.84	0
ATOM	4301	N	THR	A	560	1:088	90,547	-65:252	1,00	69,41	N
ATOM	4302	CA	THR	A	560	0,274	89,394	-65,630	1,00	71.46	C
ATOM	4303	C	THR	A	560	1,117	88.274	-66,225	1,00	73,52	C
ATOM	4304	CB	THR	A	560	-0:791	89,768	-66:654	1,00	72,20	C
ATOM	4305	OG1	THR	A	560	-1,271	88,577	-67,302	1,00	72,59	0
ATOM	4306	CG2	THR	A	560	-0,196	90.680	-67,694	1,00	66,73	C
ATOM	4307	N	VAL	A	561	0,508	87,102	-66,380	1,00	69.69	N
ATOM	4308	CA	VAL	A	561	1,120	86,006	-67,126	1,00	73,33	C
ATOM	4309	C	VAL	A	561	1,263	86:366	-68,608	1,00	78.07	C
ATOM	4310	O	VAL	A	561	2,220	85,964	-69,276	1,00	78.68	0
ATOM	4311	CB	VAL	A	561	0.296	84,719	-66.991	1,00	72,12	C
ATOM	4312	CGI	VAL	A	561	0,981	83:567	-67,685	1,00	75.71	C
ATOM	4313	CG2	VAL	A	561	0,082	84.393	-65,530	1,00	73.69	C
ATOM	4314	N	LYS	A	562	0.303	87,133	-69.117	1,00	81,69	N
ATOM	4315	CA	LYS	A	562	0,355	87,607	-70,492	1,00	78.73	C
ATOM	4316	C	LYS	A	562	1,586	88.487	-70,691	1,00	83.98	C
ATOM	4317	O	LYS	A	562	2:247	88,418	-71:726	1,00	90,79	0
ATOM	4318	CB	LYS	A	562	-0,919	88,369	-70,855	1,00	71.73	C
ATOM	4319	N	GLN	A	563	1,899	89..304	-69,693	1,00	79,57	N
ATOM	4320	CA	GLN	A	563	3:078	90,147	-69:761	1,00	79,82	C
ATOM	4321	C	GLN	A	563	4.306	89,267	-69.798	1,00	84,76	C
ATOM	4322	0	GLN	A	563	5,266	89.549	-70,506	1,00	87,16	0
ATOM	4323	CB	GLN	A	563	3,147	91,087	-68,571	1,00	81.16	C
ATOM	4324	CG	GLN	A	563	3.690	92,455	-68.899	1,00	81,52	C
ATOM	4325	CD	GLN	A	563	3,004	93:536	-68,088	1,00	81.54	C
ATOM	4326	OE1	GLN	A	563	2,347	94.410	-68,647	1,00	80.75	0
ATOM	4327	NE2	GLN	A	563	3.147	93,477	-66.759	1,00	75,14	N
ATOM	4328	N	LEU	A	564	4,258	88,184	-69,032	1,00	83.20	N
ATOM	4329	CA	LEU	A	564	5,372	87.248	-68,962	1,00	86.15	C
ATOM	4330	C	LEU	A	564	5:567	86,537	-70:298	1,00	85,17	C
ATOM	4331	O	LEU	A	564	6,691	86,356	-70,771	1,00	81.74	O
ATOM	4332	CB	LEU	A	564	5,145	86.217	-67,851	1,00	80,63	C
ATOM	4333	CG	LEU	A	564	6:218	85,132	-67.832	1,00	78,65	C
ATOM	4334	CD1	LEU	A	564	7.557	85,800	-67.572	1,00	78,81	C
ATOM	4335	CD2	LEU	A	564	5,920	84.064	-66,794	1,00	77,83	C
ATOM	4336	N	LYS	A	565	4,459	86,135	-70,901	1,00	83.09	N
ATOM	4337	CA	LYS	A	565	4.539	85,373	-72.122	1,00	83,61	C
ATOM	4338	C	LYS	A	565	5,062	86:253	-73,242	1,00	84.47	C
ATOM	4339	O	LYS	A	565	6,131	86,005	-73,787	1,00	83.19	0
ATOM	4340	CB	LYS	A	565	3.177	84,782	-72.460	1,00	81,04	C
ATOM	4341	CG	LYS	A	565	2,712	83:779	-71,418	1,00	77.89	C
ATOM	4342	CD	LYS	A	565	1,551	82.945	-71,934	1,00	78.18	C
ATOM	4343	CE	LYS	A	565	1.190	81,846	-70.963	1,00	72,42	C
ATOM	4344	NZ	LYS	A	565	-0,019	81,126	-71,398	1,00	72.69	N
ATOM	4345	N	GLU	A	566	4,328	87.313	-73,546	1,00	85.81	N
ATOM	4346	CA	GLU	A	566	4:637	88,136	-74:702	1,00	87,22	C
ATOM	4347	C	GLU	A	566	5,827	89,054	-74,477	1,00	88.75	C
ATOM	4348	O	GLU	A	566	6,721	89.130	-75,320	1,00	88,93	0

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ATOM   4349  CB   GLU A 566      3.418  88.972 -75.091  1.00 92.36      C
ATOM   4350  CG   GLU A 566      2.186  88.150 -75.417  1.00 97.52      C
ATOM   4351  CD   GLU A 566      0.939  89.008 -75.537  1.00108.75      C
ATOM   4352  OE1  GLU A 566     -0.046  88.548 -76.158  1.00113.75      0
ATOM   4353  OE2  GLU A 566      0.947  90.141 -75.003  I.00104.76      0
ATOM   4354  N    ASP A 567      5.833  89.761 -73.349  1.00 85.14      N
ATOM   4355  CA   ASP A 567      6.795  90.841 -73.154  1.00 85.91      C
ATOM   4356  C    ASP A 567      8.188  90.336 -72.758  I.00 88.86      C
ATOM   4357  O    ASP A 567      9.180  91.022 -72.990  1.00 89.93      0
ATOM   4358  CE   ASP A 567      6.276  91.837 -72.110  1.00 88.30      C
ATOM   4359  CG   ASP A 567      6.320  93.271 -72.605  I.00 94.00      C
ATOM   4360  OD2  ASP A 567      5.266  93.949 -72.575  1.00 85.33      0
ATOM   4361  OD1  ASP A 567      7.410  93.707 -73.047  1.00 96.98      0
ATOM   4362  N    TYR A 568      8.272  89.146 -72.171  1.00 83.05      N
ATOM   4363  CA   TYR A 568      9.575  88.563 -71.867  1.00 82.68      C
ATOM   4364  C    TYR A 568      9.864  87.357 -72.741  1.00 81.96      C
ATOM   4365  O    TYR A 568     10.752  87.394 -73.594  1.00 80.86      0
ATOM   4366  CB   TYR A 568      9.677  88.147 -70.394  I.00 81.71      C
ATOM   4367  CG   TYR A 568     10.970  87.415 -70.053  1.00 79.86      C
ATOM   4368  CD2  TYR A 568     10.980  86.048 -69.811  1.00 75.32      C
ATOM   4369  CD1  TYR A 568     12.179  88.100 -69.971  I.00 79.67      C
ATOM   4370  CE2  TYR A 568     12.151  85.390 -69.503  1.00 77.30      C
ATOM   4371  CE1  TYR A 568     13.355  87.450 -69.666  1.00 70.95      C
ATOM   4372  CZ   TYR A 568     13.339  86.095 -69.431  I.00 77.06      C
ATOM   4373  OH   TYR A 568     14.518  85.438 -69.123  1.00 74.87      0
ATOM   4374  O    PHE A 569     10.184  84.473 -75.361  1.00 78.54      0
ATOM   4375  N    PHE A 569      9.114  86.284 -72.515  I.00 77.70      N
ATOM   4376  CA   PHE A 569      9.410  85.020 -73.159  1.00 77.50      C
ATOM   4377  C    PHE A 569      9.372  85.106 -74.689  1.00 82.35      C
ATOM   4378  CB   PHE A 569      8.460  83.940 -72.647  1.00 79.19      C
ATOM   4379  CG   PHE A 569      9.083  83.050 -71.615  1.00 81.93      C
ATOM   4380  CD1  PHE A 569      9.859  81.965 -71.996  1.00 83.90      C
ATOM   4381  CD2  PHE A 569      8.933  83.315 -70.264  1.00 83.19      C
ATOM   4382  CE1  PHE A 569     10.454  81.141 -71.046  I.00 83.12      C
ATOM   4383  CE2  PHE A 569      9.528  82.498 -69.307  1.00 82.54      C
ATOM   4384  CZ   PHE A 569     10.290  81.408 -69.702  1.00 81.90      C
ATOM   4385  O    LYS A 570     10.243  87.083 -77.866  I.00 84.01      0
ATOM   4386  N    LYS A 570      8.458  85.906 -75.239  1.00 84.54      N
ATOM   4387  CA   LYS A 570      8.413  86.109 -76.683  1.00 77.10      C
ATOM   4388  C    LYS A 570      9.313  87.262 -77.086  I.00 80.83      C
ATOM   4389  CB   LYS A 570      6.985  86.361 -77.162  1.00 76.15      C
ATOM   4390  O    LYS A 571     12.062  89.791 -77.621  1.00 87.77      0
ATOM   4391  N    LYS A 571      9.040  88.444 -76.547  1.00 82.36      N
ATOM   4392  CA   LYS A 571      9.774  89.643 -76.930  1.00 82.14      C
ATOM   4393  C    LYS A 571     11.278  89.476 -76.729  1.00 84.95      C
ATOM   4394  CB   LYS A 571      9.266  90.855 -76.138  1.00 85.20      C
ATOM   4395  CG   LYS A 571      9.666  92.212 -76.714  I.00 78.23      C
ATOM   4396  O    ILE A 572     14.960  87.507 -75.658  1.00 85.12      0
ATOM   4397  N    ILE A 572     11.682  88.951 -75.575  1.00 85.89      N
ATOM   4398  CA.  ILE A 572     13.100  88.935 -75.214  I.00 83.52      C
ATOM   4399  C    ILE A 572     13.784  87.569 -75.331  1.00 82.00      C
ATOM   4400  CB   ILE A 572     13.308  89.455 -73.773  1.00 86.49      C
ATOM   4401  O    GLU A 573     13.493  83.261 -76.673  I.00 80.71      0
ATOM   4402  N    GLU A 573     13.072  86.480 -75.058  1.00 80.80      N
ATOM   4403  CA   GLU A 573     13.664  85.144 -75.191  1.00 78.57      C
ATOM   4404  C    GLU A 573     13.288  84.466 -76.506  I.00 80.90      C
ATOM   4405  CB   GLU A 573     13.244  84.250 -74.023  1.00 82.43      C
ATOM   4406  CG   GLU A 573     13.939  84.552 -72.716  1.00 82.79      C
ATOM   4407  CD   GLU A 573     15.204  83.747 -72.523  1.00 77.91      C
ATOM   4408  OE1  GLU A 573     16.293  84.369 -72.524  1.00 84.51      0
ATOM   4409  OE2  GLU A 573     15.106  82.505 -72.351  1.00 73.35      0
ATOM   4410  O    GLU A 574     11.820  82.739 -79.859  1.00 84.41      0
ATOM   4411  N    GLU A 574     12.709  85.247 -77.412  I.00 80.35      N
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ATOM   4412  CA   GLU  A  574     12..326    84..812   -78..758    1 .00   78..85     C
ATOM   4413  C    GLU  A  574     11 ,655    83..440   --78 ,862   1 ,00   80..70     C
ATOM   4414  CB   GLU  A  574     13 .551    84.,845   -79 .671    1 ,00   84 ,85     C
ATOM   4415  CG   GLU  A  574     14 .020    86.,262   -80. ,003   1 .00   90..17     C
ATOM   4416  CD   GLU  A  574     15.,485    86. .323  -80.,407    1 ,00   93.,74     C
ATOM   4417  OE1  GLU  A  574     16 .152    85.,263   -80.. 406   1 ,00   91 ,69     0
ATOM   4418  OE2  GLU  A  574     15..969    87.,436   -80.. 712   1 ,00   96,.17     0
ATOM   4419  O    PHE  A  575      8 ,060    83. 168   -77 ,636    1 ,00   81 .49     0
ATOM   4420  N    PHE  A  575     10..889    83..065   -77 ,845    1 ,00   79..15     N
ATOM   4421  CA   PHE  A  575     10..057    81.,873   -77 .931    1 ,00   84 ,44     C
ATOM   4422  C    PHE  A  575      8 ,608    82..255   -78.,235    I ,00   84 .31     C
ATOM   4423  CB   PHE  A  575     10..141    81..064   -76 ,639    1 ,00   85..31     C
ATOM   4424  CG   PHE  A  575     11 .461    80.,390   -76 .439    1 ,00   85 ,38     C
ATOM   4425  CD1  PHE  A  575     12..087    79.,747   -77 ,497    1 .00   84 .34     C
ATOM   4426  CD2  PHE  A  575     12.,086    80.. 414  -75 ,203    1 ,00   86..41     C
ATOM   4427  CE1  PHE  A  575     13 ..311   79.,128   -77 ..330   1 ,00   83,.93     C
ATOM   4428  CE2  PHE  A  575     13..308    79.,793   -75 ..023   1 .00   91 .57     C
ATOM   4429  CZ   PHE  A  575     13 ,928    79 .147   -76 ,093    1 ,00   86..10     C
ATOM   4430  0    ASP  A  576      4 .958    82.,043   -77 .855    1 ,00   94 ,12     0
ATOM   4431  N    ASP  A  576      7 .992    81.,553   -79 .174    1 ,00   88,.24     N
ATOM   4432  CA.  ASP  A  576      6 ,635    81. 877   -79 ,575    1 ,00   89..55     C
ATOM   4433  C    ASP  A  576      5 ..636    81.,300   -78 ,571    1 ,00   93..57     C
ATOM   4434  CB   ASP  A  576      6 ..353    81.,359   -80.. 993   1 ,00   90,.19     C
ATOM   4435  CG   ASP  A  576      7 ,188    82.. 069  -82.,058    I ,00   92 .18     C
ATOM   4436  OD1  ASP  A  576      7 .361    83.,306   -81.,972    1 ,00   99..69     0
ATOM   4437  OD2  ASP  A  576      7 .678    81.,388   -82. 985    1 ,00   94 ,97     0
ATOM   4438  O    SER  A  577      5 ,921    78.. 020  -76.,113    I ,00   92 .12     0
ATOM   4439  N    SER  A  577      5 ,563    79 .975   -78 ,509    1 ,00   92 .89     N
ATOM   4440  CA   SER  A  577      4 .605    79.,310   -77 .638    1 ,00   92 ,88     C
ATOM   4441  C    SER  A  577      5 ..189    79.,005   -76 ,267    1 .00   95..07     C
ATOM   4442  CB   SER  A  577      4 ,134    78 .005   -78 ,263    1 ,00   94 .54     C
ATOM   4443  OG   SER  A  577      5 ..087    76.,982   -78.. 006   1 ,00   97 ,37     0
ATOM   4444  O    VAL  A  578      2 .975    80.,111   -73 ,184    1 .00   83..05     0
ATOM   4445  N    VAL  A  578      4 ,862    79 .836   -75 ,277    1 ,00   92 .01     N
ATOM   4446  CA   VAL  A  578      5 ..208    79.,541   -73 .889    1 ,00   83,.89     C
ATOM   4447  C    VAL  A  578      3 ..939    79.,356   -73 .055    1 ,00   80,.56     C
ATOM   4448  CB   VAL  A  578      6 ,107    80. 645   -73 ,268    1 ,00   86..40     C
ATOM   4449  CGI  VAL  A  578      7 .311    80.,886   -74 ,153    1 ,00   85..18     C
ATOM   4450  CG2  VAL  A  578      5 ..344    81.,943   -73 .066    1 ,00   81 ,91     C
ATOM   4451  O    GLU  A  579      4 ,152    77 .210   -69.,542    I ,00   76..21     0
ATOM   4452  N    GLU  A  579      3 ,929    78 .317   -72 ,229    1 ,00   81 .74     N
ATOM   4453  CA   GLU  A  579      2 .804    78 ,072   -71 ..333   1 ,00   84 ,00     C
ATOM   4454  C    GLU  A  579      3 ..286    78.,014   -69 ..880   1 .00   80..22     C
ATOM   4455  CB   GLU  A  579      2 ,075    76 .778   -71 ,712    1 ,00   83..50     C
ATOM   4456  CG   GLU  A  579      0 ..569    76.,785   -71 ..368   1 ,00   91 ,33     C
ATOM   4457  CD   GLU  A  579     --0..314    77 ,246   -72..524    1 .00   88..67     C
ATOM   4458  OE1  GLU  A  579     -.1 ,127    76 .425   -72.,998    1 ,00   92 ..35    0
ATOM   4459  OE2  GLU  A  579     -0..201    78.,415   -72 .959    1 ,00   83,.16     0
ATOM   4460  O    ILE  A  580      1 .145    78 ,359   -66.. 580   1 ,00   69,.35     0
ATOM   4461  N    ILE  A  580      2 ,702    78 .867   -69.,034    1 ,00   79..00     N
ATOM   4462  CA   ILE  A  580      3 ..170    79.,100   -67.,660    1 ,00   71 .31     C
ATOM   4463  C    ILE  A  580      2 .368    78 ,364   -66.. 570   1 ,00   69,.32     C
ATOM   4464  CB   ILE  A  580      3 ,162    80.. 620  -67.,359    I ,00   75..80     C
ATOM   4465  CGI  ILE  A  580      4 .167    81.,342   -68.,268    1 ,00   79..41     C
ATOM   4466  CG2  ILE  A  580      3 .435    80.,914   -65. 882    1 ,00   69 ,86     C
ATOM   4467  CD1  ILE  A  580      5 ,578    80.. 770  -68.,218    I ,00   75..64     C
ATOM   4468  O    SER  A  581      3 ,756    78 .618   -63.,159    1 ,00   69..59     0
ATOM   4469  N    SER  A  581      3 .085    77 ,742   -65. 635    1 ,00   71 ,99     N
ATOM   4470  CA   SER  A  581      2 ,498    77 ,051   -64.,488    1 .00   67 .69     C
ATOM   4471  C    SER  A  581      2 ,901    77 .730   -63.,167    1 ,00   72 .04     C
ATOM   4472  CB   SER  A  581      2 .927    75.,585   -64.. 488   1 ,00   65,.84     C
ATOM   4473  OG   SER  A  581      2 .649    74 ,973   -63.,249    1 .00   69..03     0
ATOM   4474  O    GLY  A  582      2 ,477    79 .829   -59.,374    1 ,00   73..10     0
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ATOM    4475  N    GLY  A  582        2 .278   77.332  -62..058   1.00  75..24         N
ATOM    4476  CA   GLY  A  582        2 ,625   77.878  --60.,752  1,00  69..87         C
ATOM    4477  C    GLY  A  582        2 .171   79,,299  -60..446   1.00  72 ,20         C
ATOM    4478  O    VAL  A  583      --0..347   81.,151  -63..221   1.00  78..77         0
ATOM    4479  N    VAL  A  583        1 „461   79.925  -61.,384   1,00  72.79          M
ATOM    4480  CA   VAL  A  583        0 ..858  81,,236  -61..142   1.00  69,.09         C
ATOM    4481  C    VAL  A  583      --0..375   81,,437  -62..027   1,00  75..42         C
ATOM    4482  CB   VAL  A  583        1 „863   82. 377  -61.,377   1,00  64.52          C
ATOM    4483  CGI  VAL  A  583        1 .216   83.,728  -61.,117   1,00  75..42         C
ATOM    4484  CG2  VAL  A  583        2 .400   82.,338  -62.. 774  1,00  66,.82         C
ATOM    4485  O    GLU  A  584      -1 „639    84..266  -62,,628   1,00  80..99         0
ATOM    4486  N    GLU  A  584      -1 .465    81..902  -61.,423   1,00  80..77         M
ATOM    4487  CA   GLU  A  584      -2 .701    82.,183  -62. 154   1,00  77,29          C
ATOM    4488  C    GLU  A  584      -2 .597    83.,528  -62..851   1.00  76..89         C
ATOM    4489  CB   GLU  A  584      -3.,906    82..168  -61.,212   1,00  75..17         C
ATOM    4490  O    ASP  A  585      -2 .404    86,,994  -65..143   1.00  71,68          0
ATOM    4491  N    ASP  A  585      --3..599   83.,844  -63..665   1.00  71.51          N
ATOM    4492  CA.  ASP  A  585      -3.,648    85. 029  -64.,541   1,00  73..31         C
ATOM    4493  C    ASP  A  585      -2 .747    86,,238  -64..230   1.00  73,.54         C
ATOM    4494  CB   ASP  A  585      --5..100   85.,525  -64..597   1,00  83,.05         C
ATOM    4495  CG   ASP  A  585      -6.,090    84. 397  -64.,851   1,00  87.80          C
ATOM    4496  OD1  ASP  A  585      -5..828    83..557  -65.,743   1,00  90..38         0
ATOM    4497  OD2  ASP  A  585      -7 .120    84.,336  -64..148   1,00  88,.62         0
ATOM    4498  O    ARG  A  586      -1 ,071    86..342  -60,,552   1,00  74.49          0
ATOM    4499  N    AP.G A  586      -2..384    86..434  -62.,962   1,00  69..35         M
ATOM    4500  CA   ARG  A  586      -1 .539    87.,566  -62. 569   1,00  69,03          C
ATOM    4501  C    ARG  A  586      -0,,714    87..231  -61,,331   1,00  73..69         C
ATOM    4502  CB   ARG  A  586      -2.,386    88..820  -62.,307   1,00  70..98         C
ATOM    4503  O    PHE  A  587        0 .489   89.,587  -58. 708   1,00  66,65          0
ATOM    4504  N    PHE  A  587        0 ..392  87.,944  -61.,146   1.00  71.78          N
ATOM    4505  CA   PHE  A  587        1 ,259   87.713  -59,991    1,00  66..27         C
ATOM    4506  C    PHE  A  587        0 ..706  88,,374  -58..735   1.00  66,.05         C
ATOM    4507  CB   PHE  A  587        2 ,680   88.,225  -60..264   1.00  65..78         C
ATOM    4508  CG   PHE  A  587        3 „617   87. 166  -60.,781   1,00  66..44         C
ATOM    4509  CD1  PHE  A  587        4 .132   86,,207  -59..930   1.00  67,82          C
ATOM    4510  CD2  PHE  A  587        3 ..984  87.,133  -62..109   1,00  67,23          C
ATOM    4511  CE1  PHE  A  587        5 ,000   85. 222  -60.,397   1,00  66..52         C
ATOM    4512  CE2  PHE  A  587        4 ,843   86.,162  -62.,578   1,00  68..58         C
ATOM    4513  CZ   PHE  A  587        5 .352   85.,205  -61. 721   1,00  65 ,13         C
ATOM    4514  O    ASM  A  588        0 „612   90..187  -55,,432   1,00  60..52         0
ATOM    4515  M    ASM  A  588        0 „484   87.568  -57.,702   1,00  65..34         M
ATOM    4516  CA   ASN  A  588        0 .019   88.,056  -56. 409   1,00  62,60          C
ATOM    4517  C    ASN  A  588        0 ,999   89.,063  -55,787    1.00  64.21          C
ATOM    4518  CB   ASM  A  588      -0.,231    86..875  -55.,461   1,00  58..85         C
ATOM    4519  CG   ASN  A  588      -1 .427    86,,026  -55..893   1.00  67,24          C
ATOM    4520  OD1  ASN  A  588      -2 .290    86.,492  -56 .642   1.00  67.86          0
ATOM    4521  ND2  ASM  A  588      -.1 ,482    84. 783  -55.,425   1,00  70..28         M
ATOM    4522  O    ALA  A  589        3 ..304  90,,503  -57...341   1.00  59,.35         0
ATOM    4523  N    ALA  A  589        2 .267   88.,679  -55..674   1,00  61,75          N
ATOM    4524  CA.  ALA  A  589        3 „268   89. 586  -55.,135   1,00  55..01         C
ATOM    4525  C    ALA  A  589        3 ,589   90.,667  -56,155    1,00  55..37         C
ATOM    4526  CB   ALA  A  589        4 .513   88.,828  -54..737   1,00  54,86          C
ATOM    4527  O    SER  A  590        5 ,698   93..779  -54,,734   1,00  61.50          0
ATOM    4528  N    SER  A  590        4 ,163   91..778  -55.,695   1,00  48..84         M
ATOM    4529  CA   SER  A  590        4 .460   92.,898  -56. 579   1,00  47,86          C
ATOM    4530  C    SER  A  590        5 ,448   93..850  -55,,929   1,00  55..72         C
ATOM    4531  CB   SER  A  590        3 „164   93..643  -56,978    1,00  65..96         C
ATOM    4532  OG   SER  A  590        2 .334   93.,989  -55. 869   1,00  63,28          0
ATOM    4533  N    LEU  A  591        6 ..020  94.,743  -56,718    1.00  61.34          N
ATOM    4534  CA   LEU  A  591        7 „006   95..675  -56,196    1,00  63..64         C
ATOM    4535  C    LEU  A  591        6 ..460  97,,101  -56..149   1.00  65,.38         C
ATOM    4536  O    LEU  A  591        6 ..989  97.,998  -56..795   1.00  68..74         0
ATOM    4537  CB   LEU  A  591        8 „277   95. 624  -57 ,047    1,00  71.24          C
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ATOM   4538  CG   LEU A 591      9.538   94.971  -56.471  1.00 66.61      C
ATOM   4539  GDI  LEU A 591      9.262   93.567  --55.979 1.00 60.97      C
ATOM   4540  CD2  LEU A 591     10.646   94.968  -57.500  1.00 66.07      C
ATOM   4541  N    GLY A 592      5.410   97.304  -55.363  1.00 67.96      N
ATOM   4542  CA.  GLY A 592      4.716   98.578  -55.321  I.00 64.45      C
ATOM   4543  C    GLY A 592      5.506   99.721  -54.718  1.00 68.09      C
ATOM   4544  O    GLY A 592      5.444  100.844  -55.205  1.00 65.02      O
ATOM   4545  N    TH.R A 593      6.239   99.445  -53.646  I.00 65.62      N
ATOM   4546  CA   THR A 593      7.043  100.472  -52.998  1.00 66.14      C
ATOM   4547  C    THR A 593      8.155  100.941  -53.930  1.00 74.59      C
ATOM   4548  0    THR A 593      8.475  102.141  -53.962  I.00 70.78      0
ATOM   4549  CB   THR A 593      7.653   99.964  -51.661  1.00 66.41      C
ATOM   4550  OG1  THR A 593      6.596   99.707  -50.730  1.00 68.69      0
ATOM   4551  CG2  THR A 593      8.627  100.979  -51.057  1.00 61.50      C
ATOM   4552  N    TYR A 594      8.733  100.001  -54.688  1.00 68.38      N
ATOM   4553  CA   TYR A 594      9.798  100.338  -55.618  1.00 67.73      C
ATOM   4554  C    TYR A 594      9.362  101.423  -56.575  1.00 73.22      C
ATOM   4555  0    TYR A 594     10.113  102.350  -56.855  I.00 75.34      0
ATOM   4556  CB   TYR A 594     10.249   99.120  -56.417  1.00 75.08      C
ATOM   4557  CG   TYR A 594     11.234   99.469  -57.518  1.00 77.61      C
ATOM   4558  CD1  TYR A 594     12.588   99.636  -57.240  I.00 74.61      C
ATOM   4559  CD2  TYR A 594     10.809   99.644  -58.838  1.00 80.72      C
ATOM   4560  CE1  TYR A 594     13.495   99.962  -58.242  1.00 78.12      C
ATOM   4561  CE2  TYR A 594     11.710   99.968  -59.848  I.00 81.02      C
ATOM   4562  CZ   TYR A 594     13.050  100.123  -59.541  1.00 80.33      C
ATOM   4563  OH   TYR A 594     13.943  100.440  -60.536  1.00 82.50      0
ATOM   4564  N    HIS A 595      8.135  101.300  -57.070  I.00 76.33      N
ATOM   4565  CA   HIS A 595      7.579  102.253  -58.029  1.00 72.97      C
ATOM   4566  C    HIS A 595      7.163  103.587  -57.384  1.00 75.05      C
ATOM   4567  O    HIS A 595      7.301  104.637  -58.005  1.00 74.76      0
ATOM   4568  CB   HIS A 595      6.393  101.619  -58.753  1.00 72.18      C
ATOM   4569  CG   HIS A 595      6.774  100.469  -59.630  1.00 78.77      C
ATOM   4570  ND1  HIS A 595      6.588  100.480  -60.995  1.00 83.33      N
ATOM   4571  CD2  HIS A 595      7.348   99.277  -59.338  I.00 75.70      C
ATOM   4572  CE1  HIS A 595      7.025   99.342  -61.506  1.00 81.99      C
ATOM   4573  NE2  HIS A 595      7.488   98.594  -60.521  1.00 83.02      N
ATOM   4574  N    ASP A 596      6.658  103.540  -56.150  I.00 71.23      N
ATOM   4575  CA   ASP A 596      6.370  104.751  -55.381  1.00 72.41      C
ATOM   4576  C    ASP A 596      7.625  105.606  -55.277  1.00 74.71      C
ATOM   4577  O    ASP A 596      7.658  106.742  -55.751  I.00 81.22      O
ATOM   4578  CB   ASP A 596      5.852  104.419  -53.970  1.00 74.37      C
ATOM   4579  CG   ASP A 596      4.541  103.633  -53.983  1.00 74.36      C
ATOM   4580  OD2  ASP A 596      4.210  102.996  -52.959  1.00 68.33      0
ATOM   4581  OD1  ASP A 596      3.836  103.655  -55.011  1.00 75.52      0
ATOM   4582  N    LEU A 597      8.654  105.043  -54.655  1.00 74.62      N
ATOM   4583  CA   LEU A 597      9.956  105.688  -54.541  1.00 78.47      C
ATOM   4584  C    LEU A 597     10.543  106.108  -55.887  I.00 80.70      C
ATOM   4585  O    LEU A 597     11.310  107.064  -55.959  1.00 82.46      O
ATOM   4586  CB   LEU A 597     10.932  104.757  -53.837  1.00 75.39      C
ATOM   4587  CG   LEU A 597     10.520  104.437  -52.412  I.00 72.22      C
ATOM   4588  CD1  LEU A 597     11.319  103.279  -51.896  1.00 74.02      C
ATOM   4589  CD2  LEU A 597     10.748  105.653  -51.570  1.00 77.12      C
ATOM   4590  N    LEU A 598     10.189  105.401  -56.953  I.00 77.28      N
ATOM   4591  CA   LEU A 598     10.724  105.739  -58.266  1.00 81.57      C
ATOM   4592  C    LEU A 598     10.150  107.063  -58.767  1.00 83.73      C
ATOM   4593  O    LEU A 598     10.905  107.953  -59.175  I.00 83.76      0
ATOM   4594  CB   LEU A 598     10.451  104.624  -59.280  1.00 81.45      C
ATOM   4595  CG   LEU A 598     11.284  104.746  -60.559  1.00 81.79      C
ATOM   4596  CD1  LEU A 598     12.732  105.119  -60.217  1.00 78.40      C
ATOM   4597  CD2  LEU A 598     11.224  103.459  -61.394  1.00 78.13      C
ATOM   4598  N    LYS A 599      8.822  107.186  -58.734  1.00 83.93      N
ATOM   4599  CA   LYS A 599      8.154  108.443  -59.067  1.00 80.05      C
ATOM   4600  C    LYS A 599      8.695  109.592  -58.228  I.00 80.29      C
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ATOM	4601	O	LYS	A	599	9.228	110.562	-58.760	1.00	83.61	O
ATOM	4602	CB	LYS	A	599	6.645	108.331	-58.865	1.00	81.94	C
ATOM	4603	CG	LYS	A	599	5.866	107.941	-60.111	1.00	86.57	C
ATOM	4604	CD	LYS	A	599	4.402	108.373	-60.001	1.00	89.60	C
ATOM	4605	CE	LYS	A	599	4.279	109.882	-59.805	I.00	86.51	C
ATOM	4606	NZ	LYS	A	599	2.867	110.312	-59.574	1.00	87.54	N
ATOM	4607	N	ILE	A	600	8.559	109.465	-56.915	1.00	82.32	N
ATOM	4608	CA.	ILE	A	600	9.000	110.492	-55.979	I.00	85.51	C
ATOM	4609	C	ILE	A	600	10.400	111.037	-56.296	1.00	88.83	C
ATOM	4610	O	ILE	A	600	10.586	112.248	-56.431	1.00	90.11	O
ATOM	4611	CB	ILE	A	600	9.002	109.954	-54.527	I.00	88.15	C
ATOM	4612	CGI	ILE	A	600	7.633	109.378	-54.151	1.00	84.23	C
ATOM	4613	CG2	ILE	A	600	9.441	111.031	-53.552	1.00	90.73	C
ATOM	4614	CD1	ILE	A	600	6.483	110.316	-54.394	1.00	92.10	C
ATOM	4615	N	ILE	A	601	11.373	110.141	-56.452	1.00	89.11	N
ATOM	4616	CA	ILE	A	601	12.773	110.561	-56.431	1.00	88.31	C
ATOM	4617	C	ILE	A	601	13.502	110.533	-57.782	1.00	86.88	C
ATOM	4618	O	ILE	A	601	14.560	111.154	-57.923	I.00	86.26	0
ATOM	4619	CB	ILE	A	601	13.564	109.718	-55.421	1.00	84.12	C
ATOM	4620	CGI	ILE	A	601	14.102	108.444	-56.059	1.00	85.35	C
ATOM	4621	CG2	ILE	A	601	12.699	109.387	-54.221	I.00	86.45	C
ATOM	4622	CD1	ILE	A	601	15.017	107.677	-55.142	1.00	87.17	C
ATOM	4623	N	LYS	A	602	12.941	109.824	-58.760	1.00	83.97	N
ATOM	4624	CA	LYS	A	602	13.402	109.914	-60.146	I.00	87.92	C
ATOM	4625	C	LYS	A	602	14.890	109.601	-60.339	1.00	89.74	C
ATOM	4626	O	LYS	A	602	15.560	110.253	-61.138	1.00	90.43	O
ATOM	4627	CB	LYS	A	602	13.103	111.318	-60.698	I.00	85.24	C
ATOM	4628	O	ASP	A	603	17.443	106.137	-58.673	1.00	87.60	0
ATOM	4629	N	ASP	A	603	15.395	108.599	-59.622	1.00	88.59	N
ATOM	4630	CA	ASP	A	603	16.817	108.249	-59.654	1.00	89.49	C
ATOM	4631	C	ASP	A	603	17.014	106.726	-59.666	1.00	88.26	C
ATOM	4632	CB	ASP	A	603	17.530	108.877	-58.453	1.00	90.56	C
ATOM	4633	CG	ASP	A	603	19.048	108.786	-58.545	1.00	93.64	C
ATOM	4634	OD1	ASP	A	603	19.569	107.860	-59.204	I.00	85.33	0
ATOM	4635	OD2	ASP	A	603	19.718	109.647	-57.932	1.00	100.55	0
ATOM	4636	O	LYS	A	604	17.912	102.847	-59.939	1.00	83.26	0
ATOM	4637	N	LYS	A	604	16.714	106.106	-60.804	I.00	85.81	N
ATOM	4638	CA	LYS	A	604	16.648	104.649	-60.927	1.00	84.40	C
ATOM	4639	C	LYS	A	604	17.947	103.917	-60.555	1.00	86.90	C
ATOM	4640	CB	LYS	A	604	16.237	104.280	-62.359	I.00	81.85	C
ATOM	4641	CG	LYS	A	604	15.946	102.814	-62.573	1.00	76.78	C
ATOM	4642	CD	LYS	A	604	14.940	102.616	-63.680	1.00	78.19	C
ATOM	4643	CE	LYS	A	604	14.429	101.186	-63.718	1.00	77.02	C
ATOM	4644	NZ	LYS	A	604	15.491	100.230	-64.143	1.00	75.79	N
ATOM	4645	O	ASP	A	605	21.332	102.975	-58.623	1.00	79.94	0
ATOM	4646	N	ASP	A	605	19.090	104.485	-60.925	1.00	86.14	N
ATOM	4647	CA.	ASP	A	605	20.360	103.821	-60.655	I.00	85.75	C
ATOM	4648	C	ASP	A	605	20.627	103.836	-59.153	1.00	87.29	C
ATOM	4649	CB	ASP	A	605	21.506	104.485	-61.427	1.00	86.61	C
ATOM	4650	O	PHE	A	606	19.763	103.079	-55.468	I.00	83.95	0
ATOM	4651	N	PHE	A	606	20.051	104.818	-58.468	1.00	88.38	N
ATOM	4652	CA	PHE	A	606	20.146	104.880	-57.015	1.00	86.31	C
ATOM	4653	C	PHE	A	606	19.317	103.756	-56.396	I.00	85.62	C
ATOM	4654	CB	PHE	A	606	19.686	106.244	-56.505	1.00	83.72	C
ATOM	4655	CG	PHE	A	606	19.695	106.371	-55.017	1.00	82.60	C
ATOM	4656	CD2	PHE	A	606	18.552	106.125	-54.285	I.00	81.45	C
ATOM	4657	CD1	PHE	A	606	20.843	106.748	-54.350	1.00	83.96	C
ATOM	4658	CE2	PHE	A	606	18.555	106.241	-52.917	1.00	78.26	C
ATOM	4659	CE1	PHE	A	606	20.852	106.867	-52.975	1.00	83.31	C
ATOM	4660	CZ	PHE	A	606	19.707	106.611	-52.259	1.00	80.87	C
ATOM	4661	O	LEU	A	607	17.855	100.324	-55.744	1.00	87.75	0
ATOM	4662	N	LEU	A	607	18.114	103.562	-56.930	1.00	87.68	N
ATOM	4663	CA.	LEU	A	607	17.211	102.509	-56.467	I.00	87.82	C

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ATOM    4664   C    LEU  A  607        17.808   101.,125  -56,673   1.00  86..49          C
ATOM    4665   CB   LEU  A  607        15,,853  102..591  --57,,183  1,00  86..41          C
ATOM    4666   CG   LEU  A  607        14.671   103.,222  -56.430   1,00  85,.80          C
ATOM    4667   GDI  LEU  A  607        14.900   103.,148  -54,935   1.00  90..08          C
ATOM    4668   CD2  LEU  A  607        14„385   104 .658  -56,,858   1,00  82,03           C
ATOM    4669   O    ASP  A  608        20.440    98.,047  -57..351   1,00  90,.14          0
ATOM    4670   N    ASP  A  608        18..262  100,,854  -57..894   1,00  88,.96          N
ATOM    4671   CA.  ASP  A  608        18,,785   99. 534  -58,,258   1,00  85.,24          C
ATOM    4672   C    ASP  A  608        20..114   99.,210  -57.,569   1,00  84.29           C
ATOM    4673   CB   ASP  A  608        18..941   99,,437  -59.775    1,00  80,.98          C
ATOM    4674   CG   ASP  A  608        17,615    99.587   -60.,506    1,00  86..37          C
ATOM    4675   OD2  ASP  A  608        17.539   100.,435  -61.,422   1,00  88..11          0
ATOM    4676   OD1  ASP  A  608        16. 647   98,,865  -60. 163   1,00  78,38           0
ATOM    4677   O    ASN  A  609        21..475  100.,175  -54.224    1.00  87.93           0
ATOM    4678   N    ASM  A  609        20,,869  100..239  -57,,215   1,00  84.76           N
ATOM    4679   CA   ASN  A  609        22..128  100.,048  -56.518    1,00  86,.26          C
ATOM    4680   C    ASN  A  609        21..926   99.,473  -55,122    1.00  87.52           C
ATOM    4681   CB   ASN  A  609        22,,881  101. 372  -56,,432   1,00  87,55           C
ATOM    4682   CG   ASN  A  609        24..272  101.,213  -55.866    1,00  86,.63          C
ATOM    4683   OD1  ASN  A  609        24.759   100,,095  -55.696    1,00  91,91           0
ATOM    4684   ND2  ASN  A  609        24,,926  102. 333  -55,,573   1,00  83.,04          N
ATOM    4685   O    GLU  A  610        23..210   97..373  -51.,526   1,00  90..22          0
ATOM    4686   N    GLU  A  610        22.298    98,,207  -54.932    1,00  90,.71          N
ATOM    4687   CA   GLU  A  610        22.,108   97..522  -53.,650   1,00  86..20          C
ATOM    4688   C    GLU  A  610        23..049   98..023  -52.,556   1,00  88..62          C
ATOM    4689   CB   GLU  A  610        22.286    96,,011  -53. 812   1,00  84,23           C
ATOM    4690   CG   GLU  A  610        21.,198   95...303  -54.,627   1,00  88..01          C
ATOM    4691   CD   GLU  A  610        21,,451   93..795  -54,,762   1,00  86..54          C
ATOM    4692   OE1  GLU  A  610        22.530    93,,335  -54. 330   1,00  88,90           O
ATOM    4693   OE2  GLU  A  610        20..578   93.,073  -55,298    1.00  79..96          O
ATOM    4694   O    GLU  A  611        24,,111  100..646  -49„584    1,00  79..89          O
ATOM    4695   N    GLU  A  611        23..658   99.,181  -52.779    1,00  91,68           N
ATOM    4696   CA   GLU  A  611        24..545   99.,798  -51.,803   1.00  91.12           C
ATOM    4697   C    GLU  A  611        23,,733  100. 551  -50.,756   1,00  83.,68          C
ATOM    4698   CB   GLU  A  611        25.517   100.,745  -52.510    1,00  90,.85          C
ATOM    4699   CG   GLU  A  611        26..797  101,,036  -51.754    1,00  97,22           C
ATOM    4700   CD   GLU  A  611        27,,751  101. 905  -52,,558   1,00100.,95           C
ATOM    4701   OE1  GLU  A  611        27..950  101.,617  -53.,761   1,00103. .65          0
ATOM    4702   OE2  GLU  A  611        28. 290  102,,883  -51. 991   1,00104 ,96           0
ATOM    4703   O    ASN  A  612        19.,510  101.662   -49.,539   1,00  83..49          0
ATOM    4704   N    ASN  A  612        22,,600  101..076  -51,,198   1,00  86..01          N
ATOM    4705   CA   ASN  A  612        21.751   101„895   -50. 344   1,00  86,37           C
ATOM    4706   C    ASN  A  612        20..579  101.,108  -49..777   1.00  81.34           C
ATOM    4707   CB   ASN  A  612        21,,231  103..100  -51,,126   1,00  86..35          C
ATOM    4708   CG   ASK  A  612        22..236  103.,613  -52.133    1,00  87,82           C
ATOM    4709   OD1  ASN  A  612        23.,258  104.,194  -51.,766   1.00  89..39          0
ATOM    4710   ND2  ASN  A  612        21,,950  103. 404  -53,,414   1,00  89.,08          N
ATOM    4711   O    GLU  A  613        18..151   99.,417  -47.319    1,00  81,19           0
ATOM    4712   N    GLU  A  613        20..775   99,,812  -49.574    1,00  82,79           N
ATOM    4713   CA.  GLU  A  613        19,,693   98. 975  -49,,080   1,00  84,16           C
ATOM    4714   C    GLU  A  613        19.,329   99.,365  -47,649    1,00  80..91          C
ATOM    4715   CB   GLU  A  613        20..051   97,,478  -49.165    1,00  77,25           C
ATOM    4716   CG   GLU  A  613        19.,566   96.798   -50.,452   1,00  80..38          C
ATOM    4717   CD   GLU  A  613        19.,967   95.,329  -50.,555   1,00  88..79          C
ATOM    4718   OF.1 GLU  A  613        19. 078   94,,453  -50. 446   1,00  81,15           0
ATOM    4719   OE2  GLU  A  613        21.,170   95.046   -50.,758   1,00  93..92          0
ATOM    4720   N    ASP  A  614        20,,325   99.645   -46„810    1,00  75..94          N
ATOM    4721   CA   ASP  A  614        20. 056  100,,092  -45. 442   1,00  80,52           C
ATOM    4722   C    ASP  A  614        19.,303  101.,443  -45,435    1.00  78..31          C
ATOM    4723   O    ASP  A  614        18,,353  101.639   -44,672    1,00  72.14           0
ATOM    4724   CB   ASP  A  614        21...359  100.,207  -44.634    1,00  74,60           C
ATOM    4725   CG   ASP  A  614        22..161   98.,895  -44,593    1.00  88..28          C
ATOM    4726   OD1  ASP  A  614        21,,563   97. 797  -44„523    1,00  84,55           0
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ATOM   4727  OD2 ASP A 614     23.408  98.961 -44.626  1.00 91.34      O
ATOM   4728  N   ILE A 615     19.722 102.356 --46.304 1.00 78.52      N
ATOM   4729  CA  ILE A 615     19.163 103.700 -46.348  1.00 76.28      C
ATOM   4730  C   ILE A 615     17.661 103.688 -46.664  1.00 77.56      C
ATOM   4731  O   ILE A 615     16.855 104.206 -45.891  I.00 74.77      0
ATOM   4732  CB  ILE A 615     19.904 104.570 -47.389  1.00 76.26      C
ATOM   4733  CGI ILE A 615     21.414 104.530 -47.148  1.00 82.10      C
ATOM   4734  CG2 ILE A 615     19.409 106.004 -47.344  I.00 83.05      C
ATOM   4735  GDI ILE A 615     22.225 105.157 -48.265  1.00 82.00      C
ATOM   4736  N   LEU A 616     17.292 103.091 -47.796  1.00 77.93      N
ATOM   4737  CA  LEU A 616     15.897 103.032 -48.222  I.00 75.24      C
ATOM   4738  C   LEU A 616     15.050 102.137 -47.319  1.00 75.35      C
ATOM   4739  O   LEU A 616     13.825 102.206 -47.343  1.00 72.93      O
ATOM   4740  CB  LEU A 616     15.798 102.536 -49.662  1.00 72.71      C
ATOM   4741  CG  LEU A 616     16.238 103.464 -50.795  1.00 75.60      C
ATOM   4742  CD1 LEU A 616     16.784 102.669 -51.962  1.00 84.57      C
ATOM   4743  CD2 LEU A 616     15.084 104.300 -51.269  1.00 79.46      C
ATOM   4744  N   GLU A 617     15.698 101.281 -46.540  I.00 72.47      N
ATOM   4745  CA  GLU A 617     14.980 100.453 -45.583  1.00 71.91      C
ATOM   4746  C   GLU A 617     14.638 101.305 -44.379  1.00 74.71      C
ATOM   4747  0   GLU A 617     13.585 101.140 -43.766  I.00 75.00      0
ATOM   4748  CB  GLU A 617     15.813  99.243 -45.167  1.00 72.71      C
ATOM   4749  CG  GLU A 617     15.031  97.957 -45.046  1.00 73.59      C
ATOM   4750  CD  GLU A 617     14.131  97.707 -46.242  I.00 70.87      C
ATOM   4751  OE1 GLU A 617     14.586  97.857 -47.393  1.00 73.16      0
ATOM   4752  OE2 GLU A 617     12.957  97.366 -46.029  1.00 66.62      0
ATOM   4753  N   ASP A 618     15.549 102.218 -44.059  I.00 74.14      N
ATOM   4754  CA  ASP A 618     15.383 103.183 -42.985  1.00 72.66      C
ATOM   4755  C   ASP A 618     14.269 104.192 -43.289  1.00 71.59      C
ATOM   4756  O   ASP A 618     13.540 104.628 -42.391  1.00 69.40      0
ATOM   4757  CB  ASP A 618     16.707 103.905 -42.748  1.00 75.43      C
ATOM   4758  CG  ASP A 618     16.585 105.035 -41.762  1.00 69.27      C
ATOM   4759  OD2 ASP A 618     16.761 106.199 -42.164  1.00 71.58      0
ATOM   4760  OD1 ASP A 618     16.336 104.753 -40.581  I.00 75.84      0
ATOM   4761  N   ILE A 619     14.131 104.552 -44.557  1.00 70.42      N
ATOM   4762  CA  ILE A 619     13.112 105.515 -44.956  1.00 72.71      C
ATOM   4763  C   ILE A 619     11.720 104.914 -44.870  I.00 70.79      C
ATOM   4764  O   ILE A 619     10.827 105.514 -44.283  1.00 72.01      0
ATOM   4765  CB  ILE A 619     13.337 106.027 -46.382  1.00 71.92      C
ATOM   4766  CGI ILE A 619     14.666 106.768 -46.469  I.00 76.66      C
ATOM   4767  CG2 ILE A 619     12.213 106.942 -46.805  1.00 65.92      C
ATOM   4768  GDI ILE A 619     14.903 107.437 -47.797  1.00 74.25      C
ATOM   4769  N   VAL A 620     11.534 103.735 -45.459  1.00 64.52      N
ATOM   4770  CA  VAL A 620     10.250 103.059 -45.390  1.00 64.77      C
ATOM   4771  C   VAL A 620      9.840 102.801 -43.936  1.00 64.30      C
ATOM   4772  O   VAL A 620      8.661 102.855 -43.594  1.00 67.10      0
ATOM   4773  CB  VAL A 620     10.270 101.747 -46.179  I.00 55.43      C
ATOM   4774  CGI VAL A 620      9.109 100.855 -45.787  1.00 58.95      C
ATOM   4775  CG2 VAL A 620     10.198 102.036 -47.643  1.00 56.52      C
ATOM   4776  N   LEU A 621     10.821 102.570 -43.077  I.00 66.86      N
ATOM   4777  CA  LEU A 621     10.559 102.306 -41.663  1.00 65.34      C
ATOM   4778  C   LEU A 621      9.971 103.515 -40.938  1.00 73.97      C
ATOM   4779  0   LEU A 621      8.965 103.385 -40.239  I.00 75.46      0
ATOM   4780  CB  LEU A 621     11.833 101.866 -40.950  1.00 63.68      C
ATOM   4781  CG  LEU A 621     11.584 101.596 -39.474  1.00 61.50      C
ATOM   4782  CD1 LEU A 621     10.465 100.588 -39.316  I.00 55.83      C
ATOM   4783  CD2 LEU A 621     12.851 101.103 -38.844  1.00 60.58      C
ATOM   4784  N   THR A 622     10.593 104.684 -41.099  1.00 73.94      N
ATOM   4785  CA  THR A 622     10.088 105.901 -40.467  1.00 71.43      C
ATOM   4786  C   THR A 622      8.803 106.404 -41.146  1.00 73.50      C
ATOM   4787  O   THR A 622      8.055 107.174 -40.553  1.00 79.67      0
ATOM   4788  CB  THR A 622     11.154 107.031 -40.455  1.00 66.49      C
ATOM   4789  OG1 THR A 622     11.615 107.272 -41.783  I.00 62.97      0
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ATOM    4790   CG2  THR  A  622      12..337   106..671   -39..556    1.00   64.99         C
ATOM    4791   N    LEU  A  623       8„543    105..962   --42.,376   1,00   71.19         N
ATOM    4792   CA   LEU  A  623       7..309   106.,317   -43.092     I.00   74,33         C
ATOM    4793   C    LEU  A  623       6..147   105.,357   -42,764    1.00   76..44        C
ATOM    4794   0    LEU  A  623       4„979    105. 657   -43,047    1,00   73.,64        0
ATOM    4795   CB   LEU  A  623       7.531    106.,334   -44.616    I.00   73,.05        C
ATOM    4796   CG   LEU  A  623       8..388   107 ,383   -45.344    1,00   73..56        C
ATOM    4797   GDI  LEU  A  623       8„535    107. 017   -46,813    1,00   73.,14        C
ATOM    4798   CD2  LEU  A  623       7.814    108.,782   -45,218    1,00   76..13        C
ATOM    4799   N    THR  A  624       6..480   104.,196   -42.. 197   1,00   73..34        N
ATOM    4800   CA   THR  A  624       5„490    103..237   -41,705    1,00   72.31         C
ATOM    4801   C    THR  A  624       5..233   103..488   -40,209    1,00   76..19        C
ATOM    4802   O    THR  A  624       4.239    103.,031   -39.637    1,00   75,11         0
ATOM    4803   CB   THR  A  624       5..962   101.,772   -41,938    1.00   66..85        C
ATOM    4804   OG1  THR  A  624       6,031    101..507   -43,346    1,00   65..76        0
ATOM    4805   CG2  THR  A  624       5..009   100.,765   -41.297    I.00   63,.35        C
ATOM    4806   N    LEU  A  625       6..126   104.,254   -39,591    1,00   74.53         N
ATOM    4807   CA.  LEU  A  625       6„113    104 .442   -.38.,150   1,00   76..19        C
ATOM    4808   C    LEU  A  625       5..445   105.,754   -37.745    I.00   77,20         C
ATOM    4809   O    LEU  A  625       4.585    105.,786   -36.864    1,00   79,.65        O
ATOM    4810   CB   LEU  A  625       7„543    104 ..392  -.37.,615   1,00   79..13        C
ATOM    4811   CG   LEU  A  625       7.757    103..774   -36,235    1,00   76..15        C
ATOM    4812   CD2  LEU  A  625       9..228   103.,779   -35.884     1,00   76,25         C
ATOM    4813   CD1  LEU  A  625       7,202    102..372   -.36,205    1,00   66..58        C
ATOM    4814   N    PHE  A  626       5..843   106..836   -38.,402   1,00   81.57         N
ATOM    4815   CA   PHE  A  626       5..346   108.,168   -38. 070   1,00   76,50         C
ATOM    4816   C    PHE  A  626       4„393    108..690   -.39,145    1,00   79.82         C
ATOM    4817   O    PHE  A  626       4,664    108..575   -40,339    1,00   77.06         0
ATOM    4818   CB   PHE  A  626       6.523    109.,132   -37. 878   1,00   73,41         C
ATOM    4819   CG   PHE  A  626       7,567    108.,615   -36,935    1.00   73..71        C
ATOM    4820   CD1  PHE  A  626       7,370    108..673   -35.,570   1,00   70..46        C
ATOM    4821   CD2  PHE  A  626       8..733   108.,042   -37.416     I.00   74,13         C
ATOM    4822   CE1  PHE  A  626       8..322   108.,188   -34,694    1.00   73..83        C
ATOM    4823   CE2  PHE  A  626       9„690    107 .551   -.36,551    1,00   72.85         C
ATOM    4824   CZ   PHE  A  626       9.487    107 ,619   -35.189     I.00   76,.38        C
ATOM    4825   O    GLU  A  627       2.202    Ill ,989   -40.709    1,00   76,05         0
ATOM    4826   N    GLU  A  627       3„271    109.257    -.38.,712   1,00   84,39         N
ATOM    4827   CA   GLU  A  627       2,297    109.,834   -39,633    1,00   85..89        C
ATOM    4828   C    GLU  A  627       2.486    111,345    -39.694    1,00   81,20         C
ATOM    4829   CB   GLU  A  627       0„873    109.493    -.39,191    1,00   85..24        C
ATOM    4830   CG   GLU  A  627       0„598    109..923   -37.,759   1,00   85..69        C
ATOM    4831   CD   GLU  A  627      -0. 818   109.,648   -37. .300   1,00   84,62         C
ATOM    4832   OE1  GLU  A  627      --1,674    109.,259   -38..127   1.00   80..60        0
ATOM    4833   OE2  GLU  A  627      -1,081    109..820   -36,091    1,00   84.80         0
ATOM    4834   O    ASP  A  628       5..407   113.,472   -39.265    I.00   83,.73        0
ATOM    4835   N    ASP  A  628       2.982    Ill ,894   -38.,591   1.00   81.07         N
ATOM    4836   CA.  ASP  A  628       3„158    113. 332   -.38.,450   1,00   81.85         C
ATOM    4837   C    ASP  A  628       4.254    113.,880   -39..370    I.00   84,62         C
ATOM    4838   CB   ASP  A  628       3.474    113.,665   -36..998   1,00   79,.78        C
ATOM    4839   CG   ASP  A  628       3„528    115. 153   -.36,744    1,00   88..28        C
ATOM    4840   OD1  ASP  A  628       2,770    115..895   -37.,415   1,00   90..71        0
ATOM    4841   OD2  ASP  A  628       4.325    115.,578   -35.879     1,00   82,08         0
ATOM    4842   O    ARG  A  629       7,070    116..211   -41,239    1,00   90..62        0
ATOM    4843   N    ARG  A  629       3,890    114 .807   -40,259    1,00   88..64        N
ATOM    4844   CA   ARG  A  629       4.825    115.,357   -41 .246    1,00   86,61         C
ATOM    4845   C    ARG  A  629       6„014    116. 088   -40.,616   1,00   89..20        C
ATOM    4846   CB   ARG  A  629       4,102    116..303   -42.,202   1,00   87.15         C
ATOM    4847   O    GLU  A  6.30      9.088    116,161    -38. 046   1,00   87,04         0
ATOM    4848   N    GLU  A  630       5,851    116.,574   -39,390    1.00   85..53        N
ATOM    484 9  CA   GLU  A  630       6,979    117 .150   -38.,668   1,00   84.27         C
ATOM    4850   C    GLU  A  6.30      7.860    116.,041   -38.084    I.00   87,28         C
ATOM    4851   CB   GLU  A  630       6..499   118.,090   -37.,561   1.00   88..89        C
ATOM    4852   O    MET  A  631       9„773    112 .473   -.37.,883   1,00   87,18         0
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ATOM	4853	N	MET	A	631	7.231	114.958	-37.634	1.00	90.06	N
ATOM	4854	CA	MET	A	631	7.964	113.824	--37.072	1.00	85.25	C
ATOM	4855	C	MET	A	631	8.752	113.113	-38.157	1.00	85.95	C
ATOM	4856	CB	MET	A	631	7.014	112.839	-36.375	1.00	83.29	C
ATOM	4857	CG	MET	A	631	6.369	113..386	-35.099	I.00	87.45	C
ATOM	4858	SD	MET	A	631	5.752	112.124	-33.969	1.00	76.17	S
ATOM	4859	CE	MET	A	631	7.295	111.359	-33.510	1.00	73.08	C
ATOM	4860	O	ILE	A	632	11.355	112.885	-40.754	I.00	83.48	0
ATOM	4861	N	ILE	A	632	8.259	113.218	-39.389	1.00	87.08	N
ATOM	4862	CA	ILE	A	632	8.964	112.699	-40.553	1.00	84.42	C
ATOM	4863	C	ILE	A	632	10.268	113.474	-40.745	I.00	87.2.1	C
ATOM	4864	CB	ILE	A	632	8.107	112.800	-41.824	1.00	80.85	C
ATOM	4865	CGI	ILE	A	6.32	6.800	112.023	-41.653	1.00	83.87	C
ATOM	4866	CG2	ILE	A	632	8.872	112.308	-43.024	1.00	81.72	C
ATOM	4867	CD1	ILE	A	632	6.968	110.641	-41.078	1.00	79.54	C
ATOM	4868	O	GLU	A	6.33	13.596	115.252	-40.651	1.00	76.67	0
ATOM	4869	N	GLU	A	633	10.138	114.797	-40.869	1.00	86.64	N
ATOM	4870	CA.	GLU	A	633	11.266	115.714	-4.1.025	I.00	83.07	C
ATOM	4871	C	GLU	A	6.33	12.487	115.396	-40.142	1.00	81.50	C
ATOM	4872	CB	GLU	A	633	10.799	117.142	-40.747	1.00	81.43	C
ATOM	4873	O	GLU	A	634	15.259	113.562	-.37.741	I.00	86.89	0
ATOM	4874	N	GLU	A	634	12.280	115.285	-38.832	1.00	81.50	N
ATOM	4875	CA	GLU	A	634	13.382	115.080	-37.886	1.00	82.45	C
ATOM	4876	C	GLU	A	634	14.051	113.701	-.37.992	I.00	87.74	C
ATOM	4877	CB	GLU	A	634	12.887	115.291	-36.453	1.00	82.17	C
ATOM	4878	O	A.P.G	A	6.35	14.668	109.952	-40.273	1.00	9.1.17	0
ATOM	4879	N	ARG	A	635	13.274	112.681	-.38.350	I.00	85..34	N
ATOM	4880	CA	ARG	A	635	13.820	111.331	-38.478	1.00	84.34	C
ATOM	4881	C	ARG	A	6.35	14.283	111.070	-39.922	1.00	85.47	C
ATOM	4882	CB	ARG	A	635	12.788	110.289	-38.027	1.00	75.76	C
ATOM	4883	O	LEU	A	636	16.156	113.292	-43.585	1.00	80.02	0
ATOM	4884	N	LEU	A	6.36	14.259	112.115	-40.747	1.00	81.80	N
ATOM	4885	CA	LEU	A	636	14.702	112.022	-42.137	1.00	81.99	C
ATOM	4886	C	LEU	A	636	15.808	113.045	-42.425	I.00	85..30	C
ATOM	4887	CB	LEU	A	6.36	13.517	112.237	-43.087	1.00	83.66	C
ATOM	4888	CG	LEU	A	636	13.387	111.331	-44.317	1.00	83.11	C
ATOM	4889	CD1	LEU	A	636	13.440	109.862	-43.913	I.00	83.52	C
ATOM	4890	CD2	LEU	A	636	12.104	111.628	-45.081	1.00	78.10	C
ATOM	4891	O	LYS	A	6.37	19.114	115.368	-42.832	1.00	87.70	0
ATOM	4892	N	LYS	A	637	16.359	113.614	-4.1.349	I.00	89.64	N
ATOM	4893	CA	LYS	A	637	17.290	114.745	-41.404	1.00	87.75	C
ATOM	4894	C	LYS	A	6.37	18.573	114.472	-42.184	1.00	85.23	C
ATOM	4895	CB	LYS	A	637	17.656	115.188	-39.982	1.00	86.07	C
ATOM	4896	O	THR	A	638	21.227	113.214	-44.973	1.00	97.96	0
ATOM	4897	N	THR	A	6.38	19.068	113.243	-42.124	1.00	88.70	N
ATOM	4898	CA	THR	A	638	20.344	112.923	-42.763	1.00	86.56	C
ATOM	4899	C	THR	A	638	20.249	112.926	-44.283	I.00	88.00	C
ATOM	4900	CB	THR	A	6.38	20.877	111.555	-42..303	1.00	85.61	C
ATOM	4901	OG1	THR	A	638	19.817	110.590	-42.330	1.00	84.45	0
ATOM	4902	CG2	THR	A	638	2.1.430	111.654	-40.893	I.00	88.64	C
ATOM	4903	O	TYR	A	639	19.457	114.305	-47.512	1.00	86.36	0
ATOM	4904	N	TYR	A	639	19.067	112.626	-44.801	1.00	83.78	N
ATOM	4905	CA	TYR	A	639	18.917	112..345	-46.217	I.00	81.23	C
ATOM	4906	C	TYR	A	639	18.573	113.596	-47.028	1.00	86.04	C
ATOM	4907	CB	TYR	A	6.39	17.850	111.266	-46.411	1.00	77.07	C
ATOM	4908	CG	TYR	A	639	18.129	109.956	-45.690	I.00	81.28	C
ATOM	4909	CD1	TYR	A	639	17.118	109.032	-45.479	1.00	79.45	C
ATOM	49.10	CD2	TYR	A	6.39	19.401	109.640	-45.232	1.00	8.1.63	C
ATOM	4911	CE1	TYR	A	639	17.364	107.836	-44.830	1.00	78.97	C
ATOM	4912	CE2	TYR	A	639	19.650	108.449	-44.581	1.00	80.14	C
ATOM	4913	CZ	TYR	A	6.39	18.628	107.551	-44..383	1.00	77.14	C
ATOM	4914	OH	TYR	A	639	18.871	106.361	-43.743	1.00	75.43	0
ATOM	4915	N	ASP	A	644	16.848	116.513	-53.541	I.00	96.73	N

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ATOM   4916  CA   ASP  A 644      16.681 117.790 -52.867  1.00 97.16      c
ATOM   4917  C    ASP  A 644      15.194 118.129 --52.664 1.00100.71      C
ATOM   4918  O    ASP  A 644      14.334 117.249 -52.731  1.00 98.59      0
ATOM   4919  CB   ASP  A 644      17.391 118.896 -53.652  1.00 98.58      c
ATOM   4920  CG   ASP  A 644      17.795 120.079 -52.775  1.00102.84      c
ATOM   4921  OD2  ASP  A 644      16.896 120.754 -52.225  1.00104.56      0
ATOM   4922  OD1  ASP  A 644      19.012 120.343 -52.646  1.00 96.61      0
ATOM   4923  N    ASP  A 645      14.909 119.414 -52.450  1.00 99.08      N
ATOM   4924  CA   ASP  A 645      13.656 119.882 -51.842  1.00 97.28      c
ATOM   4925  c    ASP  A 645      12.341 119.521 -52.551  1.00 97.74      c
ATOM   4926  0    ASP  A 645      11.316 119.396 -51.888  1.00 98.46      0
ATOM   4927  CB   ASP  A 645      13.716 121.406 -51.673  1.00 98.82      c
ATOM   4928  N    LYS  A 646      12.347 119.376 -53.875  1.00 99.85      N
ATOM   4929  CA   LYS  A 646      11.116 119.018 -54.593  1.00 97.58      c
ATOM   4930  C    LYS  A 646      10.763 117.567 -54.323  1.00 97.88      C
ATOM   4931  O    LYS  A 646       9.589 117.180 -54.302  1.00 93.95      O
ATOM   4932  CB   LYS  A 646      11.265 119.241 -56.102  1.00 92.87      c
ATOM   4933  CG   LYS  A 646      10.081 118.744 -56.914  1.00 88.36      c
ATOM   4934  CD   LYS  A 646      10.518 118.326 -58.310  1.00 94.47      c
ATOM   4935  CE   LYS  A 646       9.346 117.840 -59.150  1.00 85.24      c
ATOM   4936  NZ   LYS  A 646       9.656 117.930 -60.600  1.00 74.93      N
ATOM   4937  O    VAL  A 647      10.334 114.216 -52.269  1.00 91.70      0
ATOM   4938  N    VAL  A 647      11.808 116.772 -54.116  1.00 99.75      N
ATOM   4939  CA   VAL  A 647      11.676 115.343 -53.894  1.00 95.36      C
ATOM   4940  C    VAL  A 647      11.194 115.067 -52.476  1.00 92.52      C
ATOM   4941  CB   VAL  A 647      13.010 114.621 -54.140  1.00 97.07      C
ATOM   4942  CGI  VAL  A 647      12.826 113.120 -54.028  1.00 96.89      C
ATOM   4943  CG2  VAL  A 647      13.563 114.989 -55.514  1.00 96.98      C
ATOM   4944  O    MET  A 648       9.281 115.546 -48.891  1.00 92.18      O
ATOM   4945  N    MET  A 648      11.736 115.803 -51.510  1.00 93.10      N
ATOM   4946  CA   MET  A 648      11.360 115.646 -50.102  1.00 94.37      C
ATOM   4947  C    MET  A 648       9.901 116.028 -49.839  1.00 94.16      C
ATOM   4948  CB   MET  A 648      12.275 116.486 -49.207  1.00 92.64      c
ATOM   4949  CG   MET  A 648      12.239 116.101 -47.737  1.00 89.78      c
ATOM   4950  SD   MET  A 648      13.239 114.637 -47.378  1.00107.06      s
ATOM   4951  CE   MET  A 648      14.905 115.231 -47.684  1.00 81.82      c
ATOM   4952  N    LYS  A 649       9.363 116.910 -50.674  1.00 96.62      N
ATOM   4953  CA   LYS  A 649       7.982 117.353 -50.528  1.00100.63      c
ATOM   4954  C    LYS  A 649       7.048 116.222 -50.932  1.00 96.88      c
ATOM   4955  O    LYS  A 649       5.979 116.040 -50.340  1.00 95.89      0
ATOM   4956  CB   LYS  A 649       7.710 118.610 -51.369  1.00 96.35      c
ATOM   4957  N    GLN  A 650       7.461 115.460 -51.940  1.00 90.16      N
ATOM   4958  CA   GLN  A 650       6.681 114.321 -52.396  1.00 92.84      c
ATOM   4959  C    GLN  A 650       6.890 113.135 -51.453  1.00 91.62      C
ATOM   4960  O    GLN  A 650       6.188 112.126 -51.551  1.00 92.81      O
ATOM   4961  CB   GLN  A 650       7.061 113.946 -53.832  1.00 89.53      c
ATOM   4962  N    LEU  A 651       7.833 113.279 -50.521  1.00 87.27      N
ATOM   4963  CA   LEU  A 651       8.243 112.170 -49.664  1.00 88.79      C
ATOM   4964  c    LEU  A 651       7.666 112.219 -48.246  1.00 89.95      c
ATOM   4965  0    LEU  A 651       7.231 111.194 -47.720  1.00 90.46      0
ATOM   4966  CB   LEU  A 651       9.770 112.105 -49.585  1.00 91.64      c
ATOM   4967  CG   LEU  A 651      10.400 110.770 -49.158  1.00 91.68      c
ATOM   4968  CD1  LEU  A 651      10.359 109.723 -50.276  1.00 92.45      c
ATOM   4969  CD2  LEU  A 651      11.818 110.983 -48.682  1.00 83.01      c
ATOM   4970  O    LYS  A 652       5.024 112.831 -45.302  1.00 91.89      0
ATOM   4971  N    LYS  A 652       7.663 113.394 -47.621  1.00 93.75      N
ATOM   4972  CA   LYS  A 652       7.093 113.529 -46.282  1.00 87.57      C
ATOM   4973  C    LYS  A 652       5.612 113.183 -46.321  1.00 86.93      c
ATOM   4974  CB   LYS  A 652       7.296 114.940 -45.733  1.00 86.61      c
ATOM   4975  CG   LYS  A 652       8.744 115.379 -45.658  1.00 87.86      c
ATOM   4976  CD   LYS  A 652       9.127 115.805 -44.247  1.00 89.70      c
ATOM   4977  CE   LYS  A 652      10.011 117.046 -44.256  1.00 86.20      c
ATOM   4978  NZ   LYS  A 652       9.266 118.261 -44.717  1.00 93.99      N
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ATOM   4979  O    ARG  A  653     2 .338  110..883  -47 .549   1 .00  92 .01        O
ATOM   4980  N    ARG  A  653     5 „025  113..269  --4 7 ,510  1 ,00  83..65        N
ATOM   4981  CA   ARG  A  653     3 ..630  112.,907  -47 .728   1 .00  86,.07        C
ATOM   4982  c    ARG  A  653     3 ..405  Ill .389  -47 .901   1 .00  91 .45        c
ATOM   4983  CB   ARG  A  653     3 „083  113. 654  -48 ,949   1 ,00  83..31        c
ATOM   4984  O    ARG  A  654     5 ..405  107 ,854  -47 .046   1 .00  84 ,09        0
ATOM   4985  N    ARG  A  654     4 .386  110.,656  -48 ..433   1 ,00  84 ,86        N
ATOM   4986  CA.  ARG  A  654     4 „197  109 .215  -48 ,619   1 ,00  84 .47        C
ATOM   4987  C    ARG  A  654     4 .358  108..457  -47 ,305   1 ,00  87 .11        C
ATOM   4988  CB   ARG  A  654     5 ..170  108.,651  -49 ..659   1 ,00  86,.87        c
ATOM   4989  CG   ARG  A  654     5 „083  107..121  -49.,855   1 ,00  83..63        c
ATOM   4990  CD   ARG  A  654     3 ..923  106..716  -50.,736   1 ,00  82 .74        c
ATOM   4991  NE   ARG  A  654     4 .023  107 ,389  -52. 027   1 ,00  90 ,96        N
ATOM   4992  CZ   ARG  A  654     3 ..309  107 .077  -53.,104   1 .00  88..12        c
ATOM   4993  NH1  ARG  A  654     2 ,432  106..081  -53.,061   1 ,00  88..35        N
ATOM   4994  NH2  ARG  A  654     3 ..481  107 ,761  -54..227   1 ,00  87 ,96        N
ATOM   4995  O    ARG  A  655     1 .521  106..321  -46 ..056   1 ,00  80..09        O
ATOM   4996  N    ARG  A  655     3 „321  108. 489  -46 ,472   1 ,00  85..84        N
ATOM   4997  CA   ARG  A  655     3 ..316  107 ,708  -45 ..240   1 .00  78,.00        C
ATOM   4998  c    ARG  A  655     2 .614  106.,364  -45 ..480   1 ,00  77 ,71        c
ATOM   4999  CB   ARG  A  655     2 „644  108. 490  -44 ,110   1 ,00  79..73        c
ATOM   5000  O    TYR  A  656     2 ..382  103.,861  -42.,858   1 ,00  69..54        0
ATOM   5001  N    TYR  A  656     3 ..263  105.,277  -45 ..053   1 ,00  65,.34        N
ATOM   5002  CA   TYR  A  656     2 „754  103..912  -45 ,231   1 ,00  68..50        C
ATOM   5003  C    TYR  A  656     2 ..149  103..346  -43 ,954   1 ,00  67 .26        C
ATOM   5004  CB   TYR  A  656     3 .870  102.,943  -45. 676   1 ,00  66 ,37        C
ATOM   5005  CG   TYR  A  656     4 „369  103..107  -47 ,083   1 ,00  62 .93        C
ATOM   5006  CD1  TYR  A  656     3 „566  102..785  -48 ,165   1 ,00  69..18        C
ATOM   5007  CD2  TYR  A  656     5 . 657  103.,555  -47 ..333   1 ,00  67 ,77        C
ATOM   5008  CE1  TYR  A  656     4 .026  102.,923  -49 ..468   1 .00  70..40        c
ATOM   5009  CE2  TYR  A  656     6 ,129  103..692  -48 ,624   1 ,00  71 .62        c
ATOM   5010  CZ   TYR  A  656     5 ...311  103.,376  -49 ..691   1 .00  70,.83        c
ATOM   5011  OH   TYR  A  656     5 ..775  103.,507  -50..980   1 .00  72 .33        0
ATOM   5012  O    TH.R A  657     0 „893   99. 549  -44 ,243   1 ,00  56..59        0
ATOM   5013  N    THR  A  657     1 .425  102..240  -44 .098   1 .00  60,.84        N
ATOM   5014  CA   THR  A  657     0 ..825  101.,568  -42..952   1 ,00  61 ,76        c
ATOM   5015  C    TH.R A  657     0 „959  100. 040  -43 ,126   1 ,00  55..95        c
ATOM   5016  CB   THR  A  657    -0..681  102.,008  -42.,764   1 ,00  58..00        c
ATOM   5017  OG1  THR  A  657    -1 ..307  101.,227  -41 .741   1 ,00  61 ,05        0
ATOM   5018  CG2  THR  A  657    -1 „479  101..849  -44 ,054   1 ,00  49 .90        c
ATOM   5019  O    GLY  A  658     3 „616   97..765  -42.,151   1 ,00  60..03        0
ATOM   5020  N    GLY  A  658     1 .168   99.,310  -42 .029   1 ,00  51 ,22        N
ATOM   5021  CA   GLY  A  658     1 ..208   97.,860  -42 ,067   1 .00  53..33        c
ATOM   5022  C    GLY  A  658     2 ,573   97..224  -41 ,781   1 ,00  58..27        c
ATOM   5023  O    TRP  A  659     2 .530   93.,294  -41 .205   1 .00  53,.16        0
ATOM   5024  N    TRP  A  659     2 .551   96.,072  -41 .116   1 .00  47 .84        N
ATOM   5025  CA.  TRP  A  659     3 „748   95. .320  -40.,782   1 ,00  50..45        c
ATOM   5026  C    TRP  A  659     3 ..617   93.,870  -41 .269   1 .00  56,.16        c
ATOM   5027  CB   TRP  A  659     3 ..986   95.,359  -39 ..279   1 ,00  54 ,13        c
ATOM   5028  CG   TRP  A  659     4 „104   96. 744  -.38.,793   1 ,00  57 .26        c
ATOM   5029  CD1  TRP  A  659     3 ..086   97.,569  -38.,401   1 ,00  51 .95        c
ATOM   5030  CD2  TRP  A  659     5 ..310   97.,498  -38..660   1 ,00  54 ,67        c
ATOM   5031  NE1  TRP  A  659     3 „589   98..781  -.38.,028   1 ,00  57 .72        N
ATOM   5032  CE2  TRP  A  659     4 .952   98..769  -38.,181   1 ,00  58..57        c
ATOM   5033  CE3  TRP  A  659     6 .662   97.,220  -38. 900   1 ,00  56 ,48        c
ATOM   5034  CZ2  TRP  A  659     5 „896   99 .765  -.37.,935   1 ,00  60..82        c
ATOM   5035  CZ3  TRP  A  659     7 ,599   98..204  -38.,655   1 ,00  51 .89        c
ATOM   5036  CH2  TRP  A  659     7 .215   99..462  -38. 180   1 ,00  58 ,39        c
ATOM   5037  O    GLY  A  660     4 .702   91.,079  -40 ..168   1 .00  53..74        0
ATOM   5038  N    GLY  A  660     4 ,726   93..291  -41 ,739   1 ,00  53..91        N
ATOM   5039  CA   GLY  A  660     4 .742   91.,977  -42 ..366   1 .00  48,.09        c
ATOM   5040  c    GLY  A  660     4 .860   90.,856  -41 .353   1 .00  49..80        c
ATOM   5041  0    ARG  A  661     6 „865   87. 268  -.39 ,679   1 ,00  54 .13        0
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ATOM   5042  N    ARG A 661       5.138  89.644 -41.805  1.00 44.59           N
ATOM   5043  CA   ARG A 661       5.202  88.521 -40.883  1.00 50.58           C
ATOM   5044  C    ARG A 661       6.640  88.101 -40.559  1.00 52.43           C
ATOM   5045  CB   ARG A 661       4.421  87.329 -41.446  1.00 51.17           C
ATOM   5046  CG   ARG A 661       2.984  87.673 -41.913  I.00 50.86           C
ATOM   5047  CD   ARG A 661       1.998  87.783 -40.739  1.00 49.77           C
ATOM   5048  NE   ARG A 661       1.993  86.571 -39.928  1.00 57.55           N
ATOM   5049  CZ   ARG A 661       1.423  86.455 -38.733  I.00 58.48           C
ATOM   5050  NH1  ARG A 661       0.804  87.494 -38.175  1.00 51.56           N
ATOM   5051  NH2  ARG A 661       1.482  85.293 -38.089  1.00 51.15           N
ATOM   5052  O    LEU A 662       9.875  90.413 -41.396  I.00 53.20           O
ATOM   5053  N    LEU A 662       7.618  88.695 -41.236  1.00 52.30           N
ATOM   5054  CA   LEU A 662       8.997  88.201 -41.134  1.00 57.50           C
ATOM   5055  C    LEU A 662      10.016  89.308 -40.886  1.00 52.18           C
ATOM   5056  CB   LEU A 662       9.381  87.418 -42.409  1.00 50.96           C
ATOM   5057  CG   LEU A 662       8.505  86.223 -42.794  1.00 49.41           C
ATOM   5058  CD1  LEU A 662       8.989  85.566 -44.054  1.00 58.15           C
ATOM   5059  CD2  LEU A 662       8.453  85.215 -41.681  I.00 53.62           C
ATOM   5060  N    SER A 663      11.050  89.002 -40.106  1.00 56.50           N
ATOM   5061  CA   SER A 663      12.119  89.970 -39.851  1.00 57.48           C
ATOM   5062  C    SER A 663      13.090  90.075 -41.003  I.00 52.35           C
ATOM   5063  O    SER A 663      13.045  89.288 -41.933  1.00 53.10           0
ATOM   5064  CB   SER A 663      12.900  89.613 -38.588  1.00 55.51           C
ATOM   5065  OG   SER A 663      13.326  88.281 -38.634  I.00 53.79           0
ATOM   5066  N    ARG A 664      13.948  91.081 -40.920  1.00 55.71           N
ATOM   5067  CA   ARG A 664      15.067  91.296 -41.837  1.00 54.49           C
ATOM   5068  C    ARG A 664      16.196  90.263 -41.630  I.00 59.48           C
ATOM   5069  O    ARG A 664      16.737  89.711 -42.581  1.00 59.68           0
ATOM   5070  CB   ARG A 664      15.599  92.707 -41.638  1.00 54.68           C
ATOM   5071  CG   ARG A 664      16.667  93.129 -42.594  1.00 61.74           C
ATOM   5072  CD   ARG A 664      17.202  94.450 -42.135  1.00 66.33           C
ATOM   5073  NE   ARG A 664      18.031  95.097 -43.134  1.00 69.96           N
ATOM   5074  CZ   ARG A 664      18.421  96.361 -43.037  1.00 75.69           C
ATOM   5075  NH1  ARG A 664      18.044  97.082 -41.992  I.00 70.34           N
ATOM   5076  NH2  ARG A 664      19.175  96.905 -43.981  1.00 77.44           N
ATOM   5077  N    LYS A 665      16.524  90.019 -40.366  1.00 51.35           N
ATOM   5078  CA.  LYS A 665      17.514  89.045 -39.978  I.00 56.07           C
ATOM   5079  C    LYS A 665      17.170  87.713 -40.608  1.00 63.82           C
ATOM   5080  O    LYS A 665      18.047  86.974 -41.053  1.00 58.18           O
ATOM   5081  CB   LYS A 665      17.575  88.892 -38.453  I.00 57.71           C
ATOM   5082  CG   LYS A 665      18.971  88.756 -37.919  1.00 62.62           C
ATOM   5083  CD   LYS A 665      19.026  87.861 -36.707  1.00 63.17           C
ATOM   5084  CE   LYS A 665      20.456  87.788 -36.192  1.00 72.29           C
ATOM   5085  NZ   LYS A 665      20.588  86.976 -34.955  1.00 82.97           N
ATOM   5086  N    LEU A 666      15.879  87.413 -40.642  1.00 56.18           N
ATOM   5087  CA   LEU A 666      15.444  86.126 -41.124  1.00 54.12           C
ATOM   5088  C    LEU A 666      15.474  86.079 -42.640  I.00 56.97           C
ATOM   5089  O    LEU A 666      15.954  85.111 -43.216  1.00 59.27           O
ATOM   5090  CB   LEU A 666      14.043  85.807 -40.608  1.00 58.24           C
ATOM   5091  CG   LEU A 666      13.424  84.558 -41.234  I.00 53.99           C
ATOM   5092  CD1  LEU A 666      14.286  83.352 -40.912  1.00 50.35           C
ATOM   5093  CD2  LEU A 666      11.993  84.367 -40.765  1.00 52.55           C
ATOM   5094  N    ILE A 667      14.975  87.125 -43.290  I.00 56.36           N
ATOM   5095  CA   ILE A 667      14.837  87.105 -44.745  1.00 58.16           C
ATOM   5096  C    ILE A 667      16.193  87.252 -45.457  1.00 59.74           C
ATOM   5097  O    ILE A 667      16.414  86.661 -46.524  I.00 59.25           0
ATOM   5098  CB   ILE A 667      13.861  88.213 -45.228  1.00 57.90           C
ATOM   5099  CGI  ILE A 667      13.802  88.278 -46.745  1.00 62.50           C
ATOM   5100  CG2  ILE A 667      14.284  89.591 -44.727  1.00 58.33           C
ATOM   5101  CD1  ILE A 667      13.577  89.707 -47.287  1.00 63.08           C
ATOM   5102  N    ASN A 668      17.106  88.011 -44.848  1.00 61.63           N
ATOM   5103  CA   ASN A 668      18.375  88.365 -45.496  1.00 60.24           C
ATOM   5104  C    ASM A 668      19.508  88.708 -44.522  I.00 56.41           C
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ATOM    5105   O    ASN  A  668       20..264    89.·635   -44·.758    1.00   57.56          O
ATOM    5106   CB   ASM  A  668       18.,143    89..547   --46.,441   1,00   63..17         C
ATOM    5107   CG   ASN  A  668       19.058     89.,533   -47·.641    1,00   63,.60         C
ATOM    5108   OD1  ASN  A  668       19..622    90.·563   -48.016     1.00   70..92         O
ATOM    5109   ND2  ASM  A  668       19.,194    88. 375   -48,270     1,00   58.,98         N
ATOM    5110   N    GLY  A  669       19.621     87.,965   -43.432     1,00   56,.59         M
ATOM    5111   CA   GLY  A  669       20..701    88.,178   -42.·496    1,00   58,.47         C
ATOM    5112   C    GLY  A  669       21.,421    86. 891   -42.,160    1,00   59.,64         C
ATOM    5113   O    GLY  A  669       22..628    86.·757   -42.·377    1,00   66..57         O
ATOM    5114   O    ILE  A  670       21.241     84.,085   -43.716     1,00   61,18          O
ATOM    5115   N    ILE  A  670       20.,681    85..936   -41,624     I,00   54.94          N
ATOM    5116   CA   ILE  A  670       21..237    84..626   -41..349    1,00   63..71         C
ATOM    5117   C    ILE  A  670       21.796     83.,964   -42.624     1,00   63,52          C
ATOM    5118   CB   ILE  A  670       20..182    83.·724   -40.688     1.00   63..92         C
ATOM    5119   CGI  ILE  A  670       19.,874    84..259   -39,303     1,00   63..31         C
ATOM    5120   CG2  ILE  A  670       20.675     82.,277   -40.565     1,00   70,.35         C
ATOM    5121   CD1  ILE  A  670       21..114    84.·574   -38.·486    1.00   63..95         C
ATOM    5122   O    ARG  A  671       23.,593    80. 708   -42.,164    1,00   62.15          0
ATOM    5123   N    ARG  A  671       22..926    83.,284   -42.493     1,00   70,.34         M
ATOM    5124   CA   ARG  A  671       23..476    82.,584   -43.638     1,00   59,.96         C
ATOM    5125   C    ARG  A  671       23.,512    81. 108   -43,328     1,00   59..49         C
ATOM    5126   CB   ARG  A  671       24..854    83..138   -43.995     1,00   63..47         C
ATOM    5127   CG   ARG  A  671       24.799     84.,616   -44.351     1,00   63,.66         C
ATOM    5128   CD   ARG  A  671       26.,127    85..258   -44,761     I,00   61.65          C
ATOM    5129   ME   ARG  A  671       25..889    86..679   -45.010     1,00   67.53          M
ATOM    5130   CZ   ARG  A  671       25. 523    87.,185   -46. 186    1,00   70,83          C
ATOM    5131   NH1  ARG  A  671       25.,295    88..494   -46.,311    I,00   59..74         N
ATOM    5132   NH2  ARG  A  671       25.,390    86..387   -47,242     1,00   64.78          N
ATOM    5133   O    ASP  A  672       25. 873    79.,378   -44.830     1,00   60,19          O
ATOM    5134   N    ASP  A  672       23..371    80.·301   -44.374     1.00   63..64         N
ATOM    5135   CA   ASP  A  672       23.,629    78.873    -44,283     1,00   61.32          C
ATOM    5136   C    ASP  A  672       25.126     78.,696   -44.143     1,00   60,.23         C
ATOM    5137   CB   ASP  A  672       23..107    78.·159   -45.511     1.00   59..01         C
ATOM    5138   CG   ASP  A  672       23.,623    76.749    -45,620     1,00   64.14          C
ATOM    5139   OD2  ASP  A  672       24..487    76.,522   -46.·489    1,00   63,.40         0
ATOM    5140   OD1  ASP  A  672       23..162    75,870    -44.850     1,00   60,.67         0
ATOM    5141   O    LYS  A  673       28.,640    78.275    -44,538     1,00   66..83         0
ATOM    5142   N    LYS  A  673       25..563    77.812    -43.244     1,00   63..43         M
ATOM    5143   CA   LYS  A  673       26. 992    77,692    -42.900     1,00   63,60          C
ATOM    5144   C    LYS  A  673       27.,856    77.416    -44,122     I,00   65..77         C
ATOM    5145   CB   LYS  A  673       27.,224    76.600    -41,851     1,00   56..44         C
ATOM    5146   O    GLN  A  674       29. 396    77,388    -47.475     1,00   70,14          0
ATOM    5147   N    GLN  A  674       27.·693    76.·231   -44.705     1.00   66..76         N
ATOM    5148   CA   GLN  A  674       28.,455    75.847    -45,894     1,00   68..33         C
ATOM    5149   C    GLN  A  674       28..373    76.,852   -47.039     1,00   68,.21         C
ATOM    5150   CB   GLN  A  674       27..992    74.485    -46.400     1.00   70..40         C
ATOM    5151   CG   GLN  A  674       28.,503    73.319    -45,589     1,00   71.30          C
ATOM    5152   CD   GLN  A  674       27.983     72.,004   -46.·112    1,00   78,.40         C
ATOM    5153   OE1  GLN  A  674       27.743     71,856    -47.318     1,00   79,.95         0
ATOM    5154   NE2  GLN  A  674       27.,789    71.038    -45,209     1,00   74.75          N
ATOM    5155   O    SER  A  675       27.·489    80.·230   -49.305     1,00   62.34          O
ATOM    5156   N    SER  A  675       27.161     77,100    -47.527     1,00   65,.02         N
ATOM    5157   CA   SER  A  675       26.,976    77.977    -48.,679    I,00   60..32         C
ATOM    5158   C    SER  A  675       27.·230    79.·457   -48.388     1,00   59..69         C
ATOM    5159   CB   SER  A  675       25. 564    77,814    -49. 229    1,00   61,50          C
ATOM    5160   OG   SER  A  675       24.,604    78.·288   -48.,299    I,00   67.40          O
ATOM    5161   O    GLY  A  676       26.,090    83.·337   -47,220     1,00   63..24         O
ATOM    5162   N    GLY  A  676       27.132     79.,860   -47.126     1,00   62,50          N
ATOM    5163   CA   GLY  A  676       27..228    81.·271   -46.774     1.00   61.23          C
ATOM    5164   C    GLY  A  676       26.,057    82.·106   -47,275     1,00   63..66         C
ATOM    5165   O    LYS  A  677       22..410    81.,743   -46.·493    1,00   58,.48         O
ATOM    5166   N    LYS  A  677       25..011    81.·452   -47.767     1.00   61.77          N
ATOM    5167   CA.  LYS  A  677       23.,887    82. 192   -48,358     1,00   64.50          C
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ATOM	5168	C	LYS	A	677	22.730	82.520	-47.398	1.00	58.61	C
ATOM	5169	CB	LYS	A	677	23.337	81.425	--49.556	1.00	61.95	C
ATOM	5170	CG	LYS	A	677	24.227	81.492	-50.771	1.00	57.32	C
ATOM	5171	CD	LYS	A	677	23.417	81.336	-52 .041	1.00	61.47	C
ATOM	5172	CE	LYS	A	677	22.767	79.975	-52 .121	I.00	56.16	C
ATOM	5173	NZ	LYS	A	677	22.024	79.807	-53.410	1.00	57.98	N
ATOM	5174	N	THR	A	678	22.123	83.691	-47.600	1.00	61.45	N
ATOM	5175	CA.	TH.R	A	678	20.859	84.041	-46.941	I.00	54.79	C
ATOM	5176	C	THR	A	678	19.667	83.451	-47.698	1.00	54.43	C
ATOM	5177	O	THR	A	678	19.758	83.140	-48.887	1.00	51.98	O
ATOM	5178	CB	THR	A	678	20.642	85.570	-46.845	I.00	60.33	C
ATOM	5179	OG1	THR	A	678	20.442	86.112	-48.163	1.00	54.44	0
ATOM	5180	CG2	THR	A	678	21.811	86.255	-46.152	1.00	54.51	C
ATOM	5181	N	ILE	A	679	18.540	83.337	-47.002	1.00	60.47	N
ATOM	5182	CA	ILE	A	679	17.293	82.857	-47.587	1.00	48.27	C
ATOM	5183	C	ILE	A	679	16.976	83.538	-48.910	1.00	52.22	C
ATOM	5184	O	ILE	A	679	16.621	82.860	-49.876	1.00	54.20	O
ATOM	5185	CB	ILE	A	679	16.115	83.049	-46.609	I.00	48.69	C
ATOM	5186	CGI	ILE	A	679	16.393	82.305	-45.295	1.00	50.29	C
ATOM	5187	CG2	ILE	A	679	14.807	82.570	-47.222	1.00	50.50	C
ATOM	5188	CD1	ILE	A	679	15.171	82.020	-44.487	I.00	50.96	C
ATOM	5189	N	LEU	A	680	17.138	84.862	-48.970	1.00	56.03	N
ATOM	5190	CA	LEU	A	680	16.793	85.613	-50.177	1.00	53.76	C
ATOM	5191	C	LEU	A	680	17.777	85.338	-51.316	I.00	56.08	C
ATOM	5192	O	LEU	A	680	17.366	85.281	-52 .478	1.00	57.51	0
ATOM	5193	CB	LEU	A	680	16.707	87.116	-49.877	1.00	55.24	C
ATOM	5194	CG	LEU	A	680	16.552	88.029	-51.099	I.00	51.57	C
ATOM	5195	CD1	LEU	A	680	15.254	87.752	-51.807	1.00	52.42	C
ATOM	5196	CD2	LEU	A	680	16.643	89.467	-50.698	1.00	51.05	C
ATOM	5197	N	ASP	A	681	19.058	85.147	-50.987	1.00	59.21	N
ATOM	5198	CA	ASP	A	681	20.035	84.598	-51.949	1.00	54.21	C
ATOM	5199	C	ASP	A	681	19.538	83.304	-52 .595	1.00	55.37	C
ATOM	5200	O	ASP	A	681	19.536	83.171	-53.818	1.00	59.24	0
ATOM	5201	CB	ASP	A	681	21.379	84.331	-51.278	I.00	54.33	C
ATOM	5202	CG	ASP	A	681	22.157	85.613	-50.970	1.00	61.78	C
ATOM	5203	OD1	ASP	A	681	21.903	86.665	-51.607	1.00	58.25	0
ATOM	5204	OD2	ASP	A	681	23.042	85.550	-50.087	I.00	67.82	0
ATOM	5205	N	PHE	A	682	19.119	82.345	-51.777	1.00	53.19	N
ATOM	5206	CA	PHE	A	682	18.574	81.095	-52.305	1.00	48.09	C
ATOM	5207	C	PHE	A	682	17.391	81.311	-53.237	I.00	52.63	C
ATOM	5208	O	PHE	A	682	17.327	80.713	-54.297	1.00	49.30	0
ATOM	5209	CB	PHE	A	682	18.160	80.171	-51.170	1.00	48.78	C
ATOM	5210	CG	PHE	A	682	19.287	79.328	-50.625	1.00	53.06	C
ATOM	5211	CD1	PHE	A	682	19.757	78.224	-51.341	1.00	57.41	C
ATOM	5212	CD2	PHE	A	682	19.882	79.629	-49.406	1.00	52.31	C
ATOM	5213	CE1	PHE	A	682	20.794	77.423	-50.850	1.00	53.40	C
ATOM	5214	CE2	PHE	A	682	20.930	78.834	-48.912	I.00	57.91	C
ATOM	5215	CZ	PHE	A	682	21.381	77.727	-49.646	1.00	54.85	C
ATOM	5216	N	LEU	A	683	16.461	82.183	-52 .834	1.00	56.76	N
ATOM	5217	CA.	LEU	A	683	15.253	82.443	-53.598	I.00	46.31	C
ATOM	5218	C	LEU	A	683	15.592	83.076	-54.932	1.00	53.02	C
ATOM	5219	O	LEU	A	683	14.937	82.819	-55.934	1.00	56.16	0
ATOM	5220	CB	LEU	A	683	14.296	83.351	-52 .815	I.00	52.86	C
ATOM	5221	CG	LEU	A	683	13.711	82.828	-51.501	1.00	54.16	C
ATOM	5222	GDI	LEU	A	683	12.791	83.881	-50.881	1.00	53.85	C
ATOM	5223	CD2	LEU	A	683	12.980	81.494	-51.683	I.00	49.33	C
ATOM	5224	N	LYS	A	684	16.619	83.913	-54.939	1.00	54.11	N
ATOM	5225	CA	LYS	A	684	17.161	84.433	-56.185	1.00	54.86	C
ATOM	5226	C	LYS	A	684	17.731	83.322	-57.105	1.00	59.09	C
ATOM	5227	O	LYS	A	684	17.395	83.266	-58.292	1.00	60.28	0
ATOM	5228	CB	LYS	A	684	18.243	85.468	-55.883	1.00	54.28	C
ATOM	5229	CG	LYS	A	684	17.700	86.801	-55.398	1.00	53.22	C
ATOM	5230	CD	LYS	A	684	18.848	87.670	-54.938	I.00	53.17	C

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ATOM   5231  CE   LYS  A 684     18.462  89.112  -54.864  1.00 54.69      C
ATOM   5232  NZ   LYS  A 684     18.748  89.636  --53.495 1.00 58.96      M
ATOM   5233  K    SER  A 685     18.583  82.452  -56.563  1.00 54.58      K
ATOM   5234  CA   SER  A 685     19.200  81.388  -57.362  1.00 57.63      C
ATOM   5235  C    SER  A 685     19.537  80.143  -56.559  1.00 55.61      C
ATOM   5236  O    SER  A 685     20.323  80.191  -55.604  1.00 53.10      O
ATOM   5237  CE   SER  A 685     20.471  81.879  -58.038  1.00 60.94      C
ATOM   5238  OG   SER  A 685     21.073  80.798  -58.741  1.00 68.18      0
ATOM   5239  O    ASP  A 686     18.672  75.571  -56.985  1.00 56.77      0
ATOM   5240  N    ASP  A 686     18.954  79.020  -56.950  1.00 53.93      N
ATOM   5241  CA   ASP  A 686     19.177  77.782  -56.204  1.00 53.30      C
ATOM   5242  C    ASP  A 686     19.292  76.609  -57.175  1.00 52.10      C
ATOM   5243  CB   ASP  A 686     18.048  77.571  -55.188  1.00 52.93      C
ATOM   5244  CG   ASP  A 686     18.251  76.354  -54.293  1.00 57.83      C
ATOM   5245  OD1  ASP  A 686     19.397  76.062  -53.868  1.00 61.58      0
ATOM   5246  OD2  ASP  A 686     17.238  75.681  -54.004  1.00 58.49      0
ATOM   5247  O    GLY  A 687     18.298  75.835  -60.209  1.00 58.45      0
ATOM   5248  N    GLY  A 687     20.086  76.798  -58.224  1.00 54.77      M
ATOM   5249  CA   GLY  A 687     20.417  75.727  -59.149  1.00 56.22      C
ATOM   5250  C    GLY  A 687     19.170  75.111  -59.742  1.00 60.71      C
ATOM   5251  0    PHE  A 688     15.675  72.548  -59.524  1.00 67.48      0
ATOM   5252  K    PHE  A 688     19.087  73.781  -59.715  1.00 59.81      K
ATOM   5253  CA   PHE  A 688     17.917  73.050  -60.220  1.00 63.73      C
ATOM   5254  C    PHE  A 688     16.810  72.884  -59.179  1.00 65.39      C
ATOM   5255  CB   PHE  A 688     18.320  71.654  -60.716  1.00 64.56      C
ATOM   5256  CG   PHE  A 688     19.145  71.665  -61.966  1.00 62.87      C
ATOM   5257  CD1  PHE  A 688     19.074  72.725  -62.848  1.00 58.02      C
ATOM   5258  CD2  PHE  A 688     19.999  70.616  -62.253  1.00 60.05      C
ATOM   5259  CE1  PHE  A 688     19.834  72.742  -63.987  1.00 59.15      C
ATOM   5260  CE2  PHE  A 688     20.762  70.627  -63.396  1.00 61.31      C
ATOM   5261  CZ   PHE  A 688     20.684  71.689  -64.261  1.00 61.25      C
ATOM   5262  O    ALA  A 689     14.032  73.596  -56.272  1.00 59.47      0
ATOM   5263  N    ALA  A 689     17.157  73.093  -57.910  1.00 66.88      N
ATOM   5264  CA.  ALA  A 689     16.246  72.844  -56.793  1.00 63.20      C
ATOM   5265  C    ALA  A 689     15.166  73.927  -56.616  1.00 56.75      C
ATOM   5266  CB   ALA  A 689     17.038  72.690  -55.498  1.00 59.18      C
ATOM   5267  O    ASM  A 690     12.511  76.165  -55.493  1.00 59.99      0
ATOM   5268  K    ASN  A 690     15.521  75.194  -56.852  1.00 58.24      K
ATOM   5269  CA   A.SK A 690     14.608  76.345  -56.647  1.00 64.33      C
ATOM   5270  C    ASM  A 690     13.736  76.197  -55.403  1.00 60.18      C
ATOM   5271  CB   ASM  A 690     13.709  76.559  -57.871  1.00 55.80      C
ATOM   5272  CG   ASN  A 690     14.409  77.309  -58.986  1.00 64.15      C
ATOM   5273  OD1  ASN  A 690     15.641  77.444  -58.991  1.00 66.24      0
ATOM   5274  ND2  ASM  A 690     13.628  77.811  -59.939  1.00 58.56      M
ATOM   5275  O    AP.G A 691     13.196  78.078  -52 .726  1.00 51.11      0
ATOM   5276  N    ARG  A 691     14.381  76.069  -54.251  1.00 54.71      M
ATOM   5277  CA.  ARG  A 691     13.679  75.748  -53.024  1.00 55.95      C
ATOM   5278  C    AP.G A 691     12.851  76.914  -52 .517  1.00 57.13      C
ATOM   5279  CB   ARG  A 691     14.662  75.315  -51.953  1.00 57.99      C
ATOM   5280  CG   ARG  A 691     14.971  73.823  -51.971  1.00 56.38      C
ATOM   5281  CD   ARG  A 691     16.102  73.501  -51.026  1.00 45.42      C
ATOM   5282  NE   ARG  A 691     17.368  74.035  -51.514  1.00 56.94      N
ATOM   5283  CZ   ARG  A 691     18.564  73.653  -51.069  1.00 52.96      C
ATOM   5284  KH 1 ARG  A 691     18.652  72.735  -50.124  1.00 53.12      K
ATOM   5285  NH2  AP.G A 691     19.666  74.185  -51.571  1.00 54.73      K
ATOM   5286  O    ASM  A 692     12.169  77.456  -49.323  1.00 56.82      O
ATOM   5287  N    ASN  A 692     11.749  76.571  -51.860  1.00 61.06      M
ATOM   5288  CA   ASN  A 692     10.838  77.547  -51.270  1.00 58.03      C
ATOM   5289  C    ASM  A 692     11.329  78.076  -49.945  1.00 50.55      C
ATOM   5290  CB   ASM  A 692      9.464  76.921  -51.058  1.00 52.33      C
ATOM   5291  CG   ASN  A 692      8.422  77.676  -51.752  1.00 54.08      C
ATOM   5292  OD1  ASM  A 692      7.270  77.253  -51.846  1.00 58.39      0
ATOM   5293  ND2  ASM  A 692      8.812  78.834  -52 .272  1.00 58.75      M
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ATOM	5294	O	PHE	A	693	11.435	78.344	-46.193	1.00	54.55	O
ATOM	5295	N	PHE	A	693	10.766	79.189	--49.491	1.00	56.29	N
ATOM	5296	CA	PHE	A	693	11.025	79.675	-48.141	1.00	50.71	C
ATOM	5297	**c**	PHE	A	693	10.675	78.586	-47.133	1.00	50.63	**c**
ATOM	5298	CB	PHE	A	693	10.232	80.967	-47.864	I.00	56.95	**c**
ATOM	5299	CG	PHE	A	693	10.159	81.344	-46.402	1.00	54.73	**c**
ATOM	5300	CD1	PHE	A	693	11.222	81.988	-45.777	1.00	58.28	**c**
ATOM	5301	CD2	PHE	A	693	9.029	81.067	-45.657	I.00	58.12	**c**
ATOM	5302	CE1	PHE	A	693	11.161	82.335	-44.428	1.00	61.09	**c**
ATOM	5303	CE2	PHE	A	693	8.959	81.424	-44.304	1.00	62.56	**c**
ATOM	5304	CZ	PHE	A	693	10.029	82.053	-43.696	I.00	60.15	**c**
ATOM	5305	O	MET	A	694	10.232	74.847	-45.705	1.00	58.27	0
ATOM	5306	N	MET	*A*	694	9.536	77.924	-47.344	1.00	47.21	N
ATOM	5307	CA	MET	A	694	9.121	76.817	-46.485	1.00	53.86	**c**
ATOM	5308	C	MET	A	694	10.055	75.623	-46.638	1.00	56.92	**c**
ATOM	5309	CB	MET	A	694	7.682	76.374	-46.790	1.00	59.70	**c**
ATOM	5310	CG	MET	A	694	6.572	77.133	-46.051	1.00	51.16	**c**
ATOM	5311	SD	MET	A	694	6.554	76.796	-44.285	I.00	52.87	S
ATOM	5312	CE	MET	A	694	7.288	78.329	-43.681	1.00	54.21	**c**
ATOM	5313	O	GLN	A	695	13.560	73.789	-46.852	1.00	57.13	0
ATOM	5314	N	GLN	A	695	10.647	75.484	-47.822	I.00	58.38	N
ATOM	5315	CA	GLN	A	695	11.598	74.400	-48.088	1.00	60.50	C
ATOM	5316	**c**	GLN	A	695	12.967	74.673	-47.463	1.00	55.56	**c**
ATOM	5317	CB	GLN	A	695	11.732	74.171	-49.600	I.00	57.77	**c**
ATOM	5318	CG	GLN	A	695	10.733	73.163	-50.158	1.00	54.15	**c**
ATOM	5319	CD	GLN	*A*	695	10.603	73.277	-51.655	1.00	59.70	**c**
ATOM	532 0	OE1	GLN	A	695	11.029	74.271	-52 .250	I.00	57.55	0
ATOM	532 1	NE2	GLN	A	695	10.009	72.266	-52 .277	1.00	53.64	N
ATOM	5322	O	LEU	*A*	696	15.512	75.615	-44.823	1.00	58.18	O
ATOM	532 3	N	LEU	A	696	13.455	75.902	-47.620	1.00	52.16	N
ATOM	532 4	CA	LEU	A	696	14.686	76.334	-46.976	1.00	52.32	C
ATOM	532 5	C	LEU	A	696	14.618	76.192	-45.447	1.00	55.89	C
ATOM	532 6	CB	LEU	A	696	14.987	77.776	-47.355	1.00	49.20	**c**
ATOM	5327	CG	LEU	A	696	15.100	78.103	-48.840	I.00	47.71	**c**
ATOM	532 8	CD1	LEU	A	696	15.400	79.562	-49.026	1.00	46.65	**c**
ATOM	532 9	CD2	LEU	A	696	16.203	77.282	-49.453	1.00	55.79	**c**
ATOM	5330	O	ILE	A	697	13.548	75.089	-41.635	I.00	57.95	0
ATOM	5331	N	1LE	A	697	13.532	76.703	-44.867	1.00	60.57	N
ATOM	5332	CA	ILE	*A*	697	13.285	76.689	-43.419	1.00	58.54	C
ATOM	5333	C	ILE	A	697	13.190	75.278	-42.792	I.00	56.18	C
ATOM	5334	CB	ILE	A	697	11.982	77.511	-43.113	1.00	62.63	C
ATOM	5335	CGI	ILE	*A*	697	12.284	79.001	-43.178	1.00	57.74	**c**
ATOM	5336	CG2	ILE	A	697	11.392	77.185	-41.766	1.00	65.13	**c**
ATOM	5337	CD1	ILE	A	697	13.709	79.311	-42.819	1.00	57.73	**c**
ATOM	5338	O	HIS	A	698	13.795	70.785	-43.221	1.00	66.48	0
ATOM	5339	N	HI S	A	698	12.731	74.286	-43.551	1.00	57.59	N
ATOM	5340	CA.	HI S	A	698	12.682	72.909	-43.040	I.00	60.53	C
ATOM	5341	C	HIS	A	698	13.784	71.964	-43.566	1.00	60.15	C
ATOM	5342	CB	HIS	A	698	11.324	72.294	-43.351	1.00	55.87	**c**
ATOM	5343	CG	HI S	A	698	10.182	73.069	-42.784	I.00	65.67	**c**
ATOM	5344	ND1	HIS	A	698	9.607	74.137	-43.441	1.00	62.83	N
ATOM	5345	CD2	HIS	A	698	9.527	72.954	-41.605	1.00	62.28	**c**
ATOM	5346	CE1	HIS	A	698	8.642	74.640	-42.695	I.00	63.42	C
ATOM	5347	ME 2	HIS	A	698	8.571	73.938	-41.578	1.00	67.92	N
ATOM	5348	O	ASP	*A*	699	17.597	72.099	-43.588	1.00	59.70	O
ATOM	5349	N	ASP	A	699	14.700	72.464	-44.389	I.00	57.08	N
ATOM	5350	CA	ASP	A	699	15.705	71.589	-44.989	1.00	61.46	C
ATOM	5351	C	ASP	*A*	699	16.830	71.245	-44.026	1.00	61.56	C
ATOM	5352	CB	ASP	A	699	16.302	72.198	-46.258	1.00	58.65	**c**
ATOM	5353	CG	ASP	A	699	17.038	71.162	-47.111	1.00	65.28	C
ATOM	5354	OD2	ASP	A	699	17.098	71.340	-48.348	1.00	64.40	0
ATOM	5355	OD1	ASP	A	699	17.550	70.164	-46.555	1.00	65.85	0
ATOM	5356	O	ASP	A	700	20.370	69.382	-42.792	I.00	68.81	0

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ATOM    5357  N    ASP  A  700      16.944   69.957  -43.739   1.00  66.08          N
ATOM    5358  CA   ASP  A  700      17.985   69.475  -42.850   1.00  68.90          C
ATOM    5359  C    ASP  A  700      19.373   69.565  -43.481   1.00  65.55          C
ATOM    5360  CB   ASP  A  700      17.676   68.045  -42.430   1.00  63.04          C
ATOM    5361  CG   ASP  A  700      16.257   67.896  -41.916   1.00  67.37          C
ATOM    5362  OD1  ASP  A  700      15.350   67.667  -42.750   1.00  70.39          0
ATOM    5363  OD2  ASP  A  700      16.051   68.033  -40.688   1.00  66.60          0
ATOM    5364  N    SER  A  701      19.439   69.856  -44.778   1.00  63.32          N
ATOM    5365  CA   SER  A  701      20.733   70.058  -45.428   1.00  68.33          C
ATOM    5366  C    SER  A  701      21.281   71.420  -45.066   1.00  68.66          C
ATOM    5367  0    SER  A  701      22.491   71.615  -44.975   1.00  71.91          0
ATOM    5368  CB   SER  A  701      20.627   69.935  -46.948   1.00  71.13          C
ATOM    5369  OG   SER  A  701      20.548   68.576  -47.340   1.00  76.48          0
ATOM    5370  N    LEU  A  702      20.372   72.364  -44.858   1.00  67.48          N
ATOM    5371  CA   LEU  A  702      20.744   73.733  -44.563   1.00  59.70          C
ATOM    5372  C    LEU  A  702      20.784   73.949  -43.065   1.00  60.81          C
ATOM    5373  O    LEU  A  702      20.284   73.126  -42.300   1.00  64.90          0
ATOM    5374  CB   LEU  A  702      19.766   74.699  -45.223   1.00  56.89          C
ATOM    5375  CG   LEU  A  702      19.604   74.442  -46.717   1.00  60.91          C
ATOM    5376  CD2  LEU  A  702      20.949   74.575  -47.428   1.00  61.68          C
ATOM    5377  CD1  LEU  A  702      18.573   75.380  -47.313   1.00  55.01          C
ATOM    5378  N    THR  A  703      21.377   75.058  -42.644   1.00  61.13          N
ATOM    5379  CA   THR  A  703      21.456   75.363  -41.230   1.00  64.26          C
ATOM    5380  C    THR  A  703      20.351   76.307  -40.742   1.00  66.34          C
ATOM    5381  O    THR  A  703      20.279   76.563  -39.538   1.00  69.43          0
ATOM    5382  CB   THR  A  703      22.825   75.990  -40.856   1.00  65.93          C
ATOM    5383  OG1  THR  A  703      23.045   77.183  -41.621   1.00  66.28          0
ATOM    5384  CG2  THR  A  703      23.959   74.995  -41.096   1.00  60.36          C
ATOM    5385  N    PHE  A  704      19.504   76.817  -41.644   1.00  59.35          N
ATOM    5386  CA   PHE  A  704      18.439   77.758  -41.237   1.00  59.60          C
ATOM    5387  C    PHE  A  704      17.530   77.142  -40.182   1.00  59.58          C
ATOM    5388  O    PHE  A  704      17.276   77.746  -39.147   1.00  66.27          0
ATOM    5389  CB   PHE  A  704      17.570   78.201  -42.418   1.00  57.76          C
ATOM    5390  CG   PHE  A  704      18.327   78.880  -43.527   1.00  60.02          C
ATOM    5391  CD1  PHE  A  704      19.107   80.000  -43.272   1.00  56.98          C
ATOM    5392  CD2  PHE  A  704      18.235   78.408  -44.835   1.00  55.18          C
ATOM    5393  CE1  PHE  A  704      19.793   80.627  -44.295   1.00  57.04          C
ATOM    5394  CE2  PHE  A  704      18.903   79.038  -45.853   1.00  50.38          C
ATOM    5395  CZ   PHE  A  704      19.689   80.142  -45.584   1.00  52.68          C
ATOM    5396  N    LYS  A  705      17.059   75.931  -40.453   1.00  59.70          N
ATOM    5397  CA   LYS  A  705      16.199   75.186  -39.539   1.00  60.67          C
ATOM    5398  C    LYS  A  705      16.750   75.125  -38.113   1.00  66.44          C
ATOM    5399  O    LYS  A  705      15.990   75.237  -37.144   1.00  66.88          0
ATOM    5400  CB   LYS  A  705      15.983   73.765  -40.077   1.00  59.01          C
ATOM    5401  CG   LYS  A  705      15.155   72.878  -39.179   1.00  63.31          C
ATOM    5402  CD   LYS  A  705      14.913   71.503  -39.789   1.00  65.60          C
ATOM    5403  CE   LYS  A  705      14.163   70.613  -38.809   1.00  64.73          C
ATOM    5404  NZ   LYS  A  705      13.514   69.464  -39.468   1.00  64.29          N
ATOM    5405  N    GLU  A  706      18.073   74.961  -38.000   1.00  67.92          N
ATOM    5406  CA   GLU  A  706      18.765   74.848  -36.714   1.00  64.47          C
ATOM    5407  C    GLU  A  706      18.935   76.209  -36.059   1.00  66.66          C
ATOM    5408  O    GLU  A  706      18.663   76.365  -34.867   1.00  70.27          0
ATOM    5409  CB   GLU  A  706      20.137   74.182  -36.883   1.00  63.80          C
ATOM    5410  N    ASP  A  707      19.397   77.188  -36.838   1.00  65.37          N
ATOM    5411  CA   ASP  A  707      19.499   78.568  -36.368   1.00  70.33          C
ATOM    5412  C    ASP  A  707      18.149   79.069  -35.823   1.00  68.60          C
ATOM    5413  O    ASP  A  707      18.113   79.802  -34.833   1.00  69.97          0
ATOM    5414  CB   ASP  A  707      19.988   79.494  -37.491   1.00  68.37          C
ATOM    5415  CG   ASP  A  707      21.505   79.605  -37.555   1.00  71.40          C
ATOM    5416  OD1  ASP  A  707      22.168   79.568  -36.492   1.00  73.62          0
ATOM    5417  OD2  ASP  A  707      22.035   79.746  -38.680   1.00  72.06          0
ATOM    5418  N    ILE  A  708      17.055   78.658  -36.473   1.00  67.93          N
ATOM    5419  CA   ILE  A  708      15.698   79.031  -36.066   1.00  65.22          C
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ATOM   5420  C    ILE A 708      15.289  78.398 -34.736  1.00 66.51           C
ATOM   5421  O    ILE A 708      14.918  79.105 --33.800  1.00 67.14          0
ATOM   5422  CB   ILE A 708      14.660  78.652 -37.138  1.00 62.45           C
ATOM   5423  CGI  ILE A 708      14.737  79.624 -38.318  1.00 63.05           C
ATOM   5424  CG2  ILE A 708      13.254  78.671 -36.556  I.00 59.01           C
ATOM   5425  GD1  ILE A 708      13.582  79.515 -39.278  1.00 55.15           C
ATOM   5426  N    GLN A 709      15.375  77.073 -34.647  1.00 68.81           N
ATOM   5427  CA.  GLN A 709      15.021  76.365 -33.414  I.00 71.01           C
ATOM   5428  C    GLN A 709      15.938  76.685 -32.225  1.00 67.88           C
ATOM   5429  O    GLN A 709      15.547  76.494 -31.072  1.00 69.06           0
ATOM   5430  CB   GLN A 709      15.003  74.861 -33.664  I.00 72.46           C
ATOM   5431  CG   GLN A 709      13.763  74.417 -34.409  1.00 76.15           C
ATOM   5432  CD   GLN A 709      14.029  73.264 -35.363  1.00 81.29           C
ATOM   5433  OE1  GLN A 709      14.740  72.303 -35.031  1.00 72.86           0
ATOM   5434  NE2  GLN A 709      13.462  73.359 -36.564  1.00 80.36           N
ATOM   5435  N    LYS A 710      17.143  77.176 -32.499  1.00 66.69           N
ATOM   5436  CA   LYS A 710      17.990  77.713 -31.442  1.00 67.12           C
ATOM   5437  C    LYS A 710      17.469  79.075 -30.960  I.00 73.16           C
ATOM   5438  O    LYS A 710      17.729  79.469 -29.831  1.00 74.31           O
ATOM   5439  CB   LYS A 710      19.436  77.849 -31.915  1.00 68.82           C
ATOM   5440  N    ALA A 711      16.731  79.780 -31.814  I.00 68.21           N
ATOM   5441  CA   ALA A 711      16.298  81.141 -31.517  1.00 69.87           C
ATOM   5442  C    ALA A 711      15.059  81.167 -30.649  1.00 70.50           C
ATOM   5443  0    ALA A 711      14.794  82.151 -29.965  I.00 75.34           0
ATOM   5444  CB   ALA A 711      16.033  81.904 -32.800  1.00 66.09           C
ATOM   5445  N    GLN A 712      14.291  80.091 -30.696  1.00 67.51           N
ATOM   5446  CA   GLN A 712      13.050  80.028 -29.951  I.00 74.01           C
ATOM   5447  C    GLN A 712      13.335  79.569 -28.520  1.00 82.38           C
ATOM   5448  O    GLN A 712      13.904  78.493 -28.302  1.00 83.88           O
ATOM   5449  CB   GLN A 712      12.055  79.113 -30.677  1.00 73.50           C
ATOM   5450  CG   GLN A 712      11.648  79.674 -32.070  1.00 69.27           C
ATOM   5451  CD   GLN A 712      10.587  78.847 -32.786  1.00 73.81           C
ATOM   5452  OE1  GLN A 712       9.798  78.143 -32.157  1.00 78.37           0
ATOM   5453  NE2  GLN A 712      10.564  78.933 -34.112  I.00 74.86           N
ATOM   5454  O    VAL A 713      12.389  78.711 -24.455  1.00 70.65           0
ATOM   5455  N    VAL A 713      12.963  80.402 -27.550  1.00 80.18           N
ATOM   5456  CA.  VAL A 713      13.313  80.168 -26.145  I.00 82.07           C
ATOM   5457  C    VAL A 713      12.164  79.488 -25.387  1.00 77.29           C
ATOM   5458  CB   VAL A 713      13.706  81.506 -25.436  1.00 76.50           C
ATOM   5459  CGI  VAL A 713      15.140  81.459 -24.927  I.00 79.91           C
ATOM   5460  CG2  VAL A 713      12.741  81.842 -24.302  1.00 75.98           C
ATOM   5461  O    ASP A 718       3.324  78.974 -19.458  1.00 77.40           0
ATOM   5462  N    ASP A 718       5.962  80.580 -19.021  1.00 90.22           N
ATOM   5463  CA   ASP A 718       4.708  80.901 -19.697  1.00 90.25           C
ATOM   5464  C    ASP A 718       3.554  80.122 -19.095  1.00 83.53           C
ATOM   5465  CB   ASP A 718       4.803  80.596 -21.190  1.00 92.22           C
ATOM   5466  CG   ASP A 718       6.009  81.241 -21.841  I.00103.00           C
ATOM   5467  OD2  ASP A 718       5.958  81.484 -23.067  1.00104.15           0
ATOM   5468  OD1  ASP A 718       7.007  81.498 -21.130  1.00103.76           0
ATOM   5469  N    SER A 719       2.831  80.749 -18.172  I.00 85.06           N
ATOM   5470  CA   SER A 719       1.714  80.095 -17.496  1.00 79.89           C
ATOM   5471  C    SER A 719       0.636  79.680 -18.484  1.00 73.51           C
ATOM   5472  0    SER A 719       0.514  80.246 -19.572  I.00 69.49           0
ATOM   5473  CB   SER A 719       1.110  81.017 -16.445  1.00 86.52           C
ATOM   5474  OG   SER A 719       0.547  82.166 -17.051  1.00 77.63           0
ATOM   5475  N    LEU A 720      -0.148  78.684 -18.104  I.00 71.21           N
ATOM   5476  CA   LEU A 720      -1.202  78.211 -18.979  1.00 69.10           C
ATOM   5477  C    LEU A 720      -2.311  79.265 -19.031  1.00 69.41           C
ATOM   5478  O    LEU A 720      -2.908  79.516 -20.088  1.00 67.96           0
ATOM   5479  CB   LEU A 720      -1.736  76.856 -18.506  1.00 68.11           C
ATOM   5480  CG   LEU A 720      -2.975  76.347 -19.252  1.00 68.46           C
ATOM   5481  CD1  LEU A 720      -2.631  75.931 -20.663  1.00 67.96           C
ATOM   5482  CD2  LEU A 720      -3.659  75.220 -18.505  I.00 65.81           C
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ATOM   5483  N    HIS  A  721      -2 .568   79.,898  -17 .893   1 .00  67 .83      N
ATOM   5484  CA   HIS  A  721      -3.,524   80..989  -17 ,867   1 ,00  67 .99      C
ATOM   5485  C    HIS  A  721      -3..147   82.,028  -18 .909   1 ,00  65,.30      C
ATOM   5486  O    HIS  A  721      --3..974  82.,410  -19..737   1 .00  67 .80      0
ATOM   5487  CB   HIS  A  721      -3.,605   81. 635  -16 ,484   1 ,00  66.,22      C
ATOM   5488  CG   HIS  A  721      -4 .518   82.,822  -16 .436   1 ,00  66,.51      C
ATOM   5489  ND1  HIS  A  721      -4 .399   83.,817  -15..491   1 ,00  63,.88      N
ATOM   5490  CD2  HIS  A  721      -5 „553   83. 182  -17 ,234   1 ,00  62 ,32      C
ATOM   5491  CE1  HIS  A  721      -5..325   84..737  -15.,705   1 ,00  67 .02      C
ATOM   5492  NE2  HIS  A  721      --6..036  84.,376  -16..758   1 ,00  63,.64      N
ATOM   5493  N    GLU  A  722      -1 ,896   82..467  -18.,885   I ,00  62 .37      N
ATOM   5494  CA   GLU  A  722      -1 .466   83..517  -19.,794   1 ,00  66..37      C
ATOM   5495  C    GLU  A  722      -1 .593   83.,098  -21 .252   1 ,00  69 ,51      C
ATOM   5496  O    GLU  A  722      -2 .015   83.,899  -22.,087   1 .00  70..54      0
ATOM   5497  CB   GLU  A  722      -0.,032   83..941  -19 ,486   1 ,00  72 .02      C
ATOM   5498  CG   GLU  A  722       0 ..057   84.,913  -18 .320   1 ,00  78,.95      C
ATOM   5499  CD   GLU  A  722       1 .479   85.,311  -17 ,980   1 .00  81 .77      C
ATOM   5500  OE1  GLU  A  722       2 „340   85. .313  -18.,889   1 ,00  74 ,31      0
ATOM   5501  OE2  GLU  A  722       1 .729   85.,629  -16 .794   1 ,00  85,.57      0
ATOM   5502  N    HIS  A  723      --1 .251  81.,849  -21 .558   1 ,00  67 ,25      N
ATOM   5503  CA.  HIS  A  723      -.1 ,329   81. 373  -22.,933   1 ,00  67 ,51      C
ATOM   5504  C    HIS  A  723      -2..758   81.,427  -23 ,441   1 ,00  66..19      C
ATOM   5505  O    HIS  A  723      --3..005  81.,903  -24 .549   1 ,00  67 ,45      0
ATOM   5506  CB   HIS  A  723      -0,,787   79 .948  -23 ,071   I ,00  72 .96      C
ATOM   5507  CG   HIS  A  723      -0..949   79..381  -24 ,448   1 ,00  71 .84      C
ATOM   5508  ND1  HIS  A  723      -0. 121   79.,723  -25. 496   1 ,00  76 ,73      N
ATOM   5509  CD2  HIS  A  723      -1 ,864   78..523  -24.,957   I ,00  68..64      C
ATOM   5510  CE1  HIS  A  723      -0.,508   79 .085  -26 ,586   1 ,00  79..65      C
ATOM   5511  NE2  HIS  A  723      -1 .568   78 ,356  -26. 288   1 ,00  73 ,56      N
ATOM   5512  N    ILE  A  724      --3..689  80.,927  -22.,630   1 .00  66..93      N
ATOM   5513  CA   ILE  A  724      -5.,119   81..003  -22.,943   1 ,00  66..13      C
ATOM   5514  C    ILE  A  724      -5..593   82.,459  -22. 987   1 ,00  67 ,16      C
ATOM   5515  O    ILE  A  724      --6..418  82.,821  -23 ,824   1 .00  66..71      O
ATOM   5516  CB   ILE  A  724      -5 „980   80. 241  -21.,915   1 ,00  63.,2.3      C
ATOM   5517  CGI  ILE  A  724      -5..549   78.,776  -21.·826   1 ,00  61 ,13      C
ATOM   5518  CG2  ILE  A  724      -7 .479   80.,359  —22 .244   1 ,00  48,.03      C
ATOM   5519  CD1  ILE  A  724      -6.,086   78 .059  -20.,588   1 ,00  54 ,24      C
ATOM   5520  N    ALA  A  725      -5..072   83.,296  -22.,097   1 ,00  60..81      N
ATOM   5521  CA   ALA  A  725      -5. 514   84.,689  -22 .075   1 ,00  65 ,83      C
ATOM   5522  C    ALA  A  725      -5.,199   85...356  -23 ,393   I ,00  66..33      C
ATOM   5523  O    ALA  A  725      -5.,891   86..285  -23 ,799   1 ,00  68..55      0
ATOM   5524  CB   ALA  A  725      -4 .865   85.,458  -20. 925   1 ,00  66 ,76      C
ATOM   5525  N    ASN  A  726      -4 .168   84.,854  -24 ,071   1 .00  68..02      N
ATOM   5526  CA   ASM  A  726      -3.,589   85..542  -25 ,222   1 ,00  65..59      C
ATOM   5527  C    ASN  A  726      -4 .122   85.,071  -26 .560   1 ,00  69,.74      C
ATOM   5528  O    ASN  A  726      --3..982  85.,764  -27 ,564   1 .00  75..24      0
ATOM   5529  CB   ASN  A  726      -2,,072   85. 406  -25 ,196   1 ,00  69.,05      C
ATOM   5530  CG   ASN  A  726      -1 .434   86.,278  -24.·122   1 ,00  82 ,83      C
ATOM   5531  OD1  ASN  A  726      -2 .103   86.,729  -23 ..179   1 ,00  81 ,47      0
ATOM   5532  ND2  ASN  A  726      -0.,136   86. 530  -24.,263   1 ,00  90.,15      N
ATOM   5533  O    LEU  A  727      -7 .112   85.,083  -27 ,388   1 ,00  66..41      0
ATOM   5534  N    LEU  A  727      -4 .732   83.,892  -26 ..578   1 ,00  68,.67      N
ATOM   5535  CA   LEU  A  727      -5.,439   83.·426  -27.,764   I ,00  64 .96      C
ATOM   5536  C    LEU  A  727      -6 ,482   84.,431  -28 ,213   1 ,00  60..23      C
ATOM   5537  CB   LEU  A  727      -6. 119   82.,093  -27 .481   1 ,00  64 ,87      C
ATOM   5538  CG   LEU  A  727      -5.,176   80.·965  -27.,081   I ,00  68..34      C
ATOM   5539  CD1  LEU  A  727      -5.,974   79 .783  -26 ,555   1 ,00  62 .47      C
ATOM   5540  CD2  LEU  A  727      -4 .311   80.,578  -28. 276   1 ,00  68 ,39      C
ATOM   5541  O    ALA  A  728      --8..991  83.,304  -29 ,235   1 .00  62 .15      O
ATOM   5542  N    ALA  A  728      -9 ,676   84..559  -29 ,515   1 ,00  57 .69      N
ATOM   5543  CA   ALA  A  728      -7 .849   85.,265  -30.·004   1 ,00  64 ,32      C
ATOM   5544  C    ALA  A  728      --9..094  84.,471  -29 ,595   1 .00  63..03      C
ATOM   5545  CB   ALA  A  728      -7 „781   85. 441  -.31.,510   1 ,00  59.,16      C
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ATOM    5546  O    GLY  A  729     -11.641  85.834  -27.381  1.00  59.53          O
ATOM    5547  N    GLY  A  729     -10.260  85.103  -29.643  1.00  61.13          N
ATOM    5548  CA   GLY  A  729     -11.505  84.430  -29.323  1.00  60.46          C
ATOM    5549  C    GLY  A  729     -12.231  85.069  -28.152  1.00  62.97          C
ATOM    5550  0    SER  A  730     -13.561  83.728  -25.406  I.00  61.10          0
ATOM    5551  N    SER  A  730     -13.514  84.749  -28.014  1.00  61.30          N
ATOM    5552  CA   SER  A  730     -14.332  85.340  -26.969  1.00  60.80          C
ATOM    5553  C    SER  A  730     -13.851  84.905  -25.607  I.00  58.62          C
ATOM    5554  CB   SER  A  730     -15.798  84.946  -27.135  1.00  69.73          C
ATOM    5555  OG   SER  A  730     -16.039  83.666  -26.573  1.00  69.25          0
ATOM    5556  O    PRO  A  731     -14.059  83.846  -21.748  I.00  56.89          0
ATOM    5557  N    FRO  A  731     -13.777  85.855  -24.661  1.00  58.25          N
ATOM    5558  CA   PRO  A  7.31    -13.401  85.544  -23.279  1.00  58.88          C
ATOM    5559  C    PRO  A  731     -14.401  84.569  -22.680  1.00  55.22          C
ATOM    5560  CB   FRO  A  731     -13.456  86.916  -22.563  1.00  58.02          C
ATOM    5561  CG   PRO  A  7.31    -13.476  87.924  -23.648  1.00  59.54          C
ATOM    5562  CD   PRO  A  731     -14.158  87.269  -24.817  1.00  61.41          C
ATOM    5563  O    ALA  A  732     -16.177  81.250  -22.315  I.00  55.45          0
ATOM    5564  N    ALA  A  7.32    -15.622  84.563  -23.210  1.00  48.26          N
ATOM    5565  CA   ALA  A  732     -16.602  83.580  -22.790  1.00  55.61          C
ATOM    5566  C    ALA  A  732     -16.111  82.162  -23.141  I.00  58.40          C
ATOM    5567  CB   ALA  A  732     -17.941  83.856  -23.424  1.00  49.02          C
ATOM    5568  O    ILE  A  733     -13.517  79.280  -23.598  1.00  52.50          0
ATOM    5569  N    ILE  A  733     -15.608  81.986  -24.359  I.00  58.66          N
ATOM    5570  CA   ILE  A  733     -15.051  80.697  -24.744  1.00  58.73          C
ATOM    5571  C    ILE  A  7.33    -13.737  80.410  -24.037  1.00  56.24          C
ATOM    5572  CB   ILE  A  733     -14.848  80.595  -26.253  I.00  62.18          C
ATOM    5573  CGI  ILE  A  733     -16.208  80.396  -26.910  1.00  76.89          C
ATOM    5574  CG2  ILE  A  7.33    -14.034  79.350  -26.612  1.00  64.38          C
ATOM    5575  CD1  ILE  A  733     -16.896  79.076  -26.484  1.00  68.22          C
ATOM    5576  O    LYS  A  734     -11.066  79.868  -21.339  1.00  48.70          0
ATOM    5577  N    LYS  A  7.34    -12.874  81.416  -23.903  1.00  54.85          N
ATOM    5578  CA   LYS  A  734     -11.581  81.163  -23.279  1.00  51.52          C
ATOM    5579  C    LYS  A  734     -11.805  80.720  -21.851  I.00  55.15          C
ATOM    5580  CB   LYS  A  7.34    -10.691  82.385  -23..317  1.00  51.95          C
ATOM    5581  CG   LYS  A  734     -10.085  82.667  -24.672  1.00  60.76          C
ATOM    5582  CD   LYS  A  734     -10.121  84.164  -24.957  I.00  60.31          C
ATOM    5583  CE   LYS  A  734      -8.773  84.825  -24.756  1.00  57.62          C
ATOM    5584  NZ   LYS  A  7.34     -8.953  86.300  -24.747  1.00  71.99          N
ATOM    5585  N    LYS  A  735     -12.833  81.282  -21.211  I.00  50.06          N
ATOM    5586  CA   LYS  A  735     -13.150  80.849  -19.864  1.00  46.70          C
ATOM    5587  C    LYS  A  735     -13..379  79.340  -19.880  1.00  48.74          C
ATOM    5588  O    LYS  A  735     -12.699  78.607  -19.161  1.00  48.82          0
ATOM    5589  CB   LYS  A  735     -14.361  81.562  -19.300  1.00  43.01          C
ATOM    5590  CG   LYS  A  7.35    -14.681  81.124  -17.879  1.00  44.51          C
ATOM    5591  CD   LYS  A  735     -15.419  82.225  -17.097  1.00  41.00          C
ATOM    5592  CE   LYS  A  735     -15.674  81.790  -15.681  I.00  42.58          C
ATOM    5593  NZ   LYS  A  7.35    -16.479  82.802  -14.943  1.00  39.29          N
ATOM    5594  N    GLY  A  736     -14.310  78.879  -20.714  1.00  47.52          N
ATOM    5595  CA.  GLY  A  736     -14.593  77.453  -20.818  I.00  49.91          C
ATOM    5596  C    GLY  A  736     -13.359  76.585  -21.039  1.00  45.10          C
ATOM    5597  O    GLY  A  736     -13.276  75.457  -20.561  1.00  49.31          0
ATOM    5598  N    ILE  A  737     -12.374  77.136  -21.730  I.00  46.25          N
ATOM    5599  CA   ILE  A  737     -11.209  76.375  -22.151  1.00  47.19          C
ATOM    5600  C    ILE  A  7.37    -10.288  76.102  -20.977  1.00  52.46          C
ATOM    5601  O    ILE  A  737      -9.738  75.013  -20.839  I.00  54.27          0
ATOM    5602  CB   ILE  A  737     -10.456  77.119  -23.255  1.00  48.68          C
ATOM    5603  CGI  ILE  A  7.37    -11.223  76.967  -24.566  1.00  49.04          C
ATOM    5604  CG2  ILE  A  737      -9.030  76.624  -23.377  1.00  47.79          C
ATOM    5605  CD1  ILE  A  737     -10.676  77.786  -25.705  1.00  56.67          C
ATOM    5606  N    LEU  A  7.38    -10.138  77.098  -20.114  1.00  51.83          N
ATOM    5607  CA   LEU  A  738      -9.335  76.922  -18.920  1.00  52.73          C
ATOM    5608  C    LEU  A  738      -9.961  75.870  -18.013  I.00  51.94          C
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ATOM   5609  O    LEU A 738     -9.275  74.966 -17.518  1.00 55.27    O
ATOM   5610  CB   LEU A 738     -9.172  78.239 -18.179  1.00 51.12    C
ATOM   5611  CG   LEU A 738     -8.408  78.203 -16.856  1.00 51.97    C
ATOM   5612  GDI  LEU A 738     -7.116  77.391 -16.984  1.00 51.41    c
ATOM   5613  CD2  LEU A 738     -8.107  79.628 -16.428  1.00 46.70    c
ATOM   5614  N    GLN A 739    -11.267  75.959 -17.817  1.00 49.85    N
ATOM   5615  CA   GLN A 739    -11.911  75.037 -16.903  1.00 48.50    c
ATOM   5616  C    GLN A 739    -11.852  73.605 -17.452  1.00 49.32    C
ATOM   5617  O    GLN A 739    -11.898  72.656 -16.686  1.00 47.57    O
ATOM   5618  CB   GLN A 739    -13.349  75.474 -16.629  1.00 43.25    c
ATOM   5619  CG   GLN A 739    -13.442  76.921 -16.131  1.00 44.04    c
ATOM   5620  CD   GLN A 739    -12.622  77.151 -14.879  1.00 41.93    c
ATOM   5621  OE1  GLN A 739    -12.841  76.509 -13.862  1.00 43.91    0
ATOM   5622  NE2  GLN A 739    -11.662  78.055 -14.954  1.00 44.86    N
ATOM   5623  N    THR A 740    -11.724  73.469 -18.772  1.00 52.28    N
ATOM   5624  CA   THR A 740    -11.662  72.161 -19.419  1.00 49.52    C
ATOM   5625  c    THR A 740    -10.348  71.511 -19.047  1.00 49.48    c
ATOM   5626  O    THR A 740    -10.325  70.385 -18.546  1.00 49.94    0
ATOM   5627  CB   THR A 740    -11.783  72.246 -20.962  1.00 49.13    c
ATOM   5628  OG1  THR A 740    -13.057  72.798 -21.314  1.00 54.29    0
ATOM   5629  CG2  THR A 740    -11.680  70.871 -21.589  1.00 45.53    c
ATOM   5630  N    VAL A 741     -9.262  72.236 -19.261  1.00 47.38    N
ATOM   5631  CA   VAL A 741     -7.946  71.749 -18.864  1.00 46.74    c
ATOM   5632  C    VAL A 741     -7.869  71.408 -17.375  1.00 48.35    c
ATOM   5633  O    VAL A 741     -7.286  70.402 -16.993  1.00 50.48    0
ATOM   5634  CB   VAL A 741     -6.847  72.770 -19.187  1.00 51.38    c
ATOM   5635  CGI  VAL A 741     -5.481  72.257 -18.744  1.00 48.17    c
ATOM   5636  CG2  VAL A 741     -6.869  73.107 -20.666  1.00 50.08    c
ATOM   5637  N    LYS A 742     -8.455  72.225 -16.511  1.00 52.26    N
ATOM   5638  CA   LYS A 742     -8.419  71.851 -15.103  1.00 50.04    c
ATOM   5639  C    LYS A 742     -9.217  70.565 -14.861  1.00 52.31    C
ATOM   5640  O    LYS A 742     -8.845  69.754 -14.018  1.00 50.34    O
ATOM   5641  CB   LYS A 742     -8.940  72.969 -14.223  1.00 46.17    c
ATOM   5642  CG   LYS A 742     -7.993  74.129 -14.082  1.00 48.49    c
ATOM   5643  CD   LYS A 742     -8.639  75.241 -13.249  1.00 50.66    c
ATOM   5644  CE   LYS A 742     -7.752  76.491 -13.185  1.00 44.34    c
ATOM   5645  NZ   LYS A 742     -7.809  77.153 -11.843  1.00 49.07    N
ATOM   5646  N    VAL A 743    -10.303  70.380 -15.611  1.00 51.62    N
ATOM   5647  CA   VAL A 743    -11.186  69.249 -15.374  1.00 47.59    C
ATOM   5648  C    VAL A 743    -10.480  67.980 -15.780  1.00 49.59    C
ATOM   5649  O    VAL A 743    -10.521  66.979 -15.079  1.00 49.02    O
ATOM   5650  CB   VAL A 743    -12.512  69.374 -16.140  1.00 45.42    C
ATOM   5651  CGI  VAL A 743    -13.180  68.020 -16.278  1.00 41.97    c
ATOM   5652  CG2  VAL A 743    -13.449  70.324 -15.421  1.00 43.88    c
ATOM   5653  N    VAL A 744     -9.812  68.041 -16.918  1.00 53.76    N
ATOM   5654  CA   VAL A 744     -9.099  66.890 -17.433  1.00 50.06    c
ATOM   5655  C    VAL A 744     -7.945  66.504 -16.497  1.00 53.97    C
ATOM   5656  O    VAL A 744     -7.743  65.321 -16.216  1.00 62.47    O
ATOM   5657  CB   VAL A 744     -8.558  67.161 -18.844  1.00 53.22    c
ATOM   5658  CGI  VAL A 744     -7.602  66.033 -19.266  1.00 53.77    c
ATOM   5659  CG2  VAL A 744     -9.711  67.323 -19.837  1.00 42.59    c
ATOM   5660  N    ASP A 745     -7.211  67.498 -16.001  1.00 48.31    N
ATOM   5661  CA   ASP A 745     -6.068  67.260 -15.137  1.00 45.36    C
ATOM   5662  C    ASP A 745     -6.467  66.612 -13.826  1.00 54.65    C
ATOM   5663  O    ASP A 745     -5.731  65.770 -13.299  1.00 63.37    O
ATOM   5664  CB   ASP A 745     -5.307  68.552 -14.849  1.00 52.54    C
ATOM   5665  CG   ASP A 745     -4.194  68.837 -15.872  1.00 66.44    C
ATOM   5666  OD1  ASP A 745     -4.343  68.514 -17.081  1.00 62.77    O
ATOM   5667  OD2  ASP A 745     -3.156  69.400 -15.451  1.00 69.28    0
ATOM   5668  N    GLU A 746     -7.618  66.978 -13.289  1.00 51.25    N
ATOM   5669  CA   GLU A 746     -8.036  66.391 -12.021  1.00 53.17    c
ATOM   5670  c    GLU A 746     -8.587  64.982 -12.244  1.00 55.43    c
ATOM   5671  O    GLU A 746     -8.468  64.120 -11.374  1.00 56.23    0
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ATOM   5672  CB  GLU  A  746     --9..055   67..301  -11 .310   1,00  52 .30        C
ATOM   5673  CG  GLU  A  746     --10,,141  66..593  -10.,485   1,00  50..35        C
ATOM   5674  CD  GLU  A  746     -10 .651   67.,446  -9 ..306   1,00  55,.97        C
ATOM   5675  OE1 GLU  A  746     -11 .752   67.,155  -8..761    1,00  49..81        0
ATOM   5676  OE2 GLU  A  746     -9.,930    68. .389  -8.,917   1,00  49..53        0
ATOM   5677  N   LEU  A  747     -9 .177    64.,741  -13.410    1,00  53,.17        N
ATOM   5678  CA  LEU  A  747     --9..679   63.,411  -13..747   1,00  56,.53        C
ATOM   5679  C   LEU  A  747     -8.,519    62. 418  -13.,914   1,00  59..70        C
ATOM   5680  O   LEU  A  747     -8..668    61.,238  -13.,613   1,00  50..32        0
ATOM   5681  CE  LEU  A  747     -10..518   63.,429  -15..025   1,00  52,80         C
ATOM   5682  CG  LEU  A  747     -11 ,960   63.. 915  -14 ,979   I,00  59..66        C
ATOM   5683  CD1 LEU  A  747     -12..598   63.,805  -16.,364   1,00  55..30        C
ATOM   5684  CD2 LEU  A  747     -12.764    63.,141  -13 .935   1,00  58,76         C
ATOM   5685  N   VAL  A  748     -7 .383    62.,911  -14 ,401   1,00  55..18        N
ATOM   5686  CA  VAL  A  748     --8.,187   62.. 102  -14 ,503   1,00  54 .48        C
ATOM   5687  C   VAL  A  748     -5..750    61.,653  -13.110    1,00  61 ,73        C
ATOM   5688  O   VAL  A  748     -5..537    60.,455  -12..873   1,00  63..11        0
ATOM   5689  CB  VAL  A  748     -5 ,053    62. 860   -15.,212   1,00  57 .32        C
ATOM   5690  CGI VAL  A  748     -3..699    62.,444  -14.689    1,00  62 ,26        C
ATOM   5691  CG2 VAL  A  748     -5..128    62.,613  -16.. 689  1,00  58,.39        C
ATOM   5692  N   LYS  A  749     -5 ,652    62. 598   -12.,180   1,00  62 .83        N
ATOM   5693  CA  LYS  A  749     -5..356    62.,249  -10.,799   1,00  62 .07        C
ATOM   5694  C   LYS  A  749     -6..390    61.,262  -10..273   1,00  62 ,28        C
ATOM   5695  0   LYS  A  749     -6.,033    60.. 265  -9.,661    I,00  69..32        0
ATOM   5696  CB  LYS  A  749     -5..312    63.,483  -9 ,917     1,00  59..65        C
ATOM   5697  CG  LYS  A  749     -4 .185    64.,459  -10. 230    1,00  64 ,58        C
ATOM   5698  CD  LYS  A  749     -4 ,059    65.. 499  -9.,102    I,00  66..39        C
ATOM   5699  CE  LYS  A  749     -3.,649    66.. 879  -9.,604    1,00  70..47        C
ATOM   5700  NZ  LYS  A  749     -4 .751    67.,904  -9. 482     1,00  74 ,76        N
ATOM   5701  N   VAL  A  750     -7 .665    61.,515  -10.,544   1,00  61 .82        N
ATOM   5702  CA  VAL  A  750     -8.,722    60.. 566  -10.,180   1,00  64 .60        C
ATOM   5703  C   VAL  A  750     -8..438    59.,169  -10.. 752  1,00  60,.19        C
ATOM   5704  O   VAL  A  750     -8..790    58.,152  -10.,153   1,00  57 .09        0
ATOM   5705  CB  VAL  A  750     -10.,120   61. 051   -10.,661   1,00  57 .06        C
ATOM   5706  CGI VAL  A  750     -11 .100   59.,889  -10.. 792  1,00  59,.17        C
ATOM   5707  CG2 VAL  A  750     -10..668   62.,076  -9.. 718    1,00  58,.93        C
ATOM   5708  O   MET  A  751     -5 ,479    56. 772   -13 ,218    1,00  69..54        0
ATOM   5709  N   MET  A  751     -7 .772    59.,133  -11 ,900    1,00  63..53        N
ATOM   5710  CA  MET  A  751     -7 .516    57,877   -12 .590    1,00  62 ,44        C
ATOM   5711  C   MET  A  751     -6.,099    57.. .355  -12.,339   I,00  64 .75        C
ATOM   5712  CB  MET  A  751     -7 ,758    58..047  -14 ,083    1,00  57 .47        C
ATOM   5713  CG  MET  A  751     -9. 218    58.,146  -14 .439    1,00  55 ,56        C
ATOM   5714  SD  MET  A  751     -10..280   57.,008  -13.,524   1,00  69..10        S
ATOM   5715  CE  MET  A  751     -10.,556   55.. 699  -14 ,712    1,00  51 .84        C
ATOM   5716  O   GLY  A  752     -2 .010    57.,161  -11 .471    1,00  80,.57        0
ATOM   5717  N   GLY  A  752     -5..592    57.,588  -11 ,138    1,00  64 .47        N
ATOM   5718  CA. GLY  A  752     -4 ,272    57. 129   -10.,764   1,00  70..26        C
ATOM   5719  C   GLY  A  752     -3..085    57.,749  -11 .482    1,00  7.1 ,90       C
ATOM   5720  O   ARG  A  753     -1 .074    59.,131  -14 .990    1,00  72 ,51        0
ATOM   5721  N   ARG  A  753     -3.,263    58. 925   -12.,078   1,00  68..72        N
ATOM   5722  CA  ARG  A  753     -2.,236    59.,573  -12.,917   1,00  70..80        C
ATOM   5723  C   ARG  A  753     -2 .007    58.,821  -14 .249    1,00  72 ,83        C
ATOM   5724  CB  ARG  A  753     -0.,901    59 .722   -12.,163   I,00  74 .89        C
ATOM   5725  CG  ARG  A  753     -0.,787    60.,897  -11 ,182    1,00  75..67        C
ATOM   5726  CD  ARG  A  753      0 .233    60.,583  -10. 071    1,00  86 ,96        C
ATOM   5727  NE  ARG  A  753      1 ,041    61.. 737  -9.,646    I,00106. .08        N
ATOM   5728  CZ  ARG  A  753      1 ,973    61.. 703  -8.,683    1,00103. .46        C
ATOM   5729  NH1 ARG  A  753      2 .218    60.,574  -8. 025     1,00103, .43        N
ATOM   5730  NH2 ARG  A  753      2 ,661    62.,798  -8.,367    1,00  96..57        N
ATOM   5731  O   HIS  A  754     -4 ,815    58.. 149  -16 ,809    1,00  68..60        O
ATOM   5732  N   HIS  A  754     -2 .867    57.,849  -14 .556    1,00  69,.14        N
ATOM   5733  CA  HIS  A  754     -2 .831    57.,158  -15.,842   1,00  68..62        C
ATOM   5734  C   HIS  A  754     -3.,607    57. 913   -16 ,934    1,00  74 .12        C
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ATOM	5735	CB	HIS	A	754	-3.404	55.745	-15.703	1.00	75.33	c
ATOM	5736	CG	HI S	A	754	-2.409	54.723	-15.240	1.00	85.69	C
ATOM	5737	ND1	HIS	A	754	-2.592	53.369	-15.431	1.00	85.03	N
ATOM	5738	CD2	HIS	A	754	-1.224	54.855	-14.595	1.00	85.29	c
ATOM	5739	CE1	HI S	A	754	-1.565	52.713	-14.922	I.00	88.92	C
ATOM	5740	NE2	HIS	A	754	-0.720	53.591	-14.408	1.00	89.60	N
ATOM	5741	O	LYS	A	755	-4.745	56.981	-19.510	1.00	72.76	O
ATOM	5742	N	LYS	A	755	-2.909	58.267	-18.011	I.00	71.62	N
ATOM	5743	CA	LYS	A	755	-3.511	58.976	-19.134	1.00	65.92	C
ATOM	5744	c	LYS	A	755	-4.654	58.178	-19.733	1.00	67.02	c
ATOM	5745	CB	LYS	A	755	-2.472	59.268	-20.213	I.00	66.33	c
ATOM	5746	CG	LYS	A	755	-1.123	59.684	-19.689	1.00	66.67	c
ATOM	5747	CD	LYS	A	755	-1.110	61.097	-19.194	1.00	71.83	c
ATOM	5748	CE	LYS	A	755	0.332	61.563	-19.082	1.00	78.53	c
ATOM	5749	NZ	LYS	A	755	1.120	61.070	-20.255	1.00	70.21	N
ATOM	5750	O	PP.0	A	756	-5.270	58.176	-23.143	1.00	65.34	O
ATOM	5751	N	PRO	A	756	-5.557	58.851	-20.468	1.00	71.82	N
ATOM	5752	CA.	PRO	A	756	-6.640	58.151	-21.167	I.00	66.96	C
ATOM	5753	C	PP.0	A	756	-6.241	57.678	-22.575	1.00	68.04	C
ATOM	5754	CB	PRO	A	756	-7.739	59.217	-21.231	1.00	62.31	c
ATOM	5755	CG	PRO	A	756	-6.996	60.472	-21.329	I.00	59.65	c
ATOM	5756	CD	PRO	A	756	-5.774	60.309	-20.464	1.00	57.98	c
ATOM	5757	O	GLU	A	757	-6.241	58.013	-26.153	1.00	65.64	0
ATOM	5758	N	GLU	A	757	-6.981	56.712	-23.118	I.00	72.33	N
ATOM	5759	CA	GLU	A	757	-6.838	56.332	-24.526	1.00	67.87	C
ATOM	5760	C	GLU	A	757	-7.104	57.561	-25.390	1.00	68.15	C
ATOM	5761	CB	GLU	A	757	-7.817	55.206	-24.910	I.00	65.90	C
ATOM	5762	CG	GLU	A	757	-7.286	53.774	-24.860	1.00	74.45	C
ATOM	5763	CD	GLU	A	757	-8.177	52.800	-25.639	1.00	76.82	c
ATOM	5764	OE1	GLU	A	757	-9.094	52.198	-25.028	1.00	74.97	0
ATOM	5765	OE2	GLU	A	757	-7.965	52.645	-26.866	1.00	75.46	0
ATOM	5766	N	ASN	A	758	-8.314	58.100	-25.236	1.00	67.37	N
ATOM	5767	CA	ASN	A	758	-8.807	59.191	-26.068	1.00	68.51	c
ATOM	5768	C	ASM	A	758	-9.359	60.387	-25.297	I.00	68.72	C
ATOM	5769	O	ASN	A	758	-9.759	60.278	-24.129	1.00	67.39	O
ATOM	5770	CB	ASN	A	758	-9.918	58.683	-26.990	1.00	69.28	c
ATOM	5771	CG	ASN	A	758	-9.473	57.547	-27.863	I.00	70.56	c
ATOM	5772	OD1	ASN	A	758	-8.277	57.266	-27.974	1.00	69.89	0
ATOM	5773	ND2	ASN	A	758	-10.432	56.893	-28.513	1.00	68.53	N
ATOM	5774	N	ILE	A	759	-9.410	61.528	-25.978	I.00	65.84	N
ATOM	5775	CA	ILE	A	759	-10.166	62.665	-25.487	1.00	55.17	C
ATOM	5776	C	ILE	A	759	-11.023	63.230	-26.612	1.00	56.14	C
ATOM	5777	O	ILE	A	759	-10.526	63.830	-27.562	1.00	58.31	O
ATOM	5778	CB	ILE	A	759	-9.264	63.752	-24.912	1.00	60.52	c
ATOM	5779	CGI	ILE	A	759	-8.539	63.225	-23.664	1.00	52.02	c
ATOM	5780	CG2	ILE	A	759	-10.116	64.984	-24.561	1.00	52.86	c
ATOM	5781	CD1	ILE	A	759	-7.352	64.070	-23.212	I.00	50.80	c
ATOM	5782	N	VAL	A	760	-12.323	63.008	-26.506	1.00	54.71	N
ATOM	5783	CA	VAL	A	760	-13.253	63.444	-27.530	1.00	56.36	c
ATOM	5784	C	VAL	A	760	-13.937	64.768	-27.146	I.00	60.73	C
ATOM	5785	O	VAL	A	760	-14.782	64.815	-26.247	1.00	59.55	0
ATOM	5786	CB	VAL	A	760	-14.323	62.372	-27.791	1.00	58.43	c
ATOM	5787	CGI	VAL	A	760	-15.225	62.800	-28.912	I.00	53.55	c
ATOM	5788	CG2	VAL	A	760	-13.662	61.034	-28.109	1.00	63.30	c
ATOM	5789	N	ILE	A	761	-13.584	65.836	-27.856	1.00	61.16	N
ATOM	5790	CA	ILE	A	761	-14.123	67.166	-27.582	I.00	59.74	C
ATOM	5791	C	ILE	A	761	-15.213	67.632	-28.544	1.00	58.20	C
ATOM	5792	O	ILE	A	761	-15.065	67.556	-29.755	1.00	62.79	O
ATOM	5793	CB	ILE	A	761	-13.027	68.224	-27.622	1.00	54.83	c
ATOM	5794	CGI	ILE	A	761	-11.762	67.713	-26.954	1.00	53.81	c
ATOM	5795	CG2	ILE	A	761	-13.507	69.477	-26.944	1.00	61.73	c
ATOM	5796	CD1	ILE	A	761	-10.598	68.641	-27.149	1.00	55.54	c
ATOM	5797	N	GLU	A	762	-16.305	68.126	-27.980	I.00	53.47	N

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ATOM    5798  CA   GLU  A  762      -17 .306   68..854  -28..731   1.00  55..92           C
ATOM    5799  C    GLU  A  762      -17,,374   70.279   -28,164    1,00  59..23           C
ATOM    5800  O    GLU  A  762      -17 .566   70.,485  -26..965   1.00  57,67            0
ATOM    5801  CB   GLU  A  762      -18..661   68.,150  -28..650   1.00  55..84           C
ATOM    5802  CG   GLU  A  762      -19,830    68. 909  -29.,280   1,00  66.,29           C
ATOM    5803  CD   GLU  A  762      -21..154   68.,718  -28..502   1.00  76,.53           C
ATOM    5804  OE1  GLU  A  762      -21 .215   69.,131  -27.322    1,00  72,25            0
ATOM    5805  OE2  GLU  A  762      -22.,129   68. 145  -29.,054   1,00  73.,74           0
ATOM    5806  O    MET  A  763      -18..753   73..163  -30.,432   1,00  61 .52           0
ATOM    5807  N    MET  A  763      -17 .162   71,269   -29..012   1,00  55,.96           N
ATOM    5808  CA   MET  A  763      -17 ,321   72.636   -28.,574   1,00  53..69           C
ATOM    5809  C    MET  A  763      -18..556   73..256  -29,221    1,00  60..78           C
ATOM    5810  CB   MET  A  763      -16. 088   73,450   -28. 903   1,00  53,69            C
ATOM    5811  CG   MET  A  763      -16..253   74,912   -28,568    1.00  55..44           C
ATOM    5812  SD   MET  A  763      -14 ,732   75.816   -28,825    1,00  63..82           S
ATOM    5813  CE   MET  A  763      -13..727   75.,131  -27.534    1.00  46,.30           C
ATOM    5814  O    ALA  A  764      -19..317   76.,570  -29..308   1.00  70..38           0
ATOM    5815  N    ALA  A  764      -19,394    73.874   -28,401    1,00  55.,59           N
ATOM    5816  CA   ALA  A  764      -20..578   74,564   -28..904   1.00  68,.60           C
ATOM    5817  C    ALA  A  764      -20..189   75,796   -29.714    1,00  67,70            C
ATOM    5818  CB   ALA  A  764      -21.,510   74.961   -27,744    1,00  68.,12           C
ATOM    5819  O    ARG  A  765      -22..761   77,989   -30..742   1,00  80..16           0
ATOM    5820  N    ARG  A  765      -20..834   75,965   -30..865   1,00  73,.23           N
ATOM    5821  CA   ARG  A  765      -20.,688   77.184   -31.,655   1,00  76..31           C
ATOM    5822  C    ARG  A  765      -21..601   78..267  -31.,065   1,00  79..72           C
ATOM    5823  CB   ARG  A  765      -21 .017   76,911   -33. 123   1,00  74,71            C
ATOM    5824  O    GLU  A  766      -23,475    80..627  -31.,852   1,00  86..11           0
ATOM    5825  N    GLU  A  766      -21.,077   79.487   -30.,916   1,00  82 .39           N
ATOM    5826  CA   GLU  A  766      -21 .752   80.,553  -30. 152   1,00  83,40            C
ATOM    5827  C    GLU  A  766      -22..972   81.,177  -30..870   1.00  85..45           C
ATOM    5828  CB   GLU  A  766      -20,731    81..641  -29,784    1,00  81 .86           C
ATOM    5829  CG   GLU  A  766      -19..428   81.,078  -29..169   1.00  82,99            C
ATOM    5830  CD   GLU  A  766      -18..460   82.,152  -28..663   1.00  82 .46           C
ATOM    5831  OE1  GLU  A  766      -17 ,514   82. 516  -29.,399   1,00  84,73            0
ATOM    5832  OE2  GLU  A  766      -18..628   82.,616  -27.517    1.00  74,85            0
ATOM    5833  O    ASN  A  767      -25..240   84.,830  -32..264   1,00  95,.83           0
ATOM    5834  N    ASM  A  767      -23,459    82. 311  -30.,365   1,00  91 ,85           N
ATOM    5835  CA   ASN  A  767      -24..669   82..933  -30.,918   1,00  91 .03           C
ATOM    5836  C    ASN  A  767      -24 .380   84.,002  -31. 963   1,00  92,11            C
ATOM    5837  CB   ASN  A  767      -25,516    83..542  -29.,805   1,00  83..76           C
ATOM    5838  O    LYS  A  775      -24,799   100..659  -38.,758   1,00102. .58           0
ATOM    5839  N    LYS  A  775      -27.244   101.,878  -36. 532   1,00  95,88            N
ATOM    5840  CA   LYS  A  775      -25..832  101.,658  -36,834    1.00100..42           C
ATOM    5841  C    LYS  A  775      -25,638   100..548  -37.,860   1,00103. .22           C
ATOM    5842  CB   LYS  A  775      -25..053  101.,325  -35..560   1.00  99,.52           C
ATOM    5843  CG   LYS  A  775      -23..710  100.,647  -35..812   1.00  90..50           C
ATOM    5844  CD   LYS  A  775      -22.,652  101. 186  -34.,871   1,00  90.,28           C
ATOM    5845  CE   LYS  A  775      -22..612  102.,713  -34..928   1.00  84,74            C
ATOM    5846  NZ   LYS  A  775      -21 .508  103.,288  -34..101   1,00  77,48            N
ATOM    5847  O    ASN  A  776      -26,521    98. 502  -41 ,060   1,00104.,34            O
ATOM    5848  N    ASN  A  776      -26..406   99.,473  -37.,709   1,00104..28            N
ATOM    5849  CA   ASN  A  776      -26..382   98.,374  -38..666   1,00105,.63            C
ATOM    5850  C    ASN  A  776      -27.,035   98..782  -.39,977    1,00104..72            C
ATOM    5851  CB   ASN  A  776      -27..089   97..143  -38.,095   1,00108..91            C
ATOM    5852  CG   ASN  A  776      -27.302    96.,057  -39.136    1,00108,.19            C
ATOM    5853  OD1  ASN  A  776      -28.,315   96..040  -.39,845    1,00104..92            O
ATOM    5854  ND2  ASN  A  776      -26,343    95..144  -39,234    1,00108..11            N
ATOM    5855  N    SER  A  777      -28. 175   99.,451  -39.870    1,00100,.81            N
ATOM    5856  CA   SER  A  777      -28..909   99.,873  -41 ,049   1,00103..69            C
ATOM    5857  C    SER  A  777      -28,198   101..020  -41,775    1,00105..17            C
ATOM    5858  O    SER  A  777      -28...351  101.,178  -42 .988   1,00103,.57            O
ATOM    5859  CB   SER  A  777      -30..334  100.,282  -40..667   1,00105..84            C
ATOM    5860  OG   SER  A  777      -31.,060    99. 180  -40.,147   1,00105.,2.1            0
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ATOM	5861	N	ARG	A	778	-27..423	101..811	-41.031	1.00105..45	N
ATOM	5862	CA	ARG	A	778	--26,653	102..914	-41,609	1,00101..53	C
ATOM	5863	C	ARG	A	778	-25..371	102.,390	-42.257	1,00103,.54	C
ATOM	5864	O	ARG	A	778	-24..783	103.,042	-43..119	1.00102..46	0
ATOM	5865	CB	ARG	A	778	-26,322	103. 965	-40.,546	1,00 96.,27	C
ATOM	5866	N	GLU	A	779	-24..942	101.,208	-41.826	1,00105,.88	N
ATOM	5867	CA	GLU	A	779	-23..834	100.,505	-42..459	1,00104,.51	C
ATOM	5868	C	GLU	A	779	-24.,291	99. 952	-43,806	1,00103.,78	C
ATOM	5869	O	GLU	A	779	-23..615	100.,117	-44,825	1,00 99..58	0
ATOM	5870	CB	GLU	A	779	-23..327	99.,372	-41.559	1,00102,.87	C
ATOM	5871	CG	GLU	A	779	-22.,066	99.693	-40.,776	I,00103..58	C
ATOM	5872	CD	GLU	A	779	-20..793	99..361	-41,549	1,00109..94	C
ATOM	5873	OE1	GLU	A	779	-19. 848	98.,812	-40. 940	1,00110 ,21	0
ATOM	5874	OE2	GLU	A	779	-20..730	99.,648	-42,763	1.00111..31	0
ATOM	5875	N	ARG	A	780	-25,454	99..304	-43,792	1,00103..77	N
ATOM	5876	CA	ARG	A	780	-26..031	98.,702	-44.988	1,00103,.30	C
ATOM	5877	C	ARG	A	780	-26..404	99.,779	-45..997	1.00100..01	C
ATOM	5878	0	ARG	A	780	-26,425	99. 540	-47,202	1,00 96.,06	0
ATOM	5879	CB	ARG	A	780	-27.260	97.,858	-44 .627	1,00 98,.76	C
ATOM	5880	N	MET	A	781	-26..686	100.,972	-45..486	1,00102,.86	N
ATOM	5881	CA.	MET	A	781	-27,089	102. 107	-46,309	1,00101.,30	C
ATOM	5882	C	MET	A	781	-25..890	102..776	-46,981	1,00 95..33	C
ATOM	5883	O	MET	A	781	-26..046	103.,490	-47.971	1,00 92,52	0
ATOM	5884	CB	MET	A	781	-27.,853	103..129	-45,460	I,00100..20	C
ATOM	5885	CG	MET	A	781	-28..653	104..124	-46,265	1,00 97.84	C
ATOM	5886	SD	MET	A	781	-29. 845	103.,309	-47.338	1,00105,.09	S
ATOM	5887	CE	MET	A	781	-.30.,412	104..712	-48.,287	I,00103..85	C
ATOM	5888	N	LYS	A	782	-24,697	102..540	-46,436	1,00 98..61	N
ATOM	5889	CA	LYS	A	782	-23 .469	103.,100	-47.003	1,00100..05	C
ATOM	5890	C	LYS	A	782	-22..830	102.,138	-48,010	1.00 97.69	C
ATOM	5891	O	LYS	A	782	-22.,008	102..543	-48,834	1,00 95..73	0
ATOM	5892	CB	LYS	A	782	-22..469	103.,454	-45..895	1,00 94,41	C
ATOM	5893	N	ARG	A	783	-23..212	100.,866	-47.951	1.00 98..23	N
ATOM	5894	CA.	ARG	A	783	-22.,759	99. 912	-48,952	1,00 93.,67	C
ATOM	5895	C	ARG	A	783	-23..680	99.,951	-50..175	1,00 94,.15	C
ATOM	5896	O	ARG	A	783	-23..308	99.,482	-51..247	1,00 96,.88	O
ATOM	5897	CB	ARG	A	783	-22.,689	98. 502	-48,370	1,00 91,41.	C
ATOM	5898	CG	ARG	A	783	-21..874	97.,540	-49,219	1,00 92.53	C
ATOM	5899	CD	ARG	A	783	-21.042	96.,616	-48. 362	1,00 90,40	C
ATOM	5900	NE	ARG	A	783	-19,903	96..072	-49.,101	I,00101..54	N
ATOM	5901	CZ	ARG	A	783	-18.,672	96..580	-49,072	1,00 96..80	C
ATOM	5902	NH1	ARG	A	783	-18. 409	97.,653	-48. 336	1,00 96,35	N
ATOM	5903	NH2	ARG	A	783	-17 .702	96.,013	-49..780	1.00 91.29	N
ATOM	5904	N	ILE	A	784	-24,874	100..521	-50.,010	1,00 91.65	N
ATOM	5905	CA	ILE	A	784	-25..823	100.,699	-51..115	1,00 89,.93	C
ATOM	5906	C	ILE	A	784	-25..557	101.,981	-51..911	1.00 93..13	C
ATOM	5907	O	ILE	A	784	-25,448	101. 958	-53.,140	1,00 90.,82	O
ATOM	5908	CB	ILE	A	784	-27.280	100.,747	-50..607	1,00 90,.88	C
ATOM	5909	CGI	ILE	A	784	-27.680	99.,417	-49..972	1,00 89,.27	C
ATOM	5910	CG2	ILE	A	784	-28,226	101. 123	-51. ,728	1,00 82,85	C
ATOM	5911	CD1	ILE	A	784	-27..271	98..220	-50.,762	1,00 88..41	C
ATOM	5912	N	GLU	A	785	-25..468	103.,098	-51..197	1,00 91,87	N
ATOM	5913	CA	GLU	A	785	-25,248	104...393	-51.,819	I,00 94.98	C
ATOM	5914	C	GLU	A	785	-23,899	104..443	-52.,549	1,00 95..54	C
ATOM	5915	O	GLU	A	785	-23 .806	104.,988	-53. 651	1,00 97,49	O
ATOM	5916	CB	GLU	A	785	-25,342	105..513	-50.,769	I,00 88..95	C
ATOM	5917	N	GLU	A	786	-22.,862	103..865	-51.,951	1,00 89..48	N
ATOM	5918	CA	GLU	A	786	-21 .527	103.,896	-52. 551	1,00 92,81	C
ATOM	5919	C	GLU	A	786	-21.,403	102.,932	-53.,737	1.00 98..36	C
ATOM	5920	O	GLU	A	786	-20,455	103..016	-54.,523	1,00 98..29	0
ATOM	5921	CB	GLU	A	786	-20..460	103.,571	-51..500	1,00 86,.83	C
ATOM	5922	N	GLY	A	787	-22..361	102.,018	-53.,860	1.00 99..18	N
ATOM	5923	CA.	GLY	A	787	-22.,362	101. 045	-54 ,938	1,00 93.,96	C

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ATOM     5924   c    GLY  A  787       -23..191  101..535  -56..Ill   1.00  94.89            c
ATOM     5925   O    GLY  A  787       --22.,794  101..395  -57.,267   1,00  95..30           O
ATOM     5926   N    ILE  A  788       -24...354  102.,103  -55..813   1,00  92,.18           N
ATOM     5927   CA   ILE  A  788       -25..164  102..753  -56..837   1.00  94.04            c
ATOM     5928   C    ILE  A  788       -24.,377  103. 862  -57 ,527   1,00  94,21            c
ATOM     5929   O    ILE  A  788       -24..320  103.,915  -58..756   1,00  92,56            0
ATOM     5930   CB   ILE  A  788       -26..452  103.,338  -56..245   1,00  92,.70           c
ATOM     5931   CGI  ILE  A  788       -27,383  102. 211  -55.,800   1,00  90.,64           c
ATOM     5932   CG2  ILE  A  788       -27..132  104..245  -57.,241   1,00  87.55            c
ATOM     5933   CD1  ILE  A  788       -27.547  101.,116  -56..825   1,00  95,.94           c
ATOM     5934   O    LYS  A  789       -21.,041  106.197  -58.,677   I,00  99..52           0
ATOM     5935   N    LYS  A  789       -23..751  104..722  -56,720   1,00  95..82           N
ATOM     5936   CA   LYS  A  789       -22.918  105.,835  -57. 195   1,00  97,05            c
ATOM     5937   c    LYS  A  789       -21..758  105..374  -58..100   1.00  97.92            c
ATOM     5938   CB   LYS  A  789       -22.,366  106..627  -55.,995   1,00  91.48            c
ATOM     5939   CG   LYS  A  789       -21..885  108.,049  -56...309   1,00  87,.67           c
ATOM     5940   CD   LYS  A  789       -20..528  108..338  -55..650   1.00  86..60           c
ATOM     5941   CE   LYS  A  789       -20.,554  109.574  -54 ,740   1,00  81 ,06           c
ATOM     5942   NZ   LYS  A  789       -20..078  110.,847  -55...396   1,00  78,.21           N
ATOM     5943   O    GLU  A  790       -20..602  102.,311  -61..200   1,00101, .55           0
ATOM     5944   N    GLU  A  790       -21.,570  104 .065  -58.,222   1,00  94,76            N
ATOM     5945   CA   GLU  A  790       -20..583  103..538  -59,152   1,00  96..98           c
ATOM     5946   c    GLU  A  790       -21 .265  102.,794  -60..289   1,00  96,.69           c
ATOM     5947   CB   GLU  A  790       -19,595  102..615  -58.,438   I,00  97,.76           c
ATOM     5948   CG   GLU  A  790       -18..203  102..602  -59,058   1,00  99..33           c
ATOM     5949   CD   GLU  A  790       -17 .411  103.,874  -58. 762   1,00105, .53           c
ATOM     5950   OE1  GLU  A  790       -16,384  104..101  -59,438   I,00106. .93           0
ATOM     5951   OE2  GLU  A  790       -17,813  104 .645  -57.,856   1,00107. .71           0
ATOM     5952   O    LEU  A  791       -24 .320  102.,859  -63. .306   1,00  99,25            0
ATOM     5953   N    LEU  A  791       -22..591  102..703  -60..227   1.00  96..83           N
ATOM     5954   CA   LEU  A  791       -23,372  102..028  -61.,262   1,00  96..68           c
ATOM     5955   C    LEU  A  791       -24..186  103.,019  -62..093   1,00  98,.06           c
ATOM     5956   CB   LEU  A  791       -24..311  100..986  -60..644   1.00  96..44           c
ATOM     5957   CG   LEU  A  791       -23,711   99. 693  -60.,088   1,00  93.,74           c
ATOM     5958   CD1  LEU  A  791       -24..797   98.,873  -59..406   1,00  92,82            c
ATOM     5959   CD2  LEU  A  791       -23..031   98.,893  -61..189   1,00  91,70            c
ATOM     5960   O    GLY  A  792       -27,495  104 .683  -63.,390   1,00  97,72            0
ATOM     5961   N    GLY  A  792       -24..743  104..031  -61.,435   1,00  96..81           N
ATOM     5962   CA   GLY  A  792       -25. 501  105.,057  -62. 127   1,00  93,43            c
ATOM     5963   C    GLY  A  792       -26.,980  104..749  -62.,269   I,00  95..96           c
ATOM     5964   O    SER  A  793       -31.,119  105..425  -61.,638   1,00  96..52           0
ATOM     5965   N    SER  A  793       -27.660  104.,579  -61. 134   1,00  96,46            N
ATOM     5966   CA   SER  A  793       -29..093  104..269  -61..097   1.00  97.45            c
ATOM     5967   C    SER  A  793       -29,953  105..185  -61.,958   1,00  94.93            c
ATOM     5968   CB   SER  A  793       -29..608  104.,342  -59..668   1,00  96,.75           c
ATOM     5969   OG   SER  A  793       -29..457  105..658  -59..162   1.00  92.45            0
ATOM     5970   O    LYS  A  797       -37.,066  105. 881  -58.,232   1,00  97,65            0
ATOM     5971   N    LYS  A  797       -35...325  107 ,244  -59..788   1,00106, .58           N
ATOM     5972   CA   LYS  A  797       -34..807  106.,603  -58..587   1,00102, .97           c
ATOM     5973   C    LYS  A  797       -35.,874  105. 715  -57 ,966   1,00102.,82            c
ATOM     5974   CB   LYS  A  797       -34..332  107 ,651  -57.,571   1,00  94.33            c
ATOM     5975   O    GLU  A  798       -35..520  104.,747  -54..160   1,00107, .01           0
ATOM     5976   N    GLU  A  798       -35.,449  104..758  -57.,149   I,00108. .09           N
ATOM     5977   CA   GLU  A  798       -36..409  104..078  -56,298   1,00105. .85           c
ATOM     5978   C    GLU  A  798       -36. 458  104.,785  -54. 957   1,00106, .22           c
ATOM     5979   CB   GLU  A  798       -36,090  102..593  -56,133   I,00102. .80           c
ATOM     5980   CG   GLU  A  798       -36,493  101..733  -57.,340   1,00  98..74           c
ATOM     5981   CD   GLU  A  798       -38. 002  101.,711  -57. 637   1,00  97,89            c
ATOM     5982   OE1  GLU  A  798       -38..775  102.,528  -57.,089   1.00  99..50           0
ATOM     5983   OE2  GLU  A  798       -38.,421  100..861  -58.,445   1,00  95..81           0
ATOM     5984   O    HIS  A  799       -37..262  106.,492  -51..290   1,00114, .17           0
ATOM     5985   N    HIS  A  799       -37..594  105.,427  -54..730   1.00109. .66           N
ATOM     5986   CA.  HIS  A  799       -37.,806  106. 298  -53.,585   1,00109.,59            c
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ATOM   5987  C    HIS  A  799    -37.613  105:720  -52.173   1,00111.85    C
ATOM   5988  CB   HIS  A  799    --39,219 106.890  -53,666   1,00107.85    C
ATOM   5989  O    PP.0 A  800    -36.473  105,348  -49,192   1.00109,21    O
ATOM   5990  N    PRO  A  800    -37.878  104:406  -51:935   1.00112.65    N
ATOM   5991  CA.  PRO  A  800    -37,862  103.947  -50,534   1,00110,64    C
ATOM   5992  C    PRO  A  800    -36.592  104,261  -49,754   1.00110,40    C
ATOM   5993  CB   PRO  A  800    -38.024  102,430  -50.664   1,00109,45    c
ATOM   5994  CG   PRO  A  800    -.38,817  102.254  -51,876   1,00107,81    c
ATOM   5995  CD   PRO  A  800    -38.348  103:326  -52.827   1,00111.22    c
ATOM   5996  O    VAL  A  801    -33,499  105,209  -47.668   1,00109,59    0
ATOM   5997  N    VAL  A  801    -.35,686  103.291  -49,691   I,00112.61    N
ATOM   5998  CA   VAL  A  801    -34.379  103:460  -49.060   1,00112.62    C
ATOM   5999  C    VAL  A  801    -34.365  104:345  -47.802   1,00110,51    C
ATOM   6000  CB   VAL  A  801    -33,374  104:047  -50:067   1.00110.18    c
ATOM   6001  O    GLU  A  802    -34,206  104.802  -43,518   1,00116.63    0
ATOM   6002  N    GLU  A  802    -35.324  104,143  -46.896   1.00110,77    N
ATOM   6003  CA   GLU  A  802    -35.351  104.887  -45.632   1.00112.05    c
ATOM   6004  C    GLU  A  802    -.34,406  104.255  -44,608   1,00111,23    C
ATOM   6005  CB   GLU  A  802    -36.774  104,962  -45,067   1.00110,48    C
ATOM   6006  O    ASN  A  803    -32.482  100,459  -42.940   1,00110,35    O
ATOM   6007  N    ASM  A  803    -.33,868  103.090  -44,976   1,00109:39    N
ATOM   6008  CA   ASN  A  803    -32.754  102,404  -44:301   1,00109.66    C
ATOM   6009  c    ASN  A  803    -33,159  101,462  -43,167   1,00110,06    c
ATOM   6010  CB   ASN  A  803    -31,719  103.411  -43,778   I,00109.27    c
ATOM   6011  O    THR  A  804    -34:960   98:440  -41:786   1,00107.00    0
ATOM   6012  N    THR  A  804    -34.243  101,766  -42.459   1,00108,10    N
ATOM   6013  CA   THR  A  804    -.34,768  100.817  -41,482   I,00106.15    C
ATOM   6014  C    THR  A  804    -35,191   99,565  -42,238   1,00106.74    C
ATOM   6015  CB   THR  A  804    -35.969  101,379  -40.690   1,00107,11    C
ATOM   6016  OG1  THR  A  804    -37:195  101:042  -41,356   1.00107.11    O
ATOM   6017  CG2  THR  A  804    -35,862  102.896  -40,544   1,00110.10    C
ATOM   6018  O    GLN  A  805    -35.590   96,548  -44.917   1.00103,40    O
ATOM   6019  N    GLN  A  805    -35.784   99.794  -43.409   1.00105.45    N
ATOM   6020  CA.  GLN  A  805    -.36,310   98.748  -44,282   1,00107,03    C
ATOM   602 1  C    GLN  A  805    -35.259   97,714  -44.695   1.00104,56    C
ATOM   6022  CB   GLN  A  805    -36.921   99,390  -45,532   1,00102,68    c
ATOM   6023  CG   GLN  A  805    -37,784  100.606  -45,243   1,00103,78    c
ATOM   602 4  CD   GLN  A  805    -37:806  101:596  -46:393   1,00106.05    c
ATOM   602 5  OE1  GLN  A  805    -36.808  102,252  -46.673   1,00106,03    0
ATOM   602 6  NE2  GLN  A  805    -.38,948  101.709  -47,062   I,00105.23    N
ATOM   602 7  O    LEU  A  806    -31,673   95.324  -44,638   1,00 96.76    O
ATOM   602 8  N    LEU  A  806    -34.000   98,149  -44.786   1,00105,28    N
ATOM   602 9  CA   LEU  A  806    -32.888   97:303  -45.243   1.00102.07    c
ATOM   6030  C    LEU  A  806    -32,588   96.101  -44,345   1,00102.16    C
ATOM   6031  CB   LEU  A  806    -31.600   98,129  -45.377   1,00102,96    C
ATOM   6032  CG   LEU  A  806    -31.436   99.175  -46:484   1.00104.26    c
ATOM   6033  CD1  LEU  A  806    -29,945   99.453  -46,722   1,00 99,91    c
ATOM   6034  CD2  LEU  A  806    -32.139   98,751  -47.773   1.00100,16    c
ATOM   6035  O    GLN  A  807    -33,180   92,485  -42.999   1,00 98,56    0
ATOM   6036  N    GLN  A  807    -.33,325   95.962  -43,245   1,00104,67    N
ATOM   6037  CA   GLN  A  807    -33.181   94.797  -42:384   1,00102.43    C
ATOM   6038  c    GLN  A  807    -33,750   93,571  -43,092   1,00 97,77    c
ATOM   6039  CB   GLN  A  807    -.33,869   95.020  -41,034   I,00101.36    c
ATOM   6040  N    ASN  A  808    -34:863   93:755  -43.807   1,00 97.25    N
ATOM   6041  CA   ASN  A  808    -35.466   92,675  -44.593   1,00100,04    C
ATOM   6042  C    ASN  A  808    -.34,483   92.131  -45,612   I,00101.25    C
ATOM   6043  O    ASN  A  808    -33,798   92.899  -46,290   1,00 98.55    O
ATOM   6044  CB   ASN  A  808    -36.736   93,141  -45.316   1,00101,20    c
ATOM   6045  CG   ASN  A  808    -37,234   92:121  -46:346   1.00101.35    c
ATOM   6046  OD1  ASN  A  808    -37,096   90.904  -46,162   1,00102.52    0
ATOM   6047  ND2  ASN  A  808    -37.807   92,618  -47.441   1.00 98,96    N
ATOM   6048  N    GLU  A  809    -34,425   90:806  -45.723   1.00101.73    N
ATOM   6049  CA.  GLU  A  809    -.33,434   90.158  -46,568   1,00 95,57    C
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ATOM 6050 C   GLU A 809 -33.667  90:406 -48.063 1.00 97.43   C
ATOM 6051 0   GLU A 809 --32,750 90.823 -48,773 1,00 96.37   O
ATOM 6052 CB  GLU A 809 -33.404  88,660 -46.278 1.00 96,88   C
ATOM 6053 CG  GLU A 809 -34.756  87:978 -46.341 1,00101,49   C
ATOM 6054 CD  GLU A 809 -34,626  86.500 -46,648 1,00104.75   C
ATOM 6055 OE1 GLU A 809 -35.634  85,876 -47.054 1.00105,09   0
ATOM 6056 OE2 GLU A 809 -33.506  85,966 -46.487 1,00103,40   0
ATOM 6057 N   LYS A 810 -34,887  90.167 -48,537 1,00 99.54   N
ATOM 6058 CA  LYS A 810 -35.182  90.276 -49.962 1,00 97,33   C
ATOM 6059 C   LYS A 810 -34.958  91,695 -50.476 1,00 97,12   C
ATOM 6060 0   LYS A 810 -34,291  91.900 -51,492 1,00 96.39   0
ATOM 6061 CB  LYS A 810 -36.615  89.833 -50:242 1,00 91.76   C
ATOM 6062 CG  LYS A 810 -36.986  88,560 -49.525 1,00 95,26   C
ATOM 6063 CD  LYS A 810 -37.507  87:518 -50.486 1.00 95.25   C
ATOM 6064 CE  LYS A 810 -37,749  86.207 -49,766 1,00 96.12   C
ATOM 6065 NZ  LYS A 810 -38.451  85,223 -50.628 1.00 98,09   N
ATOM 6066 N   LEU A 811 -35,504  92:675 -49.768 1,00 95.88   N
ATOM 6067 CA. LEU A 811 -35,340  94.060 -50,174 1,00 96.57   C
ATOM 6068 C   LEU A 811 -33.869  94,465 -50.238 1.00 96,95   C
ATOM 6069 O   LEU A 811 -33.466  95,204 -51.135 1,00 95,50   0
ATOM 6070 CB  LEU A 811 -36,086  94.994 -49,225 1,00101,17   C
ATOM 6071 CG  LEU A 811 -35.987  96:477 -49:588 1,00 97.56   C
ATOM 6072 CD1 LEU A 811 -36.536  96,700 -50.982 1,00 96,29   C
ATOM 6073 CD2 LEU A 811 -36,726  97..329 -48,573 1,00 98.78   C
ATOM 6074 N   TYR A 812 -33.067  93.980 -49:293 1,00 93.19   N
ATOM 6075 CA  TYR A 812 -31.676  94,403 -49.212 1,00 89,38   C
ATOM 6076 C   TYR A 812 -30,895  93.838 -50,383 1,00 92.35   C
ATOM 6077 O   TYR A 812 -30,048  94.522 -50,961 1,00 90.71   0
ATOM 6078 CB  TYR A 812 -31.048  93,976 -47.884 1,00 92,27   C
ATOM 6079 CG  TYR A 812 -29,606  94:407 -47.722 1.00 90.15   C
ATOM 6080 CD1 TYR A 812 -29,225  95.726 -47,937 1,00 94.38   C
ATOM 6081 CD2 TYR A 812 -28.629  93,500 -47..346 1.00 87,87   C
ATOM 6082 CE1 TYR A 812 -27:904  96:127 -47.789 1.00 90.66   C
ATOM 6083 CE2 TYR A 812 -27,308  93.891 -47,193 1,00 89.91   C
ATOM 6084 CZ  TYR A 812 -26.952  95,204 -47.419 1.00 89,69   C
ATOM 6085 OH  TYR A 812 -25.638  95,591 -47.272 1,00 93.80   0
ATOM 6086 N   LEU A 813 -31,198  92.588 -50,731 1,00 94.12   N
ATOM 6087 CA  LEU A 813 -30:599  91:925 -51:887 1,00 88.33   C
ATOM 6088 C   LEU A 813 -30.958  92,658 -53.174 1,00 86,52   C
ATOM 6089 O   LEU A 813 -30,092  92.930 -54,000 1,00 86.56   0
ATOM 6090 CB  LEU A 813 -31,054  90.463 -51,968 1,00 87.83   C
ATOM 6091 CG  LEU A 813 -30..318  89,446 -51.096 1,00 83,55   C
ATOM 6092 CD1 LEU A 813 -30.993  88:093 -51.160 1.00 84.01   C
ATOM 6093 CD2 LEU A 813 -28,881  89.326 -51,543 1,00 84.39   C
ATOM 6094 N   TYR A 814 -32 .242  92,970 -53.326 1.00 87,72   N
ATOM 6095 CA  TYR A 814 -32 ,756  93:727 -54.470 1.00 92.96   C
ATOM 6096 C   TYR A 814 -31,862  94.927 -54,810 1,00 92.99   C
ATOM 6097 O   TYR A 814 -31..351  95,033 -55.929 1,00 90,76   0
ATOM 6098 CB  TYR A 814 -34.195  94,175 -54.183 1,00 87,67   C
ATOM 6099 CG  TYR A 814 -34,845  95.037 -55,245 1,00 92.83   C
ATOM 6100 CD2 TYR A 814 -35:004  96:406 -55:053 1,00 95.33   C
ATOM 6101 CD1 TYR A 814 -35.338  94,482 -56.418 1,00 92,78   C
ATOM 6102 CE2 TYR A 814 -35,609  97.199 -56,011 1,00 92.98   C
ATOM 6103 CE1 TYR A 814 -35:947  95.272 -57:385 1,00 91.56   C
ATOM 6104 CZ  TYR A 814 -36.077  96,628 -57.176 1,00 94,15   C
ATOM 6105 OH  TYR A 814 -36,680  97.422 -58,129 1,00100,46   0
ATOM 6106 N   TYR A 815 -31,646  95.803 -53,831 1,00 96.37   N
ATOM 6107 CA  TYR A 815 -30.777  96,964 -54.007 1,00 93,36   C
ATOM 6108 C   TYR A 815 -29.327  96.529 -54.235 1.00 90.39   C
ATOM 6109 O   TYR A 815 -28,631  97.093 -55,076 1,00 91,80   0
ATOM 6110 CB  TYR A 815 -30.876  97,908 -52 .799 1.00 93,99   C
ATOM 6111 CG  TYR A 815 -32 ,133  98:770 -52 ,761 1.00 94.69   C
ATOM 6112 CD2 TYR A 815 -33,182  98.485 -51,890 1,00 96.56   C
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ATOM  6113  GDI  TYR  A  815   -32 .256   99.888  -53.580   1,00  98.77   c
ATOM  6114  CE2  TYR  A  815   --34,330   99.288  -51,851   1,00  99.41   C
ATOM  6115  CE1  TYR  A  815   -33.399   100,695  -53:550   1,00  98,31   c
ATOM  6116  CZ   TYR  A  815   -34.432   100:393  -52 ,686   1,00100.05   c
ATOM  6117  OH   TYR  A  815   -35,559   101.200  -52 ,668   1,00102,75   0
ATOM  6118  N    LEU  A  816   -28.879   95,511   -53:506   1,00  92,03   N
ATOM  6119  CA   LEU  A  816   -27.542   94,949   -53.706   1,00  88,90   c
ATOM  6120  C    LEU  A  816   -27,335   94.409   -55,123   1,00  89,47   C
ATOM  6121  O    LEU  A  816   --26.203  94,177   -55:549   1,00  91.63   0
ATOM  6122  CB   LEU  A  816   -27.281   93,830   -52 .700   1,00  88,47   c
ATOM  6123  CG   LEU  A  816   -26,925   94.219   -51,267   1,00  86.55   c
ATOM  6124  GDI  LEU  A  816   -26.842   92.965   -50:435   1,00  89.86   c
ATOM  6125  CD2  LEU  A  816   -25.607   94,973   -51.205   1,00  86,65   c
ATOM  6126  N    GLN  A  817   -28.431   94:206   -55:844   1,00  87.22   N
ATOM  6127  CA   GLN  A  817   -28,373   93.638   -57,179   1,00  88.60   C
ATOM  6128  C    GLN  A  817   -28.938   94,606   -58:206   1,00  90,09   c
ATOM  6129  O    GLN  A  817   -29.301   94:208   -59:311   1,00  93.38   0
ATOM  6130  CB   GLN  A  817   -29,128   92..311   -57,219   1,00  87,57   c
ATOM  6131  CG   GLN  A  817   -28.613   91,302   -56:209   1,00  88,27   c
ATOM  6132  CD   GLN  A  817   -29.544   90,128   -56,034   1,00  84,31   c
ATOM  6133  OE1  GLN  A  817   -29,280   89.225   -55,245   1,00  82,38   0
ATOM  6134  NE2  GLN  A  817   -30.634   90:123   -56:790   1,00  85.44   N
ATOM  6135  N    ASN  A  818   -29.007   95,877   -57.827   1,00  91,81   N
ATOM  6136  CA   ASN  A  818   -29,452   96.956   -58,712   1,00  92.70   C
ATOM  6137  C    ASN  A  818   -30.799   96.688   -59:392   1,00  93.97   C
ATOM  6138  O    ASN  A  818   -30.995   97,014   -60.560   1,00  96,86   O
ATOM  6139  CB   ASN  A  818   -28,384   97.238   -59,774   1,00  92.69   C
ATOM  6140  CG   ASN  A  818   -28,633   98.537   -60,520   1,00  97.56   C
ATOM  6141  OD1  ASN  A  818   -29.269   99,452   -59.997   1,00101,59   O
ATOM  6142  ND2  ASN  A  818   -28.157   98:613   -61:755   1,00  97.69   N
ATOM  6143  O    GLY  A  819   -33,920   94.792   -61,155   1,00  96.81   O
ATOM  6144  N    GLY  A  819   -31.729   96,100   -58:652   1,00  93,12   N
ATOM  6145  CA   GLY  A  819   -33.042   95:804   -59:188   1,00  90.86   c
ATOM  6146  C    GLY  A  819   -.33,022   94.790   -60,315   1,00  91,09   C
ATOM  6147  O    AP.G  A  820   -31.083   91,302   -59:740   1,00  85,30   O
ATOM  6148  N    ARG  A  820   -32 .004   93:927   -60.336   1,00  90,25   N
ATOM  6149  CA.  ARG  A  820   -.31,876   92.889   -61,371   1,00  91,52   C
ATOM  6150  C    ARG  A  820   -31.683   91:479   -60:804   1,00  85.28   C
ATOM  6151  CB   ARG  A  820   -30.702   93,194   -62..308   1,00  91,46   c
ATOM  6152  CG   ARG  A  820   -.30,513   94.656   -62,670   1,00  93.85   c
ATOM  6153  CD   ARG  A  820   -29,447   94.803   -63,747   1,00  95.58   c
ATOM  6154  NE   ARG  A  820   -29.760   93,989   -64.918   1,00  93,53   N
ATOM  6155  CZ   ARG  A  820   -30.688   94:308   -65:812   1,00  96.75   c
ATOM  6156  NH1  ARG  A  820   -31,392   95.424   -65,670   1,00  87.39   N
ATOM  6157  NH2  AP.G  A  820   -30.916   93,513   -66:845   1,00  96,05   N
ATOM  6158  O    ASP  A  821   -29.662   89:492   -61:936   1,00  83.17   O
ATOM  6159  N    ASP  A  821   -32 ,175   90.481   -61,534   1,00  84,84   N
ATOM  6160  CA   ASP  A  821   -31.919   89,078   -61:213   1,00  83,07   C
ATOM  6161  c    ASP  A  821   -30,414   88,804   -61,247   1,00  80,84   c
ATOM  6162  CB   ASP  A  821   -32 ,665   88.165   -62,195   1,00  82,72   c
ATOM  6163  CG   ASP  A  821   -32 .673   86.705   -61:772   1,00  81.61   c
ATOM  6164  OD2  ASP  A  821   -33.755   86,083   -61.820   1,00  83,63   0
ATOM  6165  OD1  ASP  A  821   -31,609   86:166   -61,408   1,00  82.91   0
ATOM  6166  O    MET  A  822   -27.031   85:967   -61:566   1,00  78.21   0
ATOM  6167  N    MET  A  822   -29.977   87,800   -60.499   1,00  8.1,62   N
ATOM  6168  CA   MET  A  822   -28,561   87.450   -60,454   1,00  83.92   C
ATOM  6169  C    MET  A  822   -28,209   86:251   -61:333   1,00  80.47   C
ATOM  6170  CB   MET  A  822   -28.144   87,168   -59.015   1,00  8.3,34   C
ATOM  6171  CG   MET  A  822   -27.903   88:409   -58:208   1,00  79.38   c
ATOM  6172  SD   MET  A  822   -26,253   89.046   -58,497   1,00  85.13   s
ATOM  6173  CE   MET  A  822   -25.288   87,620   -57.994   1,00  79,65   c
ATOM  6174  O    TYR  A  823   -29.088   83:748   -64.949   1,00  81.02   0
ATOM  6175  N    TYR  A  823   -29,231   85.552   -61,813   1,00  80,45   N
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ATOM   6176  CA   TYR  A  823    -29..031   84..352   -62..624   1,00  81.01    C
ATOM   6177  C    TYR  A  823    --29,393   84..570   -64.,087   1,00  81.31    C
ATOM   6178  CB   TYR  A  823    -29..856   83.,204   -62..063   1,00  78,.96    C
ATOM   6179  CG   TYR  A  823    -29..291   82.,641   -60..797   1,00  76..61    C
ATOM   6180  CD2  TYR  A  823    -30.,118   82. 113   -59.,819   1,00  78.,81    C
ATOM   6181  GD1  TYR  A  823    -27.928   82.,642   -60..573   1,00  75,.37    C
ATOM   6182  CE2  TYR  A  823    -29..597   81.,592   -58..652   1,00  80,.38    C
ATOM   6183  CE1  TYR  A  823    -27,398   82. 129   -59.,413   1,00  75.,77    C
ATOM   6184  CZ   TYR  A  823    -28..231   81..602   -58.,456   1,00  77.51    C
ATOM   6185  OH   TYR  A  823    -27.695   81.,091   -57..293   1,00  78,.37    0
ATOM   6186  O    VAL  A  824    -30.,932   88..196   -64.,837   1,00  84.63    0
ATOM   6187  N    VAL  A  824    -30..075   85..676   -64.,352   1,00  81.96    N
ATOM   6188  CA   VAL  A  824    -30. 540   85.,992   -65. 690   1,00  81,57    C
ATOM   6189  C    VAL  A  824    -30..657   87.,509   -65,815   1,00  85..06    C
ATOM   6190  CB   VAL  A  824    -31.,883   85..284   -65.,989   1,00  81.79    C
ATOM   6191  CG2  VAL  A  824    -32..782   86.,132   -66..866   1,00  87,67    C
ATOM   6192  CGI  VAL  A  824    -32..585   84.,890   -64.,697   1,00  80..89    C
ATOM   6193  O    ASP  A  825    -32.,446   89. 798   -68.,541   1,00  91,82    0
ATOM   6194  N    ASP  A  825    -30...396   88.,036   -67..006   1,00  90,.28    N
ATOM   6195  CA   ASP  A  825    -30..459   89.,475   -67..221   1,00  92,05    C
ATOM   6196  C    ASP  A  825    -31,888   89. 948   -67.,453   1,00  92,9.1    C
ATOM   6197  CB   ASP  A  825    -29..572   89.,880   -68.,396   1,00  94.52    C
ATOM   6198  CG   ASP  A  825    -29..754   91.,330   -68..790   1,00100,.63    C
ATOM   6199  OD2  ASP  A  825    -29.,386   92..226   -67.,995   1,00101..26    0
ATOM   6200  OD1  ASP  A  825    -30..275   91..574   -69.,897   1,00107..81    0
ATOM   6201  O    GLN  A  826    -33. 112   92.,067   -64. 386   1,00  99,30    0
ATOM   6202  N    GLN  A  826    -32.,467   90..521   -66.,405   1,00  92.9.3    N
ATOM   6203  CA   GLN  A  826    -33.,822   91..053   -66.,436   1,00  95..64    C
ATOM   6204  C    GLN  A  826    -33. 984   91.,995   -65. 251   1,00  96,54    C
ATOM   6205  CB   GLN  A  826    -34.848   89.,927   -66,377   1,00  90..28    C
ATOM   6206  CG   GLN  A  826    -34.,585   88..976   -65.,231   1,00  93..32    C
ATOM   6207  CD   GLN  A  826    -35..455   87.,738   -65..262   1,00  94,14    C
ATOM   6208  OE1  GLN  A  826    -36..313   87.,583   -66,133   1,00  95..68    0
ATOM   6209  NE2  GLN  A  826    -35.,236   86. 843   -64.,303   1,00  89.,84    N
ATOM   6210  O    GLU  A  827    -37..417   92.,448   -63..622   1,00  99,.25    0
ATOM   6211  N    GLU  A  827    -35..085   92.,725   -65..203   1,00  90,.83    N
ATOM   6212  CA.  GLU  A  827    -35.,326   93. 554   -64.,041   1,00  95.,16    C
ATOM   6213  C    GLU  A  827    -36,382   92.,923   -63.,149   1,00  99..64    C
ATOM   6214  CB   GLU  A  827    -35. 734   94.,967   -64. 452   1,00  95,99    C
ATOM   6215  CG   GLU  A  827    -34.,552   95..842   -64.,821   1,00  95..66    C
ATOM   6216  CD   GLU  A  827    -34.,708   97..272   -64.,349   1,00  95..48    C
ATOM   6217  OE1  GLU  A  827    -35. 791   97.,854   -64. 582   1,00  98,32    0
ATOM   6218  OE2  GLU  A  827    -33.,747   97.,808   -63.,746   1,00  92.89    0
ATOM   6219  O    LEU  A  828    -37.,548   94..608   -60.,085   1,00  95..04    0
ATOM   6220  N    LEU  A  828    -36..098   92.,906   -61..852   1,00  97,39    N
ATOM   6221  CA   LEU  A  828    -37..038   92.,393   -60.,871   1,00  97.75    c
ATOM   6222  C    LEU  A  828    -37.,984   93. 503   -60.,413   1,00  98.,56    C
ATOM   6223  CB   LEU  A  828    -36..289   91.,789   -59.683   1,00  95,.85    C
ATOM   6224  CG   LEU  A  828    -35..298   90.,679   -60..045   1,00  90,.46    C
ATOM   6225  CD1  LEU  A  828    -34.,702   90. 038   -58.,800   1,00  86.,37    C
ATOM   6226  CD2  LEU  A  828    -35.,963   89.,638   -60.,927   1,00  91.32    C
ATOM   6227  O    ASP  A  829    -40..349   93.,419   -57..697   1,00103,.09    0
ATOM   6228  N    ASP  A  829    -39,280   93..197   -60.,421   1,00102..22    N
ATOM   6229  CA   ASP  A  829    -40,320   94..131   -59,992   1,00103..13    C
ATOM   6230  C    ASP  A  829    -40. 236   94.,361   -58. 485   1,00105,.74    C
ATOM   6231  CB   ASP  A  829    -41,708   93..601   -60.,389   1,00105..02    C
ATOM   6232  CG   ASP  A  829    -42.,857   94..386   -59,755   1,00108..77    C
ATOM   6233  OD2  ASP  A  829    -43. 421   93.,906   -58. 747   1,00111,68    0
ATOM   6234  OD1  ASP  A  829    -43,215   95.,467   -60.,272   1,00108..45    0
ATOM   6235  O    ILE  A  830    -41,016   95..128   -54.,744   1,00108..35    0
ATOM   6236  N    ILE  A  830    -40.031   95.,620   -58..099   1,00106,.79    N
ATOM   6237  CA   ILE  A  830    -39,916   95.,999   -56,692   1,00105..68    C
ATOM   6238  C    ILE  A  830    -41,145   95. 588   -55.,877   1,00107.,47    C
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ATOM    6239   CB   ILE  A  830      -39..700   97..521  -56..536   1.00104..48          C
ATOM    6240   O    ASM  A  831      --43,818   93..560  -54.,279   1,00109..83          O
ATOM    6241   N    ASN  A  831      -42.333    95.,746  -56.455   1,00108,.38          N
ATOM    6242   CA   ASN  A  831      -43..577   95..447  -55.745   1.00108..10          C
ATOM    6243   C    ASM  A  831      -43,756    93. 956  -55.,445   1,00106.,93          C
ATOM    6244   CB   ASN  A  831      -44.776    95.,968  -56.540   1,00110,.47          C
ATOM    6245   O    ARG  A  832      -42..269   89.,991  -56.223   1,00101,.24          0
ATOM    6246   N    ARG  A  832      -43,824    93. 129  -56.,486   1,00107.,63          N
ATOM    6247   CA   ARG  A  832      -43..974   91..682  -56.312   1,00105..11          C
ATOM    6248   c    ARG  A  832      -42..691   91.,053  -55..762   1,00104,.65          c
ATOM    6249   CB   ARG  A  832      -44,364    91..024  -57.,640   1,00  98..94         c
ATOM    6250   O    LEU  A  833      -39..405   89..471  -54..050   1,00103..15          0
ATOM    6251   N    LEU  A  833      -42.114    91.,700  -54. 747   1,00106,.94          N
ATOM    6252   CA   LEU  A  833      -40..759   91..420  -54..263   1.00102..93          c
ATOM    6253   C    LEU  A  833      -40,506    89..973  -53.,861   1,00100..02          c
ATOM    6254   CB   LEU  A  833      -40..424   92.,326  -53..072   1,00100,.77          c
ATOM    6255   CG   LEU  A  833      -39..150   93..175  -53..168   1.00  98..97         c
ATOM    6256   CD1  LEU  A  833      -38.,703   93. 688  -51,798    1,00  98.,11         c
ATOM    6257   CD2  LEU  A  833      -38..030   92.,411  -53..844   1,00  97,83          c
ATOM    6258   O    SER  A  834      -42..698   85.,983  -53.111    1,00  95,.89         0
ATOM    6259   N    SER  A  834      -41,496    89. 301  -53.,289   1,00  98.,07         N
ATOM    6260   CA   SER  A  834      -41.274    87..908  -52..938   1,00101..18          c
ATOM    6261   c    SER  A  834      -42..251   86.,997  -53.648    1,00  98,.43         c
ATOM    6262   CB   SER  A  834      -41,347    87..698  -51.,431   1,00107..56          c
ATOM    6263   OG   SER  A  834      -40..587   86..547  -51..078   1,00108..55          0
ATOM    6264   O    ASP  A  835      -42.198    84.,541  -56. 922   1,00  91,09          0
ATOM    6265   N    ASP  A  835      -42.,576   87..382  -54.,872   1,00  99..43         N
ATOM    6266   CA   ASP  A  835      -43,144    86..445  -55.,814   1,00101..76          C
ATOM    6267   C    ASP  A  835      -41.989    85.,570  -56. 293   1,00  96,50          C
ATOM    6268   CB   ASP  A  835      -43..832   87..170  -56.975    1.00100..30          c
ATOM    6269   O    TYR  A  836      -39,152    84..801  -54.,016   1,00100..18          0
ATOM    6270   N    TYR  A  836      -40..767   85.,997  -55..966   1,00  98,.90         N
ATOM    6271   CA   TYR  A  836      -39.546    85..288  -56.353    1.00  97.75          c
ATOM    6272   C    TYR  A  836      -38.,856   84. 566  -55.,190   1,00  97,75          c
ATOM    6273   CB   TYR  A  836      -38..527   86.,245  -56.987    1,00  94,89          c
ATOM    6274   CG   TYR  A  836      -39..104   87.,441  -57..705   1,00  96,.53         c
ATOM    6275   CD1  TYR  A  836      -39,865    87. 291  -58.,858   1,00  96.,78         c
ATOM    6276   CD2  TYR  A  836      -38..853   88..728  -57..245   1,00  98..00         c
ATOM    6277   CE1  TYR  A  836      -40. 383   88.,394  -59. 517   1,00100,.10          c
ATOM    6278   CE2  TYR  A  836      -39,359    89..833  -57.,897   1,00  98..09         c
ATOM    6279   CZ   TYR  A  836      -40,123    89..662  -59,030    1,00100..85          c
ATOM    6280   OH   TYR  A  836      -40. 625   90.,764  -59. 675   1,00104,63           0
ATOM    6281   O    ASP  A  837      -35.313    84..490  -54..858   1.00  89..82         0
ATOM    6282   N    ASP  A  837      -37.,909   83..706  -55.,548   1,00  91.48          N
ATOM    6283   CA   ASP  A  837      -37..130   82.,940  -54..591   1,00  94,09          c
ATOM    6284   c    ASP  A  837      -35..894   83..698  -54..119   1.00  91.12          c
ATOM    6285   CB   ASP  A  837      -36,689    81. 604  -55.,212   1,00  90.,74         c
ATOM    6286   CG   ASP  A  837      -37..861   80.,701  -55..575   1,00  93,.84         c
ATOM    6287   OD1  ASP  A  837      -38..706   80.,429  -54..694   1,00  93,.32         0
ATOM    6288   OD2  ASP  A  837      -37.,932   80. 256  -56.,743   1,00  90.,98         0
ATOM    6289   N    VAL  A  838      -35..495   83..449  -52..880   1,00  90..35         N
ATOM    6290   CA   VAL  A  838      -34..142   83.,764  -52..451   1,00  86,.41         c
ATOM    6291   C    VAL  A  838      -33.,365   82..458  -52.,457   1,00  84.92          c
ATOM    6292   O    VAL  A  838      -33..866   81..433  -51..998   1,00  86..52         0
ATOM    6293   CB   VAL  A  838      -34. 101   84.,420  -51. 060   1,00  88,61          c
ATOM    6294   CGI  VAL  A  838      -32.,834   84..044  -50.,325   1,00  84.33          c
ATOM    6295   CG2  VAL  A  838      -34.,215   85..934  -51.,186   1,00  92.74          c
ATOM    6296   O    ASP  A  839      -29. 318   82.,302  -52. 766   1,00  82,83          0
ATOM    6297   N    ASP  A  839      -32..153   82..485  -52..998   1.00  82.96          N
ATOM    6298   CA   ASP  A  839      -31.,428   81..246  -53.,240   1,00  87.54          c
ATOM    6299   C    ASP  A  839      -29..993   81.,270  -52..726   1,00  83,.90          c
ATOM    6300   CB   ASP  A  839      -31..433   80..926  -54..737   1.00  86..08         c
ATOM    6301   CG   ASP  A  839      -30.,621   79.694   -55.,072   1,00  82,59          c
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ATOM 6302 OD2 ASP A 839 -30.053 79.648 -56.178 1.00 81.72 O
ATOM 6303 OD1 ASP A 839 --30,545 78.775 -54,229 1,00 87.30 O
ATOM 6304 O ALA A 840 -27.571 78,447 -53.508 1,00 83,03 O
ATOM 6305 N ALA A 840 -29.544 80,110 -52.253 1.00 81.75 N
ATOM 6306 CA. ALA A 840 -28,198 79.947 -51,739 1,00 81.54 C
ATOM 6307 C ALA A 840 -27.280 79,446 -52 .848 1,00 83,22 C
ATOM 6308 CB ALA A 840 -28.194 78,997 -50.559 1,00 80,84 C
ATOM 6309 O ILE A 841 -24,623 77.682 -54,842 1,00 79.48 0
ATOM 6310 N ILE A 841 -26.176 80,160 -53,044 1,00 80.77 N
ATOM 6311 CA ILE A 841 -25.233 79,887 -54.122 1,00 80,18 C
ATOM 6312 C ILE A 841 -24,550 78.537 -53,953 I,00 81.16 C
ATOM 6313 CB ILE A 841 -24.175 80.993 -54,203 1,00 82.36 C
ATOM 6314 CGI ILE A 841 -24.859 82,337 -54.458 1,00 77,37 C
ATOM 6315 CG2 ILE A 841 -23,146 80,682 -55,282 1.00 78.93 C
ATOM 6316 CD1 ILE A 841 -24,448 83.421 -53,508 1,00 76.41 C
ATOM 6317 O VAL A 842 -25.076 76,930 -50.724 1,00 81,61 0
ATOM 6318 N VAL A 842 -23,871 78,353 -52,823 1.00 81.89 N
ATOM 6319 CA. VAL A 842 -23,426 77.024 -52 ,427 1,00 78.82 C
ATOM 632 0 C VAL A 842 -24.584 76,380 -51.705 1,00 80,18 C
ATOM 632 1 CB VAL A 842 ~22.200 77,053 -51.524 1,00 79,48 C
ATOM 6322 CG2 VAL A 842 -21,053 77.721 -52 ,235 1,00 78.38 C
ATOM 632 3 CGI VAL A 842 -21.816 75,635 -51,103 1,00 81.29 C
ATOM 632 4 O PRO A 843 -25.281 74,096 -49.548 1,00 84,91 0
ATOM 6325 N PRO A 843 -25,047 75.229 -52 ,214 I,00 80.25 N
ATOM 632 6 CA PRO A 843 -26.245 74.553 -51,711 1,00 83.73 C
ATOM 632 7 C PRO A 843 -26.291 74,413 -50.188 1,00 85,86 C
ATOM 6328 CB PRO A 843 -26,166 73.192 -52 ,389 I,00 84.31 C
ATOM 632 9 CG FRO A 843 -25,540 73.503 -53,703 1,00 81.42 C
ATOM 6330 CD PRO A 843 -24.523 74,575 -53.423 1,00 78,76 C
ATOM 6331 O GLN A 844 -27.254 72,863 -46,523 1.00 93.75 0
ATOM 6332 N GLN A 844 -27,469 74.666 -49,623 1,00 84.77 N
ATOM 6333 CA GLN A 844 -27.685 74,550 -48.187 1,00 85,99 C
ATOM 6334 C GLN A 844 -27,404 73,119 -47.721 1.00 92.14 C
ATOM 6335 CB GLN A 844 -29,113 74.971 -47,823 1,00 85.16 C
ATOM 6336 O SER A 845 -25.165 69,845 -47.169 1,00 87,17 0
ATOM 6337 N SER A 845 -27.328 72,199 -48.681 1,00 89,18 N
ATOM 6338 CA. SER A 845 -26,963 70.812 -48,433 1,00 82.50 C
ATOM 6339 C SER A 845 -25,503 70,669 -48,027 1,00 84.85 C
ATOM 6340 CB SER A 845 -27.219 69.967 -49.683 1,00 86,33 C
ATOM 6341 OG SER A 845 -28,197 70.573 -50,511 I,00 95.67 0
ATOM 6342 O FHE A 846 -21,539 71.861 -46,862 1,00 81.96 0
ATOM 6343 N PHE A 846 -24.639 71,465 -48.652 1,00 84,83 N
ATOM 6344 CA PHE A 846 -23,192 71,301 -48,509 1.00 84.10 C
ATOM 6345 C FHE A 846 -22,578 72.192 -47,432 1,00 84.88 C
ATOM 6346 CB PHE A 846 -22.495 71,572 -49.842 1,00 82,87 C
ATOM 6347 CG PHE A 846 -22.818 70,569 -50.911 1.00 86.75 C
ATOM 6348 CD1 PHE A 846 -22,288 69.289 -50.860 1,00 82.66 C
ATOM 6349 CD2 PHE A 846 -23.644 70,908 -51.977 1,00 87,38 C
ATOM 6350 CE1 PHE A 846 ~22.584 68,359 -51.852 1,00 89,43 C
ATOM 6351 CE2 PHE A 846 -23,943 69.984 -52 ,975 1,00 86.76 C
ATOM 6352 CZ PHE A 846 -23,414 68,710 -52 ,912 1,00 87.93 C
ATOM 6353 O LEU A 847 -24.768 75,429 -46.127 1,00 90,86 0
ATOM 6354 N LEU A 847 -23,220 73.320 -47,153 I,00 85.11 N
ATOM 6355 CA LEU A 847 -22,674 74.287 -46,207 1,00 81.28 C
ATOM 6356 C LEU A 847 -23.779 75,046 -45.500 1,00 84,85 C
ATOM 6357 CB LEU A 847 -21,751 75.265 -46,934 I,00 84.40 C
ATOM 6358 CG LEU A 847 -21,240 76.491 -46,178 1,00 87.49 C
ATOM 6359 GDI LEU A 847 -21.108 77,666 -47.135 1,00 83,48 C
ATOM 6360 CD2 LEU A 847 -19.908 76,193 -45.491 1.00 78.20 C
ATOM 6361 O LYS A 848 -23,654 78.069 -42,485 1,00 89.14 0
ATOM 6362 N LYS A 848 -23.621 75,272 -44.201 1,00 87,39 N
ATOM 6363 CA LYS A 848 -24.594 76,073 -43.458 1.00 92.59 C
ATOM 6364 C LYS A 848 -24,230 77.568 -43,453 1,00 90.95 C
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ATOM   6365  CB   LYS  A 848    -24.719   75.559  -42.023   1.00  95.13   C
ATOM   6366  O    ASP  A 849    --25,748  80.504  -46,385   1,00  91.64   0
ATOM   6367  N    ASP  A 849    -24.556   78,270  -44.540   1,00  91,23   N
ATOM   6368  CA   ASP  A 849    -24.341   79,719  -44.613   1.00  90.73   C
ATOM   6369  C    ASP  A 849    -25,573   80.413  -45,173   1,00  87.25   C
ATOM   6370  CB   ASP  A 849    -23.114   80,056  -45.464   1,00  84,67   C
ATOM   6371  O    ASP  A 850    -28.166   83,884  -45.233   1,00  92,16   O
ATOM   6372  N    ASP  A 850    -26,440   80.885  -44,284   1,00  85,39   N
ATOM   6373  CA   ASP  A 850    -27.644   81,597  -44,704   1,00  90.61   C
ATOM   6374  C    ASP  A 850    -27.305   83,072  -44.903   1,00  88,13   C
ATOM   6375  CB   ASP  A 850    -28,769   81.422  -43,679   I,00  89.52   C
ATOM   6376  O    SER  A 851    -25.084   84.468  -47,221   1,00  86.97   0
ATOM   6377  N    SER  A 851    -26.025   83,385  -44.712   1,00  87,71   N
ATOM   6378  CA   SER  A 851    -25.474   84,724  -44,872   1.00  83.56   C
ATOM   6379  C    SER  A 851    -25,478   85.213  -46,320   1,00  89.45   C
ATOM   6380  CB   SER  A 851    -24.051   84,742  -44..334   1,00  86,94   C
ATOM   6381  OG   SER  A 851    -23.292   85,756  -44.954   1.00  89.36   O
ATOM   6382  O    ILE  A 852    -25,057   86.879  -50,034   1,00  88.52   O
ATOM   6383  N    ILE  A 852    -25.887   86,473  -46.527   1,00  90,88   N
ATOM   6384  CA   ILE  A 852    -26.069   87,054  -47.870   1,00  88,86   C
ATOM   6385  C    ILE  A 852    -24,880   86.887  -48,815   1,00  86.80   C
ATOM   6386  CB   ILE  A 852    -26.396   88,577  -47,823   1,00  86.04   C
ATOM   6387  CGI  ILE  A 852    -25.505   89,316  -46.824   1,00  85,80   C
ATOM   6388  CG2  ILE  A 852    -27,848   88.801  -47,488   I,00  86.12   C
ATOM   6389  CD1  ILE  A 852    -25.704   90.812  -46,856   1,00  78.71   C
ATOM   6390  O    ASP  A 853    -21.827   84,542  -50.454   1,00  86,03   0
ATOM   6391  N    ASP  A 853    -23,674   86.735  -48,281   I,00  85.22   N
ATOM   6392  CA   ASP  A 853    -22,547   86.439  -49,153   1,00  85.85   C
ATOM   6393  C    ASP  A 853    -22.688   85,012  -49.712   1,00  87,92   C
ATOM   6394  CB   ASP  A 853    -21.218   86,615  -48,424   1.00  85.14   C
ATOM   6395  CG   ASP  A 853    -21,045   85.630  -47,290   1,00  93.46   C
ATOM   6396  OD1  ASP  A 853    -22.067   85,278  -46.661   1,00  94,95   0
ATOM   6397  OD2  ASP  A 853    -19.894   85,205  -47.029   1.00  90.48   0
ATOM   6398  O    ASM  A 854    -26,352   82.052  -50,177   1,00  83.79   0
ATOM   6399  N    ASN  A 854    -23.777   84,334  -49..343   1,00  86,46   N
ATOM   6400  CA   ASN  A 854    -24.192   83,098  -49.994   1,00  84,74   C
ATOM   6401  C    ASM  A 854    -25,697   83.089  -50,256   1,00  84.58   C
ATOM   6402  CB   ASN  A 854    -23.803   81,890  -49,159   1,00  83.03   C
ATOM   6403  CG   ASN  A 854    -23.897   80,601  -49.938   1,00  86,12   C
ATOM   6404  OD1  ASN  A 854    -22,928   80:165  -50,565   I,00  84.27   0
ATOM   6405  ND2  ASN  A 854    -25,074   79.988  -49,918   1,00  85.72   N
ATOM   6406  N    LYS  A 855    -26.245   84,255  -50.569   1,00  80,34   N
ATOM   6407  CA   LYS  A 855    -27.671   84,355  -50,844   1.00  82.99   C
ATOM   6408  C    LYS  A 855    -27,928   85.210  -52 ,084   1,00  80.70   C
ATOM   6409  O    LYS  A 855    -27.328   86,271  -52 .262   1,00  77,16   O
ATOM   6410  CB   LYS  A 855    -28.412   84,926  -49.634   1.00  83.37   C
ATOM   6411  N    VAL  A 856    -28,820   84.737  -52 ,943   1,00  79.64   N
ATOM   6412  CA   VAL  A 856    -29.095   85,413  -54.204   1,00  83,06   C
ATOM   6413  C    VAL  A 856    -30.596   85,633  -54.359   1,00  84,41   C
ATOM   6414  0    VAL  A 856    -31,381   84.715  -54,115   1,00  87.11   0
ATOM   6415  CB   VAL  A 856    -28.542   84,592  -55,404   1,00  77.52   C
ATOM   6416  CGI  VAL  A 856    -29.364   84,821  -56.643   1,00  77,18   C
ATOM   6417  CG2  VAL  A 856    -27,070   84.916  -55,654   I,00  71.64   C
ATOM   6418  N    LEU  A 857    -30.996   86.845  -54,739   1,00  79.24   N
ATOM   6419  CA   LEU  A 857    -32.401   87,118  -55.034   1,00  83,67   C
ATOM   6420  C    LEU  A 857    -32 ,687   86.927  -56.522   I,00  82.38   C
ATOM   6421  O    LEU  A 857    -32 ,210   87.690  -57,362   1,00  81.44   0
ATOM   6422  CB   LEU  A 857    -32.783   88,532  -54.597   1,00  85,53   C
ATOM   6423  CG   LEU  A 857    -34,230   88,943  -54,879   1.00  86.79   C
ATOM   6424  CD1  LEU  A 857    -35,214   87.992  -54,210   1,00  86.82   C
ATOM   6425  CD2  LEU  A 857    -34.463   90,370  -54.421   1,00  87,61   C
ATOM   6426  N    THR  A 858    -33.463   85,899  -56.846   1.00  82.00   N
ATOM   6427  CA.  TH.R A 858    -33,682   85.531  -58,239   1,00  83.08   C
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ATOM   6428  C    THR  A  858    -35..123   85..116  -58..449   1,00  87.15     C
ATOM   6429  O    THR  A  858    --35.,791  84..671  -57.,517   1,00  86..69    0
ATOM   6430  CB   THR  A  858    -32..738   84.,381  -58..693   1.00  81,67     C
ATOM   6431  OG1  THR  A  858    -33..019   84.,019  -60.,052   1,00  82.83     0
ATOM   6432  CG2  THR  A  858    -32.,913   83. 166  -57 ,815   1,00  83..75    C
ATOM   6433  N    AP.G A  859    -35..584   85.,260  -59.689    1.00  88,.15    N
ATOM   6434  CA   ARG  A  859    -36..974   85.,013  -60..059   1,00  87,69     C
ATOM   6435  C    ARG  A  859    -37.,381   83. 550  -59.,884   1,00  91.18     C
ATOM   6436  O    ARG  A  859    -38..564   83.,238  -59,767    1,00  96..43    0
ATOM   6437  CB   ARG  A  859    -37 .204   85.,458  -61..504   1,00  90,.03    C
ATOM   6438  CG   ARG  A  859    -.38.,609   85..252  -62.,017   1,00  91.9.3    C
ATOM   6439  CD   ARG  A  859    -38..879   86..053  -63.,280   1,00  93..15    C
ATOM   6440  NE   ARG  A  859    -38. 684   87.,482  -63. 053   1,00  98,79     N
ATOM   6441  CZ   ARG  A  859    -38..946   88.,425  -63.,950   1,00  97.22     C
ATOM   6442  NH1  ARG  A  859    -38.,734   89..701  -63.,656   1,00  93..57    N
ATOM   6443  NH2  AP.G A  859    -39..423   88.,087  -65..140   1.00  98,.17    N
ATOM   6444  O    SER  A  860    -34.422    80.,614  -59..492   1,00  89..34    O
ATOM   6445  N    SER  A  860    -36,404    82. 652  -59.,844   1,00  90..18    N
ATOM   6446  CA   SER  A  860    -36..714   81.,236  -59.715    1.00  91,26     C
ATOM   6447  C    SER  A  860    -35..580   80.,419  -59.132    1,00  89,.63    C
ATOM   6448  CB   SER  A  860    -37.,054   80. 655  -61.,074   1,00  92.98     C
ATOM   6449  OG   SER  A  860    -35..841   80.,352  -61.,737   1,00  90..23    0
ATOM   6450  O    ASP  A  861    -33..283   77,361   -59.141    1,00  85,.34    0
ATOM   6451  N    ASP  A  861    -35.,927   79.488   -58.,249   1,00  94.06     N
ATOM   6452  CA   ASP  A  861    -35..020   78..411  -57.,861   1,00  90..86    C
ATOM   6453  C    ASP  A  861    -34. 439   77,768   -59. 109   1,00  86,36     C
ATOM   6454  CB   ASP  A  861    -35.,747   77..341  -57.,036   1,00  88..18    C
ATOM   6455  CG   ASP  A  861    -35.,933   77.736   -55.,589   1,00  90..87    C
ATOM   6456  OD1  ASP  A  861    -35. 194   78,627   -55. 120   1,00  88,85     0
ATOM   6457  OD2  ASP  A  861    -36..810   77,139   -54.920    1,00  95..25    0
ATOM   6458  O    LYS  A  862    -32.,771   76.674   -62.,367   1,00  82.26     0
ATOM   6459  N    LYS  A  862    -35..263   77,684   -60..142   1.00  8.3,.14    N
ATOM   6460  CA   LYS  A  862    -34.928    76.,924  -61..331   1,00  84.24     C
ATOM   6461  C    LYS  A  862    -3.3.,698   77.437   -62.,090   1,00  84.69     C
ATOM   6462  CB   LYS  A  862    -36..134   76.,901  -62..259   1.00  85,.19    C
ATOM   6463  O    ASN  A  863    -30..382   79.,568  -63..771   1,00  82,67     0
ATOM   6464  N    ASM  A  863    -3.3.,687   78.730   -62.,397   1,00  84.06     N
ATOM   6465  CA   ASN  A  863    -32..708   79.,335  -63.,305   1,00  81.02     C
ATOM   6466  C    ASN  A  863    -31. 230   79.,105  -63. 016   1,00  80,01     C
ATOM   6467  CB   ASN  A  863    -.32.,940   80..842  -63.,359   1,00  80..70    C
ATOM   6468  CG   ASN  A  863    -34.,114   81..215  -64.,237   1,00  80..21    C
ATOM   6469  OD1  ASN  A  863    -34. 245   80.,718  -65. 350   1,00  79,29     0
ATOM   6470  ND2  ASN  A  863    -34.977    82.,091  -63.,740   1,00  82.36     N
ATOM   6471  O    ARG  A  864    -27,735    76.681   -61.,958   1,00  85..85    0
ATOM   6472  N    AP.G A  864    -30..916   78.,401  -61..937   1.00  79,.38    N
ATOM   6473  CA   ARG  A  864    -29..530   78.,204  -61.,544   1,00  77.16     C
ATOM   6474  C    ARG  A  864    -28,924    76.934   -62.,126   1,00  80..9.3   C
ATOM   6475  CB   AP.G A  864    -29..422   78.,158  -60..028   1.00  76,.56    C
ATOM   6476  CG   ARG  A  864    -30..236   77,044   -59.426    1,00  83,.40    C
ATOM   6477  CD   ARG  A  864    -29.,402   76.188   -58.,507   1,00  84.38     C
ATOM   6478  ME   ARG  A  864    -28..789   76..995  -57.,466   1,00  78..25    N
ATOM   6479  CZ   ARG  A  864    -27.680    76,650   -56.835    1,00  80,.56    C
ATOM   6480  NH1  ARG  A  864    -27.,170   77.441   -55.,900   1,00  80..46    N
ATOM   6481  NH2  ARG  A  864    -27..085   75..507  -57.,149   1,00  81.42     N
ATOM   6482  O    GLY  A  865    -30. 634   73,625   -61. 729   1,00  89,49     O
ATOM   6483  N    GLY  A  865    -29.,737   76..134  -62.,808   1,00  82.51     N
ATOM   6484  CA   GLY  A  865    -29,289    74.839   -63.,289   1,00  88..79    C
ATOM   6485  C    GLY  A  865    -29. 542   73,726   -62. 283   1,00  86,65     C
ATOM   6486  O    LYS  A  866    -28,482    73.,356  -59,326    1,00  91.52     0
ATOM   6487  N    LYS  A  866    -28,531    72.896   -62.,043   1,00  85..11    N
ATOM   6488  CA   LYS  A  866    -28..659   7.1,770  -61..119   1.00  90,.06    C
ATOM   6489  C    LYS  A  866    -28..915   72.,265  -59,694    1,00  90..93    C
ATOM   6490  CB   LYS  A  866    -27,400    70.886   -61.,156   1,00  92,3.1    C
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ATOM	6491	CG	LYS	A	866	-26.961	70.453	-62.560	1.00	92.41	c
ATOM	6492	CD	LYS	A	866	--27,238	68.979	-62,829	1,00	93.87	C
ATOM	6493	CE	LYS	A	866	-27.251	68,688	-64.328	1,00	94,46	C
ATOM	6494	NZ	LYS	A	866	-27.453	67,237	-64,629	1.00100.35		N
ATOM	6495	O	SER	A	867	-28,684	72.063	-55,494	1,00	91,03	O
ATOM	6496	N	SER	A	867	-29.620	71,463	-58.900	1,00	89,20	N
ATOM	6497	CA	SER	A	867	-29.950	71,836	-57.526	1,00	90,73	C
ATOM	6498	C	SER	A	867	-28,819	71.479	-56,566	1,00	89,67	C
ATOM	6499	CB	SER	A	867	-31.242	71,151	-57,087	1,00	91.17	C
ATOM	6500	OG	SER	A	867	-32 .195	71,178	-58.136	1,00	97,88	0
ATOM	6501	O	ASP	A	868	-24,545	69.940	-56,241	1,00	82.23	0
ATOM	6502	N	ASP	A	868	-27.999	70.523	-56,973	1,00	86.42	N
ATOM	6503	CA	ASP	A	868	-26.942	69,993	-56.120	1,00	90,00	C
ATOM	6504	C	ASP	A	868	-25,573	70,612	-56,402	1.00	91.61	C
ATOM	6505	CB	ASP	A	868	-26,849	68.474	-56,299	1,00	92.05	C
ATOM	6506	CG	ASP	A	868	-26.767	68,066	-57.770	1,00	93,16	C
ATOM	6507	OD1	ASP	A	868	-27.829	67,751	-58,361	1.00	93.07	0
ATOM	6508	OD2	ASP	A	868	-25,646	68.088	-58,335	1,00	89,65	0
ATOM	6509	O	ASN	A	869	-25.120	74,648	-56.765	1,00	78,65	0
ATOM	6510	N	ASN	A	869	-25.542	71,877	-56,823	1,00	90,27	N
ATOM	6511	CA.	ASM	A	869	-24,269	72.465	-57,229	1,00	86,71	C
ATOM	6512	C	ASN	A	869	-24.161	73,971	-57,120	1,00	82.13	C
ATOM	6513	CB	ASN	A	869	-23.958	72,068	-58.673	1,00	85,39	C
ATOM	6514	CG	ASN	A	869	-22,723	71.209	-58,778	1,00	85.91	C
ATOM	6515	OD1	ASN	A	869	-22,805	69,980	-58,742	1,00	88.77	0
ATOM	6516	ND2	ASN	A	869	-21.562	71,851	-58.889	1,00	84,49	N
ATOM	6517	O	VAL	A	870	-23,497	75.265	-59,897	1,00	91.88	O
ATOM	6518	N	VAL	A	870	-22,951	74.455	-57,400	1,00	79.26	N
ATOM	6519	CA	VAL	A	870	-22.670	75,846	-57.739	1,00	80,67	C
ATOM	6520	C	VAL	A	870	-23,388	76,160	-59,055	1.00	86.36	C
ATOM	6521	CB	VAL	A	870	-21,144	76.066	-57,874	1,00	79.70	C
ATOM	6522	CGI	VAL	A	870	-20.517	74,898	-58.601	1,00	86,53	C
ATOM	6523	CG2	VAL	A	870	-20,810	77,362	-58,605	1.00	87.19	C
ATOM	6524	O	PRO	A	871	-22,664	77.235	-61,782	1,00	85,47	0
ATOM	6525	N	PRO	A	871	-23.903	77,402	-59.231	1,00	81,59	N
ATOM	6526	CA	PRO	A	871	-24.544	77,844	-60.480	1,00	83,67	C
ATOM	6527	C	PRO	A	871	-23,889	77.292	-61,741	1,00	84,88	C
ATOM	6528	CB	PRO	A	871	-24,388	79,364	-60,419	1,00	85.00	C
ATOM	6529	CG	PRO	A	871	-24.516	79,664	-58.962	1,00	82,75	C
ATOM	6530	CD	PRO	A	871	-23,975	78.458	-58,202	1,00	83.21	C
ATOM	6531	O	SER	A	872	-23,543	78.306	-64,928	1,00	85.82	0
ATOM	6532	N	SER	A	872	-24.691	76,900	-62.733	1,00	86,20	N
ATOM	6533	CA	SER	A	872	-24,195	76,221	-63,940	1.00	87.04	c
ATOM	6534	C	SER	A	872	-23,318	77.106	-64,828	1,00	86.38	C
ATOM	6535	CB	SER	A	872	-25.367	75,702	-64.767	1,00	82,79	C
ATOM	6536	OG	SER	A	872	-25.941	76,745	-65,538	1.00	83.52	0
ATOM	6537	O	GLU	A	873	-21,643	79.054	-67,941	1,00	86,15	0
ATOM	6538	N	GLU	A	873	-22.336	76,503	-65.495	1,00	88,55	N
ATOM	6539	CA	GLU	A	873	-21.429	77,252	-66.364	1,00	86,83	C
ATOM	6540	C	GLU	A	873	-22,172	78.061	-67,436	1,00	85,18	C
ATOM	6541	CB	GLU	A	873	-20,424	76,302	-67,022	1,00	89.41	C
ATOM	6542	O	GLU	A	874	-24.313	80,780	-68.800	1,00	89,00	0
ATOM	6543	N	GLU	A	874	-23,396	77.647	-67,765	1,00	82.75	N
ATOM	6544	CA	GLU	A	874	-24,232	78,382	-68,714	1,00	84.67	C
ATOM	6545	C	GLU	A	874	-24.600	79,760	-68.166	1,00	86,86	C
ATOM	6546	CB	GLU	A	874	-25,500	77.592	-69,053	1,00	83.33	C
ATOM	6547	O	VAL	A	875	-24,238	83.056	-65,967	1,00	79.05	O
ATOM	6548	N	VAL	A	875	-25.229	79,800	-66.991	1,00	84,45	N
ATOM	6549	CA	VAL	A	875	-25,551	81,081	-66,364	1.00	83.34	C
ATOM	6550	C	VAL	A	875	-24,279	81.828	-65,936	1,00	83.00	C
ATOM	6551	CB	VAL	A	875	-26.500	80,915	-65.144	1,00	85,16	C
ATOM	6552	CGI	VAL	A	875	-27.958	80,870	-65,593	1.00	87.38	C
ATOM	6553	CG2	VAL	A	875	-26,159	79.680	-64,355	1,00	84,29	C

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ATOM   6554  O    VAL  A  876    -20,960   83.585  -66.388   1.00  83.76      O
ATOM   6555  N    VAL  A  876   --23,237   81.091  -65,553   1,00  84.46      N
ATOM   6556  CA   VAL  A  876    -21.947   81,714  -65:259   1.00  80,63      C
ATOM   6557  C    VAL  A  876    -21.413   82:445  -66:489   1.00  82.55      C
ATOM   6558  CB   VAL  A  876    -20,905   80.695  -64,785   1,00  82.65      C
ATOM   6559  CG2  VAL  A  876    -21.299   80,124  -63:437   1.00  86,37      C
ATOM   6560  CGI  VAL  A  876    -19.535   81,346  -64.690   1,00  85,25      C
ATOM   6561  O    LYS  A  877    -21,381   84.696  -69,667   1,00  79.15      0
ATOM   6562  N    LYS  A  877    -21.491   81:800  -67:649   1,00  82.98      N
ATOM   6563  CA   LYS  A  877    -21.085   82,436  -68:902   1,00  82,45      C
ATOM   6564  C    LYS  A  877    -21,919   83.682  -69,220   1,00  77.58      C
ATOM   6565  CB   LYS  A  877    -21.173   81.440  -70:069   1,00  79.30      C
ATOM   6566  N    LYS  A  878    -23.223   83,627  -68.990   1,00  71,37      N
ATOM   6567  CA   LYS  A  878    -24.055   84:767  -69:366   1.00  80.34      C
ATOM   6568  C    LYS  A  878    -24,009   85.911  -68,350   1,00  78.42      C
ATOM   6569  O    LYS  A  878    -24.285   87,056  -68:698   1.00  81,22      O
ATOM   6570  CB   LYS  A  878    -25.508   84:327  -69:580   1.00  79.92      C
ATOM   6571  N    MET  A  879    -23,655   85.615  -67,102   1,00  81.05      N
ATOM   6572  CA   MET  A  879    -23.803   86,605  -66:030   1.00  81,46      C
ATOM   6573  C    MET  A  879    -22.497   87,208  -65.497   1,00  82,72      C
ATOM   6574  0    MET  A  879    -22,520   88..302 -64,926   1,00  83.77      0
ATOM   6575  CB   MET  A  879    -24.566   85.990  -64:854   1,00  81.03      C
ATOM   6576  CG   MET  A  879    -25.979   85,531  -65.169   1,00  78,89      C
ATOM   6577  SD   MET  A  879    -26,987   86.790  -65,968   1,00  79.53      S
ATOM   6578  CE   MET  A  879    -26.975   88.102  -64:745   1,00  84.68      C
ATOM   6579  N    LYS  A  880    -21..381  86,496  -65.680   1,00  82,44      N
ATOM   6580  CA   LYS  A  880    -20,081   86.843  -65,084   1,00  81.05      C
ATOM   6581  C    LYS  A  880    -19,751   88.333  -65,151   1,00  85.13      C
ATOM   6582  O    LYS  A  880    -19.214   88,919  -64.204   1,00  84,26      O
ATOM   6583  CB   LYS  A  880    -18.967   86:049  -65.766   1.00  75.03      C
ATOM   6584  N    ASM  A  881    -20,092   88.938  -66,280   1,00  87.78      N
ATOM   6585  CA   ASN  A  881    -19.862   90,356  -66:504   1.00  87,80      C
ATOM   6586  C    ASN  A  881    -20.667   91:223  -65.539   1,00  86.93      C
ATOM   6587  O    ASM  A  881    -20,108   92.057  -64,828   1,00  86.22      0
ATOM   6588  CB   ASN  A  881    -20.204   90,704  -67.953   1,00  88,37      C
ATOM   6589  CG   ASN  A  881    -19.280   91,743  -68:529   1,00  95,70      C
ATOM   6590  OD1  ASN  A  881    -19,530   92.946  -68,413   1,00100.49      0
ATOM   6591  ND2  ASN  A  881    -18.195   91:289  -69:150   1,00101.53      N
ATOM   6592  N    TYR  A  882    -21.981   91,005  -65.521   1,00  84,42      N
ATOM   6593  CA   TYR  A  882    -22,889   91:730  -64,640   1,00  85.03      C
ATOM   6594  C    TYR  A  882    -22,465   91.636  -63,178   1,00  85.46      C
ATOM   6595  O    TYR  A  882    -22.551   92,616  -62.439   1,00  85,92      O
ATOM   6596  CB   TYR  A  882    -24:319   91:207  -64.812   1.00  86.47      C
ATOM   6597  CG   TYR  A  882    -25,274   91.629  -63,710   1,00  91.46      C
ATOM   6598  CD1  TYR  A  882    -25.650   92,961  -63:549   1.00  86,45      C
ATOM   6599  CD2  TYR  A  882    -25.807   90:690  -62.834   1.00  90.87      C
ATOM   6600  CE1  TYR  A  882    -26,521   93..340 -62,538   1,00  88,01      C
ATOM   6601  CE2  TYR  A  882    -26.682   91,060  -61:827   1.00  89,30      C
ATOM   6602  CZ   TYR  A  882    -27.036   92,381  -61.684   1,00  89,33      C
ATOM   6603  OH   TYR  A  882    -27,904   92.729  -60,677   1,00  88.16      0
ATOM   6604  N    TRP  A  883    -22:003   90:455  -62:770   1,00  86.34      N
ATOM   6605  CA   TRP  A  883    -21.518   90,242  -61.407   1,00  85,25      C
ATOM   6606  C    TRP  A  883    -20,289   91:098  -61,117   1,00  85.84      C
ATOM   6607  O    TRP  A  883    -20:152   91:658  -60:028   1,00  85.85      0
ATOM   6608  CB   TRP  A  883    -21.168   88,770  -61.168   1,00  83,68      C
ATOM   6609  CG   TRP  A  883    -22,314   87:802  -61,230   1,00  79.98      C
ATOM   6610  CD1  TRP  A  883    -23,640   88.081  -61,085   1,00  81.36      C
ATOM   6611  CD2  TRP  A  883    -22.221   86,387  -61.453   1,00  78,52      C
ATOM   6612  NE1  TRP  A  883    -24:378   86:926  -61:208   1.00  82.40      N
ATOM   6613  CE2  TRP  A  883    -23,530   85.875  -61,435   1,00  72.35      C
ATOM   6614  CE3  TRP  A  883    -21.154   85,505  -61:667   1.00  81,13      C
ATOM   6615  CZ2  TRP  A  883    -23.803   84:522  -61:624   1.00  80.66      C
ATOM   6616  CZ3  TRP  A  883    -21,427   84.160  -61,858   1,00  79.82      C
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ATOM 6617 CH2  TRP A 883  -22.740 83.681 -61.833 1.00 80.09  C
ATOM 6618 N    ARG A 884 --19.395 91.185 -62.098 1.00 85.29  N
ATOM 6619 CA   AP.G A 884 -18.145 91.910 -61.925 1.00 87.95  C
ATOM 6620 C    ARG A 884  -18.421 93.381 -61.674 1.00 86.32  C
ATOM 6621 0    ARG A 884  -17.764 94.012 -60.854 1.00 87.58  0
ATOM 6622 CB   AP.G A 884 -17.236 91.739 -63.145 1.00 89.91  C
ATOM 6623 CG   ARG A 884  -15.967 92.579 -63.070 1.00 95.72  C
ATOM 6624 CD   ARG A 884  -14.914 92.184 -64.102 1.00 97.82  C
ATOM 6625 ME   ARG A 884  -14.338 90.862 -63.851 1.00100.50  N
ATOM 6626 CZ   ARG A 884  -13.417 90.598 -62.925 1.00 99.07  C
ATOM 6627 NH1  ARG A 884  -12.954 89.360 -62.782 1.00 94.05  N
ATOM 6628 NH2  ARG A 884  -12.963 91.565 -62.135 1.00 95.89  N
ATOM 6629 N    GLN A 885  -19.407 93.917 -62.382 1.00 88.58  N
ATOM 6630 CA   GLN A 885  -19.833 95.297 -62.184 1.00 89.75  C
ATOM 6631 C    GLN A 885  -20.356 95.491 -60.776 1.00 89.12  C
ATOM 6632 O    GLK A 885  -20.149 96.536 -60.163 1.00 90.31  O
ATOM 6633 CB   GLN A 885  -20.917 95.682 -63.181 1.00 86.93  C
ATOM 6634 CG   GLN A 885  -20.522 95.554 -64.628 1.00 89.35  C
ATOM 6635 CD   GLK A 885  -21.630 96.019 -65.553 1.00 95.96  C
ATOM 6636 OE1  GLN A 885  -22.799 96.091 -65.160 1.00 91.13  0
ATOM 6637 NE2  GLN A 885  -21.267 96.351 -66.789 1.00 98.83  N
ATOM 6638 N    LEU A 886  -21.065 94.482 -60.280 1.00 89.51  N
ATOM 6639 CA   LEU A 886  -21.563 94.511 -58.917 1.00 88.60  C
ATOM 6640 C    LEU A 886  -20.385 94.389 -57.967 1.00 89.04  C
ATOM 6641 O    LEU A 886  -20.356 95.042 -56.923 1.00 88.29  0
ATOM 6642 CB   LEU A 886  -22.573 93.392 -58.676 1.00 87.48  C
ATOM 6643 CG   LEU A 886  -23.950 93.553 -59.313 1.00 88.26  C
ATOM 6644 CD2  LEU A 886  -24.601 94.840 -58.861 1.00 87.13  C
ATOM 6645 GDI  LEU A 886  -24.821 92.358 -58.965 1.00 89.32  C
ATOM 6646 N    LEU A 887  -19.411 93.561 -58.343 1.00 85.34  N
ATOM 6647 CA   LEU A 887  -18.190 93.398 -57.553 1.00 88.66  C
ATOM 6648 C    LEU A 887  -17.388 94.694 -57.500 1.00 91.43  C
ATOM 6649 O    LEU A 887  -16.950 95.123 -56.430 1.00 89.43  0
ATOM 6650 CB   LEU A 887  -17.315 92.275 -58.122 1.00 86.48  C
ATOM 6651 CG   LEU A 887  -15.970 92.079 -57.423 1.00 80.52  C
ATOM 6652 CD2  LEU A 887  -15.131 91.044 -58.145 1.00 83.22  C
ATOM 6653 CD1  LEU A 887  -16.176 91.675 -55.979 1.00 80.60  C
ATOM 6654 N    ASN A 888  -17.204 95.313 -58.666 1.00 93.10  N
ATOM 6655 CA   ASN A 888  -16.437 96.550 -58.778 1.00 93.04  C
ATOM 6656 C    ASM A 888  -17.188 97.733 -58.173 1.00 91.05  C
ATOM 6657 O    ASM A 888  -16.638 98.818 -58.011 1.00 89.73  0
ATOM 6658 CB   ASN A 888  -16.081 96.829 -60.243 1.00 94.02  C
ATOM 6659 CG   ASN A 888  -14.859 96.037 -60.710 1.00 99.40  C
ATOM 6660 OD1  ASM A 888  -14.969 95.100 -61.508 1.00 98.55  0
ATOM 6661 ND2  ASN A 888  -13.685 96.417 -60.214 1.00101.22  K
ATOM 6662 N    ALA A 889  -18.451 97.516 -57.840 1.00 88.02  N
ATOM 6663 CA.  ALA A 889  -19.198 98.493 -57.081 1.00 90.48  C
ATOM 6664 C    ALA A 889  -19.148 98.107 -55.603 1.00 91.60  C
ATOM 6665 O    ALA A 889  -19.818 98.718 -54.767 1.00 91.25  O
ATOM 6666 CB   ALA A 889  -20.631 98.576 -57.581 1.00 91.43  C
ATOM 6667 N    LYS A 890  -18.339 97.089 -55.299 1.00 87.10  N
ATOM 6668 CA   LYS A 890  -18.262 96.488 -53.965 1.00 89.27  C
ATOM 6669 C    LYS A 890  -19.650 96.165 -53.403 1.00 92.10  C
ATOM 6670 O    LYS A 890  -19.877 96.263 -52.197 1.00 94.02  0
ATOM 6671 CB   LYS A 890  -17.496 97.399 -52.999 1.00 86.41  C
ATOM 6672 O    LEU A 891  -23.002 93.399 -53.081 1.00 89.08  0
ATOM 6673 N    LEU A 891  -20.568 95.783 -54.292 1.00 90.88  N
ATOM 6674 CA   LEU A 891  -21.928 95.382 -53.917 1.00 9.1.85  C
ATOM 6675 C    LEU A 891  -22.004 93.890 -53.612 1.00 88.52  C
ATOM 6676 CB   LEU A 891  -22.931 95.719 -55.028 1.00 91.01  C
ATOM 6677 CG   LEU A 891  -23.415 97.165 -55.182 1.00 9.3.52  C
ATOM 6678 GDI  LEU A 891  -24.673 97.231 -56.063 1.00 90.45  C
ATOM 6679 CD.2 LEU A 891  -23.660 97.810 -53.825 1.00 90.99  C
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ATOM   6680  O    ILE  A  892     -18.472  92.199  -53.600  1.00  84.42       O
ATOM   6681  N    ILE  A  892     --20.959 93.167  -53.987  1.00  86.07       N
ATOM   6682  CA   ILE  A  892     -20.828  91.775  -53.607  1.00  84.51       C
ATOM   6683  c    ILE  A  892     -19.410  91.524  -53.158  1.00  88.39       c
ATOM   6684  CB   ILE  A  892     -21.170  90.798  -54.750  I.00  82.66       c
ATOM   6685  CGI  ILE  A  892     -20.239  91.014  -55.944  1.00  82.84       c
ATOM   6686  CG2  ILE  A  892     -22.630  90.921  -55.150  1.00  89.04       c
ATOM   6687  GDI  ILE  A  892     -20.341  89.934  -57.001  I.00  86.70       c
ATOM   6688  O    THR  A  893     --17.636 89.147  -53.919  1.00  81.86       0
ATOM   6689  N    THR  A  893     -19.263  90.545  -52.277  1.00  86.68       N
ATOM   6690  CA   THR  A  893     -17.962  90.164  -51.785  I.00  85.6.3      C
ATOM   6691  C    THR  A  893     -17.113  89.622  -52.910  1.00  86.82       C
ATOM   6692  CB   THR  A  89.3    -18.064  89.099  -50.693  1.00  84.73       c
ATOM   6693  OG1  THR  A  893     -19.221  89.351  -49.886  1.00  86.68       0
ATOM   6694  CG2  THR  A  893     -16.811  89.112  -49.822  1.00  89.25       c
ATOM   6695  N    GLN  A  894     -15.800  89.723  -52.729  1.00  86.77       N
ATOM   6696  CA   GLN  A  894     -14.856  88.946  -53.504  1.00  90.21       c
ATOM   6697  C    GLN  A  894     -15.256  87.482  -53.439  I.00  93.18       C
ATOM   6698  O    GLK  A  894     -15..353  86.808  -54.470  1.00  94.88       O
ATOM   6699  CB   GLN  A  894     -13.434  89.113  -52.974  1.00  90.27       c
ATOM   6700  CG   GLN  A  894     -12.469  88.119  -53.573  I.00  88.63       c
ATOM   6701  CD   GLN  A  894     -12.257  88.371  -55.045  1.00  94.11       c
ATOM   6702  OE1  GLN  A  894     -11.692  89.395  -55.423  1.00  97.96       0
ATOM   6703  NE2  GLN  A  894     -12.721  87.452  -55.890  I.00  90.42       N
ATOM   6704  N    ARG  A  895     -15.492  87.000  -52.218  1.00  91.73       N
ATOM   6705  CA   A.P.G  A  895   -15.829  85.597  -52.007  1.00  93.64       C
ATOM   6706  C    ARG  A  895     -17.137  85.241  -52.700  I.00  89.12       C
ATOM   6707  O    ARG  A  895     -17.221  84.212  -53.376  1.00  86.61       O
ATOM   6708  CB   A.P.G  A  895   -15.924  85.260  -50.518  1.00  92.78       c
ATOM   6709  CG   ARG  A  895     -16.205  83.784  -50.271  1.00  88.61       c
ATOM   6710  CD   ARG  A  895     -16.309  83.460  -48.792  1.00  90.65       c
ATOM   6711  NE   ARG  A  895     -17.690  8.3.366 -48..315  1.00  89.16       N
ATOM   6712  CZ   ARG  A  895     -18.380  82.229  -48.232  1.00  90.53       c
ATOM   6713  NH1  ARG  A  895     -17.822  81.085  -48.611  I.00  91.97       N
ATOM   6714  NH2  ARG  A  895     -19.630  82.234  -47.777  1.00  91.22       N
ATOM   6715  N    LYS  A  896     -18.148  86.093  -52.539  1.00  89.46       N
ATOM   6716  CA.  LYS  A  896     -19.433  85.854  -53.184  I.00  84.48       C
ATOM   6717  C    LYS  A  896     -19.240  85.720  -54.683  1.00  83.00       C
ATOM   6718  O    LYS  A  896     -19.782  84.814  -55.295  1.00  82.09       O
ATOM   6719  CB   LYS  A  896     -20.433  86.967  -52.888  I.00  82.70       C
ATOM   6720  CG   LYS  A  896     -21.856  86.552  -53.235  1.00  84.61       C
ATOM   6721  CD   LYS  A  896     -22.840  87.701  -53.249  1.00  74.50       C
ATOM   6722  CE   LYS  A  896     -24.258  87.176  -53.343  1.00  71.84       c
ATOM   6723  NZ   LYS  A  896     -25.265  88.235  -53.072  1.00  74.85       N
ATOM   6724  N    PHE  A  897     -18.437  86.610  -55.258  1.00  85.71       N
ATOM   6725  CA   PHE  A  897     -18.116  86.552  -56.677  1.00  82.37       c
ATOM   6726  C    PHE  A  897     -17.510  85.216  -57.050  I.00  87.71       C
ATOM   6727  O    PHE  A  897     -17.837  84.641  -58.086  1.00  89.72       O
ATOM   6728  CB   PHE  A  897     -17.146  87.661  -57.067  1.00  83.36       c
ATOM   6729  CG   PHE  A  897     -16.733  87.616  -58.507  I.00  85.86       c
ATOM   6730  CD1  PHE  A  897     -17.458  88.303  -59.468  1.00  89.68       c
ATOM   6731  CD2  PHE  A  897     -15.630  86.879  -58.910  1.00  87.66       c
ATOM   6732  CE1  PHE  A  897     -17.088  88.258  -60.801  I.00  84.45       c
ATOM   6733  CE2  PHE  A  897     -15.260  86.832  -60.238  1.00  85.16       c
ATOM   6734  CZ   PHE  A  897     -15.987  87.527  -61.183  1.00  82.37       c
ATOM   6735  N    ASP  A  898     -16.602  84.731  -56.217  I.00  88.11       N
ATOM   6736  CA   ASP  A  898     -15.897  83.504  -56.539  1.00  86.41       C
ATOM   6737  C    ASP  A  898     -16.803  82.288  -56.446  1.00  85.87       c
ATOM   6738  O    ASP  A  898     -16.572  81.306  -57.140  1.00  88.55       0
ATOM   6739  CB   ASP  A  898     -14.683  83.331  -55.634  1.00  87.13       c
ATOM   6740  CG   ASP  A  898     -13.472  84.067  -56.154  1.00  94.37       c
ATOM   6741  OD2  ASP  A  898     -13.280  85.244  -55.771  1.00  95.59       0
ATOM   6742  OD1  ASP  A  898     -12.719  83.470  -56.956  I.00  98.13       0
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ATOM   6743  N    ASN A 899     -17.830  82.349 -55.597  1.00 86.19           N
ATOM   6744  CA   ASM A 899     -18.782  81.241 -55.473  1.00 82.08           C
ATOM   6745  C    ASN A 899     -19.771  81.240 -56.641  1.00 8.3.16          C
ATOM   6746  O    ASN A 899     -19.997  80.204 -57.268  1.00 80.35           0
ATOM   6747  CB   ASN A 899     -19.542  81.297 -54.139  1.00 80.61           C
ATOM   6748  CG   ASN A 899     -18.684  80.881 -52.936  1.00 84.32           C
ATOM   6749  OD1  ASN A 899     -19.010  81.200 -51.788  1.00 81.38           0
ATOM   6750  ND2  ASN A 899     -17.593  80.164 -53.196  1.00 83.75           N
ATOM   6751  N    LEU A 900     -20.352  82.406 -56.927  1.00 82.99           N
ATOM   6752  CA   LEU A 900     -21.224  82.579 -58.083  1.00 80.65           C
ATOM   6753  C    LEU A 900     -20.591  81.999 -59.341  1.00 79.82           C
ATOM   6754  O    LEU A 900     -21.253  81.373 -60.160  1.00 79.98           0
ATOM   6755  CB   LEU A 900     -21.531  84.063 -58..312  1.00 80.07           C
ATOM   6756  CG   LEU A 900     -22.732  84.744 -57.647  1.00 78.95           C
ATOM   6757  CD1  LEU A 900     -24.047  84.136 -58.095  1.00 77.96           C
ATOM   6758  CD2  LEU A 900     -22.623  84.666 -56.161  1.00 8.3.37          C
ATOM   6759  N    THR A 901     -19.286  82.195 -59.458  1.00 81.89           N
ATOM   6760  CA.  TH.R A 901     -18.572  81.953 -60.697  1.00 84.48           C
ATOM   6761  C    THR A 901     -17.860  80.604 -60.801  1.00 86.63           C
ATOM   6762  O    THR A 901     -17.468  80.194 -61.888  1.00 90.46           O
ATOM   6763  CB   TH.R A 901     -17.509  83.046 -60.921  1.00 86.58           C
ATOM   6764  OG1  THR A 901     -17.111  83.047 -62.293  1.00 91.90           0
ATOM   6765  CG2  THR A 901     -16.280  82.796 -60.056  1.00 85.65           C
ATOM   6766  N    LYS A 902     -17.683  79.908 -59.691  1.00 85.17           N
ATOM   6767  CA   LYS A 902     -16.676  78.859 -59.677  1.00 90.38           C
ATOM   6768  C    LYS A 902     -17.045  77.582 -60.426  1.00 9.1.42          C
ATOM   6769  O    LYS A 902     -16.307  76.600 -60.366  1.00 92.8.3           0
ATOM   6770  CB   LYS A 902     -16.303  78.508 -58.239  1.00 92.67           C
ATOM   6771  CG   LYS A 902     -14.802  78.600 -57.981  1.00 95.32           C
ATOM   6772  CD   LYS A 902     -14.189  79.841 -58.626  1.00 85.56           C
ATOM   6773  CE   LYS A 902     -12.679  79.787 -58.496  1.00 95.49           C
ATOM   6774  NZ   LYS A 902     -12.252  79.510 -57.089  1.00 97.36           N
ATOM   6775  N    ALA A 903     -18.159  77.585 -61.144  1.00 86.31           N
ATOM   6776  CA.  ALA A 903     -18.452  76.460 -62.018  1.00 88.18           C
ATOM   6777  C    ALA A 90.3    -17.550  76.526 -63.243  1.00 89.60           C
ATOM   6778  O    ALA A 903     -17.308  75.530 -63.930  1.00 88.19           0
ATOM   6779  CB   ALA A 903     -19.891  76.465 -62.424  1.00 90.63           C
ATOM   6780  N    GLU A 904     -17.063  77.729 -63.504  1.00 91.08           N
ATOM   6781  CA   GLU A 904     -16.208  77.996 -64.643  1.00 9.1.16          C
ATOM   6782  C    GLU A 904     -14.817  77.434 -64.391  1.00 90.67           C
ATOM   6783  O    GLU A 904     -14.121  77.034 -65.326  1.00 93.34           0
ATOM   6784  CB   GLU A 904     -16.165  79.505 -64.914  1.00 9.1.89          C
ATOM   6785  CG   GLU A 904     -14.793  80.056 -65.209  1.00 96.69           C
ATOM   6786  CD   GLU A 904     -14.508  81.330 -64.443  1.00100 .09           C
ATOM   6787  OE1  GLU A 904     -13.772  81.268 -63.426  1.00 99.35           0
ATOM   6788  OE2  GLU A 904     -15.018  82.391 -64.863  1.00 97.26           0
ATOM   6789  N    ARG A 905     -14.431  77..383 -63.118  1.00 92.52           N
ATOM   6790  CA   AP.G A 905     -13.114  76.893 -62.717  1.00 90.61           C
ATOM   6791  C    ARG A 905     -13.093  75.380 -62.518  1.00 89.14           C
ATOM   6792  0    ARG A 905     -12.051  74.809 -62.212  1.00 94.44           0
ATOM   6793  CB   ARG A 905     -12.660  77.589 -61.433  1.00 89.55           C
ATOM   6794  N    GLY A 906     -14.243  74.737 -62.691  1.00 85.89           N
ATOM   6795  CA   GLY A 906     -14.351  73..304 -62.507  1.00 83.13           C
ATOM   6796  C    GLY A 906     -15.511  72.889 -61.621  1.00 87.78           C
ATOM   6797  O    GLY A 906     -15.867  7..712  -61.558  1.00 89.56           O
ATOM   6798  O    GLY A 907     -15.900  72.135 -58.720  1.00 86.74           O
ATOM   6799  N    GLY A 907     -16.096  73.855 -60.920  1.00 88.88           N
ATOM   6800  CA   GLY A 907     -17.251  73.604 -60.073  1.00 86.92           C
ATOM   6801  C    GLY A 907     -17.013  72.636 -58.925  1.00 87.66           C
ATOM   6802  O    LEU A 908     -18.522  69.277 -57.907  1.00 87.70           0
ATOM   6803  N    LEU A 908     -18.077  72.363 -58.177  1.00 86.78           N
ATOM   6804  CA   LEU A 908     -17.993  71.455 -57.037  1.00 89.95           C
ATOM   6805  C    LEU A 908     -17.659  70.022 -57.442  1.00 86.99           C
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ATOM   6806  CB  LEU A 908     -19.304  71.468 -56.248  1.00 89.64           C
ATOM   6807  CG  LEU A 908     -19.633  72.743 -55.469  1.00 87.47           C
ATOM   6808  CD1 LEU A 908     -20.783  72.506 -54.488  1.00 84.98           C
ATOM   6809  CD2 LEU A 908     -18.400  73.261 -54.754  1.00 78.72           C
ATOM   6810  O   SER A 909     -17.633  67.582 -55.903  1.00 87.49           O
ATOM   6811  N   SER A 909     -16.401  69.644 -57.243  1.00 87.72           N
ATOM   6812  CA  SER A 909     -15.940  68.279 -57.478  1.00 85.23           C
ATOM   6813  C   SER A 909     -16.684  67.250 -56.622  1.00 88.49           C
ATOM   6814  CB  SER A 909     -14.446  68.182 -57.192  1.00 77.47           C
ATOM   6815  OG  SER A 909     -14.203  67.144 -56.269  1.00 81.58           O
ATOM   6816  O   GLU A 910     -16.513  64.382 -53.534  1.00 83.17           O
ATOM   6817  N   GLU A 910     -16.244  65.998 -56.682  1.00 82.98           N
ATOM   6818  CA  GLU A 910     -16.844  64.977 -55.837  1.00 83.47           C
ATOM   6819  C   GLU A 910     -16.019  64.835 -54.566  1.00 84.10           C
ATOM   6820  CB  GLU A 910     -16.943  63.641 -56.573  1.00 92.50           C
ATOM   6821  CG  GLU A 910     -18.096  62.755 -56.117  1.00 91.15           C
ATOM   6822  CD  GLU A 910     -19.378  63.062 -56.855  1.00 88.34           C
ATOM   6823  OE1 GLU A 910     -20.385  62.342 -56.660  1.00 87.99           O
ATOM   6824  OE2 GLU A 910     -19.375  64.028 -57.641  1.00 90.02           O
ATOM   6825  N   LEU A 911     -14.749  65.217 -54.657  1.00 84.07           N
ATOM   6826  CA  LEU A 911     -13.889  65.300 -53.486  1.00 83.34           C
ATOM   6827  C   LEU A 911     -14.242  66.569 -52.690  1.00 85.73           C
ATOM   6828  O   LEU A 911     -14.010  66.662 -51.480  1.00 81.94           O
ATOM   6829  CB  LEU A 911     -12.420  65.299 -53.901  1.00 81.11           C
ATOM   6830  N   ASP A 912     -14.813  67.542 -53.391  1.00 85.16           N
ATOM   6831  CA  ASP A 912     -15.341  68.739 -52.765  1.00 83.13           C
ATOM   6832  C   ASP A 912     -16.669  68.464 -52.069  1.00 85.25           C
ATOM   6833  O   ASP A 912     -16.933  68.987 -50.989  1.00 80.32           O
ATOM   6834  CB  ASP A 912     -15.526  69.845 -53.798  1.00 86.04           C
ATOM   6835  CG  ASP A 912     -14.222  70.430 -54.252  1.00 87.94           C
ATOM   6836  OD2 ASP A 912     -14.255  71.336 -55.118  1.00 85.29           O
ATOM   6837  OD1 ASP A 912     -13.172  69.990 -53.730  1.00 84.63           O
ATOM   6838  N   LYS A 913     -17.521  67.663 -52.699  1.00 87.40           N
ATOM   6839  CA  LYS A 913     -18.777  67.290 -52.065  1.00 87.11           C
ATOM   6840  C   LYS A 913     -18.473  66.536 -50.768  1.00 83.45           C
ATOM   6841  O   LYS A 913     -19.094  66.785 -49.743  1.00 83.15           O
ATOM   6842  CB  LYS A 913     -19.642  66.449 -53.007  1.00 86.48           C
ATOM   6843  N   ALA A 914     -17.483  65.650 -50.819  1.00 83.79           N
ATOM   6844  CA  ALA A 914     -17.049  64.875 -49.653  1.00 84.22           C
ATOM   6845  C   ALA A 914     -16.532  65.769 -48.528  1.00 81.81           C
ATOM   6846  O   ALA A 914     -16.970  65.652 -47.379  1.00 78.04           O
ATOM   6847  CB  ALA A 914     -15.976  63.873 -50.056  1.00 75.26           C
ATOM   6848  N   GLY A 915     -15.595  66.651 -48.873  1.00 80.84           N
ATOM   6849  CA  GLY A 915     -15.008  67.584 -47.928  1.00 78.62           C
ATOM   6850  C   GLY A 915     -16.033  68.427 -47.193  1.00 76.51           C
ATOM   6851  O   GLY A 915     -15.932  68.611 -45.989  1.00 76.98           O
ATOM   6852  N   PHE A 916     -17.024  68.938 -47.918  1.00 80.46           N
ATOM   6853  CA  PHE A 916     -18.084  69.729 -47.313  1.00 76.14           C
ATOM   6854  C   PHE A 916     -18.857  68.897 -46.313  1.00 78.25           C
ATOM   6855  O   PHE A 916     -19.407  69.442 -45.354  1.00 79.43           O
ATOM   6856  CB  PHE A 916     -19.041  70.287 -48.373  1.00 79.00           C
ATOM   6857  CG  PHE A 916     -18.627  71.623 -48.923  1.00 83.48           C
ATOM   6858  CD2 PHE A 916     -18.103  71.734 -50.201  1.00 82.81           C
ATOM   6859  CD1 PHE A 916     -18.764  72.774 -48.161  1.00 82.92           C
ATOM   6860  CE2 PHE A 916     -17.713  72.964 -50.702  1.00 81.21           C
ATOM   6861  CE1 PHE A 916     -18.375  74.006 -48.658  1.00 82.75           C
ATOM   6862  CZ  PHE A 916     -17.851  74.101 -49.931  1.00 78.69           C
ATOM   6863  N   ILE A 917     -18.896  67.582 -46.533  1.00 78.77           N
ATOM   6864  CA  ILE A 917     -19.590  66.667 -45.619  1.00 79.85           C
ATOM   6865  C   ILE A 917     -18.671  66.216 -44.463  1.00 75.94           C
ATOM   6866  O   ILE A 917     -19.128  66.061 -43.334  1.00 76.61           O
ATOM   6867  CB  ILE A 917     -20.157  65.419 -46.363  1.00 83.22           C
ATOM   6868  CG1 ILE A 917     -21.015  65.828 -47.567  1.00 84.04           C
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ATOM   6869  CG2  ILE  A  917    -21..008   64.,568  -45..428   1.00  82.83    C
ATOM   6870  GDI  ILE  A  917    -22.,325   66..536  --47,222   1,00  81.82    C
ATOM   6871  N    LYS  A  918    -17.383    66.,025  -44.736    1.00  72,34    N
ATOM   6872  CA   LYS  A  918    -16..396   65.,825  -43..671   1.00  72.20    c
ATOM   687 3 C    LYS  A  918    -16,,316   67. 018  -42.,709   1,00  72.94    C
ATOM   6874  O    LYS  A  918    -16..245   66.,860  -41 .487   1.00  70,.97    O
ATOM   6875  CB   LYS  A  918    -15..018   65.,582  -44.267    1,00  71,75    c
ATOM   687 6 CG   LYS  A  918    -13.,903   65. 690  -43,261    1,00  71.20    c
ATOM   6877  CD   LYS  A  918    -12..692   66.,391  -43,843    1,00  73..82    c
ATOM   6878  CE   LYS  A  918    -12..095   65.,622  -45..014   1,00  78,.55    c
ATOM   6879  NZ   LYS  A  918    -10.,854   66..272  -45,546    1,00  71.60    N
ATOM   6880  O    ARG  A  919    -17.501    70..618  -40,872    1,00  79..70    O
ATOM   6881  N    A.P.G A 919    -16. 319   68.,216  -43. 275   1,00  73,15    N
ATOM   6882  CA   ARG  A  919    -16..211   69.,432  -42,486    1.00  70..81    c
ATOM   6883  C    ARG  A  919    -17,484    69.. 721 -41,709    1,00  73..54    C
ATOM   6884  CB   ARG  A  919    -15..859   70.,617  -43..380   1.00  70,.12    C
ATOM   6885  CG   ARG  A  919    -14.370    70.,881  -43.473    1.00  70..19    c
ATOM   6886  CD   ARG  A  919    -14,055    72.016   -44 ,430    1,00  70..59    c
ATOM   6887  NE   ARG  A  919    -14.201    71,590   -45..817   1.00  80,.29    N
ATOM   6888  CZ   ARG  A  919    -15..219   71,926   -46..600   1,00  82,08    c
ATOM   6889  NH1  ARG  A  919    -16.,179   72.715   -46,133    1,00  88..04    N
ATOM   6890  NH2  ARG  A  919    -15..270   71,485   -47,850    1,00  79..42    N
ATOM   6891  O    GLN  A  920    -20..515   68.,256  -39..030   1,00  71,68    O
ATOM   6892  N    GLN  A  920    -18.,551   68..972  -41 ,982    1,00  72.55    N
ATOM   6893  CA   GLN  A  920    -19..761   69..047  -41,166    1,00  69..68    C
ATOM   6894  C    GLN  A  920    -19. 676   68.,157  -39.932    1,00  72,17    C
ATOM   6895  CB   GLN  A  920    -20.,992   68..645  -41 ,962    1,00  73..45    C
ATOM   6896  CG   GLN  A  920    -21.,490   69..663  -42.,942   1,00  73..21    C
ATOM   6897  CD   GLN  A  920    -22.568    69.,077  -43. 810   1,00  74,55    C
ATOM   6898  OE1  GLN  A  920    -23..528   68.,505  -43,306    1.00  76..20    O
ATOM   6899  NE2  GLN  A  920    -22.,401   69..179  -45,120    1,00  77.99    N
ATOM   6900  O    LEU  A  921    -17.411    66.,480  -36..725   1.00  66,.99    O
ATOM   6901  N    LEU  A  921    -18..670   67.,284  -39..896   1,00  76..57    N
ATOM   6902  CA.  LEU  A  921    -18.,551   66. 303  -38.,819   1,00  73..25    C
ATOM   6903  C    LEU  A  921    -17.333    66.,570  -37..945   1.00  68,.45    C
ATOM   6904  CB   LEU  A  921    -18..508   64.,890  -39..398   1,00  69,.53    c
ATOM   6905  CG   LEU  A  921    -19.,696   64. 524  -40.,294   1,00  72.59    c
ATOM   6906  CD1  LEU  A  921    -19..648   63.,062  -40,700    1,00  77.34    c
ATOM   6907  CD2  LEU  A  921    -21.034    64.,847  -39.635    1,00  72,58    c
ATOM   6908  O    VAL  A  922    -15.,668   69..630  -.38.,493   1,00  71.01    0
ATOM   6909  N    VAL  A  922    -16.,211   66..895  -38.,573   1,00  68..03    N
ATOM   6910  CA   VAL  A  922    -15. 058   67.,393  -37. 839   1,00  64,10    C
ATOM   6911  c    VAL  A  922    -15.,149   68.,913  -37.,638   1.00  71.54    c
ATOM   6912  CB   VAL  A  922    -13.,770   67..093  -38.,555   1,00  62.93    c
ATOM   6913  CGI  VAL  A  922    -12.615    67.,177  -37..579   1.00  67,39    c
ATOM   6914  CG2  VAL  A  922    -13..842   65.,731  -39..209   1,00  70..35    c
ATOM   6915  O    GLU  A  923    -12.,438   70.954   -37.,310   1,00  71.46    0
ATOM   6916  N    GLU  A  923    -14.629    69.,392  -36..510   1.00  73,.63    N
ATOM   6917  CA   GLU  A  923    -14.576    70,820   -36..204   1,00  70,.02    c
ATOM   6918  C    GLU  A  923    -13.,491   71.531   -37.,028   1,00  70..57    c
ATOM   6919  CB   GLU  A  923    -14,331    71,021   -34.,706   1,00  66..36    c
ATOM   6920  CG   GLU  A  923    -14.310    72.,478  -34..256   1,00  67,74    c
ATOM   6921  CD   GLU  A  923    -15.,677   73..107  -.34.,247   1,00  66..58    c
ATOM   6922  OE1  GLU  A  923    -16.,527   72..645  -33.,454   1,00  71.33    0
ATOM   6923  OF.2 GLU  A  923    -15. 903   74,054   -35. 033   1,00  66,28    0
ATOM   6924  O    THR  A  924    -11,148    75...300  -.37.,936   1,00  70..28    0
ATOM   6925  N    THR  A  924    -13.,742   72.783   -37.,413   1,00  68..61    N
ATOM   6926  CA   THR  A  924    -12.773    73,523   -38. 230   1,00  75,86    c
ATOM   6927  c    THR  A  924    -12.,227   74,810   -37.,569   1.00  70..93    c
ATOM   6928  CB   THR  A  924    -13.,385   73.887   -39,607    1,00  73..38    c
ATOM   6929  OG1  THR  A  924    -14.148    72.,781  -40..101   1.00  69,.47    0
ATOM   6930  CG2  THR  A  924    -12..288   74,222   -40..615   1.00  77.94    C
ATOM   6931  N    ARG  A  925    -12.,965   75.340   -36,596    1,00  70..00    N
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ATOM	6932	CA	ARG	A	925	-12.608	76.588	-35.911	1.00	62.60	c
ATOM	6933	C	ARG	A	925	-11.180	76.593	--35.353	1.00	61.00	c
ATOM	6934	O	ARG	A	925	-10.697	75.567	-34.878	1.00	62.86	0
ATOM	6935	CB	ARG	A	925	-13.611	76.851	-34.781	1.00	61.11	c
ATOM	6936	CG	ARG	A	925	-15.031	77.130	-35.264	I.00	66.69	c
ATOM	6937	CD	ARG	A	925	-15.973	77.444	-34.120	1.00	61.27	c
ATOM	6938	NE	ARG	A	925	-16.663	76.262	-33.612	1.00	65.52	N
ATOM	6939	CZ	ARG	A	925	-17.231	76.177	-.32.410	I.00	67.55	C
ATOM	6940	NH1	ARG	A	925	-17.848	75.058	-32.040	1.00	61.92	N
ATOM	6941	NH2	ARG	A	925	-17.174	77.206	-31.565	1.00	65.62	N
ATOM	6942	N	GLN	A	926	-10.509	77.744	-.35.441	I.00	62.95	N
ATOM	6943	CA	GLN	A	926	-9.191	77.965	-34.825	1.00	64.12	C
ATOM	6944	C	GLN	A	926	-9.184	77.721	-33.318	1.00	65.80	C
ATOM	6945	O	GLN	A	926	-8.330	76.995	-32.787	1.00	61.07	O
ATOM	6946	CB	GLN	A	926	-8.719	79.398	-35.064	1.00	67.46	c
ATOM	6947	CG	GLN	A	926	-7.482	79.574	-35.945	1.00	75.91	c
ATOM	6948	CD	GLN	A	926	-6.554	78.366	-35.992	1.00	73.14	c
ATOM	6949	OE1	GLN	A	926	-5.992	77.944	-.34.969	I.00	73.69	0
ATOM	6950	NE2	GLN	A	926	-6.369	77.816	-37.199	1.00	68.87	N
ATOM	6951	N	ILE	A	927	-10.137	78.357	-32.637	1.00	58.47	N
ATOM	6952	CA.	ILE	A	927	-10.186	78.326	-.31.185	I.00	60.25	C
ATOM	6953	C	ILE	A	927	-10.272	76.875	-30.684	1.00	58.86	C
ATOM	6954	O	ILE	A	927	-9.601	76.522	-29.715	1.00	60.93	O
ATOM	6955	CB	ILE	A	927	-11.377	79.225	-.30.629	I.00	54.45	C
ATOM	6956	CGI	ILE	A	927	-11.234	79.469	-29.135	1.00	54.90	C
ATOM	6957	CG2	ILE	A	927	-12.739	78.640	-30.933	1.00	48.69	C
ATOM	6958	CD1	ILE	A	927	-9.829	79.840	-28.687	I.00	55.01	C
ATOM	6959	N	THR	A	928	-11.049	76.028	-31.362	1.00	54.16	N
ATOM	6960	CA	THR	A	928	-11.132	74.609	-31.001	1.00	58.40	C
ATOM	6961	c	THR	A	928	-9.798	73.879	-31.218	1.00	62.29	c
ATOM	6962	O	THR	A	928	-9.403	73.036	-30.410	1.00	62.68	0
ATOM	6963	CB	THR	A	928	-12.229	73.869	-31.796	1.00	61.41	c
ATOM	6964	OG1	THR	A	928	-13.525	74.245	-31.319	1.00	60.33	0
ATOM	6965	CG2	THR	A	928	-12.086	72.382	-.31.620	I.00	62.08	c
ATOM	6966	N	LYS	A	929	-9.093	74.211	-32.296	1.00	61.65	N
ATOM	6967	CA	LYS	A	929	-7.769	73.639	-32.520	1.00	57.45	c
ATOM	6968	C	LYS	A	929	-6.814	74.026	-.31.407	I.00	60.91	C
ATOM	6969	O	LYS	A	929	-5.894	73.269	-31.099	1.00	64.27	0
ATOM	6970	CB	LYS	A	929	-7.204	74.070	-33.873	1.00	58.71	c
ATOM	6971	CG	LYS	A	929	-7.580	73.113	-.34.999	I.00	67.09	c
ATOM	6972	CD	LYS	A	929	-7.621	73.795	-36.373	1.00	78.11	c
ATOM	6973	CE	LYS	A	929	-8.600	73.085	-37.324	1.00	79.21	c
ATOM	6974	NZ	LYS	A	929	-8.458	73.503	-38.753	1.00	78.53	N
ATOM	6975	N	HIS	A	930	-7.032	75.183	-30.782	1.00	55.33	N
ATOM	6976	CA	HIS	A	930	-6.169	75.580	-29.678	1.00	59.90	c
ATOM	6977	c	HIS	A	930	-6.393	74.708	-28.448	1.00	61.14	c
ATOM	6978	O	HIS	A	930	-5.428	74.240	-27.833	I.00	56.95	0
ATOM	6979	CB	HIS	A	930	-6.365	77.056	-29.338	1.00	59.55	c
ATOM	6980	CG	HIS	A	930	-5.684	77.973	-30.300	1.00	59.89	c
ATOM	6981	ND1	HIS	A	930	-6.332	79.021	-.30.918	I.00	64.56	N
ATOM	6982	CD2	HIS	A	930	-4.416	77.984	-30.768	1.00	56.95	C
ATOM	6983	CE1	HIS	A	930	-5.488	79.640	-31.724	1.00	65.37	c
ATOM	6984	NE2	HIS	A	930	-4.320	79.026	-31.656	I.00	62.14	N
ATOM	6985	N	VAL	A	931	-7.662	74.508	-28.100	1.00	55.86	N
ATOM	6986	CA	VAL	A	931	-8.048	73.550	-27.076	1.00	57.72	C
ATOM	6987	C	VAL	A	931	-7.340	72.221	-27.287	I.00	59.86	C
ATOM	6988	O	VAL	A	931	-8.636	71.740	-26.403	1.00	57.91	O
ATOM	6989	CB	VAL	A	931	-9.559	73.270	-27.088	1.00	59.53	C
ATOM	6990	CGI	VAL	A	931	-10.000	72.656	-25.775	1.00	53.05	c
ATOM	6991	CG2	VAL	A	931	-10.322	74.531	-27.381	1.00	61.13	c
ATOM	6992	N	ALA	A	932	-7.544	71.643	-28.469	1.00	58.46	N
ATOM	6993	CA	ALA	A	932	-6.977	70.336	-28.831	1.00	63.71	c
ATOM	6994	C	ALA	A	932	-5.456	70.340	-28.742	I.00	59.16	C

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ATOM    6995   O    ALA  A  932       --4 .868    69..455   -28 ..121    1 .00   55..55          O
ATOM    6996   CB   ALA  A  932       -7 ,428     69..936   --30.,227    1 ,00   59..79          C
ATOM    6997   N    GLK  A  9.33      -4 .835     71 ,365   -29.· .32 4  1 ,00   57 ,51          N
ATOM    6998   CA   GLN  A  933       --3..393    71 ,545   -29 ..216    1 .00   59..67          C
ATOM    6999   C    GLN  A  933       -2,,917     71 .585   -27 ,770     1 ,00   62 .63          C
ATOM    7000   O    GLN  A  9.33      -1 .808     71 ,166   -27 .477     1 ,00   67 ,08          O
ATOM    7001   CB   GLN  A  933       -2 .957     72.,830   -29 ..925    1 ,00   64 ,76          C
ATOM    7002   CG   GLN  A  933       -.1 ,452    73 .112   -29.,893     1 ,00   65..12          C
ATOM    7003   CD   GLN  A  933       -1 .013     73..945   -28 ,686     1 ,00   71 .66          C
ATOM    7004   OE1  GLN  A  933       --1 .059    75 ,184   -28 ..709    1 ,00   73,.44          0
ATOM    7005   NE2  GLN  A  933       -0,,568     73..266   -27.,632     I ,00   72 .52          N
ATOM    7006   N    ILE  A  934       -3..726     72..126   -26 ,868     1 ,00   62 .73          N
ATOM    7007   CA   ILE  A  934       -3 .264     72.,351   -25. 500     1 ,00   61 ,79          C
ATOM    7008   C    ILE  A  934       --3..292    71 ,067   -24 ,732     1 .00   55..17          C
ATOM    7009   O    ILE  A  934       -2.,386     70 .768   -23 ,968     1 ,00   60..62          0
ATOM    7010   CB   ILE  A  9.34      -4 .130     73.,407   -24.· 756    1 ,00   60,.68          C
ATOM    7011   CGI  ILE  A  934       --3..801    74 ,813   -25 ,250     1 .00   57 .66          C
ATOM    7012   CG2  ILE  A  934       -3.,958     73 .306   -23 ,237     1 ,00   47 .08          C
ATOM    7013   CD1  ILE  A  9.34      -4 .957     75.,822   -25 .005     1 ,00   65,.85          C
ATOM    7014   N    LEU  A  935       -4 .358     70 ,308   -24 .940     1 ,00   54 ,82          N
ATOM    7015   CA.  LEU  A  935       -4 „508     69. 022   -24.,296     1 ,00   56..10          C
ATOM    7016   C    LEU  A  935       -3..508     68.,018   -24 ,885     1 ,00   66..36          C
ATOM    7017   O    LEU  A  935       --3..098    67.,061   -24 .227     1 ,00   65,.91          O
ATOM    7018   CB   LEU  A  935       -5.,942     68..533   -24.,449     I ,00   54 .83          C
ATOM    7019   CG   LEU  A  935       -6 .962     69..449   -23 ,749     1 ,00   45..75          C
ATOM    7020   CD2  LEU  A  935       -6. 868     69.,300   -22 .245     1 ,00   45 ,56          C
ATOM    7021   CD1  LEU  A  935       -8,,361     69..132   -24.,205     I ,00   42 .59          C
ATOM    7022   O    ASP  A  936       -0.,022     66..564   -26 ,066     1 ,00   73..20          0
ATOM    7023   N    ASP  A  936       -3 .098     68.,251   -26. 125     1 ,00   68 ,92          N
ATOM    7024   CA   ASP  A  936       -2 .175     67.,342   -26 ..781    1 .00   68..77          C
ATOM    7025   C    ASP  A  936       -0.,769     67..528   -26 ,229     1 ,00   70..75          C
ATOM    7026   CB   ASP  A  9.3 6     -2 .186     67.,551   -28 ..296    1 ,00   67 ,97          C
ATOM    7027   CG   ASP  A  936       --1 .197    66.,650   -29 ..005    1 .00   74 .34          C
ATOM    7028   OD1  ASP  A  936       -.1 ,534    65. 470   -29.,245     1 ,00   70..30          0
ATOM    7029   OD2  ASP  A  9.3 6     -0..079     67.,118   -29. ..30 6  1 ,00   77 ,87          0
ATOM    7030   N    SER  A  937       --0.· 427   68.,775   -25 ..926    1 ,00   66,.73          N
ATOM    7031   CA.  SER  A  937        0 „892     69. 099   -25 ,404     1 ,00   69..46          C
ATOM    7032   C    SER  A  937        1 .056     68.,649   -23 ,959     1 ,00   72 .22          C
ATOM    7033   O    SER  A  937        2 .171     68.,420   -23 .495     1 ,00   74 ,30          O
ATOM    7034   CB   SER  A  937        1 ,149     70..601   -25 ,494     I ,00   65..49          C
ATOM    7035   OG   SER  A  937        0 „692     71 .132   -26 ,725     1 ,00   72 .44          0
ATOM    7036   N    A.P.G A 938       -0. 058     68.,543   -23 .244     1 ,00   70 ,14          N
ATOM    7037   CA   ARG  A  938       --0..025    68.,244   -21.,817     1 .00   69..95          C
ATOM    7038   C    ARG  A  938       -0.,213     66..751   -21.,573     1 ,00   65..60          C
ATOM    7039   O    ARG  A  9.38       0 ..119    66.,244   -20 ..510    1 ,00   64 ,44          O
ATOM    7040   CB   ARG  A  938       --1 ,096    69.,059   -21. .058    1 .00   63..48          C
ATOM    7041   CG   ARG  A  938       -0.,751     70 .538   -20.,919     1 ,00   69..19          C
ATOM    7042   CD   ARG  A  9.38      -1 .891     71 ,373   -20 ...34 4  1 ,00   64 ,91          C
ATOM    7043   NE   ARG  A  938       -2 .303     70 ,919   -19. .015    1 ,00   63,.27          N
ATOM    7044   CZ   ARG  A  938       -.1 ,834    71 .418   -17 ,877     1 ,00   62 .60          C
ATOM    7045   NH1  ARG  A  938       -0.,933     72.,394   -17 ,886     1 ,00   65..94          N
ATOM    7046   NH2  ARG  A  938       -2 .264     70 ,938   -16. .725    1 ,00   59,.53          N
ATOM    7047   N    MET  A  939       -0,,734     66..039   -22.,558     I ,00   70..17          N
ATOM    7048   CA   MET  A  939       -0.,910     64..605   -22.,383     1 ,00   71 .48          C
ATOM    7049   C    MET  A  939        0 .239     63.,818   -22 .996     1 ,00   73 ,11          C
ATOM    7050   O    MET  A  939        0 „644     62..790   -22.,460     I ,00   74 .56          0
ATOM    7051   CB   MET  A  939       -2.,238     64..142   -22.,985     1 ,00   63..04          C
ATOM    7052   CG   MET  A  939       -3 .478     64.,574   -22 .202     1 ,00   66 ,59          C
ATOM    7053   SD   MET  A  939       --3.,767    63.,766   -20 ,610     1 .00   67 .70          S
ATOM    7054   CE   MET  A  939       -2.,810     64..787   -19 ,484     1 ,00   61 ,30          C
ATOM    7055   O    ASN  A  940        3 ..615    64.,925   -25 ..151    1 ,00   75,.70          0
ATOM    7056   N    ASN  A  940        0 ..760    64.,299   -24 ..119    1 .00   75..99          N
ATOM    7057   CA.  ASM  A  940        1 „704     63. 511   -24.,904     1 ,00   71 .67          C
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ATOM   7058  C    ASN  A  940      3.154   63.895  -24.661   1.00  78.13     c
ATOM   7059  CB   ASM  A  940      1,368   63.633  --26.388  1,00  62.38     C
ATOM   7060  CG   ASN  A  940      0.154   62,803  -26.774   1,00  71,15     C
ATOM   7061  OD1  ASN  A  940     -0.160   61,802  -26.119   1.00  68.70     0
ATOM   7062  ND2  ASN  A  940     -0,539   63.211  -27,838   1,00  70.97     N
ATOM   7063  O    THR  A  941      7.202   61,821  -23.767   1,00  87,51     0
ATOM   7064  N    THR  A  941      3.864   63,060  -23.897   1,00  82,94     N
ATOM   7065  CA.  THR  A  941      5.289   63.274  -23,611   1,00  87.57     C
ATOM   7066  C    THR  A  941      6.038   61,957  -23,394   1,00  85.07     C
ATOM   7067  CB   THR  A  941      5.497   64,154  -22.369   1,00  85,65     c
ATOM   7068  OG1  THR  A  941      4,577   65.254  -22,391   I,00  82.28     0
ATOM   7069  CG2  THR  A  941      6.920   64.681  -22,340   1,00  89.50     c
ATOM   7070  O    A.RG A  951      2.184   59,565  -24.147   1.00  78,82     0
ATOM   7071  N    ARG  A  951      2.687   58,652  -21.631   1.00  74.08     N
ATOM   7072  CA   ARG  A  951      2,024   57.753  -22,573   1,00  78.96     C
ATOM   7073  C    ARG  A  951      1.612   58,509  -23.844   1,00  79,75     C
ATOM   7074  CB   ARG  A  951      0.808   57,092  -21.913   1.00  79.55     c
ATOM   7075  N    GLU  A  952      0,637   57.971  -24,586   1,00  76.62     N
ATOM   7076  CA   GLU  A  952      0.142   58,628  -25.800   1,00  69,75     C
ATOM   7077  C    GLU  A  952     -1.375   58,703  -25.810   1,00  73,83     c
ATOM   7078  0    GLU  A  952     -2,048   57.672  -25,714   1,00  66.04     0
ATOM   7079  CB   GLU  A  952      0.609   57,906  -27,059   1,00  63.30     C
ATOM   7080  CG   GLU  A  952      0.590   58,772  -28.313   1,00  68,81     c
ATOM   7081  CD   GLU  A  952      1,922   59.475  -28,559   I,00  75.33     C
ATOM   7082  OE1  GLU  A  952      2.132   60.008  -29.677   1,00  69.73     0
ATOM   7083  OE2  GLU  A  952      2.762   59,495  -27.631   1,00  76,71     0
ATOM   7084  N    VAL  A  953     -1,899   59.928  -25.938   I,00  71.17     N
ATOM   7085  CA   VAL  A  953     -3,343   60.188  -25.959   1,00  60.11     C
ATOM   7086  C    VAL  A  953     -3.743   60,753  -27.327   1,00  62,30     C
ATOM   7087  O    VAL  A  953     -2.989   61,525  -27,938   1.00  58.62     0
ATOM   7088  CB   VAL  A  953     -3,760   61.185  -24,816   1,00  65.60     C
ATOM   7089  CG2  VAL  A  953     -3.326   60,667  -23.452   1,00  63,84     C
ATOM   7090  CGI  VAL  A  953     -5.269   61,482  -24.833   1.00  62.47     c
ATOM   7091  N    LYS  A  954     -4,916   60.358  -27,816   1,00  65.16     N
ATOM   7092  CA   LYS  A  954     -5.462   60,922  -29.049   1,00  62,35     C
ATOM   7093  C    LYS  A  954     -6.549   61,952  -28.745   1,00  69,11     c
ATOM   7094  0    LYS  A  954     -7,498   61.666  -27,998   1,00  70.64     0
ATOM   7095  CB   LYS  A  954     -6.032   59,824  -29,949   1,00  60.57     C
ATOM   7096  N    VAL  A  955     -6.423   63,136  -29.344   1,00  62,54     N
ATOM   7097  CA   VAL  A  955     -7,397   64.195  -29,143   I,00  63.81     C
ATOM   7098  C    VAL  A  955     -8,294   64.380  -30,375   1,00  62.90     C
ATOM   7099  O    VAL  A  955     -7.822   64,670  -31.477   1,00  58,57     0
ATOM   7100  CB   VAL  A  955     -6,677   65,508  -28,780   1.00  63.28     c
ATOM   7101  CGI  VAL  A  955     -7,671   66.613  -28,429   1,00  58.64     C
ATOM   7102  CG2  VAL  A  955     -5.725   65,248  -27.626   1,00  61,50     C
ATOM   7103  N    ILE  A  956     -9.598   64,225  -30.151   1.00  61.21     N
ATOM   7104  CA.  ILE  A  956    -10,597   64.187  -31,211   1,00  53.29     C
ATOM   7105  C    ILE  A  956    -11.623   65,309  -31.081   1,00  61,45     C
ATOM   7106  O    ILE  A  956    -12.341   65,378  -30.094   1,00  61,87     0
ATOM   7107  CB   ILE  A  956    -11,341   62.839  -31,209   1,00  57.48     C
ATOM   7108  CGI  ILE  A  956    -10,352   61,673  -31,288   1,00  66.47     C
ATOM   7109  CG2  ILE  A  956    -12,281   62,748  -32 .365   1,00  59,85     c
ATOM   7110  CD1  ILE  A  956    -10,963   60..330 -.30,885   I,00  64.06     C
ATOM   7111  N    THR  A  957    -11,712   66.176  -32 ,084   1,00  61.61     N
ATOM   7112  CA   THR  A  957    -12.650   67,284  -32.015   1,00  64,39     C
ATOM   7113  C    THR  A  957    -13,821   67.140  -.32 ,999  I,00  70.19     C
ATOM   7114  O    THR  A  957    -13,709   67.433  -34,197   1,00  69.11     0
ATOM   7115  CB   THR  A  957    -11.940   68,625  -32.253   1,00  65,64     C
ATOM   7116  OG1  THR  A  957    -11,767   68,843  -33,657   1.00  71.45     0
ATOM   7117  CG2  THR  A  957    -10,590   68.643  -31,550   1,00  62.03     C
ATOM   7118  N    LEU  A  958    -14.953   66,692  -32 .470   1,00  65,38     N
ATOM   7119  CA   LEU  A  958    -16.136   66,498  -33.274   1.00  64.37     c
ATOM   7120  C    LEU  A  958    -16,957   67.751  -33,299   1,00  63.33     C
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ATOM	7121	O	LEU	A	958	-16.790	68.631	-32 .459	1,00	70.67	O
ATOM	7122	CB	LEU	A	958	--16,994	65.367	-32 ,726	1,00	67.43	C
ATOM	7123	CG	LEU	A	958	-16.321	64,070	-32 .328	1.00	64,16	C
ATOM	7124	GDI	LEU	A	958	-17.396	63.083	-31:895	1,00	57.55	c
ATOM	7125	CD2	LEU	A	958	-15,516	63.543	-33,490	1,00	64.15	c
ATOM	7126	N	LYS	A	959	-17.864	67,828	-34.258	1.00	62,84	N
ATOM	7127	CA	LYS	A	959	-18.890	68,840	-34.211	1,00	64,78	c
ATOM	7128	C	LYS	A	959	-20,099	68.211	-33,547	1,00	64.65	c
ATOM	7129	O	LYS	A	959	-20.181	66.997	-33.432	1,00	65.07	0
ATOM	7130	CB	LYS	A	959	-19.225	69,373	-35.601	1,00	69,14	c
ATOM	7131	CG	LYS	A	959	-18,126	70.238	-.36,187	1,00	68.78	c
ATOM	7132	CD	LYS	A	959	-18.654	71.195	-37.235	1,00	64.23	c
ATOM	7133	CE	LYS	*A*	959	-17.532	72,061	-37.781	1,00	67,24	c
ATOM	7134	NZ	LYS	A	959	-17.905	72.781	-39:028	1,00	71.32	N
ATOM	7135	N	SER	A	960	-21,030	69.035	-33,089	1,00	66.08	N
ATOM	7136	CA	SER	A	960	-22.164	68,512	-32 ..358	1.00	65,52	C
ATOM	7137	c	SER	A	960	-23.172	67.810	-33.267	1,00	70.00	c
ATOM	7138	O	SER	A	960	-24,222	67.398	-32 ,795	1,00	70.46	0
ATOM	7139	CB	SER	A	960	-22.854	69,631	-31.584	1.00	69,15	c
ATOM	7140	OG	SER	A	960	-23.647	70,427	-32 .437	1,00	69,01	0
ATOM	7141	N	LYS	A	961	-22,856	67.663	-34,556	1,00	72.15	N
ATOM	7142	CA	LYS	A	961	-23.769	66.997	-35.494	1,00	71.51	C
ATOM	7143	c	LYS	A	961	-23.833	65,491	-35.293	1,00	69,32	c
ATOM	7144	0	LYS	A	961	-24,921	64.925	-.35,185	1,00	67.25	0
ATOM	7145	CB	LYS	A	961	-23.382	67.266	-36.955	1,00	77.07	c
ATOM	7146	CG	LYS	*A*	961	-24.436	66,735	-37.939	1,00	76,06	c
ATOM	7147	CD	LYS	A	961	-23,979	66.746	-.39,383	1,00	78.05	c
ATOM	7148	CE	LYS	A	961	-24,962	65.965	-40,240	1,00	77.42	c
ATOM	7149	NZ	LYS	*A*	961	-26.311	66,606	-40.208	1,00	85,66	N
ATOM	7150	N	LEU	A	962	-22.670	64.851	-35:287	1,00	63.18	N
ATOM	7151	CA	LEU	A	962	-22,598	63.424	-35,049	1,00	70.33	C
ATOM	7152	C	LEU	A	962	-23.487	63,065	-33.891	1.00	70,54	C
ATOM	7153	O	LEU	A	962	-24.507	62.400	-34.040	1,00	74.78	0
ATOM	7154	CB	LEU	A	962	-21,169	62.992	-34,744	1,00	68.88	c
ATOM	7155	CG	LEU	A	962	-20.320	62,630	-35.943	1.00	73,82	c
ATOM	7156	CD1	LEU	A	962	-18.921	62,249	-35.478	1,00	69,83	c
ATOM	7157	CD2	LEU	A	962	-20,984	61.492	-36,700	1,00	76.91	c
ATOM	7158	N	VAL	A	963	-23.094	63.574	-32 .741	1,00	68.66	N
ATOM	7159	CA	VAL	*A*	963	-23.727	63,266	-31.483	1,00	66,75	C
ATOM	7160	C	VAL	A	963	-25,221	63.548	-31,523	1,00	67.58	C
ATOM	7161	O	VAL	A	963	-26,019	62.742	-31,056	1,00	66.72	0
ATOM	7162	CB	VAL	*A*	963	-23.064	64,075	-30.367	1,00	71,75	c
ATOM	7163	CGI	VAL	A	963	-22.952	63.255	-29:105	1,00	58.61	c
ATOM	7164	CG2	VAL	A	963	-21,668	64.559	-30,835	1,00	71.16	c
ATOM	7165	N	SER	A	964	-25.598	64,683	-32 .103	1.00	68,19	N
ATOM	7166	CA	SER	A	964	-26.997	65.103	-32 .127	1,00	64.44	c
ATOM	7167	C	SER	A	964	-27,853	64.180	-32 ,991	1,00	73.22	C
ATOM	7168	O	SER	A	964	-29.046	64,005	-32 .725	1.00	73,63	O
ATOM	7169	CB	SER	A	964	-27.108	66,538	-32 .633	1,00	65,31	c
ATOM	7170	OG	SER	A	964	-28,380	67.085	-32 ,358	1,00	68.27	0
ATOM	7171	N	ASP	A	965	-27.237	63.601	-34.026	1,00	73.69	N
ATOM	7172	CA	ASP	A	965	-27.917	62,670	-34.932	1,00	75,38	c
ATOM	7173	C	ASP	A	965	-28,164	61..335	-.34,247	1,00	76.43	c
ATOM	7174	O	ASP	A	965	-29:262	60.782	-34:312	1,00	77.67	0
ATOM	7175	CB	ASP	*A*	965	-27.102	62,443	-36.213	1,00	76,95	c
ATOM	7176	CG	ASP	A	965	-27,189	63.613	-.37,181	1,00	76.93	c
ATOM	7177	OD1	ASP	A	965	-28,028	64.513	-36,950	1,00	77.19	0
ATOM	7178	OD2	ASP	*A*	965	-26.422	63,625	-38.175	1,00	77,53	0
ATOM	7179	N	PHE	A	966	-27.119	60.818	-33.617	1,00	72.76	N
ATOM	7180	CA	FHE	A	966	-27,212	59.653	-32 ,755	1,00	69.18	c
ATOM	7181	C	PHE	A	966	-28.424	59,761	-31.793	1.00	72,26	c
ATOM	7182	O	PHE	A	966	-29.178	58:815	-31:637	1,00	75.29	0
ATOM	7183	CB	PHE	A	966	-25,894	59.511	-31,999	1,00	64.58	c

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ATOM   7184   CG    PHE  A  966    -25.708   58.203   -31.305   1,00  73.05   c
ATOM   7185   CD2   PHE  A  966    --24,733  57,313   -31,734   1,00  77.18   C
ATOM   7186   GD1   PHE  A  966    -26.456   57.879   -30:185   1,00  72,66   C
ATOM   7187   CE2   PHE  A  966    -24.533   56.110   -31.084   1,00  75.32   c
ATOM   7188   CE1   PHE  A  966    -26,263   56,677   -29,533   1,00  77.36   C
ATOM   7189   CZ    PHE  A  966    -25.295   55,791   -29:981   1,00  77,23   C
ATOM   7190   N     ARG  A  967    -28.637   60.921   -31:178   1,00  74,79   N
ATOM   7191   CA.   ARG  A  967    -29,756   61,087   -30,242   1,00  75.10   C
ATOM   7192   C     ARG  A  967    -31.130   61.017   -30,927   1,00  77.41   C
ATOM   7193   O     ARG  A  967    -32 .086   60.497   -30:348   1,00  77,73   O
ATOM   7194   CB    ARG  A  967    -29,642   62,417   -29,478   1,00  73.60   C
ATOM   7195   CG    ARG  A  967    -28.560   62.477   -28,406   1,00  69.59   C
ATOM   7196   CD    ARG  A  967    -28.594   63.803   -27.653   1,00  66,37   C
ATOM   7197   NE    ARG  A  967    -29.070   63.638   -26.282   1,00  70.67   N
ATOM   7198   CZ    ARG  A  967    -28,357   63,970   -25,217   1,00  64.50   C
ATOM   7199   NH1   ARG  A  967    -27.162   64.496   -25:.381   1,00  60,21   N
ATOM   7200   NH2   ARG  A  967    -28.835   63.787   -23.998   1,00  66.89   N
ATOM   7201   N     LYS  A  968    -31,233   61,555   -32 ,143   1,00  76.05   N
ATOM   7202   CA    LYS  A  968    -32 :496   61.548   -32 :891   1,00  76,69   C
ATOM   7203   C     LYS  A  968    -32 ,744   60.178   -33:514   1,00  76,83   c
ATOM   7204   0     LYS  A  968    -33,869   59,667   -33,480   1,00  75.53   0
ATOM   7205   CB    LYS  A  968    -32 ,496   62.629   -33,977   1,00  74.19   C
ATOM   7206   N     ASP  A  969    -31:682   59.603   -34,083   1,00  75,21   N
ATOM   7207   CA    ASP  A  969    -31,695   58,237   -.34,603  1,00  78.65   C
ATOM   7208   C     ASP  A  969    -32 ,234   57,252   -33,573   1,00  82.85   C
ATOM   7209   O     ASP  A  969    -33.252   56.603   -33.805   1,00  86,67   O
ATOM   7210   CB    ASP  A  969    -30,287   57,791   -.35,032  1,00  76.35   C
ATOM   7211   CG    ASP  A  969    -29,863   58,365   -36,380   1,00  78.52   C
ATOM   7212   OD1   ASP  A  969    -30.718   58.913   -37.108   1,00  75,74   O
ATOM   7213   OD2   ASP  A  969    -28,664   58.250   -36.720   1,00  81.36   0
ATOM   7214   N     PHE  A  970    -31,559   57,159   -32 ,430   1,00  78.55   N
ATOM   7215   CA    PHE  A  970    -31:854   56.119   -31:461   1,00  75,40   C
ATOM   7216   C     PHE  A  970    -32 ,745   56.570   -30,319   1,00  75.42   c
ATOM   7217   O     PHE  A  970    -32 ,819   55,905   -29,295   1,00  80.99   0
ATOM   7218   CB    PHE  A  970    -30:554   55.571   -30:914   1,00  76,67   C
ATOM   7219   CG    PHE  A  970    -29:644   55.032   -31:969   1,00  81,20   c
ATOM   7220   CD1   PHE  A  970    -30,160   54,452   -33,111   1,00  84.64   C
ATOM   7221   CD2   PHE  A  970    -28,273   55.093   -31.819   1,00  82.41   C
ATOM   7222   CE1   PHE  A  970    -29.325   53.944   -34.080   1,00  82,37   C
ATOM   7223   CE2   PHE  A  970    -27,429   54,577   -.32 ,785  1,00  84.96   C
ATOM   7224   CZ    PHE  A  970    -27,955   54,006   -33,916   1,00  85.80   C
ATOM   7225   N     GLN  A  971    -33.429   57.692   -30.506   1,00  79,90   N
ATOM   7226   CA    GLN  A  971    -34,351   58.254   -29,505   1,00  83.40   c
ATOM   7227   C     GLN  A  971    -33,752   58,451   -28,102   1,00  84.95   C
ATOM   7228   O     GLN  A  971    -34:430   58.210   -27:099   1,00  85,47   0
ATOM   7229   CB    GLN  A  971    -35,604   57.382   -29,385   1,00  81.24   c
ATOM   7230   CG    GLN  A  971    -36,536   57,441   -30,583   1,00  84.57   C
ATOM   7231   CD    GLN  A  971    -37:557   56.315   -30:570   1,00  87,82   C
ATOM   7232   OE1   GLN  A  971    -38:392   56.228   -29:671   1,00  89,88   0
ATOM   7233   NE2   GLN  A  971    -37,477   55,433   -31,559   1,00  90.19   N
ATOM   7234   O     PHE  A  972    -31,196   61.656   -26.722   1,00  77.20   0
ATOM   7235   N     PHE  A  972    -32 .489   58.880   -28:035   1,00  85,73   N
ATOM   7236   CA    PHE  A  972    -31,890   59,378   -26,791   1,00  76.21   C
ATOM   7237   C     PHE  A  972    -32 ,134   60.868   -26,708   1,00  74.60   C
ATOM   7238   CB    PHE  A  972    -30.398   59.093   -26.742   1,00  71,44   C
ATOM   7239   CG    PHE  A  972    -30,067   57,636   -26,731   1,00  75.31   C
ATOM   7240   CD1   PHE  A  972    -30,859   56,743   -26,043   1,00  76.74   C
ATOM   7241   CD2   PHE  A  972    -28.961   57.158   -27.411   1,00  76,54   C
ATOM   7242   CE1   PHE  A  972    -30,552   55.397   -26,024   1,00  77.90   c
ATOM   7243   CE2   PHE  A  972    -28,652   55,815   -27,402   1,00  79.77   C
ATOM   7244   CZ    PHE  A  972    -29:447   54.933   -26:708   1,00  80,90   C
ATOM   7245   O     TYR  A  973    -33,251   63.160   -24,514   1,00  77.64   0
ATOM   7246   N     TYR  A  973    -33,403   61,248   -26,648   1,00  73.69   N
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ATOM   7247  CA   TYR  A  973     -33.781  62.642 -26.790  1.00 77.00         C
ATOM   7248  C    TYR  A  973     -33.231  63.519 --25.688 1.00 76.62         C
ATOM   7249  CB   TYR  A  973     -35.303  62.789 -26.826  1.00 78.41         C
ATOM   7250  CG   TYR  A  973     -35.932  62.191 -28.049  1.00 81.96         C
ATOM   7251  GDI  TYR  A  973     -35.380  62.392 -29.309  1.00 81.17         C
ATOM   7252  CD2  TYR  A  973     -37.064  61.404 -27.943  1.00 86.77         C
ATOM   7253  CE1  TYR  A  973     -35.954  61.837 -30.436  1.00 81.49         C
ATOM   7254  CE2  TYR  A  973     -37.645  60.840 -29.061  1.00 87.64         C
ATOM   7255  CZ   TYR  A  973     -37.094  61.060 -30.307  1.00 85.11         C
ATOM   7256  OH   TYR  A  973     -37.694  60.491 -31.410  1.00 81.54         0
ATOM   7257  O    LYS  A  974     -33.943  67.321 -25.873  I ,00 71.12         0
ATOM   7258  N    LYS  A  974     -32.753  64.688 -26.090  1.00 75.90         M
ATOM   7259  CA   LYS  A  974     -32.340  65.711 -25.157  1.00 67.68         C
ATOM   7260  C    LYS  A  974     -33.458  66.703 -24.933  1.00 69.92         C
ATOM   7261  CB   LYS  A  974     -31.097  66.430 -25.666  1.00 70.63         C
ATOM   7262  CG   LYS  A  974     -30.944  67.823 -25.103  1.00 70.89         C
ATOM   7263  CD   LYS  A  974     -29.502  68.250 -25.123  1.00 68.86         C
ATOM   7264  CE   LYS  A  974     -29.031  68.564 -26.516  1.00 63.78         C
ATOM   7265  NZ   LYS  A  974     -27.553  68.555 -26.562  1.00 62.06         K
ATOM   7266  O    VAL  A  975     -33.948  68.342 -21.073  1.00 79.75         0
ATOM   7267  N    VAL  A  975     -33.875  66.836 -23.681  1.00 73.52         M
ATOM   7268  CA   VAL  A  975     -34.799  67.886 -23.281  1.00 71.81         C
ATOM   7269  C    VAL  A  975     -34.116  68.757 -22.226  1.00 80.51         C
ATOM   7270  CB   VAL  A  975     -36.099  67.313 -22.737  I ,00 73.87         C
ATOM   7271  CGI  VAL  A  975     -37.121  68.412 -22.555  1.00 70.88         C
ATOM   7272  CG2  VAL  A  975     -36.628  66.256 -23.683  1.00 77.72         C
ATOM   7273  O    ARG  A  976     -32.627  71.769 -19.697  I ,00 70.40         0
ATOM   7274  M    ARG  A  976     -33.725  69.964 -22.632  1.00 76.50         M
ATOM   7275  CA   ARG  A  976     -32.767  70.769 -21.876  1.00 72.83         C
ATOM   7276  C    ARG  A  976     -33.348  71.486 -20.655  1.00 73.45         C
ATOM   7277  CB   ARG  A  976     -32.112  71.796 -22.808  1.00 73.22         C
ATOM   7278  CG   ARG  A  976     -31.069  71.207 -23.777  1.00 76.16         C
ATOM   7279  CD   ARG  A  976     -30.421  72.302 -24.642  1.00 83.85         C
ATOM   7280  NE   ARG  A  976     -31.424  73.207 -25.215  1.00 93.48         M
ATOM   7281  CZ   ARG  A  976     -31.350  74.538 -25.192  1.00 97.93         C
ATOM   7282  NH1  ARG  A  976     -32.321  75.271 -25.736  1.00101.05         N
ATOM   7283  NH2  ARG  A  976     -30.307  75.141 -24.629  1.00 98.15         M
ATOM   7284  O    GLU  A  977     -36.118  72.204 -17.411  1.00 78.44         O
ATOM   7285  N    GUI  A  977     -34.646  71.773 -20.685  1.00 77.75         K
ATOM   7286  CA   GLU  A  977     -35.295  72.533 -19.617  I ,00 72.66         C
ATOM   7287  C    GLU  A  977     -35.559  71.703 -18.370  1.00 70.17         C
ATOM   7288  CB   GLU  A  977     -36.614  73.120 -20.112  1.00 73.30         C
ATOM   7289  CG   GLU  A  977     -36.471  74.128 -21.237  1.00 76.13         C
ATOM   7290  CD   GLU  A  977     -36.294  73.474 -22.586  1.00 71.74         C
ATOM   7291  OE1  GLU  A  977     -36.176  74.195 -23.595  1.00 86.17         0
ATOM   7292  OE2  GLU  A  977     -36.282  72.236 -22.642  1.00 72.74         0
ATOM   7293  O    ILE  A  978     -34.855  70.014 -15.046  1.00 72.56         0
ATOM   7294  K    ILE  A  978     -35.147  70.446 -18.387  1.00 67.94         K
ATOM   7295  CA   ILE  A  978     -35.457  69.507 -17.318  1.00 71.72         C
ATOM   7296  C    ILE  A  978     -34.485  69.612 -16.148  1.00 71.12         C
ATOM   7297  CB   ILE  A  978     -35.437  68.061 -17.847  1.00 76.07         C
ATOM   7298  CGI  ILE  A  978     -36.442  67.888 -19.003  1.00 80.47         C
ATOM   7299  CG2  ILE  A  978     -35.652  67.061 -16.705  I ,00 77.02         C
ATOM   7300  CD1  ILE  A  978     -37.836  68.483 -18.750  1.00 74.24         C
ATOM   7301  O    A.SK A  979     -30.950  69.925 -17.459  1.00 63.22         0
ATOM   7302  N    ASM  A  979     -33.245  69.209 -16.398  I ,00 70.23         N
ATOM   7303  CA   ASM  A  979     -32.152  69.398 -15.462  1.00 64.73         C
ATOM   7304  C    ASN  A  979     -30.897  69.743 -16.247  1.00 6.1.98         C
ATOM   7305  CB   ASN  A  979     -31.945  68.154 -14.602  1.00 64.47         C
ATOM   7306  CG   ASM  A  979     -31.689  66.902 -15.426  1.00 66.03         C
ATOM   7307  OD1  ASN  A  979     -30.921  66.913 -16.388  1.00 62.91         0
ATOM   7308  ND2  ASN  A  979     -32.334  65.810 -15.040  1.00 68.02         N
ATOM   7309  O    ASM  A  980     -26.671  69.188 -17.288  1.00 54.29         0
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ATOM   7310  N    ASN  A  980    -29.764    69.831  -15.572   1.00  59.94     N
ATOM   7311  CA   ASM  A  980    --28.551   70.218  -16.260   1.00  54.80     C
ATOM   7312  C    ASN  A  980    -27.772    69.026  -16.764   1.00  52.23     C
ATOM   7313  CB   ASN  A  980    -27.673    71.061  -15.349   1.00  53.67     C
ATOM   7314  CG   ASM  A  980    -28.251    72.429  -15.101   I.00  55.74     C
ATOM   7315  OD1  ASN  A  980    -28.082    7.3.338  -15.913   1.00  52.32     0
ATOM   7316  ND2  ASK  A  980    -28.945    72.587  -13.981   1.00  60.28     K
ATOM   7317  N    TYR  A  981    -28.345    67.833  -16.631   I.00  54.75     N
ATOM   7318  C    TYR  A  981    -27.092    66.409  -18.274   1.00  50.32     C
ATOM   7319  CA   TYR  A  981    -27.577    66.597  -16.840   1.00  52.86     C
ATOM   7320  O    TYR  A  981    -26.113    65.722  -18.501   I.00  57.61     0
ATOM   7321  CB   TYR  A  981    -28.395    65.359  -16.462   1.00  58.55     C
ATOM   7322  CG   TYR  A  981    -28.560    65.091  -14.989   1.00  60.17     C
ATOM   7323  CD2  TYR  A  981    -29.232    63.963  -14.548   1.00  63.46     C
ATOM   7324  CD1  TYR  A  981    -28.043    65.953  -14.037   1.00  59.89     C
ATOM   7325  CE2  TYR  A  981    -29..399   6.3.709  -13.198   1.00  6.3.92    C
ATOM   7326  CE1  TYR  A  981    -28.198    65.707  -12.679   1.00  57.60     C
ATOM   7327  CZ   TYR  A  981    -28.876    64.584  -12.267   I.00  63.03     C
ATOM   7328  OH   TYR  A  981    -29.032    64.325  -10.921   1.00  62.57     0
ATOM   7329  N    HIS  A  982    -27.806    66.993  -19.229   1.00  52.05     K
ATOM   7330  C    HIS  A  982    -26.154    67..318  -2.1.053  I.00  50.83     C
ATOM   7331  CA   HIS  A  982    -27.526    66.814  -20.649   1.00  50.27     C
ATOM   7332  O    HIS  A  982    -25.637    66.946  -22.092   1.00  52.04     0
ATOM   7333  CB   HIS  A  982    -28.591    67.522  -21.485   I.00  51.4.1    C
ATOM   7334  CG   HIS  A  982    -28.537    69.013  -21.396   1.00  54.78     C
ATOM   7335  KD1  HIS  A  982    -29.269    69.732  -20.471   1.00  62.33     K
ATOM   7336  CD2  HIS  A  982    -27.839    69.924  -22.114   I.00  52.72     C
ATOM   7337  CEl  HIS  A  982    -29.032    71.022  -20.630   1.00  54.11     C
ATOM   7338  KF.2 HIS  A  982    -28.163    71.165  -21.617   1.00  56.17     K
ATOM   7339  N    HIS  A  983    -25.570    68.186  -20.243   1.00  51.99     K
ATOM   7340  C    HIS  A  983    -23.301    67.533  -20.376   1.00  48.19     C
ATOM   7341  CA   HIS  A  98.3   -24.248    68.686  -20.544   1.00  49.22     C
ATOM   7342  O    HIS  A  983    -22.309    67.430  -21.078   1.00  49.24     0
ATOM   7343  CB   HIS  A  983    -23.838    69.834  -19.620   I.00  45.64     C
ATOM   7344  CG   HIS  A  98.3   -24.666    7.1.069  -19.752   1.00  48.38     C
ATOM   7345  ND1  HIS  A  983    -24.447    72.014  -20.733   1.00  50.39     K
ATOM   7346  CD2  HIS  A  983    -25.690    71.539  -19.000   I.00  54.24     C
ATOM   7347  CEl  HIS  A  983    -25.311    73.003  -20.587   1.00  54.71     C
ATOM   7348  KE2  HIS  A  983    -26.074    72.742  -19.540   1.00  49.43     K
ATOM   7349  N    ALA  A  984    -2.3.629   66.666  -19.423   I.00  47.80     N
ATOM   7350  C    ALA  A  984    -23.104    64.356  -20.051   1.00  55.83     C
ATOM   7351  CA   ALA  A  984    -22.816    65.503  -19.092   1.00  50.96     C
ATOM   7352  O    ALA  A  984    -22.191    63.614  -20.442   1.00  59.19     0
ATOM   7353  CB   ALA  A  984    -23.066    65.060  -17.656   1.00  46.96     C
ATOM   7354  N    HIS  A  985    -24.381    64.196  -20..389   1.00  48.23     M
ATOM   7355  C    HIS  A  985    -24.027    63.521  -22.700   1.00  52.53     C
ATOM   7356  CA.  HIS  A  985    -24.782    63.244  -2.1.406  I.00  54.55     C
ATOM   7357  O    HIS  A  985    -23..399   62.634  -23.263   1.00  57.44     0
ATOM   7358  CB   HIS  A  985    -26.288    63.322  -21.640   1.00  56.32     C
ATOM   7359  CG   HIS  A  985    -27.100    62.914  -20.453   I.00  54.71     C
ATOM   7360  MD1  HIS  A  985    -26.599    62.109  -19.452   1.00  50.18     M
ATOM   7361  CD2  HIS  A  985    -28.380    63.192  -20.111   1.00  53.28     C
ATOM   7362  CEl  HIS  A  985    -27.535    61.912  -18.541   I.00  52.07     C
ATOM   7363  ME2  HIS  A  985    -28.623    62.561  -18.915   1.00  56.29     M
ATOM   7364  K    ASP  A  986    -24.089    64.768  -23.148   1.00  54.93     K
ATOM   7365  C    ASP  A  986    -2.1.992   64.772  -24.400   I.00  54.7.3    C
ATOM   7366  CA   ASP  A  986    -23.448    65.178  -24.390   1.00  57.80     C
ATOM   7367  O    ASP  A  986    -21.485    64.315  -25.415   1.00  59.38     0
ATOM   7368  CB   ASP  A  986    -23.569    66.687  -24.596   1.00  56.37     C
ATOM   7369  CG   ASP  A  986    -24.924    67.093  -25.119   1.00  60.58     C
ATOM   7370  OD1  ASP  A  986    -25.771    66.203  -25.311   1.00  58.16     0
ATOM   7371  OD2  ASP  A  986    -25.137    68.301  -25.349   1.00  65.96     0
ATOM   7372  N    ALA  A  987    -21.333    64.932  -23.257   I.00  56.09     M
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ATOM	7373	C	ALA	A	987	-19.766	63.037	-23.206	1.00	56.51	C
ATOM	7374	CA	ALA	A	987	--19,938	64.537	-23,106	1,00	54.78	C
ATOM	7375	O	ALA	A	987	-18.768	62,540	-23:738	1,00	57,64	0
ATOM	7376	CB	ALA	A	987	-19.404	65,020	-21,782	1.00	55.46	C
ATOM	7377	N	TYR	A	988	-20,731	62..318	-22,648	1,00	55,78	M
ATOM	7378	CA	TYR	A	988	-20.644	60,868	-22.590	1,00	63,29	C
ATOM	7379	C	TYR	A	988	-20.759	60,298	-23:998	1,00	61,50	C
ATOM	7380	0	TYR	A	988	-19,874	59.567	-24,461	1,00	56,95	0
ATOM	7381	CB	TYR	A	988	-21.733	60,292	-21,674	1,00	60.75	C
ATOM	7382	CG	TYR	A	988	-21.961	58,799	-21.854	1,00	59,82	C
ATOM	7383	CDI	TYR	A	988	-21,033	57.880	-21,404	1,00	61.76	C
ATOM	7384	CD2	TYR	A	988	-23.110	58.320	-22,476	1,00	61.10	C
ATOM	7385	CE1	TYR	A	988	-21.229	56,538	-21.569	1,00	64,56	C
ATOM	7386	CE2	TYR	A	988	-23.314	56,974	-22,646	1.00	61.96	C
ATOM	7387	CZ	TYR	A	988	-22,371	56.089	-22,191	1,00	64.10	C
ATOM	7388	OH	TYR	A	988	-22.561	54,741	-22.352	1,00	65,77	0
ATOM	7389	N	LEU	A	989	**-21.858**	60,662	-24.662	1.00	56.03	M
ATOM	7390	CA.	LEU	A	989	-22,134	60.263	-26,039	1,00	58.08	C
ATOM	7391	C	LEU	A	989	-21.001	60,641	-26.982	1,00	61,84	C
ATOM	7392	O	LEU	A	989	-20.760	59,972	-27.977	1,00	66,80	0
ATOM	7393	CB	LEU	A	989	-23,431	60.896	-26.518	1,00	52.61	C
ATOM	7394	CG	LEU	A	989	-24.633	60,659	-25,615	1,00	59.59	C
ATOM	7395	CD1	LEU	A	989	-25.845	61,453	-26.100	1,00	50,97	C
ATOM	7396	CD2	LEU	A	989	-24,937	59.173	-25,534	1,00	54.55	C
ATOM	7397	K	ASN	A	990	-20.305	61.720	-26,669	1,00	59.58	K
ATOM	7398	CA	ASN	A	990	-19.218	62,149	-27.513	1,00	58,13	C
ATOM	7399	C	ASM	A	990	-18,078	61.158	-27,447	1,00	61.76	C
ATOM	7400	O	ASM	A	990	-17,522	60.792	-28,469	1,00	62.49	0
ATOM	7401	CB	A.SM	A	990	-18.748	63,541	-27.110	1,00	54,66	C
ATOM	7402	CG	ASM	A	990	-19.181	64,580	-28.080	1.00	62.92	C
ATOM	7403	OD1	ASM	A	990	-18,461	64.882	-29,027	1,00	65.84	0
ATOM	7404	KD2	ASN	A	990	-20..386	65,127	-27.882	1,00	65,25	K
ATOM	7405	N	ALA	A	991	-17.738	60,723	-26.239	1.00	60.09	M
ATOM	7406	CA.	ALA	A	991	-16,654	59.772	-26,061	1,00	60.85	C
ATOM	7407	C	ALA	A	991	-17.023	58,412	-26.682	1,00	65,24	C
ATOM	7408	O	ALA	A	991	-16.210	57,786	-27.364	1,00	59,42	0
ATOM	7409	CB	ALA	A	991	-16,326	59.623	-24,602	1,00	53.03	C
ATOM	7410	K	VAL	A	992	-18.262	57,983	-26,439	1,00	70.03	K
ATOM	7411	CA	VAL	A	992	-18.824	56,770	-27.035	1,00	68,48	C
ATOM	7412	C	VAL	A	992	-18,686	56.807	-28,552	1,00	70.14	C
ATOM	7413	O	VAL	A	992	-18,029	55.946	-29,134	1,00	68.40	0
ATOM	7414	CB	VAL	A	992	-20..325	56,579	-26.659	1,00	70,12	C
ATOM	7415	CGI	VAL	A	992	-21.008	55,579	-27,597	1.00	63.75	C
ATOM	7416	CG2	VAL	A	992	-20,459	56.119	-25,212	1,00	69.20	C
ATOM	7417	K	VAL	A	993	-19.283	57,814	-29.191	1,00	65,45	K
ATOM	7418	CA	VAL	A	993	-19,199	57,926	-30.641	1.00	66.91	C
ATOM	7419	C	VAL	A	993	-17,754	58.163	-.31,121	1,00	69.36	C
ATOM	7420	O	VAL	A	993	-17..336	57,628	-32 .136	1,00	67,24	0
ATOM	7421	CB	VAL	A	993	-20.135	59,038	-31.153	1,00	67,83	C
ATOM	7422	CGI	VAL	A	993	-19,957	59.273	-.32 ,640	1,00	66.06	C
ATOM	7423	CG2	VAL	A	993	-21,588	58,662	-30,863	1,00	68.16	C
ATOM	7424	N	GLY	A	994	-16.975	58:927	-30.374	1,00	67,95	M
ATOM	7425	CA	GLY	A	994	-15,633	59.249	-.30,817	1,00	66.29	C
ATOM	7426	C	GLY	A	994	-14,748	58.023	-30,921	1,00	72.35	C
ATOM	7427	O	GLY	A	994	-13.967	57,860	-31.859	1,00	71,35	0
ATOM	7428	N	THR	A	995	-14,884	57.152	-29,936	1,00	71.51	M
ATOM	7429	CA	THR	A	995	-14,009	56.008	-29,783	1,00	69.32	C
ATOM	7430	C	THR	A	995	-14.395	54,853	-30.712	1,00	71,67	C
ATOM	7431	O	THR	A	995	-13,541	54,225	-31,346	1.00	68.59	0
ATOM	7432	CB	THR	A	995	-14,061	55:534	-28,355	1,00	72.06	C
ATOM	7433	OG1	THR	A	995	-15.441	55,402	-27,984	1,00	69,10	0
ATOM	7434	CG2	THR	A	995	-13.405	56,558	-27.445	1.00	68.91	C
ATOM	7435	N	ALA	A	996	-15,696	54.584	-.30,758	1,00	67.40	M

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ATOM   7436  CA   ALA. A  996     -16.285   53.599  -31.654   1.00  71.56     C
ATOM   7437  C    ALA  A  996     -15.998   53.901  -33.126   1.00  75.58     C
ATOM   7438  O    ALA  A  996     -15.780   52.997  -33.9.32  1.00  79.08     0
ATOM   7439  CE   ALA. A  996     -17.792   53.528  -31.429   1.00  70.29     C
ATOM   7440  N    LEU  A  997     -16.015   55.175  -3.3.485  I.00  73.18     N
ATOM   7441  CA   LEU  A  997     -15.825   55.543  -34.876   1.00  72.77     C
ATOM   7442  C    LEU  A  997     -14.359   55.494  -35.269   1.00  74.11     C
ATOM   7443  0    LEU  A  997     -14.039   55.310  -36.436   I.00  78..38     0
ATOM   7444  CB   LEU  A  997     -16.405   56.927  -35.153   1.00  68.58     C
ATOM   7445  CG   LEU  A  997     -17.615   56.891  -36.083   1.00  75.40     C
ATOM   7446  CDI  LEU  A  997     -18.647   57.937  -35.698   I.00  73.16     C
ATOM   7447  CD2  LEU  A  997     -17.164   57.078  -37.530   1.00  77.88     C
ATOM   7448  N    ILE  A  998     -13.460   55.654  -34.311   1.00  70.26     N
ATOM   7449  CA   ILE  A  998     -12.058   55.602  -34.655   1.00  70.08     C
ATOM   7450  C    ILE  A  998     -11.563   54.176  -34.452   1.00  76.65     C
ATOM   7451  O    ILE  A  998     -10.404   5.3.868  -34.7.34  1.00  76.85     0
ATOM   7452  CB   ILE  A  998     -11.228   56.591  -33.827   1.00  72.91     C
ATOM   7453  CGI  ILE  A  998      -9.994   57.047  -34.618   I.00  79.12     C
ATOM   7454  CG2  ILE  A  998     -10.883   56.000  -32.451   1.00  77.05     C
ATOM   7455  CD1  ILE  A  998      -8.670   56.573  -34.060   1.00  80.67     C
ATOM   7456  N    LYS  A  999     -12.450   53.306  -3.3.965  I.00  74.53     N
ATOM   7457  CA   LYS  A  999     -12.113   51.891  -33.776   1.00  79.23     C
ATOM   7458  C    LYS  A  999     -12.629   51.041  -34.947   1.00  77.32     C
ATOM   7459  0    LYS  A  999     -11.874   50.259  -35.522   I.00  77.25     0
ATOM   7460  CB   LYS  A  999     -12.670   51.373  -32.445   1.00  78.90     C
ATOM   7461  CG   LYS  A  999     -11.708   50.486  -31.647   1.00  8.3.78     C
ATOM   7462  CD   LYS  A  999     -12.187   50..339  -.30.196  I.00  91.65     C
ATOM   7463  CE   LYS  A  999     -11.945   48.936  -29.623   1.00  92.38     C
ATOM   7464  NZ   LYS  A  999     -12.840   48.649  -28.447   1.00  77.16     N
ATOM   7465  N    LYS  A1000     -13.907   51.204  -35.297   1.00  76.80     N
ATOM   7466  CA   LYS  A1000     -14.452   50.599  -36.512   1.00  77.87     C
ATOM   7467  C    LYS  A1000     -13.586   50.978  -37.709   1.00  78.96     C
ATOM   7468  O    LYS  A1000     -12.983   50.119  -38.350   1.00  81.00     0
ATOM   7469  CB   LYS  A.1000    -15.903   51.037  -.36.747  I.00  75.50     C
ATOM   7470  N    TYR  AlOOl     -13.5.13  52.277  -37.985   1.00  79.86     N
ATOM   7471  CA   TYR  AlOOl     -12.693   52.802  -39.071   1.00  78.25     C
ATOM   7472  C    TYR  A1001     -1.1.483  53.585  -38.564   I.00  76.89     C
ATOM   7473  O    TYR  AlOOl     -11.608   54.749  -38.229   1.00  79.92     0
ATOM   7474  CB   TYR  A1001     -13.5.13  53.723  -39.969   1.00  74.78     C
ATOM   7475  CG   TYR  AlOOl     -14.937   53.292  -40.236   I.00  79.14     C
ATOM   7476  CD1  TYR  AlOOl     -15.216   52.133  -40.960   1.00  77.45     C
ATOM   7477  CD2  TYR  A1001     -16.004   54.074  -39.812   1.00  7.3.97     C
ATOM   7478  CE1  TYR  AlOOl     -16.526   51.750  -41.229   1.00  76.04     C
ATOM   7479  CE2  TYR  AlOOl     -17.314   53.703  -40.076   1.00  81.12     C
ATOM   7480  CZ   TYR  AlOOl     -17.571   52.538  -40.783   1.00  81.39     C
ATOM   7481  OH   TYR  AlOOl     -18.873   52.168  -41.042   1.00  79.26     0
ATOM   7482  O    PRO  A1002      -8.668   54.488  -40.403   I.00  76.90     0
ATOM   7483  N    PRO  A1002     -10..308   52.954  -38.499   1.00  78.53     N
ATOM   7484  CA   PRO  A1002      -9.133   53.767  -38.173   1.00  71.12     C
ATOM   7485  C    PRO  A1002      -8.838   54.830  -39.235   I.00  75.54     C
ATOM   7486  CB   PRO  A1002      -8.018   52.731  -38.096   1.00  77.13     C
ATOM   7487  CG   PRO  A1002      -8.731   51.473  -37.669   1.00  73.26     C
ATOM   7488  CD   PRO  A1002     -10.045   51.509  -.38.374  I.00  74.04     C
ATOM   7489  O    LYS  A1003        y.112   58.969  -38.096   1.00  78.26     0
ATOM   7490  N    LYS  A100.3     -8.815   56.104  -38.824   1.00  87.98     N
ATOM   7491  CA   LYS  A1003      -8.537   57.246  -.39.716  I.00  82.46     C
ATOM   7492  C    LYS  A1003      -8.336   58.585  -38.971   1.00  82.90     C
ATOM   7493  CB   LYS  A100.3     -9.652   57.406  -40.758   1.00  76.42     C
ATOM   7494  CG   LYS  A1003     -10.868   58.220  -40.326   1.00  78.72     C
ATOM   7495  CD   LYS  A1003     -11.568   57.604  -39.133   1.00  74.95     C
ATOM   7496  CE   LYS  A1003     -12.890   58.271  -38.851   1.00  70.60     C
ATOM   7497  NZ   LYS  A1003     -13.908   57.907  -39.864   1.00  72.37     N
ATOM   7498  O    LEU  A.1004     -5.586   60.732  -40.771   I.00  82.78     0
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ATOM    7499   N    LEU  A1004      --7.250   59.271  -39.305   1.00  82.42           N
ATOM    7500   CA   LEU  A1004      -7.027    60.642  -38.876   1.00  77.53           C
ATOM    7501   C    LEU  A1004      -6.422    61.331  -40.095   1.00  81.46           C
ATOM    7502   CB   LEU  A1004      --6.123   60.717  -37.644   1.00  74.30           C
ATOM    7503   CG   LEU  A1004      -5.504    59.447  -.37.037   1.00  81.49           C
ATOM    7504   GD1  LEU  A1004      -6.506    58.529  -36.331   1.00  80.84           C
ATOM    7505   CD2  LEU  A1004      -4.386    59.827  -36.073   1.00  78.45           C
ATOM    7506   O    GLU  A1005      -9.713    63.761  -.39.707   1.00  77.13           0
ATOM    7507   N    GLU  A100 5     -6.783    62.581  -40.387   1.00  76.65           N
ATOM    7508   CA   GLU  A1005      -7.304    63.555  -39.436   1.00  80.24           C
ATOM    7509   C    GLU  A1005      -8.764    63.445  -.38.981   1.00  84.88           C
ATOM    7510   CB   GLU  A100 5     -7.093    64.959  -40.009   1.00  85.55           C
ATOM    7511   O    SER  A100 6     -9.931    64.059  -34.625   1.00  70.87           0
ATOM    7512   N    SER  A100 6     --8.894   62.974  -37.747   1.00  81.21           N
ATOM    7513   CA   SER  A100 6     --10.015  63.250  -36.880   1.00  69.88           C
ATOM    7514   C    SER  A100 6     -9. .363  63.425  -35.510   1.00  69.48           C
ATOM    7515   CB   SER  A100 6     -11.053   62.132  -36.895   1.00  72.04           C
ATOM    7516   OG   SER  A100 6     -12.354   62.652  -.36.666   1.00  76.46           0
ATOM    7517   O    GLU  A1007      -6. .38 9 64.724  -35.670   1.00  73.79           0
ATOM    7518   N    GLU  A1007      -8.159    62.864  -35.357   1.00  66.42           N
ATOM    7519   CA.  GLU  A1007      -7.303    63.114  -.34.197   1.00  66.14           C
ATOM    7520   C    GLU  A1007      -6.487    64.356  -34.510   1.00  66.52           C
ATOM    7521   CB   GLU  A1007      -6.395    61.914  -33.889   1.00  61.66           C
ATOM    7522   O    PHE  A1008      -2.866    66.080  -.33.715   1.00  61.28           0
ATOM    7523   N    PHE  A1008      -5.913    65.014  -33.503   1.00  68.18           N
ATOM    7524   CA   PHE  A1008      -5.290    66.329  -33.722   1.00  66.70           C
ATOM    7525   C    PHE  A1008      -3.892    66.230  -.34.374   1.00  61.21           C
ATOM    7526   CB   PHE  A1008      -5.225    67.122  -32.400   1.00  62.02           C
ATOM    7527   CG   PHE  A1008      -4.503    68.447  -32.515   1.00  61.48           C
ATOM    7528   CD1  PHE  A1008      -3.181    68.575  -32.106   1.00  61.73           C
ATOM    7529   CD2  PHE  A1008      -5.139    69.556  -33.045   1.00  61.58           C
ATOM    7530   CE1  PHE  A1008      -2.508    69.780  -32.223   1.00  60.03           C
ATOM    7531   CE2  PHE  A1008      -4.470    70.773  -33.165   1.00  63.69           C
ATOM    7532   CZ   PHE  A1008      -3.154    70.884  -.32.754   1.00  62.73           C
ATOM    7533   0    GLY  A10.30     -12.657   57.536  -57.259   1.00  87.52           0
ATOM    7534   N    GLY  A1030      -10.361   59.616  -57.240   1.00  90.29           N
ATOM    7535   CA.  GLY  A1030      -10.351   58.165  -57.171   1.00  92.18           C
ATOM    7536   C    GLY  A1030      -11.633   57.595  -56.588   1.00  92.98           C
ATOM    7537   O    LYS  A1031      -14.094   57.683  -52.902   1.00  97.60           0
ATOM    7538   N    LYS  A1031      -11.575   57.169  -55.330   1.00  96.43           N
ATOM    7539   CA   LYS  A1031      -12.762   56.694  -54.628   1.00  93.17           C
ATOM    7540   C    LYS  A1031      -13.425   57.861  -53.919   1.00  99.79           C
ATOM    7541   CB   LYS  A1031      -12.414   55.599  -53.622   1.00  95.25           C
ATOM    7542   O    ALA  A1032      -16.051   60.527  -53.070   1.00  99.71           0
ATOM    7543   N    ALA  A10.32     -13.216   59.058  -54.459   1.00  98.13           N
ATOM    7544   CA   ALA  A1032      -13.837   60.260  -53.938   1.00  94.53           C
ATOM    7545   C    ALA  A1032      -15.348   60.120  -53.993   1.00  98.04           C
ATOM    7546   CB   ALA  A10.32     -13.382   61.479  -54.721   1.00  97.40           C
ATOM    7547   O    THR  A1033      -18.764   58.713  -53.399   1.00  98.03           O
ATOM    7548   N    THR  A1033      -15.845   59.537  -55.077   1.00  98.15           N
ATOM    7549   CA   THR  A1033      -17.272   59.272  -55.196   1.00  98.55           C
ATOM    7550   C    THR  A1033      -17.732   58.430  -54.013   1.00  98.63           C
ATOM    7551   CB   THR  A1033      -17.619   58.546  -56.515   1.00100.04           C
ATOM    7552   OG1  THR  A1033      -17.181   59.334  -57.631   1.00104 .11           0
ATOM    7553   CG2  THR  A10.33     -19.123   58.322  -56.621   1.00  93.00           C
ATOM    7554   O    ALA  A1034      -17.720   57.052  -50.295   1.00  97.27           0
ATOM    7555   N    ALA  A1034      -16.942   57.407  -53.694   1.00  98.60           N
ATOM    7556   CA   ALA  A10.34     -17.224   56.512  -52.574   1.00  96.08           C
ATOM    7557   C    ALA  A1034      -16.937   57.184  -51.236   1.00  97.89           C
ATOM    7558   CB   ALA  A1034      -16.416   55.229  -52.701   1.00  96.61           C
ATOM    7559   O    LYS  A10.35     -16.227   60.453  -48.596   1.00  93.02           0
ATOM    7560   N    LYS  A1035      -15.824   57.918  -51.161   1.00  98.96           N
ATOM    7561   CA.  LYS  A1035      -15.435   58.636  -49.942   1.00  96.54           C
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ATOM   7562  C    LYS  A1035    -16..407  59..753  -49..587  1.00  95..20   C
ATOM   7563  CB   LYS  A1035    -14,022   59..204  --50.,076 1,00  96..03   C
ATOM   7564  CG   LYS  A1035    -12.918   58.,179  -49..823  1,00  99,.22   C
ATOM   7565  CD   LYS  A1035    -12..267  58.,374  -48..453  1.00  99..42   C
ATOM   7566  CE   LYS  A1035    -13.,211  58. 006  -47,315   1,00  92.80    C
ATOM   7567  NZ   LYS  A1035    -12.711   58.,480  -45..995  1,00  86,.31   N
ATOM   7568  O    TYR  A1036    -20.. 741 60.,109  -49..116  1,00  94,68    O
ATOM   7569  N    TYR  A1036    -17,437   59. 898  -50.,413  1,00  95..19   N
ATOM   7570  CA   TYR  A103 6   -18..617  60.,692  -50.,118  1,00  93..52   C
ATOM   7571  C    TYR  A1036    -19..535  59.,871  -49..190  1,00  94,20    C
ATOM   7572  CB   TYR  A103 6   -19.,294  61..086  -51.,446  1,00  94.61    C
ATOM   7573  CG   TYR  A103 6   -20.,533  61..963  -51.,391  1,00  94.97    C
ATOM   7574  GDI  TYR  A103 6   -20. 456  63.,297  -51. 023  1,00  89,72    C
ATOM   7575  CD2  TYR  A1036    -21.,777  61.,461  -51.,766  1.00  97.60    C
ATOM   7576  CEl  TYR  A1036    -21.,585  64..092  -50.,993  1,00  85..31   C
ATOM   7577  CE2  TYR  A1036    -22..909  62.,250  -51..740  1,00  92,54    C
ATOM   7578  CZ   TYR  A1036    -22..806  63.,563  -51..354  1.00  91.19    C
ATOM   7579  OH   TYR  A1036    -23.,935  64. .348  -51,333   1,00  97.92    0
ATOM   7580  O    PHE  A10.37   -20.594   58.,129  -45...305  1,00  94,00    0
ATOM   7581  N    PHE  A1037    -18..935  58.,917  -48..466  1,00  95,.50   N
ATOM   7582  CA.  PHE  A1037    -19.,651  58. 034  -47,531   1,00  95..03   C
ATOM   7583  C    PHE  A1037    -19.,866  58.,667  -46,150   1,00  98..88   C
ATOM   7584  CB   PHE  A1037    -18..908  56.,705  -47.377   1,00  92,95    C
ATOM   7585  CG   PHE  A1037    -17,854   56..693  -46.,287  1,00  98..69   C
ATOM   7586  CD1  PHE  A1037    -17,735   55..593  -45,446   1,00  99..48   C
ATOM   7587  CD2  PHE  A1037    -16. 959  57,742   -46. 126  1,00  97,85    C
ATOM   7588  CEl  PHE  A1037    -16.,768  55..551  -44,452   1,00  93..70   C
ATOM   7589  CE2  PHE  A1037    -15.,997  57..705  -45,122   1,00  97.68    C
ATOM   7590  CZ   PHE  A1037    -15. 902  56.,603  -44 .292  1,00  95,91    C
ATOM   7591  N    PHE  A1038    -19.,216  59.,809  -45,933   1.00  96..94   N
ATOM   7592  CA   PHE  A1038    -19.,496  60..652  -44,781   1,00  91.91    C
ATOM   7593  C    PHE  A10.38   -20.991   60.,958  -44 .781  1,00  95,.30   C
ATOM   7594  O    PHE  A1038    -21..576  61.,261  -43..737  1.00  97.94    0
ATOM   7595  CB   PHE  A1038    -18.,684  61. 962  -44,823   1,00  86...30   C
ATOM   7596  CG   PHE  A10.38   -17.190   61.,791  -44 .648  1,00  82,33    C
ATOM   7597  CD2  PHE  A1038    -16..641  61.,578  -43..397  1,00  81,62    C
ATOM   7598  CD1  PHE  A1038    -16.,335  61. 887  -45,729   1,00  81.27    C
ATOM   7599  CE2  PHE  A1038    -15.,269  61.,442  -43,238   1,00  74.52    C
ATOM   7600  CE1  PHE  A1038    -14.965   61.,748  -45. 569  1,00  82,04    C
ATOM   7601  CZ   PHE  A1038    -14,434   61..529  -44,322   1,00  73..28   C
ATOM   7602  O    TYR  A1039    -25.,046  60..701  -45,010   1,00  98..32   0
ATOM   7603  N    TYR  A103 9   -21.596   60.,873  -45. 966  1,00  93,19    N
ATOM   7604  CA   TYR  A1039    -23.,000  61.,215  -46,165   1.00  98..12   C
ATOM   7605  C    TYR  A1039    -23.,936  60..305  -45,375   1,00  95..65   C
ATOM   7606  CB   TYR  A10.39   -23...349 61.,161  -47 .656  1,00  93,.90   C
ATOM   7607  N    SER  A104 0   -23..491  59.,086  -45..106  1.00  95..15   N
ATOM   7608  CA.  SER  A1040    -24.,313  58. 165  -44 ,340  1,00  99.,39   C
ATOM   7609  C    SER  A104 0   -23..448  57.,206  -43..547  1,00  98,.15   C
ATOM   7610  O    SER  A1040    -23..385  57.,284  -42..318  1,00  98,.64   O
ATOM   7611  CB   SER  A1040    -25,266   57. 379  -45,261   1,00  97.70    C
ATOM   7612  OG   SER  A104 0   -24.,566  56.,422  -46,048   1,00  97.41    0
ATOM   7613  N    ASN  A1041    -22.748   56.,346  -44.282   1,00  96,.36   N
ATOM   7614  CA   ASN  A1041    -22.,200  55..090  -43,768   1,00  98..07   C
ATOM   7615  C    ASN  A1041    -21.,459  55..152  -42.,432  1,00  98..49   C
ATOM   7616  O    ASN  A1041    -21 .417   54,147   -41 .701  1,00  96,25    O
ATOM   7617  CB   ASN  A1041    -21.,271  54..473  -44 ,823  1,00  98..89   C
ATOM   7618  CG   ASN  A1041    -21.,308  52..954  -44,820   1,00  95..33   C
ATOM   7619  OD1  ASN  A1041    -20. 272  52.,299  -44 .931  1,00  97,43    O
ATOM   7620  ND2  ASN  A1041    -22.,507  52.,387  -44,691   1.00  93..05   N
ATOM   7621  N    ILE  A1042    -20.,881  56..311  -42.,107  1,00  97.58    N
ATOM   7622  CA   ILE  A104 2   -20.112   56.,438  -40..869  1,00  90,.58   C
ATOM   7623  C    ILE  A104 2   -21..042  56.,325  -39..667  1.00  89..52   C
ATOM   7624  O    ILE  A1042    -20.,620  55. 942  -.38.,580  1,00  93..96   0
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ATOM	7625	CB	ILE	A1042	-19.305	57.762	-40.811	1.00	94.48	C
ATOM	7626	CGI	ILE	A1042	--20,038	58.894	-41,540	1,00	95.90	C
ATOM	7627	CG2	ILE	A1042	-17,913	57,564	-41.416	1,00	91,84	C
ATOM	7628	GDI	ILE	A1042	-21.194	59:509	-40.776	1.00	90.77	C
ATOM	7629	N	MET	A1043	-22,316	56.636	-39,872	1,00	89,26	N
ATOM	7630	CA	MET	A1043	-23.312	56,449	-38.829	1,00	94,02	C
ATOM	7631	C	MET	A1043	-24.213	55,263	-39.159	1,00	95,35	C
ATOM	7632	0	MET	A1043	-25,246	55.058	-38,521	1,00	97,79	0
ATOM	7633	CB	MET	A1043	-24.148	57,718	-38:640	1,00	96.38	C
ATOM	7634	CG	MET	A1043	-24.324	58,124	-37.181	1,00	93,83	C
ATOM	7635	SD	MET	A1043	-22,756	58.360	-36,295	I,00	93.07	S
ATOM	7636	CE	MET	A1043	-23.380	58.873	-34,698	1,00	85.58	C
ATOM	7637	N	ASN	A1044	-23.816	54,485	-40.162	1,00	96,42	N
ATOM	7638	CA	ASN	A1044	-24.562	53:291	-40.540	1.00	94.60	C
ATOM	7639	C	ASN	A1044	-24,087	52.059	-39,760	1,00	85.58	C
ATOM	7640	O	ASN	A1044	-24.903	51,250	-39.323	1,00	80,21	0
ATOM	7641	CB	ASN	A1044	-24.466	53:049	-42.055	1.00	95.21	C
ATOM	7642	CG	ASN	A1044	-25,354	54.006	-42,865	1,00	95,22	C
ATOM	7643	OD1	ASN	A1044	-25.954	54,933	-42..314	1,00	98,01	0
ATOM	7644	ND2	ASN	A1044	-25.437	53,778	-44.175	1,00	91,81	N
ATOM	7645	O	PHE	A1045	-22,524	49.740	-36,662	1,00	82,16	O
ATOM	7646	N	PHE	A1045	-22.781	51:939	-39:536	1,00	82.09	N
ATOM	7647	CA	PHE	A1045	—22.242	50,791	-38.801	1,00	80,52	C
ATOM	7648	C	PHE	A1045	-22,806	50.691	-37,384	I,00	82.95	C
ATOM	7649	CB	PHE	A1045	-20.724	50.868	-38:721	1,00	79.63	C
ATOM	7650	CG	PHE	A1045	-20.237	51,591	-37.509	1,00	87,29	C
ATOM	7651	CD2	PHE	A1045	-20,363	52.969	-37,412	I,00	88.30	C
ATOM	7652	CD1	PHE	A1045	-19,693	50.900	-36,447	1,00	88.72	C
ATOM	7653	CE2	PHE	A1045	-19.930	53,641	-36.290	1,00	83,88	C
ATOM	7654	CE1	PHE	A1045	-19.259	51:571	-35:322	1.00	86.80	C
ATOM	7655	CZ	PHE	A1045	-19,378	52.941	-35,247	1,00	83.15	C
ATOM	7656	O	PHE	A1046	-26.114	50,307	-35.037	1,00	83,30	0
ATOM	7657	N	PHE	A1046	-23.556	51:714	-36.983	1.00	88.54	N
ATOM	7658	CA.	PHE	A1046	-24,306	51.732	-35,731	1,00	87,93	C
ATOM	7659	C	PHE	A1046	-25.656	51,047	-35.915	1,00	88,25	C
ATOM	7660	CB	PHE	A1046	-24.536	53,178	-35.251	1,00	90,38	C
ATOM	7661	CG	PHE	A1046	-23,544	53.664	-34,219	1,00	87,40	C
ATOM	7662	CD1	PHE	A1046	-23.061	52,816	-33:234	1,00	81.78	C
ATOM	7663	CD2	PHE	A1046	-23.117	54,987	-34.227	1,00	85,23	C
ATOM	7664	CE1	PHE	A1046	-22,160	53.274	-32 ,287	I,00	80.80	C
ATOM	7665	CE2	PHE	A1046	-22,212	55.452	-33,282	1,00	83.58	C
ATOM	7666	CZ	PHE	A1046	-21.737	54,596	-32..311	1,00	82,24	C
ATOM	7667	O	LYS	A1047	-26:867	48:681	-37.694	1.00	80.25	0
ATOM	7668	N	LYS	A1047	-26,282	51.321	-37,065	1,00	90.16	N
ATOM	7669	CA	LYS	A1047	-27.670	50,933	-37..351	1,00	89,03	C
ATOM	7670	C	LYS	A1047	-27.840	49:437	-37.592	1.00	86.83	C
ATOM	7671	CB	LYS	A1047	-28,207	51.709	-38,563	1,00	85,22	C
ATOM	7672	CG	LYS	A1047	-29.104	52,882	-38.213	1,00	88,18	C
ATOM	7673	CE	LYS	A1047	-29.283	53,824	-39.397	1,00	90,77	C
ATOM	7674	CE	LYS	A1047	-29,867	55.158	-38,949	1,00	81,30	C
ATOM	7675	NZ	LYS	A1047	-29:687	56.218	-39:989	1,00	88.41	N
ATOM	7676	O	THR	A1048	-30.388	46,975	-39.789	1,00	82,66	O
ATOM	7677	N	THR	A1048	-29,096	49.019	-37,694	I,00	86.97	N
ATOM	7678	CA	THR	A1048	-29:407	47.603	-37:686	1,00	88.38	C
ATOM	7679	C	THR	A1048	-30.578	47,261	-38.605	1,00	85,59	C
ATOM	7680	CB	THR	A1048	-29,721	47.151	-36,260	I,00	91.82	C
ATOM	7681	OG1	THR	A1048	-29,681	45:721	-36,185	1,00	96.97	0
ATOM	7682	CG2	THR	A1048	-31.089	47,680	-35.829	1,00	93,14	C
ATOM	7683	O	ILE	A1063	-24:281	44:325	-33:894	1.00	90.37	0
ATOM	7684	N	ILE	A1063	-24,590	42.523	-36,902	1,00	87.47	N
ATOM	7685	CA	ILE	A1063	-25.227	43,010	-35.675	1,00	78,70	C
ATOM	7686	C	ILE	A1063	-24.190	43:311	-34.589	1.00	85.86	C
ATOM	7687	CB	ILE	A.1.063	-26,258	42.007	-35,151	1,00	77,61	C

ATOM	7688	CGI	ILE	A1063	-27.366	41.805	-36.193	1.00	83.81	C
ATOM	7689	CG2	ILE	A1063	--26.829	42.461	-33.826	1.00	84.71	C
ATOM	7690	GD1	ILE	A1063	-27.776	43.066	-36.943	1.00	85.58	C
ATOM	7691	O	GLU	A1064	-19.964	42.562	-34.888	1.00	84.62	0
ATOM	7692	N	GLU	A1064	-23.200	42.440	-34.453	I.00	80.49	N
ATOM	7693	CA	GLU	A1064	-22.018	42.760	-33.673	1.00	78.26	C
ATOM	7694	C	GLU	A1064	-20.928	43.280	-34.611	1.00	86.72	C
ATOM	7695	CB	GLU	A1064	-21.518	41.535	-32 .905	I.00	73.10	C
ATOM	7696	O	THR	A1065	-18.483	45.126	-34.383	1.00	76.67	0
ATOM	7697	N	THR	A1065	-21.080	44.520	-35.093	1.00	88.96	N
ATOM	7698	CA	THR	A1065	-20.164	45.106	-36.089	I.00	85.95	C
ATOM	7699	C	THR	A1065	-18.727	45.085	-35.583	1.00	81.68	C
ATOM	7700	CB	THR	A1065	-20.554	46.566	-36.479	1.00	86.66	C
ATOM	7701	OG1	THR	A1065	-21.914	46.825	-36.108	1.00	86.83	0
ATOM	7702	CG2	THR	A1065	-20.381	46.799	-38.000	1.00	79.79	C
ATOM	7703	O	ASN	A1066	-15.602	46.286	-37.725	1.00	77.34	0
ATOM	7704	N	ASN	A1066	-17.778	45.008	-36.509	1.00	82.69	N
ATOM	7705	CA.	ASN	A1066	-16.415	44.669	-36.147	I.00	82.26	C
ATOM	7706	C	ASN	A1066	-15.362	45.593	-36.731	1.00	84.07	C
ATOM	7707	CB	ASN	A1066	-16.108	43.228	-36.578	1.00	94.74	C
ATOM	7708	O	GLY	A1067	-12.834	44.842	-38.350	I.00	99.59	0
ATOM	7709	N	GLY	A1067	-14.184	45.572	-36.111	1.00	81.66	N
ATOM	7710	CA	GLY	A1067	-13.071	46.396	-36.537	1.00	85.28	C
ATOM	7711	C	GLY	A1067	-12.423	45.870	-37.798	I.00	97.28	C
ATOM	7712	O	GLU	A1068	-9.958	44.029	-40.222	1.00	98.00	0
ATOM	7713	N	GLU	Al 068	-11.399	46.578	-38.259	1.00	98.37	N
ATOM	7714	CA	GLU	A1068	-10.701	46.186	-39.474	I.00100.23		C
ATOM	7715	C	GLU	A1068	-10.020	44.831	-39.294	1.00	99.43	C
ATOM	7716	CB	GLU	Al 068	-9.680	47.258	-39.867	1.00	98.35	C
ATOM	7717	O	THR	A1069	-8.693	42.356	-35.611	1.00	93.83	O
ATOM	7718	N	THR	A1069	-9.526	44.576	-38.086	1.00101.56		N
ATOM	7719	CA	THR	A1069	-8.786	43.350	-37.803	1.00101.04		C
ATOM	7720	C	THR	A1069	-9.365	42.570	-36.622	1.00	99.07	C
ATOM	7721	CB	THR	A1069	-7.302	43.642	-37.512	I.00101.15		C
ATOM	7722	OG1	THR	A1069	-7.174	44.242	-36.215	1.00101.85		0
ATOM	7723	CG2	THR	A1069	-6.707	44.562	-38.585	1.00100.58		C
ATOM	7724	O	GLY	A1070	-11.389	41.160	-33.426	I.00	97.91	0
ATOM	7725	N	GLY	A1070	-10.617	42.147	-36.764	1.00100.47		N
ATOM	7726	CA	GLY	A1070	-11.245	41.257	-35.805	1.00	95.37	C
ATOM	7727	C	GLY	A1070	-11.493	41.856	-34.436	I.00	96.84	C
ATOM	7728	O	GLU	A1071	-14.265	44.555	-33.813	1.00	85.32	0
ATOM	7729	N	GLU	A1071	-11.828	43.142	-34.402	1.00	95.93	N
ATOM	7730	CA	GLU	A1071	-12.067	43.837	-33.144	1.00	92.50	C
ATOM	7731	C	GLU	A1071	-13.558	44.081	-32 .918	1.00	92.66	C
ATOM	7732	CB	GLU	A1071	-11.309	45.162	-33.120	1.00	94.91	C
ATOM	7733	CG	GLU	A1071	-11.393	45.908	-31.796	1.00	98.24	C
ATOM	7734	CD	GLU	A1071	-10.388	45.406	-30.777	I.00100.32		C
ATOM	7735	OE1	GLU	A1071	-9.661	44.430	-31.081	1.00	92.31	0
ATOM	7736	OE2	GLU	A1071	-10.324	45.995	-29.674	1.00	99.36	0
ATOM	7737	O	ILE	A1072	-14.743	46.068	-30.281	I.00	91.58	0
ATOM	7738	N	ILE	A1072	-14.036	43.742	-31.724	1.00	90.58	N
ATOM	7739	CA	ILE	A1072	-15.418	44.026	-31.355	1.00	91.38	C
ATOM	7740	C	ILE	A1072	-15.559	45.510	-31.021	I.00	93.08	C
ATOM	7741	CB	ILE	A1072	-15.885	43.156	-30.167	1.00	93.18	C
ATOM	7742	CGI	ILE	A1072	-14.771	43.004	-29.121	1.00	94.64	C
ATOM	7743	CG2	ILE	A1072	-16.327	41.785	-30.664	I.00	94.59	C
ATOM	7744	CD1	ILE	A1072	-14.859	43.983	-27.953	1.00101.93		C
ATOM	7745	O	VAL	A1073	-18.250	48.991	-30.326	1.00	85.29	0
ATOM	7746	N	VAL	A1073	-16.585	46.150	-31.580	1.00	86.27	N
ATOM	7747	CA	VAL	A1073	-16.685	47.599	-31.517	1.00	85.22	C
ATOM	7748	C	VAL	A1073	-18.089	48.075	-31.138	1.00	86.06	C
ATOM	7749	CB	VAL	A1073	-16.267	48.229	-32.863	1.00	84.72	C
ATOM	7750	CGI	VAL	A1073	-16.694	49.689	-32 .930	I.00	81.53	C

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ATOM      7751    CG2   VAL   A1073        -14 .756     48..096    -33. .070    1 .00   83..88              C
ATOM      7752    N     TRP   A107 4       --19,,111    47 .458    -31.,715     1 ,00   83..00              N
ATOM      7753    CA    TP.P  A1074        -20 ..467    47 ,802    -31.. 326    1 ,00   80,.73              C
ATOM      7754    C     TRP   A1074        -21..368     46.,576    -31.,270     1 .00   86..07              C
ATOM      7755    0     TRP   A107 4       -2.1.,857    46. 095    -.32.,296    1 ,00   87 ,17              0
ATOM      7756    CB    TP.P  A1074        -21..059     48.,841    -32.. 276    1 ,00   82 ,.55             C
ATOM      7757    CG    TRP   A1074        ~22 .292     49.,495    -31.. 718    1 ,00   79,.86              C
ATOM      7758    GDI   TRP   A107 4       -23 ,568     49. 387    -.32.,185    1 ,00   83..18              C
ATOM      7759    CD2   TRP   A107 4       --22..357    50.,338    -30.,568     1 ,00   78..98              C
ATOM      7760    NE1   TRP   A1074        -24.427      50.,122    -31.. 400    1 ,00   83,.83              N
ATOM      7761    CE2   TRP   A107 4       -2.3.,703    50..712    -.30.,397    1 ,00   83..24              C
ATOM      7762    CE3   TRP   A107 4       -21..404     50..819    -29 ,669     1 ,00   75..58              C
ATOM      7763    CZ2   TP.P  A107 4       -24 .117     51 ,544    -29. .364    1 ,00   84 ,64              C
ATOM      7764    CZ3   TRP   A1074        -21..812     51.,637    -28 ..653    1 .00   76..64              C
ATOM      7765    CH2   TRP   A107 4       -23 ,157     51..996    -28 ,503     1 ,00   81 .40              C
ATOM      7766    O     ASP   A107 5       -24...380    46.,165    -28 .847     1 ,00   88,.45              0
ATOM      7767    N     ASP   A107 5       -21..583     46.,077    -30.,059     1 .00   84 .34              N
ATOM      7768    CA.   ASP   A107 5       -22.,551     45. 019    -29.,828     1 ,00   84 ,36              C
ATOM      7769    C     ASP   A1075        -23 ..949    45.,603    -29.. 844    1 ,00   8.3,.58             C
ATOM      7770    CB    ASP   A1075        ~22 .281     44 ,336    -28 .494     1 ,00   87 ,.33             C
ATOM      7771    CG    ASP   A107 5       -23 ,093     43. 079    -28 ,313     1 ,00   92 ,45              C
ATOM      7772    OD2   ASP   A107 5       -22..538     42.,101    -27 ,765     1 ,00   93..17              0
ATOM      7773    OD1   ASP   A1075        -24 .279     43.,067    -28 .721     1 ,00   92 ,.41             0
ATOM      7774    O     LYS   A107 6       -27.,831     46..694    -29.,759     1 ,00   89..90              0
ATOM      7775    N     LYS   A107 6       -24 ..664    45..455    -30.,955     1 ,00   80..86              N
ATOM      7776    CA    LYS   A107 6       -25. 935     46.,159    -31. 132     1 ,00   85 ,31              C
ATOM      7777    C     LYS   A107 6       -26.,971     45..861    -.30.,043    1 ,00   89..78              C
ATOM      7778    CB    LYS   A107 6       -26 ,528     45..841    -32.,499     1 ,00   87 .75              C
ATOM      7779    O     GLY   A107 7       -27 .855     46.,156    -26. 668     1 ,00   87 ,92              0
ATOM      7780    N     GLY   A107 7       -26 ..893    44 ,686    -29 ,425     1 .00   91 .92              N
ATOM      7781    CA    GLY   A107 7       -27 ,768     44 .390    -28 ,300     1 ,00   96..43              C
ATOM      7782    C     GLY   A107 7       -27 ..305    45.,113    -27 .044     1 ,00   92 ,.54             C
ATOM      7783    N     ARG   A107 8       -26 ..277    44 ,539    -26 ,422     1 .00   87 .17              N
ATOM      7784    CA.   ARG   A107 8       -25 ,569     45. 072    -25 ,252     1 ,00   88.,76              C
ATOM      7785    C     ARG   A107 8       -25 ..470    46.,604    -25 .082     1 ,00   91 ,27              C
ATOM      7786    O     ARG   A1078        -26 ..009    47 ,178    -24 .126     1 ,00   86,.93              O
ATOM      7787    CB    ARG   A107 8       -24.,140     44 .517    -25 ,252     1 ,00   89.,87              C
ATOM      7788    CG    ARG   A107 8       -24 ..009    43.,072    -24 ,812     1 ,00   91 .02              C
ATOM      7789    CD    ARG   A107 8       -22 .580     42.,806    -24 ..364    1 ,00   92 ,87              C
ATOM      7790    NE    ARG   A107 8       -22.,000     43..993    -2.3.,732    1 ,00   94 .63              N
ATOM      7791    CZ    ARG   A107 8       -20 ,864     44 .002    -23 ,040     1 ,00103. .51              C
ATOM      7792    NH1   ARG   A107 8       -20. 169     42.,877    -22 .879     1 ,00100, .68              N
ATOM      7793    NH2   ARG   A107 8       -20 .421     45.,138    -22.,506     1 .00   92 .45              N
ATOM      7794    N     ASP   A107 9       -24 ,766     47 .256    -26 ,002     1 ,00   87 .71              N
ATOM      7795    CA    ASP   A107 9       -24..294     48.,616    -25 .778     1 ,00   81 ,27              C
ATOM      7796    C     ASP   A1079        -25 ..376    49.,695    -25 ,915     1 .00   82 .29              C
ATOM      7797    O     ASP   A107 9       -25 ,201     50. 799    -25 ,414     1 ,00   78.,94              O
ATOM      7798    CB    ASP   A107 9       -23 ..125    48.,902    -26 .719     1 ,00   82 ,.48             C
ATOM      7799    CG    ASP   A1079        -21 .990     47 ,891    -26 .562     1 ,00   77 ,.67             C
ATOM      7800    OD1   ASP   A107 9       -2.1.,928    47 .220    -25 ,510     1 ,00   83.,86              0
ATOM      7801    OD2   ASP   A107 9       -21.,158     47 ,775    -27 ,481     1 ,00   73..23              0
ATOM      7802    N     PHE   A1080        -26 ..489    49.,385    -26 .575     1 ,00   83,.57              N
ATOM      7803    CA    PHE   A1080        -27.,643     50..296    -26.,586     1 ,00   81 .19              C
ATOM      7804    C     PHE   A1080        -28 ,239     50..436    -25 ,186     1 ,00   80..24              C
ATOM      7805    O     PHE   A1080        -28. 618     51 ,528    -24 .765     1 ,00   81 ,54              O
ATOM      7806    CB    PHE   A1080        -28.,735     49.810     -27.,544     1 ,00   82 .66              C
ATOM      7807    CG    PHE   A1080        -28 ,793     50..558    -28 ,849     1 ,00   88..54              C
ATOM      7808    GDI   PHE   A1080        -29. 708     51 ,584    -29. 035     1 ,00   85 ,76              C
ATOM      7809    CD2   PHE   A1080        -27 ,950     50.,211    -29 ,904     1 .00   92 .75              C
ATOM      7810    CEl   PHE   A1080        -29 ,775     52..257    -30.,240     1 ,00   88..11              C
ATOM      7811    CE2   PHE   A1080        -28 .005     50.,884    -31.. 110    1 ,00   89,.89              C
ATOM      7812    CZ    PHE   A1080        -28 ,920     51.,906    -31.,279     1 .00   92 .06              C
ATOM      7813    N     ALA   A1.081       -28 ,341     49. .314    -24.,479     1 ,00   80.,67              N
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ATOM  7814  CA   ALA  A1081   -28.834   49.314  -23.Ill   1.00  77.80   c
ATOM  7815  C    ALA  A1081   --27,771  49.884  -22,172   1,00  78,20   c
ATOM  7816  O    ALA  A1081   -28.100   50,563  -21:205   1,00  70,79   0
ATOM  7817  CB   ALA  A1081   -29.232   47,914  -22,688   1.00  74.95   c
ATOM  7818  N    TH.R A1082   -26,500   49.594  -22,459   1,00  77,22   N
ATOM  7819  CA   THR  A1082   -25.395   50,183  -21:720   1,00  74,83   c
ATOM  7820  c    THR  A1082   -25.546   51,709  -21.737   1,00  79,13   c
ATOM  7821  0    TH.R A1082   -25,478   52.370  -20,700   1,00  78.75   0
ATOM  7822  CB   THR  A1082   -24.021   49,781  -22,308   1,00  77.92   c
ATOM  7823  OG1  THR  A1082   -23.702   48,436  -21,935   1,00  83,90   0
ATOM  7824  CG2  THR  A1082   -22,933   50.699  -21,793   1,00  74.39   c
ATOM  7825  N    VAL  A1083   -25.789   52.251  -22,924   1,00  74.03   N
ATOM  7826  CA   VAL  A1083   -25.909   53,684  -23.107   1,00  73,17   c
ATOM  7827  c    VAL  A1083   -27.231   54,219  -22,542   1.00  74.08   c
ATOM  7828  O    VAL  A1083   -27,263   55.293  -21,952   1,00  71.63   0
ATOM  7829  CB   VAL  A1083   -25.763   54,052  -24:601   1,00  73,67   c
ATOM  7830  CGI  VAL  A1083   -26.110   55,513  -24,850   1.00  66.71   c
ATOM  7831  CG2  VAL  A1083   -24,347   53.751  -25,073   1,00  68,33   c
ATOM  7832  N    AP.G A1084   -28.321   53,474  -22.699   1,00  78,50   N
ATOM  7833  CA   ARG  A1084   -29.596   53,890  -22,105   1,00  75,07   c
ATOM  7834  C    ARG  A1084   -29,511   53.804  -20,580   1,00  74,23   c
ATOM  7835  O    ARG  A1084   -30.271   54,461  -19,874   1,00  73.03   0
ATOM  7836  CB   ARG  A1084   -30.760   53,033  ~22,619   1,00  75,75   c
ATOM  7837  N    LYS  A1085   -28,585   52:984  -20,079   1,00  72.59   N
ATOM  7838  CA   LYS  A1085   -28.407   52,830  -18,639   1,00  72.80   c
ATOM  7839  C    LYS  A1085   -27.756   54,087  -18.079   1,00  73,61   c
ATOM  7840  O    LYS  A1085   -28,323   54:766  -17,212   1,00  69.88   0
ATOM  7841  CB   LYS  A1085   -27,560   51:597  -18,312   1,00  70.73   c
ATOM  7842  N    VAL  A1086   -26.564   54,381  -18.594   1,00  67,96   N
ATOM  7843  CA   VAL  A1086   -25.864   55,619  -18.307   1.00  64.39   c
ATOM  7844  C    VAL  A1086   -26,761   56:865  -18,268   1,00  65.74   c
ATOM  7845  O    VAL  A1086   -26.731   57,619  -17:.300   1,00  68,22   0
ATOM  7846  CB   VAL  A1086   -24.766   55,845  -19.327   1.00  62.25   c
ATOM  7847  CGI  VAL  A1086   -24,229   57.252  -19,204   1,00  59,40   c
ATOM  7848  CG2  VAL  A1086   -23.673   54,829  -19:114   1,00  59,14   c
ATOM  7849  O    LEU  A1087   -30.338   59,096  -18.148   1,00  68,75   0
ATOM  7850  N    LEU  A1087   -27,578   57.084  -19,291   1,00  63,25   N
ATOM  7851  CA   LEU  A1087   -28,404   58,284  -19,297   1,00  61.57   c
ATOM  7852  C    LEU  A1087   -29.543   58,165  -18.294   1,00  66,00   c
ATOM  7853  CB   LEU  A1087   -28,981   58:578  -20,689   1,00  65.61   c
ATOM  7854  CG   LEU  A1087   -28,081   58:692  -21,923   1,00  61,50   c
ATOM  7855  GDI  LEU  A1087   -28.763   59,544  -22.987   1,00  6.3,15  c
ATOM  7856  CD2  LEU  A1087   -26,710   59,232  -21,593   1.00  60.36   c
ATOM  7857  N    SEP. A1088   -29,633   57.029  -17,607   1,00  63.97   N
ATOM  7858  CA   SEP. A1088   -30.661   56,867  -16:583   1,00  67,44   c
ATOM  7859  c    SER  A1088   -30.126   57,042  -15,158   1.00  64.25   c
ATOM  7860  0    SER  A1088   -30,915   57.170  -14,227   1,00  66,99   0
ATOM  7861  CB   SER  A1088   -31..341  55,502  -16:717   1,00  70,12   c
ATOM  7862  OG   SER  A1088   -32 .372  55,535  -17.690   1,00  72,49   0
ATOM  7863  N    MET  A1089   -28,801   57.044  -15,000   1,00  64,97   N
ATOM  7864  CA   MET  A1089   -28,150   57,298  -13,710   1,00  65.89   c
ATOM  7865  c    MET  A1089   -28.736   58,529  -13.016   1,00  66,18   c
ATOM  7866  0    MET  A1089   -28,838   59:601  -13,619   1,00  64.18   0
ATOM  7867  CB   MET  A1089   -26,640   57,487  -13,889   1,00  60.67   c
ATOM  7868  CG   MET  A1089   -25.954   56,346  -14.566   1,00  6.3,17  c
ATOM  7869  SD   MET  A1089   -24,202   56:218  -14,165   1,00  70.86   S
ATOM  7870  CE   MET  A1089   -23,459   57.438  -15,231   1,00  68.08   c
ATOM  7871  O    PRO  A1090   -29.019   61,563  -10.068   1,00  71,94   0
ATOM  7872  N    PRO  A1090   -29,135   58,376  -11,746   1.00  66.31   N
ATOM  7873  CA   FRO  A1090   -29,758   59.481  -11,014   1,00  70.45   c
ATOM  7874  C    PRO  A1090   -28.707   60,440  -10:455   1,00  67,44   c
ATOM  7875  CB   PRO  A1090   -30.527   58,765   -9,897   1.00  70.30   c
ATOM  7876  CG   PRO  A1090   -29,731   57.524   -9,640   1,00  67,18   c
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ATOM   7877  CD   PRO  A1090    -29.126   57.127  -10.968   1.00  67.17     c
ATOM   7878  O    GLN  A1091   --24,505   60.438  -11,319   1,00  59.29     O
ATOM   7879  N    GLN  A1091    -27.461   59,997  -10.441   1,00  60,34     N
ATOM   7880  CA   GLN  A1091    -26.390   60.777   -9.847   1.00  66.63     c
ATOM   7881  C    GLN  A1091    -25,333   61.237  -10,851   1,00  65,69     C
ATOM   7882  CB   GLN  A1091    -25.714   59,975   -8.733   1,00  61,52     C
ATOM   7883  CG   GLN  A1091    -24.838   60,810   -7.843   1,00  60,78     c
ATOM   7884  CD   GLN  A1091    -23,434   60.962   -8,374   1,00  59,41     c
ATOM   7885  OE1  GLN  A1091    -22.777   59,979   -8,705   1,00  57.64     0
ATOM   7886  NE2  GLN  A1091    -22.963   62,205   -8.462   1,00  56,49     N
ATOM   7887  O    VAL  A1092    -24,355   65.123  -10,517   I,00  52.96     O
ATOM   7888  N    VAL  A1092    -25.356   62.539  -11,144   1,00  60.80     N
ATOM   7889  CA   VAL  A1092    -24.318   63,191  -11.937   1,00  54,88     C
ATOM   7890  c    VAL  A1092    -23.659   64,334  -11,159   1.00  56.18     c
ATOM   7891  CB   VAL  A1092    -24,896   63.767  -13,229   1,00  58.39     c
ATOM   7892  CGI  VAL  A1092    -23.803   63,890  -14,270   1,00  58,02     c
ATOM   7893  CG2  VAL  A1092    -26.044   62,909  -13.718   1.00  62.34     c
ATOM   7894  O    ASM  A1093    -21,055   67.343  -12,095   1,00  49,06     0
ATOM   7895  N    ASN  A1093    -22.338   64,450  -11.238   1,00  53,28     N
ATOM   7896  CA   ASN  A1093    -21.630   65,555  -10.578   1,00  53,79     c
ATOM   7897  C    ASM  A1093    -21,824   66.929  -11,223   1,00  48,48     c
ATOM   7898  CB   ASN  A1093    -20.130   65,270  -10,526   1,00  50.22     c
ATOM   7899  CG   ASN  A1093    -19.818   63,966   -9.878   1,00  56,21     c
ATOM   7900  OD1  ASN  A1093    -20,345   63.645   -8,803   I,00  54.19     0
ATOM   7901  ND2  ASN  A1093    -18.958   63.183  -10,528   1,00  52.21     N
ATOM   7902  O    ILE  A1094    -22.948   70,241   -9.268   1,00  56,07     O
ATOM   7903  N    ILE  A1094    -22,817   67.663  -10,768   I,00  47.30     N
ATOM   7904  CA   ILE  A1094    -23,021   69.005  -11,303   1,00  49.88     C
ATOM   7905  C    ILE  A1094    -22.455   70,066  -10.374   1,00  49,69     C
ATOM   7906  CB   ILE  A1094    -24.498   69,258  -11,548   1.00  50.13     c
ATOM   7907  CGI  ILE  A1094    -24,939   68.462  -12,775   1,00  52.19     c
ATOM   7908  CG2  ILE  A1094    -24.768   70,711  -11.752   1,00  41,31     c
ATOM   7909  CD1  ILE  A1094    -26.377   68,657  -13.069   1.00  60.27     c
ATOM   7910  O    VAL  A1095    -20,680   73.477  -11,688   1,00  45,39     0
ATOM   7911  N    VAL  A1095    -21.414   70,762  -10.818   1,00  46,32     N
ATOM   7912  CA   VAL  A1095    -20.791   71,797  -10.000   1,00  45,17     c
ATOM   7913  C    VAL  A1095    -21,025   73.203  -10,546   1,00  44,25     c
ATOM   7914  CB   VAL  A1095    -19.264   71,615   -9,898   1,00  47.62     c
ATOM   7915  CGI  VAL  A1095    -18.647   72,799   -9.136   1,00  41,12     c
ATOM   7916  CG2  VAL  A1095    -18,893   70.272   -9,267   I,00  44.61     c
ATOM   7917  O    LYS  A1096    -20,069   76.164   -8,383   1,00  43.21     0
ATOM   7918  N    LYS  A1096    -21.577   74,097   -9.724   1,00  41,81     N
ATOM   7919  CA   LYS  A1096    -21.616   75,520  -10,047   1.00  36.17     c
ATOM   7920  C    LYS  A1096    -20,331   76.158   -9,562   1,00  36.81     C
ATOM   7921  CB   LYS  A1096    -22.818   76,207   -9.392   1,00  39,87     c
ATOM   7922  CG   LYS  A1096    -23.612   77,176  -10.276   1.00  41.98     c
ATOM   7923  CD   LYS  A1096    -22,755   78.237  -10,946   1,00  44,28     c
ATOM   7924  CE   LYS  A1096    -23.589   79,440  -11.427   1,00  44,28     c
ATOM   7925  NZ   LYS  A1096    -24.549   79,086  -12.503   1,00  47,68     N
ATOM   7926  O    LYS  A1097    -19,206   79.559   -9,524   1,00  38,09     O
ATOM   7927  N    LYS  A1097    -19.537   76,716  -10,457   1,00  34.09     N
ATOM   7928  CA   LYS  A1097    -18.295   77,363  -10.064   1,00  37,50     c
ATOM   7929  C    LYS  A1097    -18,542   78.581   -9,132   I,00  42.09     C
ATOM   7930  CB   LYS  A1097    -17,533   77.792  -11,319   1,00  37.70     C
ATOM   7931  CG   LYS  A1097    -16.103   78,243  -11.120   1,00  37,59     C
ATOM   7932  CD   LYS  A1097    -15,592   78.759  -12,431   I,00  38.00     C
ATOM   7933  CE   LYS  A1097    -14,202   79.321  -12,368   1,00  39.74     C
ATOM   7934  NZ   LYS  A1097    -14.049   80,484  -11.500   1,00  39,99     N
ATOM   7935  O    THR  A1098    -16,031   80,479   -7,586   1.00  41.83     O
ATOM   7936  N    THR  A1098    -18,030   78.496   -7,899   1,00  40.33     N
ATOM   7937  CA   THR  A1098    -18.148   79,575   -6.920   1,00  39,53     C
ATOM   7938  c    THR  A1098    -17.210   80,708   -7.278   1.00  45.50     c
ATOM   7939  CB   THR  A1098    -17,847   79.120   -5,501   1,00  41,93     c
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ATOM	7940	OG1	THR	A1098	-16.463	78.789	-5.400	1.00	59.41	O
ATOM	7941	CG2	THR	A1098	-18.712	77.916	-5.117	1.00	32.77	C
ATOM	7942	O	GLU	A1099	-18.427	84.538	-6.389	1.00	38.92	O
ATOM	7943	N	GLU	A1099	-17.752	81.928	-7.268	1.00	36.57	N
ATOM	7944	CA.	GLU	A1099	-17.028	83.090	-7.742	1.00	44.64	C
ATOM	7945	C	GLU	A1099	-17.296	84.302	-6.834	1.00	48.07	C
ATOM	7946	CB	GLU	A1099	-17.411	83.413	-9.203	1.00	42.84	C
ATOM	7947	CG	GLU	A1099	-16.981	82.334	-10.219	1.00	47.48	C
ATOM	7948	CD	GLU	A1099	-17.120	82.746	-11.693	1.00	49.59	C
ATOM	7949	OE1	GLU	A1099	-17.987	83.582	-12.025	1.00	48.04	0
ATOM	7950	OE2	GLU	A1099	-16.347	82.216	-12.530	1.00	51.25	0
ATOM	7951	O	VAL	AllOO	-16.199	87.446	-8.001	1.00	37.06	0
ATOM	7952	N	VAL	AllOO	-16.225	85.032	-6.544	1.00	41.36	N
ATOM	7953	CA	VAL	AllOO	-16.319	86.322	-5.899	1.00	43.86	C
ATOM	7954	C	VAL	AllOO	-16.796	87.327	-6.930	1.00	41.86	C
ATOM	7955	CB	VAL	AllOO	-14.958	86.785	-5.301	1.00	44.09	C
ATOM	7956	CG2	VAL	AllOO	-14.536	85.873	-4.187	1.00	42.64	C
ATOM	7957	CGI	VAL	AllOO	-15.053	88.201	-4.794	1.00	42.38	C
ATOM	7958	O	GLN	All01	-17.057	90.694	-6.574	1.00	45.71	0
ATOM	7959	N	GLN	A1101	-17.889	88.022	-6.617	1.00	40.81	N
ATOM	7960	CA.	GLN	A1101	-18.438	89.021	-7.535	1.00	38.50	C
ATOM	7961	C	GLN	A1101	-17.504	90.207	-7.602	1.00	42.73	C
ATOM	7962	CB	GLN	A1101	-19.844	89.443	-7.105	1.00	35.82	C
ATOM	7963	CG	GLN	All01	-20.817	88.252	-7.038	1.00	37.00	C
ATOM	7964	CD	GLN	A1101	-20.789	87.448	-8.315	1.00	45.09	C
ATOM	7965	OE1	GLN	A1101	-21.340	87.872	-9.326	1.00	48.52	0
ATOM	7966	NE2	GLN	All01	-20.095	86.310	-8.297	1.00	39.64	N
ATOM	7967	O	THR	A1102	-18.122	92.705	-10.428	1.00	47.00	O
ATOM	7968	N	THR	All02	-17.168	90.648	-8.812	1.00	40.26	N
ATOM	7969	CA	THR	All02	-16.357	91.852	-8.963	1.00	43.91	C
ATOM	7970	C	THR	A1102	-17.029	92.916	-9.892	1.00	43.58	C
ATOM	7971	CB	THR	All02	-14.940	91.507	-9.484	1.00	41.26	C
ATOM	7972	OG1	THR	All02	-14.967	91.302	-10.904	1.00	41.76	O
ATOM	7973	CG2	THR	A1102	-14.391	90.265	-8.766	1.00	41.07	C
ATOM	7974	O	GLY	All03	-16.959	96.890	-9.204	1.00	41.40	O
ATOM	7975	N	GLY	A1103	-16.397	94.069	-10.047	1.00	39.63	N
ATOM	7976	CA.	GLY	A1103	-17.005	95.125	-10.851	1.00	49.19	C
ATOM	7977	C	GLY	A1103	-17.576	96.351	-10.129	1.00	44.26	C
ATOM	7978	O	GLY	A1104	-20.476	96.967	-8.388	1.00	40.48	O
ATOM	7979	N	GLY	All04	-18.756	96.788	-10.575	1.00	49.33	N
ATOM	7980	CA	GLY	A1104	-19.353	98.053	-10.173	1.00	32.25	C
ATOM	7981	C	GLY	A1104	-19.928	97.990	-8.777	1.00	41.39	C
ATOM	7982	0	PHE	A1105	-22.228	98.187	-5.605	1.00	46.19	0
ATOM	7983	N	FHE	A1105	-19.817	99.088	-8.029	1.00	41.23	N
ATOM	7984	CA	PHE	A1105	-20.283	99.140	-6.640	1.00	40.19	C
ATOM	7985	C	PHE	A1105	-21.779	98.876	-6.516	1.00	41.13	C
ATOM	7986	CB	PHE	A1105	-19.932	100.494	-6.012	1.00	41.31	C
ATOM	7987	CG	PHE	A1105	-18.460	100.718	-5.850	1.00	40.58	C
ATOM	7988	CD1	PHE	A1105	-17.593	99.638	-5.805	1.00	42.47	C
ATOM	7989	CD2	PHE	A1105	-17.943	101.989	-5.763	1.00	37.72	C
ATOM	7990	CE1	PHE	A1105	-16.244	99.818	-5.671	1.00	41.14	C
ATOM	7991	CE2	PHE	A1105	-16.589	102.193	-5.636	1.00	38.64	C
ATOM	7992	CZ	PHE	All05	-15.739	101.107	-5.584	1.00	51.82	C
ATOM	7993	O	SEP.	A1106	-23.860	99.958	-y.653	1.00	47.44	0
ATOM	7994	N	SER	A1106	-22.548	99.381	-7.464	1.00	43.71	N
ATOM	7995	CA	SER	All06	-23.993	99.278	-7.388	1.00	42.69	C
ATOM	7996	C	SER	A1106	-24.595	99.649	-8.720	1.00	46.77	C
ATOM	7997	CB	SER	A1106	-24.532	100.214	-6.327	1.00	47.35	C
ATOM	7998	OG	SER	A1106	-24.558	101.510	-6.878	1.00	45.00	0
ATOM	7999	O	LYS	A1107	-25.793	102.271	-9.241	1.00	51.24	0
ATOM	8000	N	LYS	A1107	-25.927	99.656	-8.794	1.00	48.90	N
ATOM	8001	CA	LYS	A1107	-26.632	100.151	-9.960	1.00	46.07	C
ATOM	8002	C	LYS	A1107	-26.170	101.567	-10.197	1.00	56.61	C

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ATOM   8003  CB   LYS  A1107    -28.142  100.102   -9.759  1.00  50.25    C
ATOM   8004  CG   LYS  A1107   --28,774   98.782  -10,033  1,00  52.95    C
ATOM   8005  CD   LYS  A1107    -30.295   98,862  -10.012  1.00  61,40    C
ATOM   8006  CE   LYS  A1107    -30..853   99.824  -11.077  1.00  72.93    C
ATOM   8007  NZ   LYS  A1107    -31,452  101.067  -10,476  1,00  72,62    N
ATOM   8008  O    GLU  A1108    -26.275  105,634  -11.719  1.00  48,74    O
ATOM   8009  N    GLU  A1108    -26.190  101,999  -11.452  1,00  57,89    N
ATOM   8010  CA.  GLU  A1108    -25,645  103..311  -11,786  1,00  51,33    C
ATOM   8011  C    GLU  A1108    -26.655  104.465  -11;686  1,00  52.20    C
ATOM   8012  CE   GLU  A1108    -25.041  103,269  -13.182  1,00  54,96    C
ATOM   8013  CG   GLU  A1108    -23,784  102.460  -13,259  I,00  50.96    C
ATOM   8014  CD   GLU  A1108    -22.711  103;120  -14;095  1,00  57.35    C
ATOM   8015  OE1  GLU  A1108    -22.899  104,288  -14.496  1,00  67,64    0
ATOM   8016  OE2  GLU  A1108   -21..667  102;476  -14,347  1.00  66.53    0
ATOM   8017  O    SEP. A1109    -28,834  105.458   -9,045  1,00  57.43    0
ATOM   8018  N    SER  A1109    -27.928  104,134  -11.553  1.00  52,18    N
ATOM   8019  CA   SER  A1109    -28.955  105;156  -11.432  1,00  53.62    C
ATOM   8020  C    SER  Al109     -28,788  105.983  -10,154  1,00  52,13    C
ATOM   8021  CB   SER  A1109    -30..341  104,515  -11.476  1.00  57,24    C
ATOM   8022  OG   SER  A1109    -30.389  103,354  -10.657  1,00  64,06    O
ATOM   8023  O    ILE  Al110     -30,626  109.256   -9,521  1,00  48,48    0
ATOM   802 4  N    ILE  A1110    -28.561  107,277  -10.315  1,00  48.71    N
ATOM   802 5  CA   ILE  A1110    -28.501  108,165   -9.169  1,00  53,16    C
ATOM   802 6  C    ILE  Al110     -29,938  108.547   -8,779  I,00  56.58    C
ATOM   802 7  CB   ILE  A1110    -27.659  109.393   -9;479  1,00  54.11    C
ATOM   802 8  CGI  ILE  A1110    -26.188  108,988   -9.541  1,00  54,98    C
ATOM   802 9  CG2  ILE  Al110     -27,826  110.410   -8,409  I,00  57.43    C
ATOM   8030  CD1  ILE  A1110    -25,291  109.865  -10,401  1,00  60.05    C
ATOM   8031  O    LEU  A1111    -31.050  110,050   -5.946  1,00  57,62    0
ATOM   8032  N    LEU  Ai m     -30..398  108;033   -7,637  1.00  54.25    N
ATOM   8033  CA   LEU  A1m      -31,798  108,177   -7,245  1,00  54.46    C
ATOM   8034  C    LEU  Ai m     -32 .008  109,492   -6.481  1.00  57,56    C
ATOM   8035  CB   LEU  Ai m     -32..239  106;972   -6.402  1.00  54.60    C
ATOM   8036  CG   LEU  A1m      -31,906  105.561   -6,919  1,00  61,46    C
ATOM   8037  CD1  LEU  Ai m     -32 .000  104,542   -5.799  1.00  66,98    C
ATOM   8038  CD2  LEU  Ai m     -32 .783  105,121   -8.081  1,00  57,08    C
ATOM   8039  O    PRO  Al112     -33,522  109.996   -3,634  1,00  60,89    0
ATOM   8040  N    PRO  A1112    -33.263  109;993   -6;438  1,00  55.38    N
ATOM   8041  CA   PRO  A1112    -33.599  111,232   -5.710  1,00  57,87    C
ATOM   8042  C    PRO  AU I2     -33,518  111.105   -4,182  I,00  65.24    C
ATOM   8043  CB   FRO  A1112    -35,043  Ill.517   --8,132  1,00  52.30    C
ATOM   8044  CG   PRO  A1112    -35.288  110,644   -7..340  1,00  53,66    C
ATOM   8045  CD   PRO  A1112    -34.425  109;447   -7.157  1.00  48.36    C
ATOM   8046  O    LYS  A1113    -35,723  Ill.604   -2,045  1,00  74.43    0
ATOM   8047  N    LYS  Al113     -33.462  112,254   -3.508  1.00  66,95    N
ATOM   8048  CA   LYS  A1113   -33..411  112;301   -2.052  1,00  69.13    C
ATOM   8049  C    LYS  A1113    -34,624  111.582   -1,474  1,00  74,48    C
ATOM   8050  CB   LYS  Al113     -33.338  113,747   -1.544  1.00  70,52    C
ATOM   8051  CG   LYS  A1113    -34.642  114.532   -1.648  1,00  71,95    C
ATOM   8052  CD   LYS  A1113    -34,472  115.955   -1,160  1,00  72,17    C
ATOM   8053  CE   LYS  Al113     -35.779  116;720   -1;277  1,00  66.86    C
ATOM   8054  NZ   LYS  A1113    -35.658  118,077   -0.694  1,00  74,96    N
ATOM   8055  O    ARG  Al114     -34,457  110.793    2,304  I,00  88.88    0
ATOM   8056  N    ARG  Al114     -34.404  110.921   -0;347  1,00  78.86    N
ATOM   8057  CA   ARG  A1114    -35.403  110,037    0.225  1,00  87,40    C
ATOM   8058  C    ARG  Al114     -35,295  110.071    1,750  I,00  91.62    C
ATOM   8059  CB   ARG  A1114    -35,206  108.618   -0,311  1,00  89.01    C
ATOM   8060  CG   ARG  A1114    -36.435  107,743   -0..302  1,00  93,38    C
ATOM   8061  CD   ARG  A1114    -36;015  106;301   -0.119  1.00  99.17    C
ATOM   8062  NE   ARG  A1114    -36,274  105.483   -1,296  1,00  97.66    N
ATOM   8063  CZ   ARG  Al114     -35.680  104,319   -1;532  1.00104,74    C
ATOM   8064  NH1  ARG  A1114    -35.978  103;631   -2.628  1.00115.51    N
ATOM   8065  NH2  ARG  Al114     -34,778  103.848   -0,676  1,00  97,03    N
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ATOM   8066   O    ASN  A1115     -34 .688  108.,000    5 ,422   1 .00  95..81          O
ATOM   8067   N    ASN  A1115     --36 ,139  109..298    2 ,426   1 ,00  95..31          N
ATOM   8068   CA   ASN  Alii 5    -36 ..079  109..211    3 .878   1 ,00  96,.63          C
ATOM   8069   C    ASN  A1115     -35 ..323  107 ,958    4 ,368   1 .00  96..83          C
ATOM   8070   CB   ASN  A1115     -37.,493  109 .247    4 ,464   1 ,00  94 ,65          C
ATOM   8071   CG   ASN  Alii 5    -37..522  109.,796    5 .881   1 ,00  98,.01          C
ATOM   8072   OD1  ASN  A1115     -36 ..808  110.,745    6 .203   1 ,00100, .26         0
ATOM   8073   ND2  ASN  A1115     -38.,342  .10 9 .193   6 ,737   I ,00  95.,99          N
ATOM   8074   O    SEP. Alii 6    -32.,577  106.,619    3 ,906   1 ,00101. .78         0
ATOM   8075   N    SER  A1116     -35..376  106.,867    3 .595   1 ,00100, .26         N
ATOM   807 6  CA   SER  All I6    -.34.,751  .105.. 581   .3.,966   I ,00101. .14         C
ATOM   8077   C    SER  A1116     -33.,258  105.,669    4 ,289   1 ,00  99..89          C
ATOM   8078   CB   SER  A1116     -34. 932  104.,545    2.847   I ,00  95 ,30          C
ATOM   8079   OG   SER  A1116     -36 ,294  104.,360    2 ,510   1 .00105. .71         0
ATOM   8080   O    ASP  A1117     -29 ,484  103.. 382   4 ,270   1 ,00  97 .54          0
ATOM   8081   N    ASP  Alii 7    -32.. 755  104.,662    4 .995   1 ,00  96,.65          N
ATOM   8082   CA   ASP  A1117     -31.,329  104.,566    5 ,269   1 .00  97 .11          C
ATOM   8083   C    ASP  All 17    -30.,689  .103. 646    4 ,231   I ,00  98.,93          C
ATOM   8084   CB   ASP  Alii 7    -31.. 080  104.,054    6 .691   1 ,00  96,.96          C
ATOM   8085   O    LYS  A1118     -29 .003  102.,195    1.077   1 ,00  90,.62          O
ATOM   8086   N    LYS  All 18    -3.1.,519  .103. 177    3 ,299   I ,00  99.,80          N
ATOM   8087   CA   LYS  Alii 8    -31.,114  102.. 259    2 ,234   1 ,00  90..67          C
ATOM   8088   C    LYS  A1118     -30.. 036  102.,826    1.301   1 ,00  88,.11          C
ATOM   8089   CB   LYS  All 18    -.32.,339  101.. 856   1 ,404   I ,00  83..56          C
ATOM   8090   O    LEU  A1119     -27 ,708  105.,324    1 ,134   1 ,00  77 .86          0
ATOM   8091   N    LEU  A11i9     -30. 280  104.,020    0 .771   I ,00  80 ,34          N
ATOM   8092   CA   LEU  All I9    -29.,472  .104.. 575  -0.,308   I ,00  75..95          C
ATOM   8093   C    LEU  A1119     -28 ,013  104 .849    0 ,051   1 ,00  73..23          C
ATOM   8094   CB   LEU  A1119     -30. 114  105.,870   -0. 8.18   I ,00  74 ,50          C
ATOM   8095   CG   LEU  A1119     -31.,605  105.,796   -1 ,180   1 .00  83..59          C
ATOM   8096   CD1  LEU  A1119     -32.,131  107.. 161  -1 ,620   1 ,00  78..02          C
ATOM   8097   CD2  LEU  Alii 9    -31.. 900  104.,729   -2 .240   1 ,00  79,.66          C
ATOM   8098   O    ILE  A112 0    -26 ,081  106.,879   -1 ,848   1 .00  71 .33          0
ATOM   8099   N    ILE  AU20      -27 ,123  .104 .559   -0.,893   I ,00  71 ,12          N
ATOM   8100   CA   ILE  A112 0    -25 .697  104.,815   -0.. 737   1 ,00  72 ,54          C
ATOM   8101   C    ILE  A1120     -25 .403  106.,271   -1 .033   1 ,00  68,.41          C
ATOM   8102   CB   ILE  AU20      -24.,832  .103. 948   -1 ,690   I ,00  69.,56          C
ATOM   8103   CGI  ILE  A112 0    -25 ,410  102.,544   -1 ,843   1 ,00  68..33          C
ATOM   8104   CG2  ILE  A1120     -23 .381  103.,903   -1 .207   I ,00  65 ,42          C
ATOM   8105   CD1  ILE  AU20      -25 ,409  101.. 775  -0.,566   I ,00  73..25          C
ATOM   8106   O    ALA  A1121     -21.,956  107.. 768  -1 ,733   1 ,00  70..50          0
ATOM   8107   N    ALA  A112.1    -24 .373  106 ,817   -0. 398   I ,00  69 ,30          N
ATOM   8108   CA   ALA  A1121     -24 ,002  108.,217   -0.,583   1 .00  71 .51          C
ATOM   8109   C    ALA  A1121     -23 ,015  108.. 385  -1 ,733   1 ,00  69..34          C
ATOM   8110   CB   ALA  A1121     -23 .407  108.,778    0 .706   I ,00  66,.45          C
ATOM   8111   O    ARG  A1122     -20 ,123  109.,988   -4 ,021   1 .00  63..32          0
ATOM   8112   N    ARG  AU22      -23 ,354  .10 9 .226  -2.,705   I ,00  65.,15          N
ATOM   8113   CA   ARG  A1122     -22. 442  109.,504   -3.. 811   I ,00  61 ,15          C
ATOM   8114   C    ARG  A1122     -21 .130  110.,130   -3.. 360   1 ,00  63,.20          C
ATOM   8115   CB   ARG  AU22      -23 ,094  110 .427   -4 ,820   I ,00  54 ,77          C
ATOM   8116   CG   ARG  A1122     -24 ,330  109.,876   -5.,430   1 ,00  56..21          C
ATOM   8117   CD   ARG  A1122     -25 .050  110.,973   -6.. 170   1 ,00  57 ,18          C
ATOM   8118   NE   ARG  AU22      -24.,248  111 .5.13   -7 ,253   I ,00  54 .10          N
ATOM   8119   CZ   ARG  A1122     -24 ,464  112.,694   -7 ,823   1 ,00  57 .31          C
ATOM   8120   NH1  ARG  A1122     -25. 457  113 ,477   -7 .393   I ,00  47 ,56          N
ATOM   8121   NH2  ARG  AU22      -2.3.,677  113 .094   -8.,816   I ,00  56..30          N
ATOM   8122   O    LYS  A112 3    -21.,024  110.. 750    0 ,329   1 ,00  65..87          O
ATOM   8123   N    LYS  A1123     -21 .146  110 ,877   -2 .266   I ,00  63 ,77          N
ATOM   8124   CA   LYS  A1123     -19.,899  Ill ,342    -1 ,688   1 .00  60..08          C
ATOM   8125   C    LYS  A112 3    -19 ,958  Ill .088    -0.,197   1 ,00  68..39          C
ATOM   8126   CB   LYS  A112 3    -19 .662  112.,812   -1 .993   I ,00  67 ,12          C
ATOM   8127   CG   LYS  A1123     -19.,441  113.,110   -3.,465   1 .00  62 .85          C
ATOM   8128   CD   LYS  AU23      -18 ,126  112.570    -3.,959   I ,00  56.,40          C
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ATOM     8129   CE    LYS  A1123      -17 .846   113..080     -5..361    1 .00  49..06          C
ATOM     8130   NZ    LYS  A112 3     --16,,474  112..763     -5.,813    1 ,00  54 .86          N
ATOM     8131   O     LYS  A112 4     -20 ..571  Ill ,523     3 ..422    1 ,00  77 ,47          O
ATOM     8132   N     LYS  A1124      -18..811   Ill ,210     0 ..474    1 .00  71 .65          N
ATOM     8133   CA.   LYS  A1124      -18.,743   110. 997     .1. .,922  1 ,00  75..75          C
ATOM     8134   C     LYS  A112 4     -19..699   Ill ,944     2 .647     1 ,00  75,.98          C
ATOM     8135   CE    LYS  A1124      -17 .309   Ill ,198     2 .432     1 ,00  69,.49          C
ATOM     8136   O     ASP  A1125      -22.,018   115. 749     2 ,356     1 ,00  81 .10          0
ATOM     8137   N     ASP  A112 5     -19..544   113.,228     2 ,352     1 ,00  73..33          N
ATOM     8138   CA    ASP  A1125      -20 ..289  114 ,266     3 ..034    1 ,00  71 ,12          C
ATOM     8139   C     ASP  AU25       -21.,586   114 .601     2 ,321     1 ,00  75..14          C
ATOM     8140   CB    ASP  A112 5     -19..425   115.,521     3 ,166     1 ,00  72 .27          C
ATOM     8141   O     TP.P A1126      -24 .816   111 ,903     0 .810     1 ,00  68 ,99          0
ATOM     8142   N     TRP  A1126      -22..208   113.,614     1 ,679     1 .00  71 .28          N
ATOM     8143   CA    TRP  A112 6     -23 ,478   113..851     0 ,999     1 ,00  68..37          C
ATOM     814 4  C     TP.P A112 6     -24..553   112.,906     1 .459     1 ,00  69,.91          C
ATOM     8145   CB    TRP  A1126      -23 ..352  113.,712     -0.,512    1 .00  62 .43          C
ATOM     8146   CG    TRP  A1126      -22.,600   114. 790     - .1. .,186 1 ,00  65..00         C
ATOM     8147   CD1   TP.P A112 6     -22..015   115.,872     -0.. 609   1 ,00  67 ,98          C
ATOM     8148   CD2   TRP  A1126      -22 ..344  114 ,896     -2 .594    1 ,00  67 ,45          C
ATOM     8149   NE1   TRP  A1126      -2.1.,409  116. 655     - .1. .,568 1 ,00  70..58         N
ATOM     8150   CE2   TRP  A112 6     -21..593   116.,071     -2.,795    1 ,00  69..63          C
ATOM     8151   CE3   TRP  A1126      ~22 .677   114 ,106     -3.. 704   1 ,00  59,.47          C
ATOM     8152   CZ2   TRP  A112 6     -21.,165   116..476     -4 ,066    1 ,00  64 .3.3         C
ATOM     8153   CZ3   TRP  A112 6     -22..255   114 .508     -4 ,954    1 ,00  60..12          C
ATOM     8154   CH2   TRP  A1126      -21 .502   115.,679     -5. 128    1 ,00  59 ,32          C
ATOM     8155   O     ASP  A1127      -27.,868   113.. 408    1 ,457     1 ,00  73..66          0
ATOM     8156   N     ASP  A112 7     -25 ,204   113..239     2 ,561     1 ,00  74 .72          N
ATOM     8157   CA    ASP  A1127      -26. .321  112.,432     3 .023     1 ,00  7.1. ,.06       C
ATOM     8158   C     ASP  A1127      -27 ,460   112.,383     1 ,999     1 .00  71 .45          C
ATOM     8159   CB    ASP  A112 7     -26 ,846   112..953     4 ,355     1 ,00  66..66          C
ATOM     8160   CG    ASP  A112 7     -27 .759   Ill ,964     5 .020     1 ,00  74 ,75          C
ATOM     8161   OD1   ASP  A1127      -28 ..851  Ill ,718     4 ,463     1 .00  75..45          0
ATOM     8162   OD2   ASP  AU27       -27 ,381   111 .411     6 ,079     1 ,00  78..60          0
ATOM     8163   O     PRO  A112 8     -31..405   Ill ,202     0 .501     1 ,00  74 ,82          0
ATOM     8164   N     PRO  A1128      -27 .966   Ill ,175     1 .727     1 ,00  75,.63          N
ATOM     8165   CA.   PRO  A1128      -29.,046   110. 944     0 ,758     1 ,00  70..73          C
ATOM     8166   C     PRO  A112 8     -30.,427   Ill ,364     1 ,238     1 ,00  74 .04          C
ATOM     8167   CB    PRO  A112 8     -28. 998   109.,422     0 .540     1 ,00  71 ,26          C
ATOM     8168   CG    PRO  A1128      -27.,592   109 .031     0 ,907     1 ,00  72 .40          C
ATOM     8169   CD    FRO  A112 8     -27 ,251   109..929     2 ,062     1 ,00  72 .38          C
ATOM     8170   O     LYS  A112 9     -33. 163   114 ,073     1 .789     1 ,00  68 ,00          0
ATOM     8171   N     LYS  A1129      -30..530   Ill ,871     2 ,459     1 .00  74 .88          N
ATOM     8172   CA    LYS  A112 9     -31.,813   112..409     2 ,903     1 ,00  80..55          C
ATOM     8173   C     LYS  A112 9     -32..039   113.,724     2 .162     1 ,00  7.3,.37         C
ATOM     8174   CB    LYS  A1129      -31..844   112.,612     4 ,423     1 .00  80..30          C
ATOM     8175   O     LYS  All 30     -.3 1. .,147 116. 291    - .1. .,053 1 ,00  72 .03         0
ATOM     817 6  N     LYS  All.30     -30..930   114 ,418     1 .931     1 ,00  70,.39          N
ATOM     817 7  CA    LYS  A1130      -30..925   115.,706     1 .267     1 ,00  73,.72          C
ATOM     8178   C     LYS  All 30     -.30.,554  115. 607     -0.,218    1 ,00  72 .47          C
ATOM     8179   CB    LYS  A1130      -29 ,954   116.,647     1 ,991     1 ,00  73..35          C
ATOM     8180   CG    LYS  A1130      -30..317   116.,872     3 . 457    1 ,00  69,.67          C
ATOM     8181   CD    LYS  A1130      -29.,457   117 .928     4 ,120     1 ,00  69..79          C
ATOM     8182   CE    LYS  A1130      -28 ,050   117 .423     4 ,401     1 ,00  71 .79          C
ATOM     8183   NZ    LYS  All.30     -27 .295   118.,340     5 . .302   1 ,00  66 ,43          N
ATOM     8184   O     TYR  A1131      -28.,634   113..515     -.3.,864   1 ,00  65..12          0
ATOM     8185   N     TYR  A1131      -29 ,603   114 .733     -0.,540    1 ,00  69..68          N
ATOM     8186   CA    TYR  A1131      -28. 945   114 ,753     -1 .843    1 ,00  69 ,39          C
ATOM     8187   C     TYR  A1131      -29 ,152   113.,529     -2 ,757    1 .00  68..91          C
ATOM     8188   CB    TYR  A1131      -27 ,443   114 .956     -1 ,627    1 ,00  65..10          C
ATOM     8189   CG    TYR  A1131      -27 .097   116.,270     -0.. 949   1 ,00  70,.18          C
ATOM     8190   CD2   TYR  A1131      -27 ..131  117 ,466     -1 ,657    1 .00  67 .92          C
ATOM     8191   CD1   TYR  A1131      -26 ,747   116. .319    0 ,394     1 ,00  73..69          C
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ATOM	8192	CE2	TYR	A1131	-26,821	118.676	-1.057	1.00	67.88	C
ATOM	8193	CEl	TYR	A1131	--26,435	117.535	1,010	1,00	72.22	C
ATOM	8194	CZ	TYR	A1131	-26.472	118,704	0:277	1,00	72,83	C
ATOM	8195	OH	TYR	A1131	-26,161	119,911	0,864	1.00	76.72	0
ATOM	8196	O	GLY	AU 32	-27.845	110.666	-2,649	1,00	67,86	0
ATOM	8197	N	GLY	Al l 32	-29.895	112,515	-2:.317	1,00	69,93	N
ATOM	8198	CA	GLY	A1132	-30.114	Ill,323	-3.131	1,00	62.93	C
ATOM	8199	C	GLY	A1132	-28,916	110.374	-3,196	1,00	70,68	C
ATOM	8200	O	GLY	A1133	-29.275	106,797	-5,407	1,00	63.00	0
ATOM	8201	N	GLY	A1133	-29.085	109,233	-3:871	1,00	65,30	N
ATOM	8202	CA	GLY	AU 33	-27,994	108.285	-4,014	1,00	57.38	C
ATOM	8203	C	GLY	A1133	-28.274	106.963	-4,715	1,00	58.03	C
ATOM	8204	O	PHE	A1134	-27.996	103,738	-3.052	1,00	63,83	0
ATOM	8205	N	PHE	A1134	-27.365	106,011	-4,542	1.00	58.32	N
ATOM	8206	CA	PHE	A1134	-27,498	104.703	-5,184	1,00	60.23	C
ATOM	8207	C	PHE	Al l 34	-28.157	103,681	-4:266	1,00	59,94	C
ATOM	8208	CB	PHE	A1134	-26,132	104,164	-5,608	1.00	54.26	C
ATOM	8209	CG	PHE	A1134	-25,281	105.144	-6,363	1,00	53,44	C
ATOM	8210	CD1	PHE	Al l 34	-25.543	105,431	-7:694	1,00	52,07	C
ATOM	8211	CD2	PHE	A1134	-24.195	105,748	-5.754	1,00	50,68	C
ATOM	8212	CEl	PHE	A1134	-24,733	106..306	-8,391	1,00	46,31	C
ATOM	8213	CE2	PHE	A1134	-23,391	106.623	-6,442	1,00	44.11	C
ATOM	8214	CZ	PHE	A1134	-23.658	106,906	-7.754	1,00	45,39	C
ATOM	8215	O	ASP	AU 35	-27,765	100..353	-5,522	1,00	54.60	0
ATOM	8216	N	ASP	A1135	-28,883	102.736	-4,842	1,00	55.27	N
ATOM	8217	CA	ASP	A1135	-29.285	101,570	-4.074	1,00	61,24	C
ATOM	8218	C	ASP	AU 35	-28,628	100.291	-4,642	1,00	58.31	C
ATOM	8219	CB	ASP	A1135	-30,822	101.460	-4,009	1,00	67.15	C
ATOM	8220	CG	ASP	A1135	-31.469	101,004	-5.325	1,00	78,68	C
ATOM	8221	OD2	ASP	A1135	-30,791	100,899	-6,374	1.00	75.65	0
ATOM	8222	OD1	ASP	A1135	-32 ,694	100.742	-5,297	1,00	93.29	0
ATOM	8223	O	SEP.	A1136	-26.420	97,579	-5:646	1,00	62,14	0
ATOM	8224	N	SER	A1136	-29,026	99,146	-4,105	1.00	58.28	N
ATOM	8225	CA.	SER	Al l 36	-28,547	97.848	-4,576	1,00	62,83	C
ATOM	8226	C	SER	A1136	-27.019	97,717	-4:577	1,00	56,22	C
ATOM	8227	CB	SER	A1136	-29.080	97,572	-5:993	1,00	64,10	C
ATOM	8228	OG	SER	Al l 36	-.30,380	98.117	-6,180	1,00	72,60	0
ATOM	8229	O	PRO	A1137	-25,407	95.151	-3,523	1,00	49.13	0
ATOM	8230	N	PRO	A1137	-26..383	97,770	-3.395	1,00	50,03	N
ATOM	8231	CA	PRO	Al 137	-24,939	97.510	-3,378	1,00	54.25	C
ATOM	8232	C	FRO	A1137	-24,648	96.073	-3,823	1,00	51.09	C
ATOM	8233	CB	PRO	A1137	-24.546	97,739	-1.910	1,00	47,16	C
ATOM	8234	CG	PRO	A1137	-25,703	98,477	-1,324	1.00	50.20	C
ATOM	8235	CD	FRO	A1137	-26,906	98.042	-2,050	1,00	48.94	C
ATOM	8236	O	THR	Al l 38	-21..334	94,376	-3:509	1,00	43,45	0
ATOM	8237	N	THR	A1138	-23,579	95,897	-4,583	1.00	49.52	N
ATOM	8238	CA.	TH.R	A1138	-23,202	94.553	-5,011	1,00	45,00	C
ATOM	8239	C	TKR	Al l 38	-22..374	93,860	-3:928	1,00	44,79	C
ATOM	8240	CB	THR	A1138	-22.410	94,574	-6.341	1,00	48,81	C
ATOM	8241	OG1	THR	A1138	-23,172	95.256	-7,352	1,00	52,23	0
ATOM	8242	CG2	THR	A1138	-22,114	93,142	-6,809	1,00	49.46	C
ATOM	8243	O	VAL	A1139	-21.171	90,362	-4.107	1,00	46,93	0
ATOM	8244	N	VAL	Al l 39	-22,841	92:696	-3,474	1,00	42.94	N
ATOM	8245	CA	VAL	A1139	-22,079	91,897	-2,515	1,00	43.96	C
ATOM	8246	C	VAL	A1139	-20.937	91,110	-3.177	1,00	40,04	C
ATOM	8247	CB	VAL	Al l 39	-22,994	90:939	-1,768	1,00	45.70	C
ATOM	8248	CGI	VAL	A1139	-22,188	89.955	-0,967	1,00	44.44	C
ATOM	8249	CG2	VAL	A1139	-23.915	91,737	-0.839	1,00	47,92	C
ATOM	8250	O	ALA	A1140	-18,419	88,223	-3,691	1.00	42.84	0
ATOM	8251	N	ALA	A1140	-19,702	91.302	-2,709	1,00	43.03	N
ATOM	8252	CA	ALA	A1140	-18.548	90,596	-3:280	1,00	46,99	C
ATOM	8253	C	ALA	A1140	-18.535	89,116	-2,859	1.00	43.83	C
ATOM	8254	CB	ALA	Al l 40	-17,256	91.282	-2,885	1,00	49,75	C

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ATOM     8255   O    TYR  A1141      -19.307    88.826     0.977   1.00  47.50              O
ATOM     8256   N    TYR  A1141      --18.680   88.882    -1.560   1.00  48.21              N
ATOM     8257   CA   TYR  A1141      -18.842    87.545    -0.976   1.00  46.53              C
ATOM     8258   C    TYR  A1141      -19.371    87.734     0.431   1.00  47.47              C
ATOM     8259   CB   TYR  All 41     -17.526    86.730    -0.943   1.00  38.83              C
ATOM     8260   CG   TYR  A1141      -16..337   87.472    -0..379  1.00  44.47              C
ATOM     8261   CD1  TYR  A1141      -16.132    87.586     0.999   1.00  51.15              C
ATOM     8262   CD2  TYR  All 41     -15.421    88.070    -1.221   1.00  45.78              C
ATOM     8263   CE1  TYR  A1141      -15.042    88.286     1.511   1.00  45.34              C
ATOM     8264   CE2  TYR  A1141      -14.331    88.750    -0.724   1.00  48.66              C
ATOM     8265   CZ   TYR  All 41     -14.145    88.856     0.638   1.00  50.41              C
ATOM     8266   OH   TYR  A1141      -13.049    89.546     1.094   1.00  50.94              0
ATOM     8267   O    SER  A1142      -18.413    85.450     2.937   1.00  49.80              0
ATOM     8268   N    SER  A1142      -19.874    86.663     1.019   1.00  44.16              N
ATOM     8269   CA   SER  A1142      -20.359    86.723     2.374   1.00  42.39              C
ATOM     8270   C    SER  A1142      -19..353   86.122     3..337   1.00  46.78              C
ATOM     8271   CB   SER  A1142      -21.682    86.010     2.495   1.00  42.98              C
ATOM     8272   OG   SER  All 42     -22.651    86.701     1.771   1.00  43.25              0
ATOM     8273   O    VAL  A114 3     -20..370   86.036     7.173   1.00  56.67              0
ATOM     8274   N    VAL  A1143      -19.532    86.385     4.617   1.00  45.83              N
ATOM     8275   CA.  VAL  All 43     -18.603    85.853     5.583   1.00  45.10              C
ATOM     8276   C    VAL  A114 3     -19.411    85.388     6.768   1.00  46.70              C
ATOM     8277   CB   VAL  A1143      -17.524    86.873     5.997   1.00  53.16              C
ATOM     8278   CG2  VAL  All 43     -16.459    87.052     4.900   1.00  40.46              C
ATOM     8279   CGI  VAL  A114 3     -16.860    86.413     7.228   1.00  61.25              C
ATOM     8280   0    LEU  A114 4     -17.810    84.539     9.671   1.00  52.03              0
ATOM     8281   N    LEU  All 44     -19.066    84.203     7.260   1.00  60.06              N
ATOM     8282   CA   LEU  A114 4     -19.659    83.667     8.467   1.00  58.22              C
ATOM     8283   C    LEU  A114 4     -19.033    84.392     9.625   1.00  55.37              C
ATOM     8284   CB   LEU  A114 4     -19.411    82.167     8.591   1.00  55.09              C
ATOM     8285   CG   LEU  A114 4     -19.909    81.536     9.894   1.00  55.24              C
ATOM     8286   CD1  LEU  A114 4     -21.431    81.546     9.927   1.00  56.17              C
ATOM     8287   CD2  LEU  A114 4     -19.367    80.124    10.058   1.00  60.50              C
ATOM     8288   O    VAL  All 45     -21.224    84.970    13.114   1.00  56.89              0
ATOM     8289   N    VAL  A114 5     -19.863    84.857    10.549   1.00  53.39              N
ATOM     8290   CA   VAL  A1145      -19.334    85.522    11.722   1.00  58.29              C
ATOM     8291   C    VAL  All 45     -19.999    84.988    12.978   1.00  58.56              C
ATOM     8292   CB   VAL  A114 5     -19.479    87.063    11.631   1.00  59.93              C
ATOM     8293   CGI  VAL  A114 5     -20.542    87.444    10.632   1.00  56.44              C
ATOM     8294   CG2  VAL  All 45     -19.737    87.676    13.011   1.00  58.61              C
ATOM     8295   O    VAL  A114 6     -17.674    84.945    16.276   1.00  68.89              0
ATOM     8296   N    VAL  A114 6     -19.145    84.494    13.866   1.00  66.35              N
ATOM     8297   CA   VAL  A114 6     -19.557    83.962    15.150   1.00  68.18              C
ATOM     8298   C    VAL  A114 6     -18.907    84.851    16.191   1.00  68.64              C
ATOM     8299   CB   VAL  A114 6     -19.145    82.481    15..328   1.00  71.29              C
ATOM     8300   CGI  VAL  A114 6     -19.616    81.941    16.671   1.00  67.93              C
ATOM     8301   CG2  VAL  All 46     -19.717    81.645    14.201   1.00  66.20              C
ATOM     8302   O    ALA  A114 7     -21.487    86.386    18.862   1.00  71.67              0
ATOM     8303   N    ALA  A1147      -19.751    85.541    16.945   1.00  67.18              N
ATOM     8304   CA.  ALA  All 47     -19.281    86.544    17.880   1.00  73.19              C
ATOM     8305   C    ALA  A114 7     -20.386    86.964    18.837   1.00  74.49              C
ATOM     8306   CB   ALA  A1147      -18.750    87.745    17.133   1.00  73.32              C
ATOM     8307   O    LYS  All 48     -20.646    90.641    19.473   1.00  74.63              0
ATOM     8308   N    LYS  A114 8     -20.077    87.971    19.639   1.00  77.29              N
ATOM     8309   CA   LYS  A114 8     -21.067    88.518    20.539   1.00  78.56              C
ATOM     8310   C    LYS  All 48     -21.464    89.893    20.026   1.00  75.47              C
ATOM     8311   CB   LYS  A114 8     -20.524    88.580    21.964   1.00  76.58              C
ATOM     8312   O    VAL  A114 9     -24.518    91.600    21.836   1.00  74.92              0
ATOM     8313   N    VAL  A1149      -22.732    90.218    20.181   1.00  76.02              N
ATOM     8314   CA   VAL  A114 9     -23.169    91.557    19.843   1.00  79.22              C
ATOM     8315   C    VAL  A114 9     -23.778    92.232    21.073   1.00  75.09              C
ATOM     8316   CB   VAL  A1149      -24.173    91.540    18.666   1.00  75.99              C
ATOM     8317   CGI  VAL  All 49     -25.545    90.991    19.098   1.00  74.23              C
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ATOM 8318 CG2 VAL A1149 -24.301 92;930 18.076 1.00 83.98 C
ATOM 8319 O GLU A1150 --25,886 94.598 20,726 1,00 76.75 O
ATOM 832 0 N GLU A1150 -23.426 93,499 21:292 1,00 77,38 N
ATOM 832 1 CA GLU A1150 -24.130 94;299 22,288 1.00 76.39 C
ATOM 8322 C GLU A1150 -25,571 94.242 21,860 1,00 74,20 C
ATOM 832 3 CB GLU A1150 -23.612 95,737 22..354 1,00 73,63 C
ATOM 832 4 O LYS A1151 -29.009 93,012 24.374 1,00 81,61 O
ATOM 8325 N LYS A1151 -26,433 93.735 22,735 1,00 73,80 N
ATOM 832 6 CA LYS A1151 -27.822 93,490 22,365 1,00 76.49 C
ATOM 832 7 C LYS A1151 -28.792 93,826 23.482 1,00 81,79 C
ATOM 832 8 CB LYS AU 51 -28,013 92.031 21,955 1,00 80.38 C
ATOM 832 9 O GLY Al l52 -29.361 97,583 24.074 1,00 79.33 0
ATOM 8330 N GLY A1152 -29.387 95,015 23.414 1,00 76,40 N
ATOM 8331 CA GLY Al l52 -30.342 95.446 24.413 1.00 74.31 C
ATOM 8332 C GLY A1152 -30,204 96.925 24,687 1,00 81.60 C
ATOM 8333 O LYS A1153 -28.995 100,200 26.117 1,00 93,32 0
ATOM 8334 N LYS A1153 -31.035 97.449 25.590 1.00 82.64 N
ATOM 8335 CA. LYS A1153 -.30,964 98.860 25,961 1,00 85,22 C
ATOM 8336 C LYS A1153 -29.560 99,160 26.451 1,00 85,24 C
ATOM 8337 CB LYS A1153 -32 .002 99,228 27.033 1,00 77,28 C
ATOM 8338 O SER AU 54 -28,230 96.534 29,214 1,00 87,20 0
ATOM 8339 N SER A1154 -29.003 98.230 27.225 1,00 85.81 N
ATOM 8340 CA SER A1154 -27.608 98,277 27.691 1,00 91,68 C
ATOM 8341 C SER Al 154 -27,319 97.080 28,591 1,00 86.10 C
ATOM 8342 CB SER A1154 -27.303 99.577 28.466 1,00 96.09 C
ATOM 8343 OG SER A1154 -27..339 100,730 27.632 1,00 90,12 0
ATOM 8344 O LYS Al 155 -23,367 95..334 26,895 1,00 75.38 0
ATOM 8345 N LYS A1155 -26,074 96.628 28,636 1,00 83.57 N
ATOM 8346 CA LYS A1155 -25.064 96,891 27.632 1,00 78,74 C
ATOM 8347 C LYS A1155 -24.447 95.507 27.462 1.00 76.84 C
ATOM 8348 CB LYS A1155 -24,059 97.950 28,082 1,00 73.15 C
ATOM 8349 O LYS A1156 -24.757 93,281 25.580 1,00 76,89 0
ATOM 8350 N LYS A1156 -25.191 94.525 27,972 1.00 78.06 N
ATOM 8351 CA. LYS Al l56 -24,836 93.107 27,957 1,00 71,85 C
ATOM 8352 C LYS A1156 -24.623 92,564 26.558 1,00 72,35 C
ATOM 8353 CB LYS A1156 -25.923 92,288 28.660 1,00 73.48 C
ATOM 8354 O LEU A1157 -25,171 88.719 25,813 1,00 72,62 0
ATOM 8355 N LEU A1157 -24.297 91.281 26.466 1,00 80.62 N
ATOM 8356 CA LEU A1157 -23.945 90,681 25.185 1,00 73,41 C
ATOM 8357 C LEU Al 157 -24,751 89.420 24,904 1,00 73.00 C
ATOM 8358 CB LEU A1157 -22,451 90.365 25,136 1,00 68.63 C
ATOM 8359 CG LEU A1157 -21.500 91,535 25.407 1,00 68,53 C
ATOM 8360 CD1 LEU A1157 -20.069 91.172 25.099 1.00 64.79 C
ATOM 8361 CD2 LEU A1157 -21,889 92.754 24,610 1,00 69.84 C
ATOM 8362 O LYS A1158 -24..310 88,147 21.202 1.00 77,34 0
ATOM 8363 N LYS A1158 -24.992 89.159 23.630 1.00 76.07 N
ATOM 8364 CA. LYS A1158 -25,578 87.901 23,201 1,00 76,09 C
ATOM 8365 C LYS A1158 -24.687 87,390 22.101 1,00 75,11 C
ATOM 8366 CB LYS A1158 -27.017 88,070 22.708 1,00 80,07 C
ATOM 8367 N SER Al l59 -24,314 86.120 22,192 1,00 80,07 N
ATOM 8368 CA SER A1159 -23.411 85.529 21.220 1,00 78.21 C
ATOM 8369 C SER A1159 -24.225 85,283 19.969 1,00 72,15 C
ATOM 8370 0 SER Al l59 -25,416 84.959 20,055 1,00 66.47 0
ATOM 8371 CB SER A1159 -22.788 84.239 21.758 1,00 78.90 C
ATOM 8372 OG SER A1159 -21.440 84,098 21..331 1,00 78,22 0
ATOM 8373 N VAL Al 160 -23,619 85.471 18,803 1,00 69.78 N
ATOM 8374 CA VAL A1160 -24,409 85.344 17,578 1,00 69.47 C
ATOM 8375 C VAL A1160 -23.674 84,621 16.488 1,00 64,36 C
ATOM 8376 O VAL Al l60 -22.450 84.706 16.369 1.00 67.28 0
ATOM 8377 CB VAL A1160 -24,872 86.726 17,005 1,00 67.48 C
ATOM 8378 CGI VAL Al l60 -26.089 87,263 17.758 1.00 63,19 C
ATOM 8379 CG2 VAL Al l60 -23.736 87.729 16.990 1.00 63.73 C
ATOM 8380 O LYS A1161 -25,913 83.873 13,235 1,00 60,40 0
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ATOM     8381   N     LYS  All 61     -24.450   83.898   15.695   1.00  64.03          N
ATOM     8382   CA    LYS  A1161      --23.961  83.285   14.480   1.00  65.03          C
ATOM     8383   C     LYS  All 61     -24.689   83.954   13..331   1.00  62.77          C
ATOM     8384   CB    LYS  All 61     -24.208   81.771   14.480   1.00  68.27          C
ATOM     8385   CG    LYS  A1161      -23.565   81.031   13.329   I.00  61.73          C
ATOM     8386   CD    LYS  All 61     -24.291   79.722   13.062   1.00  68.35          C
ATOM     8387   CE    LYS  A1161      -24.118   78.727   14.182   1.00  68.39          C
ATOM     8388   NZ    LYS  A1161      -24 .862  77.461   13.923   I.00  65.92          N
ATOM     8389   O     GLU  All 62     -22.654   85.233   10.037   1.00  55.60          O
ATOM     8390   N     GLU  All 62     -23.951   84.637   12.467   1.00  58.78          N
ATOM     8391   CA    GLU  All 62     -24 .613  85.404   11.427   I.00  62.60          C
ATOM     8392   C     GLU  All 62     -23.869   85.416   10.091   1.00  58.02          C
ATOM     8393   CB    GLU  A1162      -24.839   86.840   11.924   1.00  60.62          C
ATOM     8394   CG    GLU  All 62     -25.988   86.955   12.912   1.00  65.33          C
ATOM     8395   CD    GLU  All 62     -26.234   88.365   13.403   1.00  70.39          C
ATOM     8396   OE1   GLU  All 62     -25.457   89.280   13.039   1.00  64.73          0
ATOM     8397   OE2   GLU  All 62     -27.215   88.546   14.158   1.00  72.45          0
ATOM     8398   O     LEU  A1163      -25.041   87.941    7.213   I.00  52.12          0
ATOM     8399   N     LEU  A1163      -24.640   85.630    9.026   1.00  59.23          N
ATOM     8400   CA    LEU  A1163      -24.141   85.774    7.667   1.00  54.99          C
ATOM     8401   C     LEU  A1163      -24 .040  87.247    7.242   I.00  54.09          C
ATOM     8402   CB    LEU  All 63     -25.061   85.033    6.708   1.00  50.92          C
ATOM     8403   CG    LEU  A1163      -24.405   84.712    5.373   1.00  54.21          C
ATOM     8404   CDI   LEU  A1163      -23.193   83.857    5.652   I.00  50.31          C
ATOM     8405   CD2   LEU  All 63     -25.382   83.993    4.461   1.00  51.65          C
ATOM     8406   O     LEU  A1164      -21.202   88.666    4.647   1.00  49.44          0
ATOM     8407   N     LEU  A1164      -22 .842  87.706    6.886   I.00  57.16          N
ATOM     8408   CA    LEU  All 64     -22 .634  89.106    6.538   1.00  54.24          C
ATOM     8409   C     LEU  A1164      -22.154   89.328    5.100   1.00  57.55          C
ATOM     8410   CB    LEU  All 64     -21 .621  89.742    7.503   1.00  57.54          C
ATOM     8411   CG    LEU  All 64     -21 .314  91.237    7.287   1.00  61.37          C
ATOM     8412   CD1   LEU  All 64     -22.471   92.110    7.744   1.00  53.13          C
ATOM     8413   CD2   LEU  All 64     -19 .996  91.674    7.945   1.00  58.92          C
ATOM     8414   O     GLY  A1165      -21.327   92.790    3.492   I.00  59.26          0
ATOM     8415   N     GLY  All 65     -22.780   90.302    4.421   1.00  50.02          N
ATOM     8416   CA    GLY  A1165      -22.392   90.689    3.075   1.00  43.50          C
ATOM     8417   C     GLY  A1165      -21.239   91.668    3.014   I.00  47.03          C
ATOM     8418   O     ILE  Al166      -18.861   91.903   -0.176   1.00  45.65          0
ATOM     8419   N     ILE  A1166      -20.142   91.243    2.421   1.00  40.25          N
ATOM     8420   CA    ILE  All 66     -19.016   92.112    2.211   I.00  37.27          C
ATOM     8421   C     ILE  Al166      -19.124   92.634    0.787   1.00  47.64          C
ATOM     8422   CB    ILE  Al166      -17.683   91.383    2.429   1.00  46.88          C
ATOM     8423   CGI   ILE  Al166      -17 .661  90.710    3.807   1.00  45.79          C
ATOM     8424   CG2   ILE  Al166      -16.495   92.330    2.251   1.00  47.23          C
ATOM     8425   CD1   ILE  Al166      -17.790   91.668    4.972   1.00  50.79          C
ATOM     8426   O     THR  All 67     -17 .464  94.833   -0.790   1.00  42.95          0
ATOM     8427   N     TH.R A1167      -19.538   93.899    0.667   I.00  47.05          N
ATOM     8428   CA    THR  All 67     -19.827   94.546   -0.602   1.00  38.98          C
ATOM     8429   C     THR  A1167      -18 .558  94.819   -1.356   1.00  40.39          C
ATOM     8430   CB    TH.R A1167      -20 .596  95.924   -0.411   I.00  44.41          C
ATOM     8431   OG1   THR  All 67     -19.725   96.915    0.171   1.00  44.52          0
ATOM     8432   CG2   THR  All 67     -21 .807  95.738    0.446   1.00  41.09          C
ATOM     8433   O     ILE  A1168      -15 .621  96.634   -3.053   I.00  50.36          0
ATOM     8434   N     ILE  All 68     -18.710   95.081   -2.642   1.00  37.94          N
ATOM     8435   CA    ILE  A1168      -17.564   95.319   -3.487   1.00  41.73          C
ATOM     8436   C     ILE  A1168      -16.834   96.563   -3.008   I.00  40.65          C
ATOM     8437   CB    ILE  A1168      -18.000   95.423   -4.967   1.00  37.41          C
ATOM     8438   CGI   ILE  A1168      -18 .463  94.047   -5.445   1.00  44.60          C
ATOM     8439   CG2   ILE  All 68     -16 .883  95.963   -5.834   1.00  36.47          C
ATOM     8440   CD1   ILE  A1168      -18.766   93.922   -6.940   1.00  43.10          C
ATOM     8441   O     MET  Al169      -15.142   99.121   -0.590   1.00  58.86          0
ATOM     8442   N     MET  Al169      -17 .582  97.540   -2.526   1.00  45.87          N
ATOM     8443   CA.   MET  All 69     -17 .001  98.795   -2.069   I.00  45.65          C
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ATOM    8444  C    MET  A1169      -16.237   98.589  -0.750  1.00 54.66           C
ATOM    8445  CB   MET  Al169      --18.104   99.837  -1.912  1.00 48.10           C
ATOM    8446  CG   MET  Al169      -17.688  101.269  -2.020  1.00 51.36           C
ATOM    8447  SD   MET  Al169      -19.190  102.310  -2.032  1.00 66.31           S
ATOM    8448  CE   MET  All 69     -19.509  102.621  -0.291  1.00 57.16           C
ATOM    8449  O    GLU  A117 0     -14.131   96.477   2..323  1.00 60.29           0
ATOM    8450  N    GLU  A117 0     -16.797   97.801   0.175  1.00 51.71           N
ATOM    8451  CA.  GLU  All 70     -16.140   97.495   1.461  1.00 52.95           C
ATOM    8452  C    GLU  A117 0     -14.941   96.531   1.392  1.00 57.56           C
ATOM    8453  CB   GLU  A117 0     -17.147   96.892   2.449  1.00 53.48           C
ATOM    8454  CG   GLU  All 70     -18.219   97.841   2.965  1.00 51.50           C
ATOM    8455  CD   GLU  A117 0     -19.408   97.099   3.568  1.00 61.72           C
ATOM    8456  OE1  GLU  A1170      -19.486   95.857   3.415  1.00 57.48           0
ATOM    8457  OE2  GLU  A117 0     -20.276   97.757   4.189  1.00 67.08           0
ATOM    8458  O    ARG  A1171      -11.866   94.108   1.348  1.00 57.40           0
ATOM    8459  N    AP.G A1171      -14.825   95.768   0..306  1.00 58.62           N
ATOM    8460  CA   ARG  A1171      -13.974   94.575   0.311  1.00 53.17           C
ATOM    8461  C    ARG  All 71     -12.504   94.853   0.617  1.00 53.64           C
ATOM    8462  CB   ARG  A1171      -14.091   93.854  -1.028  1.00 49.57           C
ATOM    8463  CG   ARG  A1171      -13.274   92.588  -1.150  1.00 46.49           C
ATOM    8464  CD   ARG  All 71     -13.223   92.157  -2.596  1.00 54.81           C
ATOM    8465  ME   ARG  A1171      -12.379   90.986  -2.802  1.00 59.51           N
ATOM    8466  CZ   ARG  A1171      -11.934   90.592  -3.987  1.00 62.02           C
ATOM    8467  NH1  ARG  All 71     -12.237   91.293  -5.073  1.00 56.46           N
ATOM    8468  NH2  ARG  A1171      -11.173   89.510  -4.081  1.00 57.65           N
ATOM    8469  O    SER  A1172       -9.203   95.999   2.211  1.00 62.84           0
ATOM    8470  N    SER  AU72       -11.966   95.916   0.051  1.00 53.83           N
ATOM    8471  CA   SER  A1172      -10.554   96.221   0.226  1.00 53.34           C
ATOM    8472  C    SER  A1172      -10.214   96.471   1.694  1.00 57.55           C
ATOM    8473  CB   SER  A1172      -10.171   97.439  -0.611  1.00 53.75           C
ATOM    8474  OG   SER  A1172       -8.900   97.280  -1.214  1.00 63.98           0
ATOM    8475  O    SER  A117 3      -9.998   96.009   5.403  1.00 69.60           0
ATOM    8476  N    SER  A117 3     -11.069   97.208   2.374  1.00 60.60           N
ATOM    8477  CA.  SER  All 73     -10.783   97.537   3.750  1.00 63.09           C
ATOM    8478  C    SER  A117 3     -10.865   96.271   4.577  1.00 63.08           C
ATOM    8479  CB   SER  A1173      -11.745   98.600   4.280  1.00 60.10           C
ATOM    8480  OG   SER  All 73     -12.699   98.020   5.136  1.00 60.27           0
ATOM    8481  O    PHE  A117 4     -10.280   92.960   5.938  1.00 64.22           0
ATOM    8482  N    PHE  A117 4     -11.898   95.476   4..326  1.00 64.54           N
ATOM    8483  CA   PHE  All 74     -12.091   94.226   5.045  1.00 61.58           C
ATOM    8484  C    PHE  A117 4     -10.869   93.322   4.935  1.00 60.51           C
ATOM    8485  CB   PHE  A117 4     -13..338   93.510   4.542  1.00 55.51           C
ATOM    8486  CG   PHE  A117 4     -13.562   92.175   5.182  1.00 54.40           C
ATOM    8487  CD2  PHE  A117 4     -13.179   91.003   4.534  1.00 57.21           C
ATOM    8488  CD1  PHE  A117 4     -14.164   92.083   6.419  1.00 55.92           C
ATOM    8489  CE2  PHE  A117 4     -13.380   89.752   5.126  1.00 53.13           C
ATOM    8490  CE1  PHE  All 74     -14.369   90.854   7.016  1.00 59.55           C
ATOM    8491  CZ   PHE  A117 4     -13.975   89.679   6..362  1.00 54.00           C
ATOM    8492  O    GLU  A1175       -7.144   91.805   4.433  1.00 68.90           0
ATOM    8493  N    GLU  All 75     -10.456   92.997   3.723  1.00 61.25           N
ATOM    8494  CA   GLU  A117 5      -9.354   92.056   3.553  1.00 62.55           C
ATOM    8495  C    GLU  A1175       -8.042   92.582   4.132  1.00 65.45           C
ATOM    8496  CB   GLU  All 75      -9.168   91.708   2.072  1.00 54.24           C
ATOM    8497  CG   GLU  A117 5     -10.386   91.047   1.482  1.00 53.03           C
ATOM    8498  CD   GLU  A117 5     -10.220   90.723   0.019  1.00 60.47           C
ATOM    8499  OE1  GLU  All 75      -9.261   91.238  -0.606  1.00 58.28           0
ATOM    8500  OE2  GLU  A117 5     -11.048   89.943  -0.505  1.00 63.60           0
ATOM    8501  O    LYS  A117 6      -5.452   93.943   6.819  1.00 73.87           0
ATOM    8502  N    LYS  A117 6      -7.928   93.896   4.292  1.00 68.35           N
ATOM    8503  CA   LYS  A117 6      -6.687   94.464   4.817  1.00 75.04           C
ATOM    8504  C    LYS  A117 6      -6.565   94.119   6.295  1.00 77.29           C
ATOM    8505  CB   LYS  A117 6      -6.637   95.983   4.628  1.00 67.75           C
ATOM    8506  N    ASM  All 77      -7.724   93.986   6.945  1.00 70.10           N
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ATOM    8507   CA   ASN  A117 7    --7.791    93.858    8.391   1.00  60.07          C
ATOM    8508   C    ASM  A117 7    -9.197     93.491    8.858   1.00  60.79          C
ATOM    8509   O    ASN  A117 7    -9.930     94.351    9..3.14 1.00  68.52          0
ATOM    8510   CB   ASN  A117 7    --7.335    95.173    9.004   1.00  60.41          C
ATOM    8511   CG   ASN  All 77    -7.078     95.092   10.494   I.00  69.89          C
ATOM    8512   OD1  ASN  A117 7    -7.7.14    94.318   11.230   1.00  68.13          0
ATOM    8513   ND2  ASN  A1177     --6.155    95.937   10.962   1.00  67.10          N
ATOM    8514   N    PRO  All 78    -9.588     92.207    8.738   I.00  61.08          N
ATOM    8515   CA   PRO  A117 8    -10 .996   91.869    8.996   1.00  58.83          C
ATOM    8516   C    PRO  A117 8    -11 .496   92.089   10.414   1.00  66.73          C
ATOM    8517   0    PRO  All 78    -12 .615   92.576   10.585   I.00  68.92          0
ATOM    8518   CB   PRO  A117 8    -11 .077   90.381    8.639   1.00  56.35          C
ATOM    8519   CG   PRO  A1178     -9.688     89.951    8.3.15  1.00  56.88          C
ATOM    8520   CD   PRO  A117 8    -8.891     91.140    8.002   1.00  55.77          C
ATOM    8521   N    ILE  A117 9    -10.698    91.749   11.418   1.00  72.03          N
ATOM    8522   CA   ILE  A117 9    -11.178    9.1.819  12.794   1.00  7.1.32         C
ATOM    8523   C    ILE  A117 9    -11 .490   93.272   13.195   1.00  71.33          C
ATOM    8524   O    ILE  All 79    -12 .518   93.548   13.824   I.00  67.53          0
ATOM    8525   CB   ILE  A117 9    -10.164    9.1.185  13.770   1.00  75.31          C
ATOM    8526   CGI  ILE  A117 9    -10 .671   91.302   15.207   1.00  75.27          C
ATOM    8527   CG2  ILE  All 79    -8.777     91.792   13.586   I.00  77.9.3         C
ATOM    8528   CD1  ILE  A117 9    -11 .997   90.588   15.426   1.00  81.03          C
ATOM    8529   N    ASP  A1180     -10 .617   94.197   12.807   1.00  69.85          N
ATOM    8530   CA   ASP  A1180     -10 .875   95.606   13.053   I.00  69.49          C
ATOM    8531   C    ASP  A1180     -12 .146   96.016   12.302   1.00  70.49          C
ATOM    8532   O    ASP  A1180     -13 .068   96.551   12.9.18  1.00  68.91          O
ATOM    8533   CB   ASP  A1180     -9.670     96.467   12.651   I.00  70.8.3         C
ATOM    8534   CG   ASP  A1180     -8.587     96.505   13.738   1.00  73.61          C
ATOM    8535   OD1  ASP  A1180     -8.932     96.258   14.9.15  1.00  74.86          0
ATOM    8536   OD2  ASP  A1180     -7.405     96.792   13.432   1.00  66.88          0
ATOM    8537   N    FHE  A1181     -12 .210   95.699   11.000   1.00  71.62          N
ATOM    8538   CA   PHE  A1181     -13.400    95.929   10.159   1.00  66.29          C
ATOM    8539   C    PHE  A1181     -14 .683   95.526   10.872   1.00  64.43          C
ATOM    8540   O    PHE  A1181     -15 .706   96.206   10.784   I.00  64.84          0
ATOM    8541   CB   PHE  A1181     -13.289    95.154    8.820   1.00  6.3.39         C
ATOM    8542   CG   PHE  A1181     -14.437    95.422    7.845   1.00  62.83          C
ATOM    8543   CD1  PHE  A1181     -15 .705   94.896    8.051   I.00  59.89          C
ATOM    8544   CD2  PHE  A1181     -14.235    96.196    6.726   1.00  63.94          C
ATOM    8545   CE1  PHE  A118.1    -16.730    95.157    7.181   1.00  62.63          C
ATOM    854 6  CE2  PHE  A1181     -15 .270   96.456    5.838   I.00  62..30         C
ATOM    8547   CZ   FHE  A1181     -16.516    95.937    6.070   1.00  60.51          C
ATOM    8548   N    LEU  A1182     -14.6.14   94.405   11.574   1.00  69.20          N
ATOM    8549   CA   LEU  All 82    -15 .795   93.745   12.106   1.00  69.67          C
ATOM    8550   C    LEU  A1182     -16.252    94.277   13.460   1.00  65.24          C
ATOM    8551   O    LEU  All 82    -17.444    94.247   13.774   1.00  61.90          0
ATOM    8552   CB   LEU  All 82    -15 .518   92.245   12.204   1.00  69.95          C
ATOM    8553   CG   LEU  All 82    -15 .631   91.446   10.909   I.00  69.11          C
ATOM    8554   CD1  LEU  All 82    -14.711    90.219   10.943   1.00  65.32          C
ATOM    8555   CD2  LEU  A1182     -17.092    91.051   10.707   1.00  60.22          C
ATOM    8556   N    GLU  All 83    -15 .308   94.729   14.279   I.00  67.85          N
ATOM    8557   CA   GLU  A1183     -15 .691   95.378   15.531   1.00  73.34          C
ATOM    8558   C    GLU  A1183     -16 .452   96.657   15.169   1.00  67.06          C
ATOM    8559   0    GLU  A1183     -17.472    96.991   15.784   I.00  67.0.1         0
ATOM    8560   CB   GLU  A1183     -14.468    95.671   16.412   1.00  73.56          C
ATOM    8561   N    ALA  A1184     -15 .981   97.317   14.110   1.00  6.3.29         N
ATOM    8562   CA   ALA  A1184     -16.571    98.559   13.617   I.00  68.7.1         C
ATOM    8563   C    ALA  A1184     -18.047    98.460   13.219   1.00  63.38          C
ATOM    8564   O    ALA  A1184     -18.675    99.479   12.997   1.00  6.3.82         O
ATOM    8565   CB   ALA  A1184     -15 .761   99.079   12.445   1.00  65.74          C
ATOM    8566   N    LYS  A1185     -18.610    97.259   13.131   1.00  62.51          N
ATOM    8567   CA   LYS  All 8 5   -20.0.16   97.137   12.740   1.00  65.10          C
ATOM    8568   C    LYS  A1185     -20.878    96.533   13.847   1.00  71.92          C
ATOM    8569   O    LYS  All 85    -22 .022   96.134   13.603   I.00  69.98          0
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ATOM   8570  CB   LYS  A1185     -20.148   96.312   11.459  1.00  72.43           C
ATOM   8571  CG   LYS  A1185    --19.349   96.870   10.274  1.00  75.49           C
ATOM   8572  CD   LYS  A1185     -19.709   96.195    8.955  1.00  66.31           C
ATOM   8573  CE   LYS  A1185     -21.161   96.445    8.584  1.00  73.98           C
ATOM   8574  NZ   LYS  A1185     -21.368   96.400    7.098  1.00  76.87           N
ATOM   8575  O    GLY  A1186     -21.348   93.978   17.528  1.00  75.13           O
ATOM   8576  N    GLY  A1186     -20.329   96.480   15.062  1.00  70.66           N
ATOM   8577  CA.  GLY  All86     -21.057   95.958   16.209  1.00  73.64           C
ATOM   8578  C    GLY  A1186     -20.683   94.544   16.654  1.00  76.21           C
ATOM   8579  O    TYR  A1187     -16.917   92.955   16.811  1.00  75.26           O
ATOM   8580  N    TYR  All87     -19.634   93.971   16.060  1.00  72.32           N
ATOM   8581  CA   TYR  A1187     -19.245   92.587   16.349  1.00  74.40           C
ATOM   8582  C    TYR  A1187     -17.993   92.494   17.210  1.00  77.92           C
ATOM   8583  CE   TYR  A1187     -18.989   91.800   15.056  1.00  69.82           c
ATOM   8584  CG   TYR  Al187     -20.220   91.407   14.286  1.00  65.61           C
ATOM   8585  CD1  TYR  A1187     -21.260   90.723   14.899  1.00  64.02           C
ATOM   8586  CD2  TYR  A1187     -20.340   91.717   12.938  1.00  65.01           c
ATOM   8587  CE1  TYR  A1187     -22.399   90.359   14.185  1.00  65.61           C
ATOM   8588  CE2  TYR  A1187     -21.474   91.370   12.215  1.00  64.79           C
ATOM   8589  CZ   TYR  A1187     -22.500   90.692   12.838  1.00  67.13           C
ATOM   8590  OH   TYR  A1187     -23.623   90.345   12.112  1.00  58.29           0
ATOM   8591  O    LYS  A1188     -18.111   89.516   19.683  1.00  78.63           0
ATOM   8592  N    LYS  A1188     -18.116   91.879   18.381  1.00  75.35           N
ATOM   8593  CA   LYS  All88     -16.914   91.538   19.135  1.00  83.65           C
ATOM   8594  C    LYS  A1188     -17.037   90.139   19.726  1.00  82.66           C
ATOM   8595  CB   LYS  A1188     -16.628   92.576   20.229  1.00  83.68           C
ATOM   8596  CG   LYS  All88     -15.162   93.026   20.293  1.00  82.20           C
ATOM   8597  CD   LYS  A1188     -15.059   94.496   20.709  1.00  88.46           C
ATOM   8598  CE   LYS  A1188     -13.618   95.010   20.660  1.00  92.13           C
ATOM   8599  NZ   LYS  A1188     -13.517   96.486   20.894  1.00  67.40           N
ATOM   8600  O    GLU  A1189     -16.078   86.245   19.520  1.00  75.44           O
ATOM   8601  N    GLU  A1189     -15.919   89.673   20.276  1.00  81.12           N
ATOM   8602  CA   GLU  A1189     -15.743   88.295   20.723  1.00  86.22           C
ATOM   8603  C    GLU  All89     -15.690   87.413   19.483  1.00  81.66           C
ATOM   8604  CB   GLU  A1189     -16.860   87.854   21.683  1.00  87.08           C
ATOM   8605  CG   GLU  A1189     -17.085   88.779   22.892  1.00  87.79           C
ATOM   8606  CD   GLU  All89     -16.039   88.604   24.004  1.00  91.44           C
ATOM   8607  OE1  GLU  A1189     -14.829   88.446   23.695  1.00  82.73           0
ATOM   8608  OF.2 GLU  A1189     -16.441   88.633   25.194  1.00  84.46           0
ATOM   8609  N    VAL  AU90      -15.185   88.007   18.399  1.00  82.87           N
ATOM   8610  CA   VAL  A1190     -15.109   87.391   17.078  1.00  77.05           C
ATOM   8611  C    VAL  All90     -14.054   86.312   17.015  1.00  70.57           C
ATOM   8612  O    VAL  A1190     -12.861   86.601   17.131  1.00  71.30           0
ATOM   8613  CB   VAL  A1190     -14.792   88.443   15.985  1.00  75.94           C
ATOM   8614  CGI  VAL  All90     -14.304   87.772   14.701  1.00  74.36           C
ATOM   8615  CG2  VAL  A1190     -16.004   89.307   15.710  1.00  74.89           C
ATOM   8616  N    LYS  A1191     -14.483   85.070   16.828  1.00  71.95           N
ATOM   8617  CA   LYS  All91     -13.526   83.986   16.632  1.00  68.00           C
ATOM   8618  c    LYS  A1191     -12.938   84.115   15.238  1.00  67.28           c
ATOM   8619  0    LYS  A1191     -13.629   83.893   14.244  1.00  71.26           0
ATOM   8620  CB   LYS  All91     -14.188   82.624   16.829  1.00  66.69           C
ATOM   8621  N    LYS  All92     -11.672   84.513   15.173  1.00  65.93           N
ATOM   8622  CA   LYS  All92     -10.981   84.690   13.907  1.00  67.55           C
ATOM   8623  C    LYS  All92     -11.075   83.404   13.101  1.00  72.45           C
ATOM   8624  O    LYS  All92     -11.380   83.422   11.912  1.00  70.81           O
ATOM   8625  CB   LYS  All92      -9.510   85.074   14.136  1.00  66.11           C
ATOM   8626  N    ASP  Al193     -10.846   82.283   13.787  1.00  80.52           N
ATOM   8627  CA   ASP  All93     -10.753   80.963   13.170  1.00  77.62           C
ATOM   8628  C    ASP  A1193     -12.098   80.478   12.656  1.00  71.03           C
ATOM   8629  O    ASP  Al193     -12.208   79.374   12.148  1.00  73.86           0
ATOM   8630  CB   ASP  All93     -10.186   79.939   14.168  1.00  78.25           C
ATOM   8631  CG   ASP  A1193      -8.670   80.028   14.318  1.00  85.68           C
ATOM   8632  OD1  ASP  A1193      -7.966   80.234   13.302  1.00  86.76           0
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ATOM   8633  OD2  ASP  A1193    --8.180   79.874   15.460   1.00  86.57        O
ATOM   8634  N    LEU  All 94   --13.130  81.291   12.794   1.00  68.60        N
ATOM   8635  CA   LEU  All 94   -14.426   80.882   12.287   1.00  68.94        C
ATOM   8636  C    LEU  A1194    -14.908   81.778   11.158   1.00  68.48        C
ATOM   8637  O    LEU  A1194    -16.084   81.749   10.792   I.00  64.93        0
ATOM   8638  CB   LEU  All 94   -15.448   80.856   13.410   1.00  6.3.89        C
ATOM   8639  CG   LEU  A1194    -15.339   79.654   14.339   1.00  68.37        C
ATOM   8640  GDI  LEU  A1194    -16.640   79.473   15.107   I.00  68.36        C
ATOM   8641  CD2  LEU  All 94   -15.005   78.414   13.530   1.00  69.47        C
ATOM   8642  N    ILE  A1195    -13.996   82.565   10.597   1.00  65.73        N
ATOM   8643  CA   ILE  AU95     -14.366   83.478    9.525   I.00  66.28        C
ATOM   8644  C    ILE  A1195    -14.245   82.769    8.180   1.00  65.03        C
ATOM   8645  O    ILE  A1195    -13.180   82.727    7.558   1.00  72.25        O
ATOM   8646  CB   ILE  A1195    -13.510   84.756    9.564   1.00  68.80        C
ATOM   8647  CGI  ILE  A1195    -13.910   85.603   10.779   1.00  68.56        C
ATOM   8648  CG2  ILE  All 95   -13.700   85.574    8..315  1.00  65.50        C
ATOM   8649  CD1  ILE  A1195    -12.940   86.709   11.093   1.00  62.22        C
ATOM   8650  N    ILE  All 96   -15.353   82.176    7.763   I.00  58.00        N
ATOM   8651  CA   ILE  A1196    -15.451   81.460    6.498   1.00  57.99        C
ATOM   8652  C    ILE  A1196    -15.901   82.357    5.323   1.00  53.83        C
ATOM   8653  0    ILE  All 96   -16.949   83.012    5.392   I.00  48.15        0
ATOM   8654  CB   ILE  A1196    -16.431   80.301    6.646   1.00  55.59        C
ATOM   8655  CGI  ILE  A1196    -16.014   79.439    7.837   1.00  61.67        C
ATOM   8656  CG2  ILE  All 96   -16.515   79.508    5.361   I.00  58.04        C
ATOM   8657  CD1  ILE  A1196    -16.823   78.191    8.006   1.00  60.68        C
ATOM   8658  N    LYS  A1197    -15.075   82.397    4.278   1.00  52.08        N
ATOM   8659  CA   LYS  A1197    -15.396   83.032    3.000   I.00  49.03        C
ATOM   8660  C    LYS  All 97   -16.469   82.244    2.267   1.00  51.06        C
ATOM   8661  O    LYS  A1197    -16.277   81.083    1.932   1.00  55.14        0
ATOM   8662  CB   LYS  A1197    -14.164   83.126    2.109   1.00  47.87        C
ATOM   8663  CG   LYS  All 97   -13.902   84.500    1.506   1.00  59.45        C
ATOM   8664  CD   LYS  All 97   -13.197   84.400    0.143   1.00  57.78        C
ATOM   8665  CE   LYS  A1197    -11.988   85.334    0.027   1.00  65.21        C
ATOM   8666  NZ   LYS  A1197    -11.628   85.581   -1.403   I.00  64.07        N
ATOM   8667  O    LEU  All 98   -19.770   84.018    0.021   1.00  4.3.91        0
ATOM   8668  N    LEU  All 98   -17.594   82.887    2.004   1.00  45.96        N
ATOM   8669  CA.  LEU  A1198    -18.671   82.257    1.282   I.00  44.07        C
ATOM   8670  C    LEU  All 98   -18.973   83.075    0.020   1.00  44.85        C
ATOM   8671  CB   LEU  A1198    -19.898   82.135    2.174   1.00  47.11        C
ATOM   8672  CG   LEU  AU98     -19.764   81.205    3.381   I.00  47.41        C
ATOM   867 3 CD1  LEU  A1198    -20.859   81.491    4.402   1.00  40.15        C
ATOM   8674  CD2  LEU  A1198    -19.806   79.719    2.938   1.00  50.85        C
ATOM   8675  O    PRO  A1199    -20.605   82.214   -2.286   1.00  43.11        0
ATOM   8676  N    FRO  A1199    -18.304   82.742   -1.074   1.00  44.57        N
ATOM   8677  CA   PRO  A1199    -18.582   83.499   -2.299   1.00  4.1.52        C
ATOM   8678  C    PRO  A1199    -19.932   83.066   -2.868   1.00  43.59        C
ATOM   867 9 CB   PRO  All 99   -17.411   83.109   -3.220   I.00  44.99        C
ATOM   8680  CG   PRO  A1199    -17.021   81.725   -2.755   1.00  4.3.72        C
ATOM   8681  CD   PRO  A1199    -17.301   81.678   -1.271   1.00  42.24        C
ATOM   8682  O    LYS  A1200    -20.626   81.404   -5.573   I.00  47..30        0
ATOM   8683  N    LYS  A1200    -20.330   83.637   -3.990   1.00  45.25        N
ATOM   8684  CA   LYS  A1200    -21.630   83.301   -4.533   1.00  47.06        C
ATOM   8685  C    LYS  A1200    -21.631   81.861   -5.028   I.00  43.23        C
ATOM   8686  CB   LYS  A1200    -22.004   84.268   -5.660   1.00  41.70        C
ATOM   8687  CG   LYS  A1200    -23.453   84.179   -6.083   1.00  43.48        C
ATOM   8688  CD   LYS  A1200    -23.774   85.291   -7.066   I.00  44.83        C
ATOM   8689  CE   LYS  A1200    -25.134   85.113   -7.676   1.00  42.98        C
ATOM   8690  NZ   LYS  A1200    -25.266   86.062   -8.813   1.00  46.25        N
ATOM   8691  N    TYR  A1201    -22.760   81.180   -4.824   1.00  42.85        N
ATOM   8692  CA   TYR  A1201    -23.037   79.795   -5.250   1.00  45.27        C
ATOM   8693  C    TYR  A1201    -22.430   78.760   -4.279   1.00  49.75        C
ATOM   8694  O    TYR  A1201    -22.220   77.609   -4.645   1.00  50.94        0
ATOM   8695  CB   TYR  A 1.201  -22.553   79.525   -6.685   I.00  39.44        C
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ATOM	8696	**CG**	TYR	A1201	-22..990	80..552	-7 .715	1 .00	42 .10	c
ATOM	8697	GDI	TYR	A1201	--24 ,330	80..785	-7 ,977	1 ,00	44 .16	C
ATOM	8698	CD2	TYR	A1201	-22..051	81.,283	-8..433	1 ,00	42 ,.16	c
ATOM	8699	CE1	TYR	A1201	-24 ..723	81.,728	-8.,905	1 .00	44 .49	c
ATOM	8700	CE2	TYR	A.1201	-22.,426	82. 216	-9.,367	1 ,00	40..19	c
ATOM	8701	CZ	TYR	A1201	-23 ..776	82.,444	-9 .593	1 ,00	47 ,.89	c
ATOM	8702	OH	TYR	A1201	-24 .164	83.,376	-10..528	1 ,00	44 ,.13	0
ATOM	8703	N	SER	A1202	-22.,158	79 .178	-3.,041	1 ,00	54 .72	M
ATOM	8704	CA	SEP.	A1202	-21..686	78..263	-2..003	1 ,00	48..83	c
ATOM	8705	c	SER	A1202	—22 .795	77 ,302	-1 .664	1 ,00	51 ,22	c
ATOM	8706	0	SER	A1202	-23 ,925	77 .718	-.1 ,415	1 ,00	52 .28	0
ATOM	8707	CB	SER	A1202	-21..248	79.,011	-0.,749	1 ,00	51 .15	c
ATOM	8708	OG	SER	A1202	-20. 209	79.,925	-1 .026	1 ,00	54 ,36	0
ATOM	8709	N	LEU	A1203	-22..448	76.,021	-1 ,638	1 .00	46..67	N
ATOM	8710	CA	LEU	A1203	-23 ,413	74 .934	-1 ,522	1 ,00	51 .47	c
ATOM	8711	C	LEU	A1203	-23 ..776	74 ,582	-0..082	1 .00	54 ,.18	c
ATOM	8712	O	LEU	A1203	-22..919	74 ,577	0 ,787	1 .00	52 .14	0
ATOM	8713	CB	LEU	A1203	-22.,848	73 .691	-2.,217	1 ,00	55..69	c
ATOM	8714	CG	LEU	A1203	-23 ..826	72.,547	-2 .434	1 .00	49,.42	c
ATOM	8715	CD1	LEU	A1203	-25 ..105	73 ,153	-2 .971	1 ,00	51 ,80	c
ATOM	8716	CD2	LEU	A1203	-23 ,242	71 .536	-3.,392	1 ,00	49.,8.1	c
ATOM	8717	N	FHE	A1204	-25 ..041	74 ,254	0 ,160	1 ,00	55..58	M
ATOM	8718	CA	PHE	A1204	-25 ..485	73 ,828	1 .493	1 ,00	54 ,.64	c
ATOM	8719	C	PHE	A1204	-26..491	72 .705	1 ,387	1 ,00	58..25	c
ATOM	8720	O	PHE	A1204	-27 ..474	72.,827	0 ,652	1 ,00	59..52	0
ATOM	8721	CB	PHE	A1204	-26. 121	74 ,993	2 .278	1 ,00	54 ,54	c
ATOM	8722	CG	PHE	A1204	-25 ,171	76.. 101	2 ,577	1 ,00	56..84	c
ATOM	8723	CD1	FHE	A1204	-24 ,405	76 .077	3 ,728	1 ,00	58..76	c
ATOM	8724	CD2	PHE	A1204	-25. 011	77 ,146	1 .692	1 ,00	58 ,05	c
ATOM	8725	CE1	PHE	A1204	-23 ..506	77 ,082	4 ,003	1 .00	56..19	c
ATOM	8726	CE2	FHE	A1204	-24 ,115	78 .155	1 ,959	1 ,00	58..75	c
ATOM	8727	CZ	PHE	A1204	-23 ...360	78.,120	3 ..116	1 .00	58,.06	c
ATOM	8728	O	GLU	A1205	-27 ..450	71 ,131	4 .549	1 .00	60..81	0
ATOM	8729	N	GLU	A1205	-26 ,262	71 .614	2 ,116	1 ,00	57 ,36	M
ATOM	8730	CA	GLU	A1205	-27 .282	70.,579	2 .224	1 .00	57 ,.96	c
ATOM	8731	c	GLU	A1205	-28 ..038	70 ,759	3 ..535	1 ,00	61 ,.42	c
ATOM	8732	CB	GLU	A1205	-26 ,678	69. 176	2 ,138	1 ,00	57 ,89	c
ATOM	8733	CG	GLU	A120 5	-27 ,728	68..066	2 ,117	1 ,00	59..33	c
ATOM	8734	CD	GLU	A1205	-27 .150	66.,705	1 .735	1 ,00	68 ,29	c
ATOM	8735	OE1	GLU	A1205	-27.,827	65.. 683	1 ,983	1 ,00	66..29	0
ATOM	8736	OE2	GLU	A1205	-26 ,028	66.. 661	1 ,181	1 ,00	68..85	0
ATOM	8737	O	LEU	A120 6	-30. 255	68.,255	4 .737	1 ,00	65 ,70	0
ATOM	8738	N	LEU	A1206	-29 ,342	70.,510	3 ,501	1 .00	61 .52	N
ATOM	8739	CA	LEU	A1206	-30.,183	70 .638	4 ,674	1 ,00	60..45	c
ATOM	8740	C	LEU	A1206	-30..872	69.,299	4 .920	1 .00	65,.10	c
ATOM	8741	CB	LEU	A1206	-31..179	71 ,786	4 ,489	1 .00	64 .15	c
ATOM	8742	CG	LEU	A120 6	-30.,459	73 .145	4 ,423	1 ,00	62 .96	c
ATOM	8743	CD1	LEU	A1206	-30..010	7.3.,534	3 ..016	1 .00	56,.49	c
ATOM	8744	CD2	LEU	A1206	-31.. 274	74 ,261	5 ..053	1 ,00	65,.60	c
ATOM	8745	O	GLU	A1207	-33.,575	68. 023	3 ,381	1 ,00	74 .40	0
ATOM	8746	N	GLU	A1207	-32.,137	69.,309	5 ..323	1 ,00	65..10	M
ATOM	8747	CA	GLU	A1207	-32.. 815	68.,050	5 ..635	1 ,00	70,.73	c
ATOM	8748	C	GLU	A1207	-33.,306	67.. .368	4 ,377	1 ,00	72 ,35	c
ATOM	8749	CB	GLU	A1207	-33.,993	68..281	6 ,583	1 ,00	70..81	c
ATOM	8750	CG	GLU	A1207	-35. 274	68.,711	5 .884	1 ,00	74 ,26	c
ATOM	8751	CD	GLU	A1207	-35..214	70.. 122	5 ,314	1 ,00	72 .70	c
ATOM	8752	OE1	GLU	A1207	-34.,192	70 .815	5 ,494	1 ,00	75..32	0
ATOM	8753	OE2	GLU	A1207	-36. 204	70.,547	4 .684	1 ,00	72 ,.96	0
ATOM	8754	O	ASN	A1208	-33.,766	65.,171	0 ,925	1 .00	77 .05	0
ATOM	8755	M	ASM	A1208	-33.,416	66.. 046	4 ,430	1 ,00	77 .22	M
ATOM	8756	CA	ASN	A1208	-33.. 920	65.,245	3 ...313	1 .00	75,.81	c
ATOM	8757	c	ASN	A1208	-33.,223	65.,501	1 .984	1 .00	73..18	c
ATOM	8758	CB	ASM	A1208	-35.,420	65. 465	3 ,143	1 ,00	80..29	c

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ATOM   8759  CG   ASN  A1208    -36..226   64.,728    4.185   1.00  84.47        C
ATOM   8760  OD1  ASM  A1208    --35.,812  63..666    4,666   1,00  77.88        0
ATOM   8761  ND2  ASN  A1208    -37..379   65.,285    4.548   1.00  80,.51       N
ATOM   8762  O    GLY  A1209    -30..680   67.,680   -0..946   1.00  66..92       0
ATOM   8763  N    GLY  A1209    -32,,034   66. 094    2,046   1,00  71.19        N
ATOM   8764  CA   GLY  A1209    -31..177   66.,231    0..879   1.00  70,.54       C
ATOM   8765  C    GLY  A1209    -31..342   67.,507    0..078   1,00  68,.39       C
ATOM   8766  0    ARG  A1210    -30.,618   70.637     0,980   1,00  63..41       0
ATOM   8767  N    ARG  A1210    -32..221   68.,402    0..521   1,00  64.21        N
ATOM   8768  CA   ARG  A1210    -32..422   69.,627   -0..231   1,00  65,.89       C
ATOM   8769  C    ARG  A1210    -31.,217   70..529   -0.,087   1,00  65..49       C
ATOM   8770  CB   ARG  A1210    -33..697   70..359    0..193   1,00  64.60        C
ATOM   8771  CG   ARG  A1210    -33. 867   70.,545    1.659    1,00  67,.43       C
ATOM   8772  CD   ARG  A1210    -35..049   71.436     1,930   1.00  71.40        C
ATOM   8773  NE   ARG  A1210    -34.,732   72.834     1,675   1,00  74.09        N
ATOM   8774  CZ   ARG  A1210    -34..547   73.,739    2.630   1.00  74,.72       C
ATOM   8775  NH1  ARG  A1210    -34.257    74.988     2.311   1.00  68..38       N
ATOM   8776  NH2  ARG  A1210    -34..658   73.392     3,906   1,00  78..01       N
ATOM   8777  N    LYS  A1211    -30..861   71,166    -1.192   1.00  66,.13       N
ATOM   8778  CA   LYS  A1211    -29..681   71,997    -1.236   1,00  60,.74       C
ATOM   8779  C    LYS  A1211    -30.,047   73.422    -1,581   1,00  60..03       C
ATOM   8780  O    LYS  A1211    -31..015   73.,678   -2..293   1,00  64.56        0
ATOM   8781  CB   LYS  A1211    -28..678   71,435    -2.239   1,00  59,.71       C
ATOM   8782  CG   LYS  A1211    -28.,237   70..027   -1,894   1,00  57,.21       C
ATOM   8783  CD   LYS  A1211    -27..291   69..448   -2..936   1,00  54.32        C
ATOM   8784  CE   LYS  A1211    -26. 786   68.,081   -2.490   1,00  61,.11       C
ATOM   8785  NZ   LYS  A1211    -26.,036   67...353  -3.,567   1,00  70..37       N
ATOM   8786  N    ARG  A1212    -29,278    74.352    -1,041   1,00  59..27       N
ATOM   8787  CA   ARG  A1212    -29. 415   75,747    -1.395   1,00  55,.40       C
ATOM   8788  C    ARG  A1212    -28,032    76..253   -1,788   1.00  52.58        C
ATOM   8789  O    ARG  A1212    -27,042    75.798    -1,236   1,00  53..12       0
ATOM   8790  CB   ARG  A1212    -29..989   76.,560   -0..230   1.00  54,.46       C
ATOM   8791  CG   ARG  A1212    -31..350   76..097    0.959    1.00  56..15       C
ATOM   8792  CD   ARG  A1212    -32.,480   76.647    -0.,580   1,00  55..65       C
ATOM   8793  NE   ARG  A1212    -33..412   75.,580   -0..936   1.00  66,.95       N
ATOM   8794  CZ   ARG  A1212    -34..718   75,619    -0.. 714  1,00  69,.23       C
ATOM   8795  NH1  ARG  A1212    -35.,261   76.679    -0.,144   1,00  79..12       N
ATOM   8796  NH2  ARG  A1212    -35.,483   74,600    -1.059   1,00  69..77       N
ATOM   8797  N    MET  A1213    -27.968    77,179    -2.746   1,00  58,.91       N
ATOM   8798  CA   MET  A1213    -26.,732   77.898    -3.,047   1,00  53..86       C
ATOM   8799  C    MET  A1213    -26,871    79.354    -2.,625   1,00  54.95        C
ATOM   8800  O    MET  A1213    -27.957    79.,907   -2.691    1,00  56,14        0
ATOM   8801  CB   MET  A1213    -26,397    77.825    -4,531    1.00  52.40        C
ATOM   8802  CG   MET  A1213    -26,078    76.429    -5.,037   1,00  56..83       C
ATOM   8803  SD   MET  A1213    -25..477   76.,464   -6..739   1.00  52,.60       S
ATOM   8804  CE   MET  A1213    -26..856   77,318    -7.495    1,00  45..46       C
ATOM   8805  N    LEU  A1214    -25,782    79.980    -2.,187   1,00  58..75       N
ATOM   8806  CA   LEU  A1214    -25..826   81.,401   -1.841    1.00  49,.14       C
ATOM   8807  C    LEU  A1214    -25..953   82.,246   -3..082   1,00  53,.62       C
ATOM   8808  0    LEU  A1214    -25,199    82. 061   -4,029    1,00  53..49       0
ATOM   8809  CB   LEU  A1214    -24..566   81.,850   -1.092    1,00  53..45       C
ATOM   8810  CG   LEU  A1214    -24.432    81.,886    0..438   1,00  60,.96       C
ATOM   8811  CD1  LEU  A1214    -25,651    82..483    1,086    1,00  60..65       C
ATOM   8812  CD2  LEU  A1214    -23..183   82..688    0..847   1,00  51.90        C
ATOM   8813  N    ALA  A1215    -26. 885   83.,190   -3.075    1,00  55,19        N
ATOM   8814  CA   ALA  A1215    -26.,905   84.,223   -4,101    1,00  49.05        C
ATOM   8815  C    ALA  A1215    -26,278    85..499   -3.,565   1,00  52..51       C
ATOM   8816  O    ALA  A1215    -25. 749   86.,310   -4..318   1,00  53,51        0
ATOM   8817  CB   ALA  A1215    -28,306    84..477   -4.565    1.00  52.06        C
ATOM   8818  O    SEP. A1216    -26,778    85..600    0,284    1,00  65..05       0
ATOM   8819  N    SEP. A1216    -26..332   85.,650   -2.248    1.00  50,.51       N
ATOM   8820  CA   SER  A1216    -25..829   86..824   -1,538    1.00  48..17       C
ATOM   8821  C    SER  A1216    -26,109    86. 581   -0.,070   1,00  60..07       C
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ATOM	8822	CB	SER	A1216	-26.510	88.110	-1.983	1.00	52.60	C
ATOM	8823	OG	SEP.	A1216	--27,865	88.074	-1,596	1,00	55.53	O
ATOM	8824	O	ALA	A1217	-27.453	86,999	3.892	1,00	62,23	0
ATOM	8825	N	ALA	A1217	-25.640	87,482	0.784	1.00	58.82	N
ATOM	8826	CA.	ALA	A1217	-25,778	87.301	2,224	1,00	57.53	C
ATOM	8827	C	ALA	A1217	-27.224	87,233	2.707	1,00	55,90	C
ATOM	8828	CE	ALA	A1217	-25.049	88,409	2.954	1,00	56,88	C
ATOM	8829	O	GLY	A1218	-31,743	86.567	1,588	1,00	67.65	0
ATOM	8830	N	GLY	A1218	-28.185	87,421	1,799	1,00	56.62	N
ATOM	8831	CA	GLY	A1218	-29.596	87,447	2.154	1,00	53,78	C
ATOM	8832	C	GLY	A1218	-30,567	86.673	1,264	1,00	60.76	C
ATOM	8833	N	GLU	A1219	-30.099	86.130	0,148	1,00	59.35	N
ATOM	8834	CA	GUI	A1219	-30.948	85,279	-0.684	1,00	57,29	C
ATOM	8835	C	GLU	A1219	-30.249	83,951	-1,086	1.00	60.47	C
ATOM	8836	O	GLU	A1219	-29,012	83.874	-1,129	1,00	55.05	0
ATOM	8837	CB	GLU	A1219	-31.383	86,052	-1.921	1,00	56,40	C
ATOM	8838	CG	GLU	A1219	-32,348	85,285	-2.776	1.00	62.73	C
ATOM	8839	CD	GLU	A1219	-32,745	86.027	-4,028	1,00	73.38	C
ATOM	8840	OE1	GLU	A1219	-33.205	85,351	-4.983	1,00	74,64	0
ATOM	8841	OE2	GLU	A1219	-32.609	87,277	-4.051	1,00	74,10	0
ATOM	8842	N	LEU	A1220	-31,043	82.909	-1,347	1,00	56.97	N
ATOM	8843	CA	LEU	A1220	-30.511	81,615	-1,769	1,00	51.75	C
ATOM	8844	C	LEU	A1220	-31.134	81,185	-3.087	1,00	57,84	C
ATOM	8845	0	LEU	A1220	-32,011	81.865	-3,628	1,00	57,70	0
ATOM	8846	CB	LEU	A1220	-30.767	80.529	-0,716	1,00	50.37	C
ATOM	8847	CG	LEU	A1220	-30.240	80,677	0.716	1,00	54,98	C
ATOM	8848	CD1	LEU	A1220	-30,980	79.740	1,653	1,00	47,21	C
ATOM	8849	CD2	LEU	A1220	-28,735	80.441	0,792	1,00	51.82	C
ATOM	8850	N	GLN	A1221	-30.668	80,049	-3.591	1,00	50,36	N
ATOM	8851	CA	GLN	A1221	-31,170	79,460	-4,815	1.00	51.72	C
ATOM	8852	C	GLN	A1221	-31,349	77.958	-4,650	1,00	58.85	C
ATOM	8853	O	GLN	A1221	-30.776	77,355	-3.730	1.00	56,59	0
ATOM	8854	CB	GLN	A1221	-30.213	79,717	-5.970	1,00	56.49	C
ATOM	8855	CG	GLN	A1221	-29,649	81.112	-6,062	1,00	52.46	C
ATOM	8856	CD	GLN	A1221	-28.849	81,303	-7.339	1.00	52,70	C
ATOM	8857	OE1	GLN	A1221	-28.336	80,346	-7.918	1,00	47,67	0
ATOM	8858	NE2	GLN	A1221	-28,756	82.534	-7,791	1,00	49.28	N
ATOM	8859	N	LYS	A1222	-32.110	77,348	-5.559	1,00	59.24	N
ATOM	8860	CA	LYS	A1222	-32.301	75,899	-5.548	1,00	58,35	C
ATOM	8861	C	LYS	A1222	-30,984	75.191	-5,814	1,00	56.96	C
ATOM	8862	O	LYS	A1222	-30,207	75.628	-8,655	1,00	57.41	O
ATOM	8863	CB	LYS	A1222	-33.353	75,483	-6.576	1,00	61,61	C
ATOM	8864	CG	LYS	A1222	-34,771	75,923	-6,191	1.00	64.90	C
ATOM	8865	CD	LYS	A1222	-35,257	77.090	-7,017	1,00	66.58	C
ATOM	8866	CE	LYS	A1222	-35.978	76,624	-8.271	1.00	68,35	C
ATOM	8867	NZ	LYS	A1222	-35.871	77,612	-9.372	1.00	66.74	N
ATOM	8868	O	GLY	A1223	-28,609	71.210	-5,666	1,00	58.52	O
ATOM	8869	N	GLY	A1223	-30.727	74,109	-5.088	1,00	56,30	N
ATOM	8870	CA	GLY	A1223	-29.469	73,398	-5.226	1,00	57,95	C
ATOM	8871	C	GLY	A1223	-29,590	71.955	-5,683	1,00	61.98	C
ATOM	8872	O	ASN	A1224	-32,045	71,110	-8,518	1,00	66.50	0
ATOM	8873	N	ASN	A1224	-30.795	71,560	-6.087	1,00	60,80	N
ATOM	8874	CA	ASN	A1224	-31,052	70.195	-6,529	1,00	59.77	C
ATOM	8875	C	ASN	A1224	-31,509	70.139	-7,977	1,00	63.46	C
ATOM	8876	CB	ASN	A1224	-32.115	69,517	-5.656	1,00	63,41	C
ATOM	8877	CG	ASN	A1224	-31,913	69.767	-4,178	1,00	61.91	C
ATOM	8878	OD1	ASN	A1224	-32,034	70.900	-3.,713	1,00	65.79	O
ATOM	8879	ND2	ASN	A1224	-31.641	68,713	-3.424	1,00	57,54	N
ATOM	8880	O	GLU	A1225	-32,717	66,686	-9,071	1.00	67.57	O
ATOM	8881	N	GLU	A1225	-31,296	68.978	-8.578	1,00	64.88	N
ATOM	8882	CA	GLU	A1225	-31.734	68,661	-9.927	1.00	65.08	C
ATOM	8883	C	GLU	A1225	-32.827	67,636	-9.841	1.00	67.57	C
ATOM	8884	CB	GLU	A1225	-30,594	68.077	-10,762	1,00	68.09	C

ATOM	8885	CG	GLU	A1225	-29..340	68..920	-10..825	1.00	65..19	C
ATOM	8886	CD	GLU	A1225	--29,451	70.047	-11,827	1,00	65..44	C
ATOM	8887	OE.1	GLU	A1225	-28..447	70.,754	-12.031	1,00	67,96	0
ATOM	8888	OE2	GLU	A1225	-30..536	70.,224	~12.425	1.00	71.55	0
ATOM	8889	O	LEU	A1226	-34.,468	66. 124	-13.,061	1,00	69..14	0
ATOM	8890	N	LEU	A122 6	-33..870	67.,803	-10..640	1,00	67,59	N
ATOM	8891	CA	LEU	A1226	-34..862	66.,751	-10..772	1,00	70..94	C
ATOM	8892	C	LEU	A1226	-34.,463	65. 779	-11,883	1,00	73..06	C
ATOM	8893	CB	LEU	A122 6	-36,234	67.,347	-11,032	1,00	73..97	C
ATOM	8894	CG	LEU	A1226	-37 .340	66.,398	-11 .484	1,00	75,.91	C
ATOM	8895	CD1	LEU	A1226	-.37.,467	65.. 194	-10.,577	1,00	75..35	C
ATOM	8896	CD2	LEU	A122 6	-38.,643	67..180	-11,523	1,00	80..60	C
ATOM	8897	O	ALA	A1227	-34. 901	61.,509	-12 .653	1,00	8.1,13	0
ATOM	8898	N	ALA	A1227	-34,121	64.,560	-11,483	1.00	72.49	N
ATOM	8899	CA	ALA	A1227	-33.,627	63.. 541	-12.,398	1,00	73..82	C
ATOM	8900	C	ALA	A1227	-34..742	62.,682	-13..0.18	1,00	82,36	C
ATOM	8901	CB	ALA	A1227	-32.,633	62.,650	-11 .670	1.00	70..35	C
ATOM	8902	O	LEU	A1228	-35,023	61. 498	-16,197	1,00	87.4.1	0
ATOM	8903	N	LEU	A1228	-35..495	63.,259	-13.. 962	1,00	84,98	N
ATOM	8904	CA	LEU	A1228	-36..548	62.,536	-14 .687	1,00	82,59	C
ATOM	8905	C	LEU	A1228	-36,005	61. 354	-15 ,459	1,00	86..76	C
ATOM	8906	CB	LEU	A122 8	-37.,275	63..452	-15.,666	1,00	80..43	C
ATOM	8907	CG	LEU	A1228	-38..603	64.,034	-15.. 195	1,00	87,82	C
ATOM	8908	CD1	LEU	A1228	-.39,441	64.. 492	-16.,382	1,00	87.83	C
ATOM	8909	CD2	LEU	A122 8	-39..362	63.,031	-14 ,341	1,00	87.81	C
ATOM	89.10	N	PRO	A122 9	-36. 651	60.,182	-15. 309	1,00	92,56	N
ATOM	8911	CA	PRO	A1229	-.36,219	58.. 972	-16.,027	1,00	87.4.1	C
ATOM	8912	C	FRO	A1229	-36,384	59.. 150	-17 ,530	1,00	82 .41	C
ATOM	89.13	O	PRO	A122 9	-37. 190	59.,978	-17 .946	1,00	84,84	0
ATOM	8914	CB	PRO	A1229	-37..152	57.,882	-15.,482	1.00	87.90	C
ATOM	8915	CG	FRO	A1229	-37.,709	58.. 456	-14 ,187	1,00	84.94	C
ATOM	8916	CD	PRO	A122 9	-37..8.13	59.,922	-14 .439	1,00	84,81	C
ATOM	8917	N	SER	A1230	-35,633	58.,391	-18..321	1.00	87.01	N
ATOM	8918	CA.	SER	A.1230	-35.,599	58. 555	-19,776	1,00	85..50	C
ATOM	8919	C	SER	A12.30	-36..974	58.,491	-20.439	1,00	88,.25	C
ATOM	8920	O	SER	A1230	-37 .222	59.,186	-21 .426	1,00	90,.32	0
ATOM	8921	CB	SER	A.1230	-34.,696	57. 495	-20.,402	1,00	85..83	C
ATOM	8922	OG	SER	A1230	-33.,384	57.,544	-19.,865	1,00	87.97	0
ATOM	8923	N	LYS	A1231	-37. 862	57,661	-19. 895	1,00	89,02	N
ATOM	8924	CA	LYS	A1231	-.39,189	57..444	-20.,479	1,00	83..46	C
ATOM	8925	C	LYS	A1231	-39,981	58..733	-20,578	1,00	83..98	C
ATOM	8926	O	LYS	A1231	-40. 526	59.,057	-21 .637	1,00	87,53	0
ATOM	8927	CB	LYS	A1231	-39,978	56.,417	-19.,661	1.00	84.81	C
ATOM	8928	N	TYR	A1232	-40,044	59.. 468	-19.,473	1,00	81 .51	N
ATOM	8929	CA	TYR	A12.32	-40..776	60.,729	-19.. 433	1,00	87,60	C
ATOM	8930	C	TYR	A1232	-40..114	61.,805	-20,283	1.00	86..22	C
ATOM	8931	O	TYR	A1232	-40.,766	62. 753	-20.,726	1,00	87.59	0
ATOM	8932	CB	TYR	A12.32	-40..908	61.,208	-17 .992	1,00	93,.70	C
ATOM	8933	CG	TYR	A1232	-41..774	60.,314	-17 .127	1,00	95,.11	C
ATOM	8934	CD1	TYR	A1232	-42.,611	59. 366	-17 ,692	1,00	91 .61	C
ATOM	8935	CD2	TYR	A1232	-41.759	60..433	-15.,750	1,00	93..00	C
ATOM	8936	CE1	TYR	A1232	-43..401	58.,555	-16.. 913	1,00	93,.09	C
ATOM	8937	CE2	TYR	A1232	-42.,549	59.635	-14,954	1,00	93..99	C
ATOM	8938	CZ	TYR	A1232	-43,369	58.,696	-15.,540	1,00	95..44	C
ATOM	8939	OH	TYR	A1232	-44 .147	57,891	-14 .755	1,00	96,83	0
ATOM	8940	N	VAL	A1233	-.38.,813	61..636	-20.,506	1,00	89..01	N
ATOM	8941	CA	VAL	A1233	-38.,015	62..546	-21.,322	1,00	86..58	C
ATOM	8942	C	VAL	A1233	-38. 360	62.,393	-22.803	1,00	8.1,43	C
ATOM	8943	O	VAL	A1233	-38.,665	63.,375	-23,473	1.00	81.90	0
ATOM	8944	CB	VAL	A1233	-36,504	62.. 301	-21.,107	1,00	84.56	C
ATOM	8945	CGI	VAL	A1233	-35..673	63.,191	-22.002	1,00	81.05	C
ATOM	8946	CG2	VAL	A1233	-36..145	62..537	-19.,660	1.00	86..19	C
ATOM	8947	N	ASM	A1234	-38.,313	61. 161	-23,303	1,00	82.66	N

ATOM	8948	CA	ASN	A1234	-38..682	60..870	-24..690	1.00	83..45	C
ATOM	8949	C	ASM	A1234	--40,,089	61..317	-25,008	1,00	81.14	C
ATOM	8950	O	ASN	A1234	-40..342	61.,918	-26.048	1,00	80,.19	O
ATOM	8951	CB	ASN	A1234	-38..565	59..380	-24,981	1.00	79..83	C
ATOM	8952	CG	ASN	A1234	-37.,148	58. 886	-24.,908	1,00	80..49	C
ATOM	8953	OD1	ASN	A1234	-36..209	59,606	-25.242	1,00	81,74	0
ATOM	8954	ND2	ASN	A1234	-36..981	57.,647	-24.468	1,00	82,27	N
ATOM	8955	N	PHE	A1235	-41,000	61. 007	-24.,094	1,00	81.57	N
ATOM	8956	CA	PHE	A123 5	-42..404	61..352	-24,254	1,00	81.53	C
ATOM	8957	C	PHE	A1235	-42..597	62.,843	-24.363	1,00	86,.11	C
ATOM	8958	0	PHE	A1235	-43,331	63...324	-25,227	I,00	89..62	0
ATOM	8959	CB	PHE	A123 5	-43..234	60..833	-23,084	1,00	85..80	C
ATOM	8960	CG	PHE	A1235	-44 .666	61.,254	-23 .138	1,00	85,02	C
ATOM	8961	CD2	PHE	A1235	-45..595	60..495	-23,820	1.00	88..43	C
ATOM	8962	CD1	PHE	A1235	-45,085	62. 417	-22.,521	1,00	91,00	C
ATOM	8963	CE2	PHE	A1235	-46..913	60.,882	-23.878	1,00	91,77	C
ATOM	8964	CE1	PHE	A1235	-46..400	62.,813	-22.,580	1.00	90..92	C
ATOM	8965	CZ	PHE	A1235	-47,318	62. 046	-23,257	1,00	96..21	C
ATOM	8966	N	LEU	A123 6	-41 .970	63.,571	-23.449	1,00	87,92	N
ATOM	8967	CA	LEU	A1236	-42..039	65.,021	-23.462	1,00	85,.81	C
ATOM	8968	C	LEU	A123 6	-41,517	65. 583	-24.,782	1,00	84.91	C
ATOM	8969	O	LEU	A123 6	-42..074	66.,536	-25,329	1,00	84.00	0
ATOM	8970	CB	LEU	A1236	-41.251	65.,597	-22.289	1,00	84,96	C
ATOM	8971	CG	LEU	A1236	-42.,097	65..973	-21.,077	I,00	89..04	C
ATOM	8972	CD1	LEU	A123 6	-41.279	66..781	-20,085	1,00	89..73	C
ATOM	8973	CD2	LEU	A1236	-43. .329	66.,754	-21 .510	1,00	86,67	C
ATOM	8974	N	TYR	A1237	-40.,452	64..984	-25,299	I,00	80..64	N
ATOM	8975	CA	TYR	A1237	-39,864	65..476	-26,531	1,00	83..47	C
ATOM	8976	C	TYR	A1237	-40. 807	65.,306	-27.707	1,00	83,12	C
ATOM	8977	O	TYR	A1237	-41.096	66.,260	-28,423	1.00	81.46	0
ATOM	8978	CB	TYR	A1237	-38.,550	64..764	-26,842	1,00	80..97	C
ATOM	8979	CG	TYR	A1237	-38..037	65.,145	-28.205	1,00	84,24	C
ATOM	8980	CD2	TYR	A1237	-38..157	64.,283	-29,285	1.00	83..61	C
ATOM	8981	CD1	TYR	A1237	-37.,470	66. .391	-28,422	1,00	82.14	C
ATOM	8982	CE2	TYR	A1237	-37..705	64.,645	-30.536	1,00	85,.46	C
ATOM	8983	CE1	TYR	A1237	-37 .018	66.,759	-29.665	1,00	85,.24	C
ATOM	8984	CZ	TYR	A1237	-37.,137	65. 883	-.30.,718	1,00	86..78	C
ATOM	8985	OH	TYR	A1237	-36..683	66..252	-31.,959	1,00	88..10	0
ATOM	8986	N	LEU	A1238	-41 .252	64.,070	-27.911	1,00	83,43	N
ATOM	8987	CA	LEU	A1238	-42.,109	63. 734	-29.,034	I,00	81.45	C
ATOM	8988	C	LEU	A1238	-43,409	64..512	-28,965	1,00	82,53	C
ATOM	8989	O	LEU	A1238	-43. 718	65.,266	-29. 879	1,00	85,38	0
ATOM	8990	CB	LEU	A1238	-42..380	62.,235	-29,071	1.00	73..46	C
ATOM	8991	CG	LEU	A1238	-41 ,094	61. 429	-29,267	1,00	79..91	C
ATOM	8992	CD1	LEU	A1238	-41 .278	60.,002	-28.840	1,00	77,45	C
ATOM	8993	CD2	LEU	A1238	-40..623	61.,490	-30.,708	1.00	79..14	C
ATOM	8994	N	ALA	A1239	-44 ,145	64. 352	-27,870	1,00	80..56	N
ATOM	8995	CA	ALA	A123 9	-45..443	65.,005	-27.696	1,00	86,.33	C
ATOM	8996	C	ALA	A1239	-45..412	66.,499	-28.035	1,00	90,.18	C
ATOM	8997	0	ALA	A1239	-46,386	67. 059	-28,546	1,00	93..22	0
ATOM	8998	CB	ALA	A123 9	-45..933	64.,803	-26,275	1,00	88..08	C
ATOM	8999	N	SER	A1240	-44.272	67.,124	-27.761	1,00	90,.39	N
ATOM	9000	CA	SER	A1240	-44 ,077	68. 547	-27.,990	I,00	91.17	C
ATOM	9001	C	SER	A124 0	-43..769	68.,828	-29,456	1,00	88..60	C
ATOM	9002	O	SER	A124 0	-43. 860	69.,966	-29. 914	1,00	86,83	0
ATOM	9003	CB	SER	A1240	-42.,945	69. 066	-27.,096	I,00	92 .44	C
ATOM	9004	OG	SER	A124 0	-43,236	70.359	-26,591	1,00	97.53	0
ATOM	9005	O	HIS	A1241	-43. 729	66.,204	-33. 202	1,00	94,29	0
ATOM	9006	N	HIS	A1241	-43..392	67.,777	-30.,179	1.00	90..64	N
ATOM	9007	CA	HIS	A1241	-43,036	67..878	-31.,592	1,00	94.46	C
ATOM	9008	C	HIS	A1241	-44 .066	67.,147	-32. 477	1,00	95,.22	C
ATOM	9009	CB	HIS	A1241	-41.620	67.,320	-31.,814	1.00	89..36	C
ATOM	9010	CG	HIS	A1241	-40.,525	68. 257	-.31.,398	1,00	89..66	C

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ATOM   9011  ND1  HIS  A1241    -40..673   69.,173  -30..377   1.00  91..79     M
ATOM   9012  CD2  HIS  A1241    --39,266   68..424  -31.,869   1,00  87..12     C
ATOM   9013  CE1  HIS  A1241    -39..555   69.,861  -30..237   1,00  85,.78     C
ATOM   9014  NE2  HIS  A1241    -38..686   69.,428  -31.,131   1.00  88..94     M
ATOM   9015  O    TYR  A1242    -46,350    65.939   -35.,275   1,00  92.,24     O
ATOM   9016  N    TYR  A1242    -45..318   67.,600  -32..411   1,00  96,.87     N
ATOM   9017  CA   TYR  A1242    -46..433   66.,948  -33.102    1,00  98,.73     C
ATOM   9018  C    TYR  A1242    -46,286    66.979   -34.,621   1,00  93.,95     C
ATOM   9019  CB   TYR  A1242    -47,759    67.,600  -32.,698   1,00  93..49     C
ATOM   9020  O    PRO  A1249    -41.743    58.,556  -40.958    1,00109,.13     0
ATOM   9021  N    PRO  A1249    -39,285    59.028   -42.,241   I,00108..61     M
ATOM   9022  CA   PRO  A124 9   -40,407    58.,354  -42.,907   1,00108..52     C
ATOM   9023  C    PRO  A124 9   -41.720    58.,620  -42 .189    1,00107 ,41     C
ATOM   9024  CB   PRO  A1249    -40,042    56.,863  -42..813   1.00106..80     C
ATOM   9025  CG   FRO  A124 9   -38.,584   56..831  -42.,461   1,00108..51     C
ATOM   9026  CD   PRO  A124 9   -38...336  58.,068  -41 .656    1,00110,.30     C
ATOM   9027  O    GLU  A1250    -45,405    57.,605  -40,881    1.00102..81     0
ATOM   9028  N    GLU  A1250    -42.,790   58.900   -42.,932   1,00106.,22     M
ATOM   9029  CA   GLU  A1250    -44 .115   59.,025  -42 ...327  1,00102,.38     C
ATOM   9030  C    GLU  A1250    -44.519    57.,680  -41.732    1,00102,.59     C
ATOM   9031  CB   GLU  A1250    -45,147    59.499   -4.3.,348   1,00  96.,89     C
ATOM   9032  N    ASP  A1251    -43,850    56.,623  -42.,196   1,00107..94     N
ATOM   9033  CA   ASP  A1251    -43.960    55.,285  -41.615    1,00108,.92     C
ATOM   9034  C    ASP  A1251    -43,510    55..294  -40.,162   I,00109..09     C
ATOM   9035  O    ASP  A1251    -44,279    54.,964  -39,259    1,00110..72     0
ATOM   9036  CB   ASP  A1251    -43.124    54,280   -42 .408    1,00104 ,74     C
ATOM   9037  N    ASM  A1252    -42.,260   55..680  -.39,938    I,00106..68     M
ATOM   9038  CA   ASM  A1252    -41,764    55..807  -38.,580   1,00104..61     C
ATOM   9039  C    A.SM A1252    -42 .407   56.,969  -37.827    1,00105,.23     C
ATOM   9040  O    ASM  A1252    -42,672    56.,856  -36,630    1.00107..68     0
ATOM   9041  CB   ASM  A1252    -40,253    55..970  -38.,579   1,00105..30     C
ATOM   9042  CG   ASN  A1252    -39.594    55.,138  -37..513   1,00101,.54     C
ATOM   9043  OD1  ASM  A1252    -38.,631   54.,427  -37.,781   1.00104..17     0
ATOM   9044  ND2  ASM  A1252    -40.,128   55.199   -36,294    1,00100.,14     M
ATOM   9045  N    GLU  A1253    -42 .668   58.,074  -38..525   1,00101,.90     N
ATOM   9046  CA   GLU  A1253    -43.267    59.,255  -37 .903    1,00  98,.88     C
ATOM   9047  C    GLU  A1253    -44 ,693   58.986   -37.,433   1,00102.,60     C
ATOM   9048  O    GLU  A1253    -45,257    59.,753  -36,651    1,00101..18     O
ATOM   9049  CB   GLU  A1253    -43.253    60.,437  -38.868    1,00  99,.37     C
ATOM   9050  N    GLM  A1254    -45,277    57..898  -.37.,921   I,00105..62     M
ATOM   9051  CA   GLN  A1254    -46,570    57..447  -37.,426   1,00104..34     C
ATOM   9052  C    GLM  A1254    -46.368    56.,485  -36.264    1,00104 ,36     C
ATOM   9053  O    GLM  A1254    -47,078    56.,559  -35,261    1.00103..15     0
ATOM   9054  CB   GLN  A1254    -47,380    56..779  -38.,538   1,00102..59     C
ATOM   9055  N    LYS  A1255    -45..380   55.,598  -36.401    1,00103,.63     N
ATOM   9056  CA   LYS  A1255    -45,051    54.,606  -35,379    1.00  99..78     C
ATOM   9057  C    LYS  A1255    -44 ,657   55.275   -34.,070   1,00106.,60     C
ATOM   9058  O    LYS  A1255    -44 .574   54.,621  -33..030   1,00107,.34     O
ATOM   9059  CB   LYS  A1255    -43.915    53.,696  -35..854   1,00101,.68     C
ATOM   9060  N    GLN  A125 6   -44 ,415   56.582   -34.,132   1,00106.,53     M
ATOM   9061  CA   GLN  A125 6   -44,000    57.,350  -32.,966   1,00104..92     C
ATOM   9062  C    GLN  A1256    -45.126    58.,236  -32..451   1,00105,.25     C
ATOM   9063  0    GLN  A1256    -45,284    58...397  -31.,244   I,00105..06     0
ATOM   9064  CB   GLN  A125 6   -42.,766   58..189  -33.,294   1,00100..65     C
ATOM   9065  CG   GLN  A1256    -41.474    57,384   -33.318    1,00  98,.22     C
ATOM   9066  CD   GLN  A1256    -40.,336   58..153  -.3.3.,944  I,00  97..14     C
ATOM   9067  OE1  GLN  A1256    -40,516    59..294  -34.,378   1,00  92..91     0
ATOM   9068  NE2  GLN  A1256    -39.156    57,534   -34.001    1,00  92,.48     N
ATOM   9069  N    LEU  A1257    -45..929   58.,792  -33.,353   1.00104..69     M
ATOM   9070  CA   LEU  A1257    -47,142    59..482  -32.,923   1,00104..06     C
ATOM   9071  C    LEU  A1257    -48..054   58.,449  -32..245   1,00106,.58     C
ATOM   9072  O    LEU  A1257    -49,009    58.,802  -31.,556   1.00104..72     0
ATOM   9073  CB   LEU  A1257    -47,846    60.164   -34.,102   1,00  99.,80     C
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ATOM	9074	CG	LEU	A1257	-48..338	61..610	-33..920	1.00 99..55	c
ATOM	9075	CD2	LEU	A1257	--47,180	62..582	-33.,697	1,00 95..67	c
ATOM	9076	GD1	LEU	A1257	-49..355	61.,723	-32..793	1.00 97,.57	c
ATOM	9077	N	PHE	A1258	-47.722	57..171	-32.,438	1.00105..73	N
ATOM	9078	CA.	PHE	A1258	-48,439	56. 045	-.31.,845	1,00106.,46	C
ATOM	9079	C	PHE	A1258	-48..194	55.,918	-30...346	1.00103,.17	C
ATOM	9080	O	PHE	A1258	-49..110	56.,122	-29..549	1,00102,.72	O
ATOM	9081	CB	PHE	A1258	-48,039	54. 740	-.32.,536	1,00106.,54	c
ATOM	9082	N	VAL	A125 9	-46..964	55.,563	-29..973	1,00102..28	N
ATOM	9083	CA	VAL	A1259	-46..567	55.,470	-28..563	1,00 99,.80	c
ATOM	9084	C	VAL	A1259	-46.,971	56..733	-27.,799	I,00100..02	c
ATOM	9085	O	VAL	A125 9	-47.367	56..679	-26,632	1,00 95..27	0
ATOM	9086	CB	VAL	A1259	-45. 044	55.,225	-28. 425	1,00 97,.84	c
ATOM	9087	CGI	VAL	A1259	-44.278	55.,962	-29,511	1.00 98..83	c
ATOM	9088	CG2	VAL	A1259	-44,544	55..607	-27,042	1,00 97..28	c
ATOM	9089	N	GLU	Al260	-46..908	57.,866	-28..489	1.00 99,.95	N
ATOM	9090	CA	GLU	A1260	-47.366	59..129	-27..939	1.00 96..91	c
ATOM	9091	C	GLU	A12 60	-48,791	59. 013	-27,403	1,00100.,73	c
ATOM	9092	O	GLU	Al260	-49..013	59,120	-26..197	1.00101,.17	0
ATOM	9093	CB	GLU	A1260	-47.285	60.,222	-29..003	1,00 99,.27	c
ATOM	9094	CG	GLU	A12 60	-47,002	61. 609	-28,451	1,00 95.,9.1	c
ATOM	9095	CD	GLU	A12 60	-48..260	62.,407	-28..170	1,00 98..83	c
ATOM	9096	OE1	GLU	A1260	-48..358	63.,553	-28..657	1,00 99,.21	0
ATOM	9097	OE2	GLU	A1260	-49.,149	61..897	-27.,460	I,00103..52	0
ATOM	9098	N	GLU	A12 61	-49..751	58..785	-28,296	1,00101..41	N
ATOM	9099	CA	GLN	A12 61	-51. 152	58.,677	-27.898	1,00100,.23	c
ATOM	9100	C	GLN	A1261	-51.,383	57..486	-26.,981	I,00102..08	c
ATOM	9101	O	GLN	A1261	-52.,281	57..508	-26,141	1,00106..09	0
ATOM	9102	CB	GLN	A12 61	-52. 049	58.,564	-29. 123	1,00100,.40	c
ATOM	9103	CG	GLN	A1261	-51.,673	59..519	-30..225	1.00103..69	c
ATOM	9104	CD	GLN	A1261	-52.,857	60..286	-30.,756	1,00110..42	c
ATOM	9105	OE1	GLN	Al261	-53..103	60.,313	-31..965	1.0011.3,.23	0
ATOM	9106	NE2	GLN	A1261	-53..601	60..925	-29,855	1.00108..93	N
ATOM	9107	N	HIS	A1262	-50.,558	56. 456	-27,146	1,00 99.,52	N
ATOM	9108	CA	HIS	A12 62	-50..654	55.,236	-26...355	1.00100,.57	c
ATOM	9109	c	HIS	A1262	-50..324	55.,463	-24.876	1,00100,.92	c
ATOM	9110	O	HIS	A1262	-50.,575	54. 596	-24.,035	1,00 97.,20	0
ATOM	9111	CB	HIS	A12 62	-49..720	54.,169	-26..929	1,00100..32	c
ATOM	9112	CG	HIS	A1262	-50. 391	52.,860	-27.211	1,00105,.41	c
ATOM	9113	ND1	HIS	A1262	-49.,728	51..654	-27.,139	I,00111..60	N
ATOM	9114	CD2	HIS	A1262	-51.,663	52..569	-27,574	1,00106..66	c
ATOM	9115	CE1	HIS	A1262	-50. 563	50.,675	-27.440	1,00114 ,73	c
ATOM	9116	NE2	HIS	A1262	-51.,744	51..204	-27,709	1.00115..66	N
ATOM	9117	O	LYS	A1263	-50.,354	59..029	-23,112	1,00 92..47	0
ATOM	9118	N	LYS	A1263	-49..756	56,622	-24..557	1.00102,.44	N
ATOM	9119	CA	LYS	A1263	-49..282	56..863	-23..200	1.00 97..51	c
ATOM	9120	C	LYS	A12 63	-49.,975	58. 031	-22.,500	1,00 95.,08	C
ATOM	9121	CB	LYS	A1263	-47 .768	57.,081	-23..199	1.00 92,.53	C
ATOM	9122	CG	LYS	A1263	-46..956	55.,803	-23..082	1,00 92,.34	c
ATOM	9123	CD	LYS	A12 63	-47,147	54. 894	-24.,283	1,00 89.,54	c
ATOM	9124	CE	LYS	A12 63	-46..056	53.,873	-24,379	1,00 84..25	c
ATOM	9125	NZ	LYS	A1263	-45..945	53.,131	-23..099	1,00 87,.44	N
ATOM	9126	O	HIS	A1264	-50.,529	60..609	-18.,897	I,00 97..06	O
ATOM	9127	N	HIS	A12 64	-50..102	57..870	-21..190	1,00 95..68	N
ATOM	9128	CA	HIS	A1264	-50. 893	58.,719	-20. 312	1,00 94,.06	C
ATOM	9129	C	HIS	A1264	-50.,025	59.712	-19,572	I,00 97..26	C
ATOM	9130	CB	HIS	A12 64	-51.,617	57..840	-19,306	1,00 91..43	C
ATOM	9131	CG	HIS	A1264	-50. 758	56.,737	-18. 771	1,00 93,.75	C
ATOM	9132	ND1	HIS	A1264	-50.,529	55..569	-19.,468	1.00 90..24	N
ATOM	9133	CD2	HIS	A12 64	-50.,039	56..637	-17,627	1,00 96..10	C
ATOM	9134	CE1	HIS	A12 64	-49..725	54.,789	-18.768	1.00 90,.32	C
ATOM	9135	NE2	HIS	A1264	-49..413	55..414	-17 .646	1.00 93..16	N
ATOM	9136	O	TYR	A12 65	-47,182	61. 896	-17 ,362	1,00 95.,16	O

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ATOM    9137   N    TYR  A1265      -48 ..716    59..534   -19. .734    1 .00  97 .90          N
ATOM    9138   CA   TYR  A1265      --47 ,662    60..112   -18.,891     1 ,00  95..93          C
ATOM    9139   C    TYR  Al265      -47 .862     61.,525   -18 ..3.18   1 .00  95,.11          C
ATOM    9140   CB   TYR  A1265      -46 ..347    60.,075   -19. .679    1 .00  90..54          C
ATOM    9141   CG   TYR  A.1265     -45 ,796     58. 674   -19 ,849     1 ,00  89.,40          C
ATOM    9142   GD1  TYR  Al265      -46. .242    57.,633   -19 .047     1 .00  90,.45          C
ATOM    9143   CD2  TYR  A1265      -44 .829     58.,392   -20 ..802    1 ,00  88,.33          C
ATOM    9144   CE1  TYR  A.1265     -45 ,743     56. 352   -19 ,190     1 ,00  90.,51          C
ATOM    9145   CE2  TYR  A12 65     -44 .323     57.,110   -20 ,949     1 ,00  82 .19          C
ATOM    9146   CZ   TYR  A1265      -44 .786     56.,096   -20 ..143    1 ,00  84 ,89          C
ATOM    9147   OH   TYR  A1265      -44 ,290     54..820   -20. ,277    I ,00  83..04          0
ATOM    9148   N    LEU  A12 66     -48 ,788     62..299   -18.,880     1 ,00  95..41          N
ATOM    914 9  CA   LEU  Al266      -49. 051     63.,660   -18. 400     1 ,00100, .92          C
ATOM    9150   C    LEU  A1266      -49 ,312     63.,733   -16.,891     1 .00101. .92          C
ATOM    9151   O    LEU  A1266      -48 ,916     64..688   -16 ,224     1 ,00100. .76          0
ATOM    9152   CB   LEU  Al266      -50. .250    64.,277   -19 .126     1 .00  95,.50          C
ATOM    9153   CG   LEU  A1266      -50. .352    64.,206   -20 ..646    1 .00  95..77          C
ATOM    9154   CD1  LEU  A.1266     -51 ,315     65. 278   -21. ,148    1 ,00  95.,88          C
ATOM    9155   CD2  LEU  Al266      -49 ..000    64.,363   -21. .289    1 .00  92 ,44          C
ATOM    9156   N    ASP  A1267      -49 ..996    62.,727   -16. .364    1 ,00103, .54          N
ATOM    9157   CA.  ASP  A1267      -50. ,330    62. 702   -14 ,950     1 ,00.105.,25          C
ATOM    9158   C    ASP  A12 67     -49 ,106     62.,301   -14 ,116     1 ,00104. .07          C
ATOM    9159   O    ASP  A1267      -48 ..935    62.,771   -12. .990    1 ,00106, .08          0
ATOM    9160   CB   ASP  A1267      -51.,506     61..744   -14 ,694     I ,00.105..37          C
ATOM    9161   CG   ASP  A12 67     -52.,690     62..426   -14 ,017     1 ,00107. .64          C
ATOM    9162   OD2  ASP  A1267      -52. 868     62.,227   -12 .793     1 ,00114  ,11          0
ATOM    9163   OD1  ASP  A1267      -5.3.,450    63..145   -14 ,706     I ,00102. .29          0
ATOM    9164   N    GLU  A1268      -48 ,246     61..453   -14 ,674     1 ,00  98..99          N
ATOM    9165   CA   GLU  A1268      -47 .131     60.,907   -13. 905     1 ,00  98 ,54          C
ATOM    9166   c    GLU  A1268      -45 ..965    61.,899   -13.,750     1 .00100. .11          c
ATOM    9167   O    GLU  A1268      -45 ,266     61..891   -12.,735     1 ,00  97 .62          0
ATOM    9168   CB   GLU  Al268      -46. .649    59.,599   -14 .546     1 .00  96,.87          C
ATOM    9169   CG   GLU  A1268      -47 .623     58.,426   -14 .388     1 .00  96..43          c
ATOM    9170   CD   GLU  A12 68     -47 ,193     57. 162   -15.,135     1 ,00  98.,3.1         C
ATOM    9171   OE1  GLU  Al268      -46. .066    57.,121   -15 .673     1 .00  96,.95          0
ATOM    9172   OE2  GLU  A1268      -47 .991     56.,200   -15. .187    1 ,00100, .27          0
ATOM    917 3  N    ILE  A1269      -45 ,763     62. 751   -14 ,751     1 ,00  98.,02          N
ATOM    9174   CA   ILE  A12 69     -44 ,708     63.,759   -14 .693     1 ,00  96..69          C
ATOM    9175   C    ILE  A1269      -45. 089     64.,853   -13. 709     1 ,00  93 ,55          C
ATOM    917 6  O    ILE  A1269      -44 ,259     65...343  -12.,948     I ,00  93..16          0
ATOM    9177   CB   ILE  A1269      -44 ,432     64..382   -16 ,086     1 ,00  97 .18          C
ATOM    9178   CGI  ILE  A1269      -43. 411     63.,543   -16. 841     1 ,00  93 ,95          C
ATOM    9179   CG2  ILE  A1269      -43 .949     65.,819   -15.,971     1 .00  95..28          C
ATOM    9180   CD1  ILE  A1269      -44 ,045     62..575   -17 ,792     1 ,00  96..38          C
ATOM    9181   N    ILE  A1270      -46. ..360   65.,228   -13 .730     1 .00  97 ,39          N
ATOM    9182   CA   ILE  A1270      -46 ..899    66.,163   -12. .754    1 .00  96..71          c
ATOM    9183   C    ILE  A127 0     -46 ,632     65. 635   -11 ,346     1 ,00  94 ,96          C
ATOM    9184   O    ILE  A1270      -46. .248    66.,383   -10 .452     1 .00  90,.77          0
ATOM    9185   CB   ILE  A1270      -48 ..398    66.,377   -12. .973    1 ,00  96,.13          C
ATOM    9186   CGI  ILE  A127 0     -48 ,636     67. 148   -14 ,276     1 ,00  99.,47          C
ATOM    9187   CG2  ILE  A127 0     -49 ,011     67..115   -11 ,798     1 ,00  99..13          C
ATOM    9188   CD1  ILE  A1270      -48 ..557    68.,666   -14 .134     1 ,00  94 ,91          C
ATOM    9189   N    GLU  A1271      -46.,808     64..328   -11 ,171     I ,00  98..04          N
ATOM    9190   CA   GLU  A1271      -46 ,511     63..671    -9 ,904     1 ,00  99..61          C
ATOM    9191   C    GLU  A1271      -45. 0.17    63.,793    -9. 583     1 ,00  99 ,45          C
ATOM    9192   O    GLU  A1271      -44 ,640     64..139    -8.,460     I ,00  99..79          0
ATOM    9193   CB   GLU  A1271      -46 ,936     62..195    -9.,945     1 ,00  99..39          C
ATOM    9194   CG   GLU  A1271      -47 .492     61.,657    -8. 628     1 ,00101  ,42          C
ATOM    9195   CD   GLU  A1271      -48 ,947     62.,051    -8.,389     1 .00106. .95          c
ATOM    9196   OE1  GLU  A1271      -49 ,842     61..262    -8.,766     1 ,00108. .02          0
ATOM    9197   OE2  GLU  A1271      -49 ..197    63.,138    -7 ..8.18    1 .00100, .15          0
ATOM    9198   N    GLN  A1272      -44 ..180    63.,510   -10. .578    1 .00  97 .41          N
ATOM    9199   CA.  GLN  A127 2     -42.,733     63. 663   -10. ,458    1 ,00  93.,90          C
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ATOM    9200   C    GLN  A1272     -42..358    65..051    -9..952    1.00  92.75         C
ATOM    9201   O    GLN  A1272     --41,704    65..201    -8..922    1,00  93..57        0
ATOM    9202   CB   GLN  A1272     -42 .071    63.,404   -11.808     1.00  89,.41        C
ATOM    9203   CG   GLN  A1272     -42..088    61.,962   -12..214    1.00  85..31        C
ATOM    9204   CD   GLN  A127 2    -40.,965    61. 217   -11,581     1,00  85.,0.1       C
ATOM    9205   OE1  GLN  A1272     -39..901    61.,783   -11.342     1.00  89,.35        0
ATOM    9206   NE2  GLN  A1272     -41.182     59.,945   -11 .286    1,00  86,.66        N
ATOM    9207   N    ILE  A127 3    -42.,794    66. 064   -10.,684    1,00  87.64         N
ATOM    9208   CA   1LE  A127 3    -42..493    67.,442   -10.,346    1,00  90..89        C
ATOM    9209   C    ILE  A1273     -42..969    67.,831    -8..934    1,00  94,99         C
ATOM    9210   0    ILE  A1273     -42.,268    68..544    -8..211    I,00  92.98         0
ATOM    9211   CB   ILE  A127 3    -43..115    68.,391   -11,387     1,00  87.18         C
ATOM    9212   CGI  ILE  A127 3    -42 .420    68.,212   -12.740     1,00  87,.11        C
ATOM    9213   CG2  ILE  A1273     -43..023    69.,825   -10.,928    1.00  80..93        C
ATOM    9214   CD1  ILE  A1273     -42.,909    69..160   -13.,820    1,00  83..34        C
ATOM    9215   N    SER. A1274     -44 .143    67.,347    -8..533    1.00  95,.82        N
ATOM    9216   CA   SER  A1274     -44.682     67.,679    -7.214     1,00  92.77         C
ATOM    9217   C    SER  A127 4    -43,972     66. 911    -6.,091    1,00  93..32        C
ATOM    9218   O    SER  A1274     -43..790    67.,442    -4.995     1.00  92,64         O
ATOM    9219   CB   SER  A1274     -46..188    67.,419    -7.174     1,00  95,.47        C
ATOM    9220   OG   SER  A127 4    -46,489     66. 102    -7,591     1,00  94.63         0
ATOM    9221   N    GLU  A127 5    -43..563    65..673    -6.365     1,00  92.11         N
ATOM    9222   CA   GLU  A1275     -42.. 721   64.,923    -5..431    1,00  92,64         C
ATOM    9223   C    GLU  A1275     -41 ,439    65..698    -5.,121    I,00  92.56         C
ATOM    9224   O    GLU  A127 5    -40..926    65..670    -4,003     1,00  92.05         0
ATOM    9225   CB   GLU  A1275     -42 .371    63.,540    -6. 005    1,00100,.19         C
ATOM    9226   CG   GLU  A1275     -41 ,421    62..689    -5.,140    I,00  98..52        C
ATOM    9227   CD   GLU  A127 5    -40,784     61..524    -5.,911    1,00102. .39        C
ATOM    9228   OE1  GLU  A1275     -40. 852    61.,528    -7.161     1,00100,.58         0
ATOM    9229   OE2  GLU  A1275     -40..212    60.,609    -5..270    1.00  98..88        0
ATOM    9230   N    PHE  A127 6    -40,930     66..389    -9,132     1,00  92.28         N
ATOM    9231   CA   PHE  A127 6    -39..687    67.,133    -6..027    1.00  87,66         C
ATOM    9232   C    PHE  A1276     -39..915    68.,417    -5..243    1.00  83..42        C
ATOM    9233   0    PHE  A127 6    -39,205     68. 706    -4,281     1,00  80..54        0
ATOM    9234   CB   PHE  A127 6    -39.154     67.,434    -7.428     1.00  8.3,.35       C
ATOM    9235   CG   PHE  A1276     -37 .718    67.,872    -7.471     1,00  76,62         C
ATOM    9236   CD2  PHE  A127 6    -37.,397    69. 205    -7,654     1,00  74.61         C
ATOM    9237   CD1  PHE  A127 6    -36,692     66.,952    -7,377     1,00  74.30         C
ATOM    9238   CF.2 PHE  A1276     -36. 082    69.,615    -7.732     1,00  73,07         C
ATOM    9239   CE1  PHE  A1276     -35.,366    67...359   -7,441     I,00  72.12         C
ATOM    9240   CZ   PHE  A127 6    -35.,065    68..694    -7,621     1,00  71.06         C
ATOM    9241   N    SER  A1277     -40. 924    69.,175    -5. 655    1,00  83,47         N
ATOM    9242   CA   SER  A1277     -41 ,215    70.,457    -5.,030    1.00  86..55        C
ATOM    9243   C    SER  A1277     -41 ,470    70.333    -3.,536    1,00  84.24         C
ATOM    9244   O    SER  A1277     -40.836     71,027    -2.739     1.00  85,.19        0
ATOM    9245   CB   SER  A1277     -42,416     71,126    -5..699    1,00  89..39        C
ATOM    9246   OG   SER  A127 7    -42.,762    72..323    -5,017     1,00  88..50        0
ATOM    9247   N    LYS  A1278     -42 ..385   69.,443    -3..162    1.00  85,.94        N
ATOM    9248   CA   LYS  A1278     -42..764    69.,280    -1.760     1,00  87,46         C
ATOM    9249   C    LYS  A127 8    -41 ,563    68. 888    -0.,890    1,00  86..80        C
ATOM    9250   O    LYS  A127 8    -41,480     69.,272     0,279     1,00  86..54        0
ATOM    9251   CB   LYS  A1278     -43..888    68.,246    -1.627     1,00  86,.38        C
ATOM    9252   N    ARG  A1279     -40.,622    68..147    -1,465     I,00  82.30         N
ATOM    9253   CA   ARG  A127 9    -39,431     67..749    -0.,721    1,00  79..29        C
ATOM    9254   C    ARG  A127 9    -38. .392   68.,866    -0. 676    1,00  80,04         C
ATOM    9255   O    ARG  A1279     -37.,736    69..088     0,339     I,00  79.56         0
ATOM    9256   CB   ARG  A1279     -38.,801    66..492    -1,333     1,00  77.47         C
ATOM    9257   CG   ARG  A127 9    -37. 777    65.,815    -0. 428    1,00  78,21         C
ATOM    9258   CD   ARG  A1279     -37.,226    64.,531    -1,027     1.00  76..65        C
ATOM    9259   NE   ARG  A1279     -36,295     64..817    -2.,117    1,00  85..72        N
ATOM    9260   CZ   ARG  A127 9    -35...364   63.,976    -2.561     1.00  84,.10        C
ATOM    9261   NH1  ARG  A1279     -35..227    62.,775    -2.005     1.00  79..35        N
ATOM    9262   NH2  ARG  A127 9    -34.,572    64. .343   -3.,567     1,00  80..10        N
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ATOM  9263  N    VAL  A1280   -38.252  69:576  -1,784  1.00 78.72   N
ATOM  9264  CA   VAL  A1280   --37,056 70.359  -1,999  1,00 72.49   C
ATOM  9265  C    VAL  A1280   -37.323  71,819  -2.320  1,00 78,71   C
ATOM  9266  O    VAL  A1280   -36.697  72.701  -1.739  1.00 82.24   0
ATOM  9267  CB   VAL  A1280   -36,236  69.749  -3,126  1,00 71,02   c
ATOM  9268  CGI  VAL  A1280   -35.066  70,614  -3.417  1,00 73,53   c
ATOM  9269  CG2  VAL  A1280   -35.790  68,368  -2.733  1,00 68,21   c
ATOM  9270  N    ILE  A1281   -38,242  72.087  -3,238  1,00 75,63   M
ATOM  9271  CA   ILE  A1281   -38.456  73.464  -3.656  1,00 76.25   c
ATOM  9272  c    ILE  A1281   -39.154  74,232  -2.548  1,00 81,78   c
ATOM  9273  0    ILE  A1281   -38,855  75.407  -2,311  I,00 80.47   0
ATOM  9274  CB   ILE  A1281   -39.268  73.553  -4.959  1,00 76.86   c
ATOM  9275  CGI  ILE  A1281   -38.569  72,762  -6.071  1,00 77,91   c
ATOM  9276  CG2  ILE  A1281   -39.457  74.990  -5.370  1.00 75.66   c
ATOM  9277  CD1  ILE  A1281   -37,056  72.956  -8,128  1,00 73.22   c
ATOM  9278  O    LEU  A1282   -41.447  76,409  -0.362  1,00 87,07   0
ATOM  9279  N    LEU  A1282   -40.059  73.548  -1,852  1.00 81.80   N
ATOM  9280  CA.  LEU  A1282   -40,793  74.128  -0,721  1,00 84.07   C
ATOM  9281  C    LEU  A1282   -41.490  75,424  -1.108  1,00 86,29   c
ATOM  9282  CB   LEU  A1282   -39.866  74,379   0.473  1,00 80,47   c
ATOM  9283  CG   LEU  A1282   -39,489  73.204   1,381  1,00 82.15   c
ATOM  9284  CD2  LEU  A1282   -38.073  73.409   1.887  1,00 79.62   c
ATOM  9285  CD1  LEU  A1282   -39.616  71,854   0.681  1,00 75,27   c
ATOM  9286  O    ALA  A1283   -45,039  75.987  -3,696  I,00 95,87   0
ATOM  9287  N    ALA  A1283   -42.121  75.416  -2.280  1,00 86.38   M
ATOM  9288  CA   ALA  A1283   -42.902  76,555  -2.750  1,00 90,94   C
ATOM  9289  C    ALA  A1283   -44,394  76.236  -2,675  I,00 93.82   c
ATOM  9290  CB   ALA  A1283   -42,501  76.930  -4,167  1,00 90.63   c
ATOM  9291  O    ASP  A1284   -47.997  75,782  -2.829  1,00 93,55   0
ATOM  9292  N    ASP  A1284   -44.920  76.252  -1.451  1.00 90.68   N
ATOM  9293  CA   ASP  A1284   -46,296  75.870  -1,148  1,00 91.21   c
ATOM  9294  C    ASP  A1284   -47..327  76,492  -2.077  1,00 95,44   c
ATOM  9295  CB   ASP  A1284   -46.628  76.249   0.292  1.00 95.55   c
ATOM  9296  CG   ASP  A1284   -45,579  75.771   1,273  1,00100,69   c
ATOM  9297  OD1  ASP  A1284   -45.364  74,536   1..347  1,00 88,46   0
ATOM  9298  OD2  ASP  A1284   -44.980  76,628   1.969  1,00 99,73   0
ATOM  9299  O    ALA  A1285   -49,220  77.715  -4,921  1,00 99.53   0
ATOM  9300  N    ALA  A1285   -47.443  77.816  -2.015  1,00 96.59   M
ATOM  9301  CA   ALA  A1285   -48.390  78,567  -2.842  1,00 96,75   C
ATOM  9302  C    ALA  A1285   -48,273  78.221  -4,326  I,00 98.37   c
ATOM  9303  CB   ALA  A1285   -48,191  80.068  -2,639  1,00 96.17   c
ATOM  9304  N    ASN  A1286   -47.101  78,484  -4.903  1,00 99,14   N
ATOM  9305  CA   ASN  A1286   -46.842  78.270  -6.327  1.00 95.35   c
ATOM  9306  C    ASM  A1286   -47,224  76.895  -8,858  1,00 98.46   c
ATOM  9307  O    ASN  A1286   -47.812  76,792  -7.934  1,00101,07   0
ATOM  9308  CB   ASN  A1286   -45.368  78.512  -6.628  1.00 92.64   c
ATOM  9309  CG   ASM  A1286   -45,096  79.918  -7,088  1,00 95.27   c
ATOM  9310  OD1  ASN  A1286   -45.839  80,845  -6.765  1,00 93,75   0
ATOM  9311  ND2  ASK  A1286   -44.032  80,089  -7.862  1,00 97,70   N
ATOM  9312  N    LEU  A1287   -46,881  75.844  -6,119  1,00 94.59   M
ATOM  9313  CA   LEU  A1287   -47.191  74.485  -6.552  1,00 94.21   c
ATOM  9314  c    LEU  A1287   -48.693  74,270  -6.638  1,00 98,78   c
ATOM  9315  0    LEU  A1287   -49,188  73.579  -7,526  I,00 97.78   0
ATOM  9316  CB   LEU  A1287   -46.578  73.462  -5.602  1,00 93.20   c
ATOM  9317  CG   LEU  A1287   -46.780  71,996  -5.987  1,00 93,25   c
ATOM  9318  CD1  LEU  A1287   -46,392  71.760  -7,432  I,00 90.66   c
ATOM  9319  CD2  LEU  A1287   -45,972  71.090  -5,074  1,00 90.26   c
ATOM  932 0 N    ASP  A1288   -49.415  74,872  -5.701  1,00102,27   N
ATOM  932 1 CA   ASP  A1288   -50.865  74.741  -5.663  1.00102.68   c
ATOM  9322  C    ASP  A1288   -51,498  75.471  -8,849  1,00100,21   c
ATOM  932 3 O    ASP  A1288   -52 ..384  74,937  -7.507  1,00102,18   0
ATOM  932 4 CB   ASP  A1288   -51.414  75.270  -4,336  1.00101.28   c
ATOM  9325  CG   ASP  A1288   -50,701  74.672  -3,120  1,00106.19   c
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ATOM   9326  OD1  ASP  A1288   -50.089   73.583   -3.238   1.00107.39   O
ATOM   9327  OD2  ASP  A1288  --50.753   75.300   -2,038   1,00106.70   O
ATOM   9328  K    LYS  A1289   -51.023   76,683   -7.127   1,00 99,47   K
ATOM   9329  CA   LYS  A1289   -51,468   77,440   -8.296   1.00 98.56   C
ATOM   9330  C    LYS  A1289   -51,059   76.742   -9,594   1,00100,40   C
ATOM   9331  O    LYS  A1289   -51.686   76,937  -10:636   1,00 99,85   0
ATOM   9332  CB   LYS  A1289   -50.908   78:864   -8:262   1,00 94,61   C
ATOM   9333  CG   LYS  A1289   -51,291   79.700   -9:461   1,00 91,73   C
ATOM   9334  CD   LYS  A1289   -51.011   81,163   -9.230   1,00 89.19   C
ATOM   9335  CE   LYS  A1289   -51.383   81,982  -10.457   1,00 96,64   C
ATOM   9336  NZ   LYS  A1289   -51,489   83:441  -10,169   1,00 90.46   N
ATOM   9337  K    VAL  A1290   -50.009   75,925   -9,515   1,00 97.88   K
ATOM   9338  CA   VAL  A1290   -49.566   75,108  -10.641   1,00 97,76   C
ATOM   9339  C    VAL  A1290   -50.550   73,984  -10.924   1.00 99.50   C
ATOM   9340  O    VAL  A1290   -50,969   73.782  -12,063   1,00 99.68   0
ATOM   9341  CB   VAL  A1290   -48.168   74,485  -10:388   1,00 97,75   C
ATOM   9342  CGI  VAL  A1290   -47.970   73,229  -11,221   1.00 93.69   C
ATOM   9343  CG2  VAL  A.1290  -47,084   75.472  -10,686   1,00 95:31   C
ATOM   9344  K    LEU  A1291   -50.919   73,252   -9:879   1,00101.26   K
ATOM   9345  CA   LEU  A1291   -51.712   72,042  -10.047   1,00101.94   C
ATOM   9346  C    LEU  A1291   -53,164   72.355  -10,401   1,00105,26   C
ATOM   9347  O    LEU  A1291   -53.834   71,554  -11.061   1,00101,99   0
ATOM   9348  CB   LEU  A1291   -51.628   71,186   -8.783   1,00101.51   C
ATOM   9349  CG   LEU  A1291   -50,224   70:596   -8,582   1,00 95.72   C
ATOM   9350  CD1  LEU  A1291   -50.149   69,656   -7:385   1,00 84.37   C
ATOM   9351  CD2  LEU  A1291   -49.788   69,888   -9.851   1,00 96,07   C
ATOM   9352  N    SER  A1292   -53.632   73:531   -9,976   1,00107:00   N
ATOM   9353  CA   SEP. A1292   -54,971   74.017  -10,314   1,00104.00   C
ATOM   9354  C    SER  A1292   -55.073   74,348  -11.802   1,00106,29   C
ATOM   9355  O    SER  A1292   -55,894   73,772  -12,524   1,00107,86   0
ATOM   9356  CB   SER  A1292   -55,329   75.253   -9,480   1,00105,59   C
ATOM   9357  OG   SER  A1292   -54.658   76,410   -9:950   1,00103,30   0
ATOM   9358  O    ALA  A1293   -53.824   74,631  -15,791   1,00105,60   0
ATOM   9359  N    ALA  A1293   -54,226   75.271  -12,255   1,00105,36   N
ATOM   9360  CA   ALA  A1293   -54.196   75,666  -13:661   1,00103,27   C
ATOM   9361  C    ALA  A1293   -53.725   74,532  -14.569   1,00103,26   C
ATOM   9362  CB   ALA  A1293   -53,316   76.876  -13,846   1,00 99,80   C
ATOM   9363  O    TYR  A1294   -54,289   71,720  -16,574   1,00100.71   0
ATOM   9364  N    TYR  A1294   -53.203   73,463  -13.978   1,00100.73   N
ATOM   9365  CA   TYR  A1294   -52 ,838   72:293  -14,758   1,00100,32   C
ATOM   9366  C    TYR  A1294   -54,078   71.659  -15,359   1,00102.17   C
ATOM   9367  CB   TYR  A1294   -52.092   71,262  -13.912   1,00 98,61   C
ATOM   9368  CG   TYR  A1294   -52 ,064   69,899  -14,557   1.00 95.61   C
ATOM   9369  CD2  TYR  A1294   -52 ,559   68.789  -13,897   1,00 97.22   C
ATOM   9370  CD1  TYR  A1294   -51.550   69,725  -15:833   1,00 95,00   C
ATOM   9371  CE2  TYR  A1294   -52 .537   67,544  -14,485   1.00 96.56   C
ATOM   9372  CE1  TYR  A.1294  -51,531   68.489  -16,428   1,00 95,40   C
ATOM   9373  CZ   TYR  A1294   -52 .023   67,401  -15:751   1,00 9.3,93   C
ATOM   9374  OH   TYR  A1294   -52 .000   66,165  -16,344   1,00 97,16   0
ATOM   9375  O    ASM  A1295   -57,633   70.790  -16,686   1,00 97,28   0
ATOM   9376  K    ASN  A1295   -54,888   71,048  -14,494   1,00103.84   K
ATOM   9377  CA   ASN  A1295   -56.094   70,342  -14,912   1,00102,71   C
ATOM   9378  C    ASM  A1295   -57,057   71,227  -15,694   1,00100,57   C
ATOM   9379  CB   ASN  A1295   -56,798   69,744  -13,697   1,00 99.94   C
ATOM   9380  CG   ASN  A1295   -56.334   68,341  -13.402   1,00 98,97   C
ATOM   9381  OD1  ASM  A1295   -55.926   67.613  -14,305   1,00102.55   0
ATOM   9382  ND2  ASK  A1295   -56,398   67.947  -12,139   1,00 99.42   K
ATOM   9383  O    LYS  A1296   -58.740   73:680  -18.233   1,00106.19   0
ATOM   9384  N    LYS  A1296   -57,204   72,475  -15.252   1.00102.18   N
ATOM   9385  CA   LYS  A1296   -58,017   73.481  -15,944   1,00101,49   C
ATOM   9386  C    LYS  A1296   -57.813   73,439  -17.456   1,00104,29   C
ATOM   9387  CB   LYS  A1296   -57,694   74,877  -15,405   1.00102.43   C
ATOM   9388  CG   LYS  A1296   -58,176   76.031  -16,270   1,00104,89   C
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ATOM    9389   CD   LYS  A1296      -58..344    77.303   -15..445    1,00106..00        C
ATOM    9390   CE   LYS  A1296      --57.,121   77.581   -14,581     1,00105..99        C
ATOM    9391   NZ   LYS  A1296      -57..420    78.,518  -13.459     1,00111,.48        N
ATOM    9392   O    HIS  A1297      -54.964     71,225   -20,316     1,00  99..09       O
ATOM    9393   N    HIS  A12 97     -56.,596    73.103   -17,866     1,00102.,96        N
ATOM    9394   CA   HIS  A1297      -56..309    72.,900  -19.269     1,00101,.81        C
ATOM    9395   C    HIS  A1297      -55..853    71,468   -19..499    1,00  99,.16       C
ATOM    9396   CB   HIS  A12 97     -55.,247    73.885   -19,758     1,00100.,74        C
ATOM    9397   CG   HIS  A12 97     -55..430    75.,279  -19.,242    1,00102..90        C
ATOM    9398   ND1  HIS  A1297      -54..976    75,680   -18..004    1,00102,.44        N
ATOM    9399   CD2  HIS  A1297      -56,013     76...369  -19,798     I,00105..02        C
ATOM    9400   CE1  HIS  A12 97     -55..268    76..954  -17,819     1,00104..80        C
ATOM    9401   NE2  HIS  A1297      -55. 898    77,396   -18. 893    1,00105,.70        N
ATOM    9402   O    ARG  A1298      -56..917    67.,547  -20,731     1,00102..58        O
ATOM    9403   N    ARG  A1298      -56,460     70.528   -18.,773    1,00  96..26       N
ATOM    9404   CA   ARG  A1298      -56..238    69.,105  -19.038     1,00101,.42        C
ATOM    9405   C    ARG  A1298      -57..091    68.,654  -20,220     1,00102..45        C
ATOM    9406   CB   ARG  A12 98     -56.,550    68. 247  -17,807     1,00  98.,8.1      C
ATOM    9407   O    ASP  A1299      -58...343   68.,937  -24..116    1,00  99,.59       0
ATOM    9408   N    ASP  A1299      -58..012    69.,523  -20.644     1,00101,.15        N
ATOM    9409   CA.  ASP  A1299      -58.,873    69. 272  -21.,803    1,00  99.,32       C
ATOM    9410   C    ASP  A12 99     -58..182    69.,637  -23,118     1,00100..59        C
ATOM    9411   CB   ASP  A1299      -60..189    70,048   -21 .676    1,00101,.72        C
ATOM    9412   O    LYS  A1300      -55.,150    69..258  -23,693     I,00103..49        0
ATOM    9413   N    LYS  A1300      -57..428    70.,738  -23,116     1,00100..96        N
ATOM    9414   CA   LYS  A1300      -56. 588    71,117   -24 .254    1,00  98,.27       C
ATOM    9415   C    LYS  A1300      -55.,603    69..970  -24.,595    I,00102..58        C
ATOM    9416   CB   LYS  A1300      -55.,850    72.425   -23,944     1,00  93..22       C
ATOM    9417   O    PRO  A130.1     -52. 709    69.,051  -25. 054    1,00103,.41        0
ATOM    9418   N    PRO  A1301      -55..267    69.,791  -25,896     1,00102..74        N
ATOM    9419   CA   FRO  A1301      -54.,623    68..565  -26,410     1,00101..40        C
ATOM    9420   C    PRO  A1301      -53..226    68.,278  -25.860     1,00102,.57        C
ATOM    9421   CB   PRO  A1301      -54.541     68.,824  -27,915     1,00  98..06       C
ATOM    9422   CG   PRO  A1301      -54 ,428    70.296   -28,019     1,00  95.,92       C
ATOM    9423   CD   PRO  A1301      -55..323    70.,839  -26.934     1,00100,.67        C
ATOM    9424   O    ILE  A1302      -49..442    68.,089  -25.256     1,00100,.59        0
ATOM    9425   N    ILE  A1302      -52.,620    67. 182  -26,319     1,00104.,50        N
ATOM    9426   CA   ILE  A1302      -51..337    66.,720  -25,782     1,00102..68        C
ATOM    9427   C    ILE  A1302      -50. 178    67.,653  -26. 139    1,00102 ,32        C
ATOM    9428   CB   ILE  A1302      -51.,006    65..287  -26.,267    I,00102..07        C
ATOM    9429   CGI  ILE  A1302      -51.,948    64..274  -25,612     1,00101..64        C
ATOM    9430   CG2  ILE  A1302      -49. 571    64.,928  -25. 937    1,00  99,.87       C
ATOM    9431   CD1  ILE  A1302      -51..601    62.,821  -25,887     1,00  91..99       C
ATOM    9432   O    ARG  A1303      -48,024     70.768   -26,775     1,00101..11        0
ATOM    9433   N    ARG  A1303      -50..025    67.,960  -27.425     1,00102,.66        N
ATOM    9434   CA   ARG  A1303      -48..977    68.,868  -27,882     1,00  99..95       C
ATOM    9435   C    ARG  A1303      -49.,051    70.190   -27,128     1,00101.,86        C
ATOM    9436   CB   ARG  A1303      -49..083    69.,113  -29..392    1,00  92,.75       C
ATOM    9437   N    GLU  A1304      -50..271    70,654   -26.870     1,00104,.44        N
ATOM    9438   CA.  GLU  A1304      -50.,481    71.907   -26,147     1,00104.,95        C
ATOM    9439   C    GLU  A1304      -50.,323    71,715   -24,641     1,00102..92        C
ATOM    9440   O    GLU  A1304      -50..059    72.,673  -23.913     1,00103,.41        O
ATOM    9441   CB   GLU  A1304      -51.,863    72.486   -26.,459    I,00102..78        C
ATOM    9442   N    GLU  A130 5     -50.,485    70.,477  -24,182     1,00102..47        N
ATOM    9443   CA   GLN  A1305      -50. 295    70.,159  -22.773     1,00100,.28        C
ATOM    9444   C    GLN  A1305      -48.,842    69..777  -22.,509    I,00100..28        C
ATOM    9445   O    GLN  A1305      -48,371     69..857  -21.,374    1,00  95..16       O
ATOM    9446   CB   GLN  A1305      -51. 230    69.,028  -22.332     1,00  99,.89       C
ATOM    9447   N    ALA  A130 6     -48,135     69.,367  -23,563     1,00102..25        N
ATOM    9448   CA   ALA  A1306      -46,733     68..957  -23,443     1,00  99..18       C
ATOM    9449   C    ALA  A130 6     -45.789     70.,152  -23.498     1,00  97,.31       C
ATOM    9450   O    ALA  A130 6     -44,805     70.,204  -22.,763    1,00  94..99       0
ATOM    9451   CB   ALA  A1306      -46,373     67. 954  -24.,530    1,00  95.,99       C
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ATOM    9452  O    GLU  A1307      -44.226    73..657  -22..802   1.00  95..79           O
ATOM    9453  N    GLU  A1307      --46„090   71.107   -24,373    1,00  97.84            N
ATOM    9454  CA   GLU  A1307      -45..302   72.,328  -24..478   1,00  97,20            C
ATOM    9455  c    GLU  A1307      -45..251   73..073  -23..153   1.00  96..10           c
ATOM    9456  CB   GLU  A1307      -45,872    73.247   -25,565    1,00100..24           c
ATOM    9457  CG   GLU  A1307      -45..276   73.,055  -26..954   1,00104,.61           c
ATOM    9458  CD   GLU  A1307      -44.687    74,343   -27.518    1,00109,.58           c
ATOM    9459  OE1  GLU  A1307      -44 ,933   74.637   -28,710    1,00110..29           0
ATOM    9460  OE2  GLU  A1307      -43..974   75..055  -26.770    1,00109..77           0
ATOM    9461  N    ASN  A1308      -46..360   73,044   —22.423    1,00  94,87            N
ATOM    9462  CA   ASN  A1308      -46.,488   73..821  -21.,197   I,00  94.52            C
ATOM    9463  C    ASN  A1308      -46..009   73..101  -19..926   1,00  90..50           C
ATOM    9464  O    ASN  A1308      -45. 665   73,750   -18. 939   1,00  88,81            O
ATOM    9465  CB   ASN  A1308      -47.941    74..268  -21..033   1.00  94.37            c
ATOM    9466  CG   ASN  A1308      -48,228    75.569   -21.,738   1,00  94.09            c
ATOM    9467  OD1  ASN  A1308      -49..230   76.,215  -21..471   1,00100,.10           0
ATOM    9468  ND2  ASN  A1308      -47.343    75..967  -22..633   1.00  94.66            N
ATOM    9469  N    ILE  A1309      -45,987    71.772   -19,946    1,00  89..98           N
ATOM    9470  CA   ILE  A130 9     -45...349  71,009   -18.875    1,00  90,.61           C
ATOM    9471  c    ILE  A1309      -43..888   71,427   -18..759   1,00  88,.73           c
ATOM    9472  0    ILE  A1309      -43,361    71.631   -17,669    1,00  83..76           0
ATOM    9473  CB   ILE  A130 9     -45..423   69..485  -19..123   1,00  86..23           c
ATOM    9474  CGI  ILE  A1309      -46..828   68.,962  -18..838   1,00  88,.51           c
ATOM    9475  CG2  ILE  A130 9     -44 ,419   68..746  -18.,251   I,00  83..49           c
ATOM    9476  CD1  ILE  A130 9     -47.182    68..957  -17.378    1,00  90..79           c
ATOM    9477  N    ILE  A131 0     -43. 245   71,563   -19. 910   1,00  88,80            N
ATOM    9478  CA   ILE  A131 0     -41,846    71.927   -19,972    I,00  86..99           C
ATOM    9479  C    ILE  A1310      -41,627    73.320   -19,385    1,00  80..97           C
ATOM    9480  O    ILE  A131 0     -40. 604   73,577   -18. 754   1,00  82,32            O
ATOM    9481  CB   ILE  A1310      -41.348    71..826  -21..420   1.00  83..46           c
ATOM    9482  CGI  ILE  A1310      -41 ,238   70.350   -21.,808   1,00  78..62           c
ATOM    9483  CG2  ILE  A1310      -40..016   72.,517  -21..602   1,00  76,.02           c
ATOM    9484  CD1  ILE  A1310      -41..189   70..121  -23..292   1.00  85..76           c
ATOM    9485  N    HIS  A1311      -42.,602   74.205   -19,544    1,00  84.05            N
ATOM    9486  CA   HIS  A1311      -42.527    75.,510  -18.894    1,00  83,.65           c
ATOM    9487  c    HIS  A1311      -42..418   75,351   -17.371    1,00  81,87            c
ATOM    9488  0    HIS  A1311      -41,892    76.225   -16,690    1,00  82.06            0
ATOM    9489  CB   HIS  A1311      -43.749    76..372  -19..230   1,00  87.46            c
ATOM    9490  CG   HIS  A1311      -43. 728   76,975   -20. 601   1,00  90,02            c
ATOM    9491  ND1  HIS  A131 1     -42.,864   76..566  -21.,592   I,00  88..42           N
ATOM    9492  CD2  HIS  A1311      -44,482    77.962   -21.,144   1,00  91.72            c
ATOM    9493  CE1  HIS  A1311      -43. 084   77,276   -22.687    1,00  89,54            c
ATOM    9494  NE2  HIS  A1311      -44..060   78..130  -22..440   1.00  87.38            N
ATOM    9495  N    LEU  A1312      -42.,913   74.231   -16,848    1,00  84.78            N
ATOM    9496  CA   LEU  A1312      -43..049   74,032   -15.401    1,00  83,.68           C
ATOM    9497  c    LEU  A1312      -41 .747   73..683  -14 .685   1.00  80..92           c
ATOM    9498  O    LEU  A1312      -41,628    73.894   -13,478    1,00  81.15            0
ATOM    9499  CB   LEU  A1312      -44 .069   72.,924  -15.100    1,00  86,.97           c
ATOM    9500  CG   LEU  A1312      -45..546   73,048   -15..467   1,00  82,41            c
ATOM    9501  CD1  LEU  A1312      -46,243    71.724   -15.,217   1,00  86..61           c
ATOM    9502  CD2  LEU  A1312      -46.191    74..139  -14..644   1,00  86..20           c
ATOM    9503  N    PHE  A1313      -40.780    73,130   -15..407   1,00  77,80            N
ATOM    9504  CA   PHE  A1313      -39,514    72.762   -14,777    I,00  78..04           C
ATOM    9505  C    PHE  A1313      -38..746   73..995  -14..322   1,00  73..87           C
ATOM    9506  O    PHE  A1313      -37. 849   73,902   -13.491    1,00  67,55            O
ATOM    9507  CB   PHE  A1313      -38.,676   71.918   -15.,719   I,00  71.39            C
ATOM    9508  CG   PHE  A1313      -39.196    70.532   -15.,879   1,00  76..34           c
ATOM    9509  CD2  PHE  A131 3     -38. 572   69.,472  -15. 248   1,00  74,68            c
ATOM    9510  CD1  PHE  A1313      -40.332    70..287  -16..641   1.00  81.39            c
ATOM    9511  CE2  PHE  A1313      -39,056    68..187  -15.,379   1,00  80..88           c
ATOM    9512  CE1  PHE  A1313      -40..825   69.,002  -16.778    1,00  83,.56           c
ATOM    9513  CZ   PHE  A1313      -40..184   67..948  -16..146   1.00  83..85           c
ATOM    9514  N    THR  A1314      -39,131    75.152   -14 ,850   1,00  67.79            N
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ATOM   9515  CA   THR  A1314    -38..688   76..430  -14 .314   1 .00  72 .78   C
ATOM   9516  C    THR  A1314    --38.,905  76.501   -12.,796   1,00  73..73   C
ATOM   9517  O    THR  A1314    -38..207   77,218   -12 .084   1 ,00  74 ,79   0
ATOM   9518  CB   THR  A1314    -39..422   77,586   -15..002   1.00  75..82   C
ATOM   9519  OG1  THR  A1314    -39,177    77.528   -16,415    1,00  76..48   0
ATOM   9520  CG2  THR  A1314    -38..963   78.,930  -14 .465   1,00  69,.52   C
ATOM   9521  N    LEU  A1315    -39..867   75,737   -12..297   1,00  76,68    K
ATOM   9522  CA.  LEU  A1315    -40.,066   75.620   -10.,861   1,00  75..95   C
ATOM   9523  C    LEU  A1315    -38..988   74,752   -10.,235   1,00  73..48   C
ATOM   9524  O    LEU  A1315    -38..515   75,036    -9..141   1,00  71,62    0
ATOM   9525  CB   LEU  A1315    -41 ,444   75..036  -10.,560   1,00  79.41    C
ATOM   9526  CG   LEU  A1315    -41.729    74.637    -9,116    1,00  77.28    C
ATOM   9527  GDI  LEU  A1315    -42 .887   75,457    -8. 566   1,00  81 ,12   C
ATOM   9528  CD2  LEU  A1315    -42 ..013  73.,142    -9.,019   1.00  75..84   C
ATOM   9529  N    THR  A1316    -38.,598   73.712   -10,,965   1,00  73..95   K
ATOM   9530  CA   THR  A1316    -37..748   72.,635  -10..469   1,00  70,.99   C
ATOM   9531  C    THR  A1316    -36..254   72.,891  -10..672   1.00  73..25   C
ATOM   9532  0    THR  A1316    -35.,398   72.123   -10.,215   1,00  76..26   0
ATOM   9533  CB   THR  A1316    -38..103   71,311   -11 .178   1,00  72 ,72   C
ATOM   9534  OG1  THR  A1316    -37 .949   70,,229  -10..266   1,00  76 ,47   0
ATOM   9535  CG2  THR  A1316    -37.,200   71.061   -12.,400   1,00  71.93    C
ATOM   9536  K    ASN  A1317    -35..946   73.,972  -11 ,371   1,00  71.35    K
ATOM   9537  CA   ASK  A1317    -34..611   74,152   -11 .920   1,00  69,.91   C
ATOM   9538  C    ASM  A1317    -.33.,597  74.662   -10.,918   1,00  67 .43   C
ATOM   9539  O    ASK  A1317    -33..833   75..676  -10.,235   1,00  59..46   0
ATOM   9540  CB   ASN  A1317    -34. 659   75,110   -13. 119   1,00  66,31    C
ATOM   9541  CG   ASM  A1317    -.34.,742  74 ..381  -14,453    1,00  69..05   C
ATOM   9542  OD1  ASK  A1317    -34.,428   73.190   -14 ,554   1,00  69..08   0
ATOM   9543  KD2  ASN  A1317    -35. 154   75,100   -15. 487   1,00  72 ,11   K
ATOM   9544  O    LEU  A1318    -31..255   76.,364  -11 ,622   1.00  67.29    0
ATOM   9545  N    LEU  A1318    -32.,473   73.945   -10,,842   1,00  59..69   K
ATOM   9546  CA   LEU  A1318    -31..275   74,447   -10..175   1,00  60,.72   C
ATOM   9547  C    LEU  A1318    -31..058   75.,928  -10..493   1.00  62 .01   C
ATOM   9548  CB   LEU  A1318    -30.,057   73.635   -10.,603   1,00  63..47   C
ATOM   9549  CG   LEU  A1318    -28..666   73.,962  -10..051   1,00  63,.31   C
ATOM   9550  CD2  LEU  A1318    -27.710    74,197   -11 .189   1,00  60,.71   C
ATOM   9551  CD1  LEU  A1318    -28,168    72.825    -9.,208   1,00  62 .85   C
ATOM   9552  O    GLY  A1319    -32..328   78.,842   -8.,732   1,00  62 .70   0
ATOM   9553  K    GLY  A1319    -30. 689   76,720    -9. 502   1,00  55,90    K
ATOM   9554  CA   GLY  A1319    -.30.,332  78..088   -9.,793   1,00  51.01    C
ATOM   9555  C    GLY  A1319    -31.,385   79.115    -9,,458   1,00  60..82   C
ATOM   9556  O    ALA  A132 0   -33. 898   80.,703  -11 .144   1,00  70,45    0
ATOM   9557  N    ALA  A132 0   -31..192   80.,316   -9..985   1.00  60..98   N
ATOM   9558  CA   ALA  A1320    -32.,088   81..434   -9,,754   1,00  61.67    C
ATOM   9559  C    ALA  A132 0   -33..548   81.,093  -10..028   1,00  70,.21   C
ATOM   9560  CB   ALA  A132 0   -31..667   82.,611  -10..618   1.00  62 .48   C
ATOM   9561  O    PRO  A1321    -35.,701   83. 356   -10.,300   1,00  66..27   0
ATOM   9562  K    PRO  A1321    -34..400   81.,221   -8..997   1,00  73,.47   K
ATOM   9563  CA   PRO  A1321    -35..852   81.,249   -9..191   1,00  71,27    C
ATOM   9564  C    PRO  A1321    -36,250    82. 261   -10.,256   1,00  66..55   C
ATOM   9565  CB   PRO  A1321    -36..375   81.,662   -7,818    1,00  68..58   C
ATOM   9566  CG   PRO  A1321    -35..382   81.,072   -6..881   1,00  67,96    C
ATOM   9567  CD   PRO  A1321    -.34.,043  81..198   -7,,567   1,00  66..89   C
ATOM   9568  O    ALA  A1322    -39,520    81..250  -12.,315   1,00  81.84    0
ATOM   9569  K    ALA  A1322    -37. 170   8.1.,875  -11 .129   1,00  71. ,99   K
ATOM   9570  CA   ALA  A1322    -.37.,685  82..781  -12.,149   1,00  78..47   C
ATOM   9571  C    ALA  A1322    -39,120    82..401  -12,,503   1,00  82.53    C
ATOM   9572  CB   ALA  A1322    -36. 805   82.,758  -13. 379   1,00  75,13    C
ATOM   9573  O    ALA  A132 3   -40,717    82.,333  -15.,524   1.00  85..18   0
ATOM   9574  N    ALA  A1323    -39,886    83..364  -13,,012   1,00  79..97   K
ATOM   9575  CA   ALA  A1323    -41 ..300  83.,156  -13...336   1,00  82,94    C
ATOM   9576  C    ALA  A132 3   -41 .529   82.,310  -14 .602   1.00  81.01    C
ATOM   9577  CB   ALA  A132 3   -41 ,983   84. 502   -13.,484   1,00  86..23   C
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ATOM   9578  O    PHE  A132 4    -45.309   80.895  -15 . 111   1.00  90.23       O
ATOM   9579  N    FHE  A1324     --42.649  81.587  -14 . 644   1.00  80.91       N
ATOM   9580  CA   PHE  A132 4    -43.003   80.731  -15 . 782   1.00  83.99       C
ATOM   9581  C    PHE  A132 4    -44.514   80.665  -16 . 026   1.00  92.00       C
ATOM   9582  CB   PHE  A132 4    -42 . 462  79.318  -15 . 580   1.00  81.52       C
ATOM   9583  CG   PHE  A132 4    -42 . 962  78.637  -14 . .331   1.00  84.02       C
ATOM   9584  CD1  PHE  A1324     -42.645   79.126  -13 . 070   1.00  82.58       C
ATOM   9585  CD2  PHE  A132 4    -43.716   77.482  -14 . 415   1.00  85.77       C
ATOM   9586  CE1  PHE  A132 4    -43.095   78.499  -11 . 924   1.00  82.13       C
ATOM   9587  CE2  PHE  A1324     -44.160   76.844  -13 . 266   1.00  88.09       C
ATOM   9588  CZ   PHE  A132 4    -43.847   77. .358  -12 . 019   1.00  83.96       C
ATOM   9589  O    LYS  A132 5    -46.257   78.213  -18 . 711   1.00  96.62       0
ATOM   9590  N    LYS  A132 5    -44 . 905  80.337  -17 . 259   1.00  94.64       N
ATOM   9591  CA   LYS  A132 5    -46.317   80.368  -17 . 648   1.00  93.84       C
ATOM   9592  C    LYS  A132 5    -46.891   78.998  -18 . 005   1.00  98.15       C
ATOM   9593  CB   LYS  A132 5    -46 . 515  81.317  -18 . 832   1.00  95.93       C
ATOM   9594  O    TYR  A132 6    -51 . 107  78.497  -18 . 044   1.00103 .37       0
ATOM   9595  N    TYR  A132 6    -48.093   78.720  -17 . 499   1.00  99.75       N
ATOM   9596  CA   TYR  A132 6    -48 . 889  77.578  -17 . 946   1.00  98.81       C
ATOM   9597  C    TYR  A132 6    -50 . 120  78.101  -18 . 677   1.00103 .43       C
ATOM   9598  CB   TYR  A132 6    -49 . 311  76.691  -16 . 780   1.00  95.93       C
ATOM   9599  CG   TYR  A132 6    -49.672   75.278  -17 . 193   1.00  98.33       C
ATOM   9600  CD1  TYR  A132 6    -48.694   74.395  -17 . 615   1.00  93.50       C
ATOM   9601  CD2  TYR  A132 6    -50 . 985  74.826  -17 . 154   1.00100 .03       C
ATOM   9602  CE1  TYR  A132 6    -49.006   73.102  -17 . 990   1.00  95.00       C
ATOM   9603  CE2  TYR  A132 6    -51 . 307  73.526  -17 . 533   1.00  96.67       C
ATOM   9604  CZ   TYR  A132 6    -50 . 310  72.671  -17 . 949   1.00  96.46       C
ATOM   9605  OH   TYR  A132 6    -50 . 600  71.376  -18 . 326   1.00  96.14       0
ATOM   9606  O    PHE  A132 7    -50 . 177  80.982  -20 . 711   1.00109 .01       0
ATOM   9607  N    PHE  A132 7    -50.041   78.095  -20.009    1.00105 .69       N
ATOM   9608  CA   FHE  A132 7    -51 . 025  78.735  -20 . 887   1.00104 .54       C
ATOM   9609  C    PHE  A132 7    -51 . 142  80.228  -20 . 535   1.00108 .85       C
ATOM   9610  CB   PHE  A132 7    -52 . 379  78.014  -20. 811    1.00102 .81       C
ATOM   9611  CG   PHE  A132 7    -52 . 322  76.554  -21 . 241   1.00102 .63       C
ATOM   9612  CD1  PHE  A132 7    -52 . 523  76.192  -22. 567    1.00103 .07       C
ATOM   9613  CD2  PHE  A1327     -52 . 072  75.547  -20 . 317   1.00  96.59       C
ATOM   9614  CE1  PHE  A132 7    -52 . 472  74.858  -22 . 958   1.00103 .47       C
ATOM   9615  CE2  PHE  A132 7    -52 . 020  74.217  -20 . 707   1.00  97.38       C
ATOM   9616  CZ   PHE  A132 7    -52 . 222  73.873  -22 . 024   1.00  97.97       C
ATOM   9617  O    ASP  A132 8    -51 . 757  83.422  -17 . 819   1.00106 .09       0
ATOM   9618  N    ASP  A132 8    -52 . 303  80.662  -20 . 048   1.00111 .60       N
ATOM   9619  CA   ASP  A132 8    -52 . 489  82.070  -19 . 678   1.00110 .52       C
ATOM   9620  C    ASP  A132 8    -52 . 134  82.308  -18 . 210   1.00109 .39       C
ATOM   9621  CB   ASP  A132 8    -53 . 928  82.526  -19 . 963   1.00109 .07       C
ATOM   9622  CG   ASP  A132 8    -54 . 947  81.404  -19 . 800   1.00109 .32       C
ATOM   9623  OD1  ASP  A132 8    -55. 916   81.366  -20. 589    1.00110 .65       0
ATOM   9624  OD2  ASP  A132 8    -54 . 787  80.565  -18 . 883   1.00107 .66       0
ATOM   9625  O    TKR  A132 9    -49.630   80.648  -16 . 111   1.00103 .62       0
ATOM   9626  N    THR  A132 9    -52 . 249  81.250  -17. 409    1.00105 .81       N
ATOM   9627  CA.  THR  A132 9    -51 . 937  81.325  -15 . 988   1.00105 .49       C
ATOM   9628  C    THR  A132 9    -50.439   81.513  -15 . 778   1.00105 .80       C
ATOM   9629  CB   THR  A132 9    -52 . 411  80.073  -15 . 228   1.00107 .70       C
ATOM   9630  OG1  THR  A132 9    -53 . 838  80.113  -15 . 082   1.00103 .53       0
ATOM   9631  CG2  THR  A132 9    -51 . 764  80.018  -13 . 845   1.00103 .89       C
ATOM   9632  N    THR  A1330     -50 . 087  82.658  -15 . 210   1.00108 .15       N
ATOM   9633  CA   THR  A1330     -48 . 701  83.056  -15 . 060   1.00  99.97       C
ATOM   9634  C    THR  A1330     -48.330   83.124  -13 . 570   1.00  99.09       C
ATOM   9635  O    THR  A1330     -49.123   83.585  -12 . 744   1.00  96.96       0
ATOM   9636  CB   THR  A1330     -48.465   84.407  -15 . 772   1.00102 .30       C
ATOM   9637  OG1  THR  A1330     -47.105   84.818  -15. 615    1.00102 .97       0
ATOM   9638  CG2  TKR  A13.30    -49.406   85.485  -15 . 232   1.00103 .50       C
ATOM   9639  N    ILE  A1331     -47.135   82.642  -13 . 228   1.00  97.81       N
ATOM   9640  CA.  ILE  A1331     -46.731   82.492  -11 . 825   1.00  91.73       C
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ATOM	9641	C	ILE	A1331	-45.540	83:347	-11.420	1.00	87.80	C
ATOM	9642	O	ILE	A1331	--44,433	83.124	-11,894	1,00	87.15	O
ATOM	9643	CB	ILE	A1331	-46.361	81,041	-11.507	1,00	88,98	C
ATOM	9644	CGI	ILE	A1331	-47.306	80:085	-12.220	1.00	92.30	C
ATOM	9645	CG2	ILE	A1331	-46,389	80.810	-10,017	1,00	86,76	C
ATOM	9646	GD1	ILE	A1331	-46.999	78,663	-11.940	1,00	89,84	C
ATOM	9647	N	ASP	A1332	-45.763	84,307	-10.530	1,00	90,24	N
ATOM	9648	CA.	ASP	A1332	-44,673	85.129	-10,031	1,00	85.13	C
ATOM	9649	C	ASP	A1332	-43.617	84.230	-9:405	1,00	91.63	C
ATOM	9650	O	ASP	A1332	-43.945	83,212	-8.789	1,00	92,52	O
ATOM	9651	CB	ASP	A1332	-45,183	86.152	-9,020	I,00	88.07	C
ATOM	9652	N	ARG	A1333	-42.348	84.579	-9:588	1,00	90.57	N
ATOM	9653	CA	ARG	A1333	-41.275	83,803	-8.984	1,00	87,05	C
ATOM	9654	C	ARG	A1333	-41.269	84:036	-7:482	1.00	87.27	C
ATOM	9655	O	ARG	A1333	-41,507	85.151	-7,010	1,00	91.84	0
ATOM	9656	CB	ARG	A1333	-39.917	84,170	-9.589	1,00	84,58	C
ATOM	9657	CG	ARG	A1333	-39.458	85:576	-9.269	1.00	86.20	C
ATOM	9658	CD	ARG	A1333	-38,163	85.925	-9,964	1,00	82,00	C
ATOM	9659	NE	ARG	A1333	-37.782	87,304	-9,694	1,00	82,46	N
ATOM	9660	CZ	ARG	A1333	-36.837	87,955	-10.358	1,00	90,58	C
ATOM	9661	NH1	ARG	A1333	-36,181	87.346	-11,340	1,00	94,11	N
ATOM	9662	NH2	ARG	A1333	-36.552	89.214	-10:051	1,00	90.55	N
ATOM	9663	N	LYS	A1334	-41.024	82,978	-6.725	1,00	85,47	N
ATOM	9664	CA	LYS	A1334	-40,894	83.122	-5,285	I,00	88.89	C
ATOM	9665	C	LYS	A1334	-39.436	82.897	-4:902	1,00	85.95	C
ATOM	9666	O	LYS	A1334	-38.885	81,819	-5.118	1,00	80,02	O
ATOM	9667	CB	LYS	A1334	-41,817	82.144	-4,555	I,00	92,96	C
ATOM	9668	N	ARG	A1335	-38,799	83.920	-4,352	1,00	83.18	N
ATOM	9669	CA	ARG	A1335	-37.385	83,799	-4.062	1,00	79,51	C
ATOM	9670	C	ARG	A1335	-37:109	83:506	-2,593	1.00	78.83	C
ATOM	9671	O	ARG	A1335	-37,875	83.878	-1,701	1,00	78.51	0
ATOM	9672	CB	ARG	A1335	-36.645	85,061	-4.504	1,00	80,01	C
ATOM	9673	CG	ARG	A1335	-37.263	86:339	-4.044	1.00	83.75	C
ATOM	9674	CD	ARG	A1335	-37,057	87.425	-5,076	1,00	87,81	C
ATOM	9675	NE	ARG	A1335	-35.837	88,194	-4.850	1,00	87,30	N
ATOM	9676	CZ	ARG	A1335	-35.240	88,924	-5.787	1,00	86,65	C
ATOM	9677	NH1	ARG	A1335	-34,136	89.609	-5,506	1,00	82,48	N
ATOM	9678	NH2	ARG	A1335	-35:746	88:961	-7:014	1,00	86.99	N
ATOM	9679	N	TYR	A1336	-35.999	82,820	-2.350	1,00	76,44	N
ATOM	9680	CA	TYR	A1336	-35,626	82.452	-1,003	I,00	66.21	C
ATOM	9681	C	TYR	A1336	-34,956	83.619	-0,312	1,00	66.13	C
ATOM	9682	O	TYR	A1336	-33.735	83,761	-0.353	1,00	67,85	0
ATOM	9683	CB	TYR	A1336	-34:724	81:236	-1.035	1.00	67.42	C
ATOM	9684	CG	TYR	A1336	-35,356	80.064	-1,744	1,00	65.61	C
ATOM	9685	CD1	TYR	A1336	-36.460	79,422	-1.209	1,00	68,11	C
ATOM	9686	CD2	TYR	A1336	-34.844	79.591	-2,937	1.00	62.72	C
ATOM	9687	CE1	TYR	A1336	-37,033	78.347	-1,842	1,00	69,86	C
ATOM	9688	CE2	TYR	A1336	-35.410	78,514	-3.574	1,00	63,72	C
ATOM	9689	CZ	TYR	A1336	-36.500	77,892	-3.019	1,00	67,93	C
ATOM	9690	OH	TYR	A1336	-37,074	76.820	-3,651	1,00	72,51	0
ATOM	9691	O	THR	A1337	-34:307	86:469	2:945	1,00	75.05	0
ATOM	9692	N	THR	A1337	-35.779	84,449	0.321	1,00	69,71	N
ATOM	9693	CA	THR	A1337	-35,343	85.698	0,940	I,00	69.80	C
ATOM	9694	C	THR	A1337	-34:690	85.508	2:299	1,00	67.19	C
ATOM	9695	CB	THR	A1337	-36.528	86,656	1.120	1,00	71,77	C
ATOM	9696	OG1	THR	A1337	-37,408	86.131	2,123	I,00	74.44	0
ATOM	9697	CG2	THR	A1337	-37,289	86.794	-0,181	1,00	69.15	C
ATOM	9698	O	SER	A1338	-32.862	82,046	3.229	1,00	67,30	0
ATOM	9699	N	SER	A1338	-34:571	84:267	2:743	1.00	72.17	N
ATOM	9700	CA	SER	A1338	-34,010	83.997	4,058	1,00	66.97	C
ATOM	9701	C	SER	A1338	-32 .813	83,043	3:947	1,00	69,73	C
ATOM	9702	CB	SER	A1338	-35.089	83:417	4:978	1.00	64.79	C
ATOM	9703	OG	SER	A1338	-34,633	83.276	6,309	1,00	70,51	0

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ATOM   9704  N    THR  A133 9   -31..740   83..367    4.660   1.00  65..42   N
ATOM   9705  CA   THR  A1339    --30.,549  82..538    4,688   1,00  65..30   C
ATOM   9706  C    THR  A13.3 9  -30..286   82.,036    6..097  1.00  71,07    C
ATOM   9707  O    THR  A133 9   -29..221   81.,478    6..364  1.00  66..63   0
ATOM   9708  CB   THR  A1339    -29.,305   83. 294    4,190   1,00  65..32   C
ATOM   9709  OG1  THR  A13.3 9  -29..197   84.,557    4.864   1.00  61,48    0
ATOM   9710  CG2  THR  A1339    -29..384   83.,529    2.681   1,00  65,.20   C
ATOM   9711  N    LYS  A1340    -31.,253   82. 259    6,991   1,00  67.25    N
ATOM   9712  CA   LYS  A134 0   -31..198   81.,724    8,347   1,00  68..72   C
ATOM   9713  C    LYS  A1340    -30..869   80.,230    8..286  1,00  72,53    C
ATOM   9714  0    LYS  A134 0   -29.,913   79.760     8,915   1,00  75..45   0
ATOM   9715  CB   LYS  A134 0   -32..529   81..950    9,062   1,00  73..84   C
ATOM   9716  CG   LYS  A134 0   -32. 456   82.,301    10. 551 1,00  79,02    C
ATOM   9717  CD   LYS  A134 0   -33..858   82.,724    11,049  1.00  81.92    C
ATOM   9718  CE   LYS  A134 0   -33.,927   82..937    12.,557 1,00  83..74   C
ATOM   9719  NZ   LYS  A134 0   -35..316   83.,282    12.999  1.00  90,.87   N
ATOM   9720  N    GLU  A1341    -31..649   79.,509    7.487   1.00  67.52    N
ATOM   9721  CA.  GLU  A1341    -31.,527   78.064     7,329   1,00  65..83   C
ATOM   9722  C    GLU  A1341    -30..107   77,536     7.283   1.00  65,.00   C
ATOM   9723  O    GLU  A1341    -29..793   76,491     7.846   1.00  69,.34   0
ATOM   9724  CB   GLU  A1341    -32.,223   77.641     6,047   1,00  69..10   C
ATOM   9725  CG   GLU  A1341    -33..595   77,070     6,256   1,00  78..43   C
ATOM   9726  CE   GLU  A1341    -34..137   76,479     4.981   1,00  83,.12   C
ATOM   9727  OE1  GLU  A1341    -.33.,360  76..426    3,999   1,00  74.79    0
ATOM   9728  OE2  GLU  A1341    -35.,323   76..073    4,960   1,00  88..00   0
ATOM   9729  N    VAL  A134 2   -29. 260   78,290     6.605   1,00  66,84    N
ATOM   9730  CA   VAL  A1342    -27.,982   77.810     6,119   1,00  64.77    C
ATOM   9731  C    VAL  A1342    -26,946    77.741     7,240   1,00  68..75   C
ATOM   9732  O    VAL  A134 2   -26. 000   76,948     7.200   1,00  63,93    0
ATOM   9733  CB   VAL  A1342    -27,527    78.,719    4,968   1.00  62.60    C
ATOM   9734  CGI  VAL  A1342    -26,059    78.982     5,005   1,00  68..68   C
ATOM   9735  CG2  VAL  A134 2   -27.962    78.,131    3..644  1.00  61,79    C
ATOM   9736  N    LEU  A134 3   -27..165   78.,554    8..264  1.00  70..73   N
ATOM   9737  CA.  LEU  A1343    -26,251    78.643     9,390   1,00  68..29   C
ATOM   9738  C    LEU  A1343    -26..142   77,349     10..209 1.00  68,.50   C
ATOM   9739  O    LEU  A1343    -25..097   77,077     10..795 1,00  67,98    0
ATOM   9740  CB   LEU  A1343    -26,682    79.794     10.,290 1,00  67.52    C
ATOM   9741  CG   LEU  A1343    -26,521    81.,131    9,588   1,00  65..64   C
ATOM   9742  GDI  LEU  A134 3   -27.118    82.,229    10. 414 1,00  64,25    C
ATOM   9743  CD2  LEU  A134 3   -25,051    81...385   9,344   1,00  66..59   C
ATOM   9744  N    ASP  A1344    -27,210    76.561     10.,264 1,00  65..01   N
ATOM   9745  CA   ASP  A134 4   -27.160    75,292     10. 998 1,00  72,44    C
ATOM   9746  C    ASP  A134 4   -27..178   74,091     10.,064 1.00  68..32   C
ATOM   9747  O    ASP  A1344    -27,808    73.086     10.,364 1,00  68..98   0
ATOM   9748  CB   ASP  A1344    -28..327   75.,193    11.985  1.00  70,.54   C
ATOM   9749  CG   ASP  A134 4   -28..232   76.,218    13..103 1.00  77.61    C
ATOM   9750  OD1  ASP  A134 4   -27,107    76.423     13.,622 1,00  71.39    0
ATOM   9751  OD2  ASP  A1344    -29..280   76.,823    13..456 1.00  81,04    0
ATOM   9752  N    ALA  A1345    -26.477    74,208     8..940  1,00  67,11    N
ATOM   9753  CA.  ALA  A1345    -26,558    73.242     7,851   1,00  58..27   C
ATOM   9754  C    ALA  A1345    -25,155    72.,790    7,437   1,00  60..17   C
ATOM   9755  O    ALA  A1345    -24.171    73,202     8..046  1,00  60,.30   0
ATOM   9756  CB   ALA  A134 5   -27.,303   73..849    6,671   1,00  55..88   C
ATOM   9757  N    THR  A1346    -25,048    71.951     6,410   1,00  52.25    N
ATOM   9758  CA   THR  A134 6   -23 .735   71,457     6.003   1,00  56,48    C
ATOM   9759  C    THR  A134 6   -23,178    72.173     4,781   1,00  56..82   C
ATOM   9760  O    THR  A134 6   -23,652    71.963     3,666   1,00  60..60   0
ATOM   9761  CB   THR  A134 6   -23 .769   69.,947    5.691   1,00  57,45    C
ATOM   9762  OG1  THR  A134 6   -24,320    69.,252    6,805   1.00  64.67    0
ATOM   9763  CG2  THR  A134 6   -22.,364   69.414     5,418   1,00  57.07    C
ATOM   9764  N    LEU  A134 7   -22..169   73.,010    4.992   1.00  5.3,.42   N
ATOM   9765  CA   LEU  A134 7   -21. .452  73.,642    3..890  1.00  53..51   C
ATOM   9766  C    LEU  A134 7   -20.,602   72.605     3,136   1,00  57.74    C
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ATOM   9767  O    LEU A1347    -19.866  71.820   3.750  1.00 54.41      O
ATOM   9768  CB   LEU A1347    -20.572  74.786   4.405  1.00 50.92      C
ATOM   9769  CG   LEU A1347    -19.522  75.320   3.429  1.00 54.16      C
ATOM   9770  CD2  LEU A1347    -18.477  76.176   4.121  1.00 49.16      c
ATOM   9771  GDI  LEU A1347    -20.171  76.072   2.253  I.00 51.55      c
ATOM   9772  N    ILE A1348    -20.701  72.610   1.807  1.00 55.91      N
ATOM   9773  CA   ILE A1348    -19.973  71.648   0.988  1.00 52.51      c
ATOM   9774  C    ILE A1348    -19.008  72.319   0.027  I.00 49.10      C
ATOM   9775  O    ILE A1348    -19.438  72.911  -0.952  1.00 52.75      O
ATOM   9776  CB   ILE A1348    -20.938  70.783   0.183  1.00 50.14      c
ATOM   9777  CGI  ILE A1348    -21.903  70.072   1.115  I.00 53.11      c
ATOM   9778  CG2  ILE A1348    -20.196  69.755  -0.636  1.00 49.25      c
ATOM   9779  GDI  ILE A1348    -22.890  69.196   0.380  1.00 53.69      c
ATOM   9780  N    HIS A1349    -17.711  72.232   0.317  1.00 49.53      N
ATOM   9781  CA   HIS A1349    -16.662  72.656  -0.613  1.00 49.34      C
ATOM   9782  C    HIS A1349    -16.378  71.580  -1.659  1.00 55.72      C
ATOM   9783  O    HIS A1349    -16.078  70.435  -1.311  1.00 54.92      O
ATOM   9784  CB   HIS A1349    -15.355  72.976   0.123  I.00 49.40      C
ATOM   9785  CG   HIS A1349    -15.476  74.078   1.123  1.00 59.01      c
ATOM   9786  ND1  HIS A1349    -15.742  75.382   0.762  1.00 56.78      N
ATOM   9787  CD2  HIS A1349    -15.372  74.072   2.474  I.00 56.16      C
ATOM   9788  CE1  HIS A1349    -15.795  76.131   1.848  1.00 56.13      C
ATOM   9789  NE2  HIS A1349    -15.580  75.360   2.900  1.00 59.53      N
ATOM   9790  N    GLN A1350    -16.438  71.952  -2.933  I.00 49.43      N
ATOM   9791  CA   GLN A1350    -16.276  70.992  -4.008  1.00 45.08      C
ATOM   9792  C    GLN A1350    -15.098  71.336  -4.860  1.00 49.26      C
ATOM   9793  O    GLM A1350    -14.908  72.499  -5.177  I.00 48.30      0
ATOM   9794  CB   GLN A1350    -17.503  70.953  -4.900  1.00 50.94      c
ATOM   9795  CG   GLN A1350    -18.840  70.703  -4.223  1.00 46.71      c
ATOM   9796  CD   GLN A1350    -19.966  70.777  -5.236  1.00 48.43      c
ATOM   9797  OE1  GLN A1350    -20.427  71.862  -5.571  1.00 55.92      0
ATOM   9798  NE2  GLN A1350    -20.386  69.627  -5.757  1.00 50.99      N
ATOM   9799  N    SER A1351    -14.295  70.333  -5.226  1.00 46.57      N
ATOM   9800  CA.  SER A1351    -13.333  70.494  -6.311  I.00 47.34      C
ATOM   9801  C    SER A1351    -14.073  70.668  -7.646  1.00 48.04      C
ATOM   9802  O    SER A1351    -15.298  70.542  -7.717  1.00 44.44      O
ATOM   9803  CB   SER A1351    -12.401  69.300  -6.399  I.00 47.42      C
ATOM   9804  OG   SER A1351    -13.142  68.153  -6.754  1.00 53.98      O
ATOM   9805  O    ILE A1352    -15.882  70.635 -11.150  1.00 52.83      O
ATOM   9806  N    ILE A1352    -13.317  70.940  -8.700  I.00 45.44      N
ATOM   9807  CA   ILE A1352    -13.889  71.347  -9.975  1.00 43.65      C
ATOM   9808  C    ILE A1352    -14.839  70.285 -10.561  1.00 53.47      C
ATOM   9809  CB   ILE A1352    -12.763  71.694 -10.990  1.00 42.30      c
ATOM   9810  CGI  ILE A1352    -13.311  72.482 -12.163  1.00 40.31      c
ATOM   9811  CG2  ILE A1352    -12.060  70.461 -11.479  1.00 47.77      c
ATOM   9812  GDI  ILE A1352    -12.246  72.960 -13.074  1.00 43.78      c
ATOM   9813  O    THR A1353    -17.398  66.863 -10.276  I.00 54.38      0
ATOM   9814  N    THR A1353    -14.517  69.006 -10.345  1.00 45.52      N
ATOM   9815  CA   THR A1353    -15.331  67.884 -10.819  1.00 44.74      c
ATOM   9816  C    THR A1353    -16.456  67.521  -9.875  I.00 44.77      c
ATOM   9817  CB   THR A1353    -14.486  66.576 -11.001  1.00 48.11      c
ATOM   9818  OG1  THR A1353    -13.995  66.133  -9.719  1.00 47.72      0
ATOM   9819  CG2  THR A1353    -13.328  66.806 -11.946  I.00 49.55      c
ATOM   9820  O    GLY A1354    -17.671  65.758  -5.963  1.00 52.77      0
ATOM   9821  N    GLY A1354    -16.322  67.877  -8.605  1.00 45.64      N
ATOM   9822  CA   GLY A1354    -17.290  67.465  -7.602  I.00 46.68      C
ATOM   9823  C    GLY A1354    -16.973  66.157  -6.892  1.00 47.90      C
ATOM   9824  O    LEU A1355    -15.383  63.531  -4.480  1.00 50.16      O
ATOM   9825  N    LEU A1355    -15.929  65.473  -7.327  1.00 44.32      N
ATOM   9826  CA   LEU A1355    -15.653  64.150  -6.792  1.00 52.55      C
ATOM   9827  C    LEU A1355    -15.044  64.281  -5.384  1.00 51.75      C
ATOM   9828  CB   LEU A1355    -14.728  63.363  -7.757  1.00 51.18      c
ATOM   9829  CG   LEU A1355    -15.334  63.111  -9.150  I.00 49.45      c
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ATOM   9830  CD2  LEU  A1355    -16.389   62.048   -9.094   1.00  47.73   C
ATOM   9831  GDI  LEU  A1355   --14.306   62.774  -10.210   1.00  45.22   C
ATOM   9832  O    TYR  A1356    -14.169   67.799   -3.595   1.00  53.35   O
ATOM   9833  N    TYR  A1356    -14.174   65.271   -5.216   1.00  52.74   N
ATOM   9834  CA.  TYR  A1356    -13.525   65.550   -3.948   I.00  49.63   C
ATOM   9835  C    TYR  A1356    -14.227   66.648   -3.194   1.00  52.30   C
ATOM   9836  CB   TYR  A1356    -12.087   65.982   -4.170   1.00  51.10   C
ATOM   9837  CG   TYR  A1356    -11.261   64.958   -4.863   I.00  51.09   C
ATOM   9838  GDI  TYR  A1356    -11.270   63.636   -4.437   1.00  52.45   C
ATOM   9839  CD2  TYR  A1356    -10.480   65.309   -5.959   1.00  52.61   C
ATOM   9840  CE1  TYR  A1356    -10.496   62.674   -5.081   I.00  60.77   C
ATOM   9841  CE2  TYR  A1356     -9.712   64.371   -6.615   1.00  62.88   C
ATOM   9842  CZ   TYR  A1356     -9.719   63.047   -6.173   1.00  64.89   C
ATOM   9843  OH   TYR  A1356     -8.962   62.112   -6.835   1.00  63.15   0
ATOM   9844  N    GLU  A1357    -14.867   66.319   -2.088   1.00  54.17   N
ATOM   9845  CA   GLU  A1357    -15.489   67.374   -1.332   1.00  48.34   C
ATOM   9846  C    GLU  A1357    -15.022   67.399    0.123   1.00  56.36   C
ATOM   9847  O    GLU  A1357    -14.576   66.382    0.666   I.00  56.99   0
ATOM   9848  CB   GLU  A1357    -17.022   67.281   -1.441   1.00  50.95   C
ATOM   9849  CG   GLU  A1357    -17.687   65.965   -1.151   1.00  49.22   C
ATOM   9850  CD   GLU  A1357    -19.157   65.976   -1.580   I.00  60.45   C
ATOM   9851  OE1  GLU  A1357    -20.053   65.682   -0.745   1.00  63.81   0
ATOM   9852  OE2  GLU  A1357    -19.427   66.290   -2.764   1.00  58.19   0
ATOM   9853  N    THR  A1358    -15.057   68.597    0.708   I.00  55.47   N
ATOM   9854  CA   THR  A1358    -14.855   68.815    2.133   1.00  50.61   C
ATOM   9855  C    THR  A1358    -16.148   69.388    2.646   1.00  54.05   C
ATOM   9856  O    THR  A1358    -16.520   70.484    2.224   I.00  54.18   0
ATOM   9857  CB   THR  A1358    -13.712   69.814    2.441   1.00  52.10   C
ATOM   9858  OG1  THR  A1358    -12.464   69.319    1.957   1.00  55.79   0
ATOM   9859  CG2  THR  A1358    -13.598   70.054    3.939   1.00  54.21   C
ATOM   9860  N    ARG  A1359    -16.840   68.686    3.541   1.00  53.02   N
ATOM   9861  CA   ARG  A1359    -18.068   69.246    4.093   1.00  55.73   C
ATOM   9862  C    ARG  A1359    -17.957   69.638    5.580   1.00  60.54   C
ATOM   9863  0    ARG  A1359    -17.420   68.900    6.413   I.00  56.03   0
ATOM   9864  CB   ARG  A1359    -19.260   68.297    3.893   1.00  52.34   C
ATOM   9865  CG   ARG  A1359    -18.926   66.896    3.484   1.00  63.22   C
ATOM   9866  CD   ARG  A1359    -20.193   66.029    3.371   I.00  66.67   C
ATOM   9867  ME   ARG  A1359    -20.869   66.182    2.090   1.00  61.70   N
ATOM   9868  CZ   ARG  A1359    -22.124   65.817    1.854   1.00  61.22   C
ATOM   9869  NH1  ARG  A1359    -22.842   65.278    2.819   I.00  65.71   N
ATOM   9870  NH2  ARG  A1359    -22.667   65.997    0.650   1.00  62.83   N
ATOM   9871  N    ILE  A1360    -18.487   70.820    5.888   1.00  54.68   N
ATOM   9872  CA   ILE  A1360    -18.436   71.381    7.227   1.00  55.23   C
ATOM   9873  C    ILE  A1360    -19.816   71.490    7.843   1.00  57.79   C
ATOM   9874  O    ILE  A1360    -20.629   72.264    7.369   1.00  62.49   O
ATOM   9875  CB   ILE  A1360    -17.821   72.769    7.210   1.00  55.72   C
ATOM   9876  CGI  ILE  A1360    -16.481   72.734    6.478   I.00  47.38   C
ATOM   9877  CG2  ILE  A1360    -17.738   73.329    8.635   1.00  52.67   C
ATOM   9878  CD1  ILE  A1360    -15.409   72.060    7.248   1.00  54.45   C
ATOM   9879  N    ASP  A1361    -20.092   70.727    8.892   I.00  58.70   N
ATOM   9880  CA   ASP  A1361    -21.361   70.867    9.592   1.00  59.16   C
ATOM   9881  C    ASP  A1361    -21.318   72.168   10.370   1.00  62.19   C
ATOM   9882  0    ASP  A1361    -20.441   72.361   11.205   I.00  67.14   0
ATOM   9883  CB   ASP  A1361    -21.600   69.682   10.519   1.00  61.83   C
ATOM   9884  CG   ASP  A1361    -22.960   69.725   11.210   1.00  73.19   C
ATOM   9885  OD1  ASP  A1361    -23.848   70.527   10.820   I.00  74.36   0
ATOM   9886  OD2  ASP  A1361    -23.145   68.924   12.154   1.00  74.83   0
ATOM   9887  O    LEU  A1362    -22.711   75.365   12.875   1.00  67.36   0
ATOM   9888  N    LEU  A1362    -22.248   73.076   10.102   1.00  67.74   N
ATOM   9889  CA   LEU  A1362    -22.197   74.384   10.757   1.00  66.62   C
ATOM   9890  C    LEU  A1362    -22.928   74.440   12.104   1.00  64.35   C
ATOM   9891  CB   LEU  A1362    -22.748   75.468    9.830   1.00  63.63   C
ATOM   9892  CG   LEU  A1362    -21.891   75.908    8.645   I.00  65.54   C
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ATOM   9893  GDI  LEU  A1362    -22.353  77.288   8.195  1.00 64.90       C
ATOM   9894  CD2  LEU  A1362    -20.388  75.883   8.955  1.00 59.07       C
ATOM   9895  O    SEP. A1363    -23.763  73.209  16.007  1.00 77.59       0
ATOM   9896  N    SER  A1363    -23.775  73.458  12.399  1.00 70.10       N
ATOM   9897  CA.  SER  A1363    -24.427  73.407  13.707  1.00 68.13       C
ATOM   9898  C    SER  A1363    -23.418  73.162  14.837  1.00 67.76       C
ATOM   9899  CB   SER  A1363    -25.529  72.335  13.736  1.00 66.35       C
ATOM   9900  OG   SER  A1363    -25.149  71.141  13.070  1.00 68.57       0
ATOM   9901  O    GLR  A1364    -19.232  73.902  16.323  1.00 81.65       0
ATOM   9902  N    GLN  A1364    -22.164  72.922  14.499  1.00 66.01       N
ATOM   9903  CA   GLN  A1364    -21.156  72.726  15.528  1.00 75.35       C
ATOM   9904  C    GLR  A1364    -20.283  73.950  15.680  1.00 78.81       C
ATOM   9905  CB   GLN  A1364    -20.292  71.511  15.212  1.00 73.08       C
ATOM   9906  CG   GLN  A1364    -21.057  70.217  15.320  1.00 76.45       C
ATOM   9907  CD   GLN  A1364    -20.510  69.165  14.400  1.00 80.50       C
ATOM   9908  OE1  GLN  A1364    -19.298  68.918  14.370  1.00 83.20       0
ATOM   9909  NE2  GLN  A1364    -21.397  68.541  13.623  1.00 75.80       N
ATOM   9910  O    LEU  A1365    -20.353  78.354  16.260  1.00 77.77       O
ATOM   9911  N    LEU  A1365    -20.704  75.043  15.064  1.00 75.17       N
ATOM   9912  CA   LEU  A1365    -19.950  76.272  15.166  1.00 72.49       C
ATOM   9913  C    LEU  A1365    -20.795  77.251  15.961  1.00 74.82       C
ATOM   9914  CB   LEU  A1365    -19.583  76.825  13.786  1.00 69.25       C
ATOM   9915  CG   LEU  A1365    -18.859  75.898  12.799  1.00 72.61       C
ATOM   9916  CD1  LEU  A1365    -18.123  76.704  11.743  1.00 69.38       C
ATOM   9917  CD2  LEU  A1365    -17.896  74.920  13.479  1.00 71.28       C
ATOM   9918  O    GLY  A1366    -21.412  78.868  18.651  1.00 79.67       0
ATOM   9919  N    GLY  A1366    -22.007  76.826  16.318  1.00 71.74       N
ATOM   9920  CA   GLY  A1366    -22.855  77.601  17.205  1.00 80.22       C
ATOM   9921  C    GLY  A1366    -22.195  77.917  18.537  1.00 82.53       C
TER
ATOM   9922  P       G B   1     -8.966  70.152 -39.923  1.00 87.23       P
ATOM   9923  OP1     G B   1     -6.786  68.677 -40.111  1.00 89.82       0
ATOM   9924  OP2     G B   1     -7.265  71.006 -41.109  1.00 81.10       0
ATOM   9925  OP3     G B   1     -8.076  70.351 -38.959  1.00 91.73       0
ATOM   9926  05'     G B   1     -5.644  70.710 -39.226  1.00 74.25       0
ATOM   9927  C5'     G B   1     -5.393  70.470 -37.847  1.00 74.53       C
ATOM   9928  C4'     G B   1     -3.924  70.575 -37.505  1.00 77.47       C
ATOM   9929  04'     G B   1     -3.179  69.518 -38.186  1.00 76.51       0
ATOM   9930  C3'     G B   1     -3.209  71.861 -37.920  1.00 71.81       C
ATOM   9931  03'     G B   1     -3.419  72.957 -37.037  1.00 74.46       0
ATOM   9932  C2'     G B   1     -1.761  71.396 -38.007  1.00 74.79       C
ATOM   9933  02'     G B   1     -1.216  71.185 -36.712  1.00 79.33       0
ATOM   9934  CI'     G B   1     -1.949  70.029 -38.659  1.00 72.84       C
ATOM   9935  N9      G B   1     -2.051  70.173 -40.129  1.00 70.42       N
ATOM   9936  C8      G B   1     -3.169  69.991 -40.920  1.00 68.97       C
ATOM   9937  N7      G B   1     -2.951  70.231 -42.187  1.00 67.96       N
ATOM   9938  C5      G B   1     -1.608  70.596 -42.244  1.00 63.09       C
ATOM   9939  C4      G B   1     -1.043  70.578 -40.981  1.00 64.95       C
ATOM   9940  Nl      G B   1      0.509  71.269 -42.963  1.00 55.74       N
ATOM   9941  C2      G B   1      0.977  71.220 -41.664  1.00 61.17       C
ATOM   9942  N3      G B   1      0.233  70.871 -40.621  1.00 61.05       N
ATOM   9943  C6      G B   1     -0.792  70.963 -43.353  1.00 57.84       C
ATOM   9944  06      G B   1     -1.123  71.047 -44.546  1.00 60.74       0
ATOM   9945  N2      G B   1      2.263  71.539 -41.457  1.00 58.48       N
ATOM   9946  05'     G B   2     -2.231  74.895 -38.169  1.00 67.99       O
ATOM   9947  C4'     G B   2      0.166  75.121 -38.120  1.00 64.65       C
ATOM   9948  C3'     G B   2      0.267  76.370 -38.975  1.00 61.96       C
ATOM   9949  C2'     G B   2      1.409  75.999 -39.917  1.00 63.39       C
ATOM   9950  P       G B   2     -3.657  74.452 -37.612  1.00 76.47       P
ATOM   9951  OP1     G B   2     -3.971  75.327 -36.452  1.00 74.52       0
ATOM   9952  OP2     G B   2     -4.570  74.403 -38.789  1.00 72.60       0
ATOM   9953  C5'     G B   2     -1.096  74.935 -37.325  1.00 60.47       C
ATOM   9954  04'     G B   2      0.331  74.047 -39.093  1.00 65.22       0
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ATOM    9955  03'   G B   2       0.497  77.555 -38.234  1.00 62.01           O
ATOM    9956  02'   G B   2       2.656  76.076 -39.246  1.00 61.62           O
ATOM    9957  CI'   G B   2       1.101  74.524 -40.189  1.00 60.68           C
ATOM    9958  N9    G B   2       0.366  74.376 -41.465  1.00 56.24           N
ATOM    9959  C8    G B   2      -0.961  74.100 -41.683  1.00 57.83           C
ATOM    9960  N1    G B   2      -1.281  74.093 -42.954  1.00 58.89           N
ATOM    9961  C5    G B   2      -0.094  74.384 -43.626  1.00 62.13           C
ATOM    9962  C4    G B   2       0.926  74.565 -42.714  1.00 60.29           C
ATOM    9963  Ml    G B   2       1.543  74.810 -45.250  1.00 62.14           N
ATOM    9964  C2    G B   2       2.485  74.975 -44.269  1.00 64.30           C
ATOM    9965  N3    G B   2       2.224  74.862 -42.970  1.00 65.35           N
ATOM    9966  C6    G B   2       0.205  74.499 -45.022  1.00 63.16           C
ATOM    9967  06    G B   2      -0.544  74.371 -45.997  1.00 65.30           O
ATOM    9968  N2    G B   2       3.726  75.278 -44.679  1.00 63.75           N
ATOM    9969  05'   A B   3       1.381  79.079 -40.052  1.00 66.00           O
ATOM    9970  C4'   A B   3       3.579  79.499 -40.972  1.00 64.40           C
ATOM    9971  C3'   A B   3       3.127  80.693 -41.795  1.00 60.65           C
ATOM    9972  C2'   A B   3       3.689  80.388 -43.181  1.00 65.30           C
ATOM    9973  P     A B   3       0.277  79.001 -38.908  1.00 62.19           P
ATOM    9974  OF1   A B   3       0.653  80.010 -37.881  1.00 71.43           0
ATOM    9975  OP2   A B   3      -1.057  79.107 -39.555  1.00 64.13           0
ATOM    9976  C5'   A B   3       2.763  79.203 -39.740  1.00 62.34           C
ATOM    9977  04'   A B   3       3.508  78.382 -41.901  1.00 66.06           0
ATOM    9978  03'   A B   3       3.577  81.921 -41.265  1.00 60.25           0
ATOM    9979  02'   A B   3       5.063  80.763 -43.270  1.00 64.19           0
ATOM    9980  CI'   A B   3       3.582  78.858 -43.230  1.00 60.94           C
ATOM    9981  N9    A B   3       2.401  78.372 -43.980  1.00 61.91           N
ATOM    9982  C8    A B   3       1.245  77.800 -43.497  1.00 56.84           C
ATOM    9983  N7    A B   3       0.404  77.436 -44.436  1.00 57.87           N
ATOM    9984  C5    A B   3       1.039  77.780 -45.622  1.00 61.93           C
ATOM    9985  C4    A B   3       2.274  78.351 -45.353  1.00 62.05           C
ATOM    9986  Nl    A B   3       1.544  78.109 -47.900  1.00 62.52           N
ATOM    9987  C2    A B   3       2.706  78.628 -47.491  1.00 63.20           C
ATOM    9988  N3    A B   3       3.170  78.792 -46.254  1.00 62.84           N
ATOM    9989  C6    A B   3       0.677  77.657 -46.976  1.00 61.75           C
ATOM    9990  N6    A B   3      -0.467  77.135 -47.404  1.00 61.15           N
ATOM    9991  05'   A B   4       3.238  83.565 -43.145  1.00 60.97           O
ATOM    9992  C4'   A B   4       4.722  84.181 -44.934  1.00 58.20           C
ATOM    9993  C3'   A B   4       3.677  85.049 -45.600  1.00 59.03           C
ATOM    9994  C2'   A B   4       3.760  84.597 -47.047  1.00 57.11           C
ATOM    9995  P     A B   4       2.804  83.275 -41.645  1.00 65.99           P
ATOM    9996  OP1   A B   4       3.334  84.365 -40.786  1.00 67.47           0
ATOM    9997  OP2   A B   4       1.344  82.995 -41.647  1.00 63.31           0
ATOM    9998  C5'   A B   4       4.555  83.991 -43.452  1.00 61.80           C
ATOM    9999  04'   A B   4       4.574  82.907 -45.605  1.00 64.56           0
ATOM   10000  03'   A B   4       3.899  86.437 -45.419  1.00 59.84           0
ATOM   10001  02'   A B   4       4.908  85.151 -47.663  1.00 59.21           0
ATOM   10002  CI'   A B   4       3.986  83.103 -46.873  1.00 59.88           C
ATOM   10003  N9    A B   4       2.727  82.337 -46.955  1.00 60.67           N
ATOM   10004  C8    A B   4       1.923  81.852 -45.954  1.00 59.47           C
ATOM   10005  N7    A B   4       0.874  81.197 -46.398  1.00 61.04           N
ATOM   10006  C5    A B   4       0.993  81.260 -47.778  1.00 60.73           C
ATOM   10007  C4    A B   4       2.133  81.953 -48.133  1.00 62.80           C
ATOM   10008  Ml    A B   4       0.634  81.010 -50.091  1.00 69.45           N
ATOM   10009  C2    A B   4       1.763  81.701 -50.286  1.00 63.24           C
ATOM   10010  N3    A B   4       2.581  82.212 -49.378  1.00 66.47           N
ATOM   10011  C6    A B   4       0.211  80.763 -48.832  1.00 65.87           C
ATOM   10012  N6    A B   4      -0.917  80.067 -48.672  1.00 68.07           N
ATOM   10013  05'   A B   5       2.429  87.360 -47.269  1.00 56.05           O
ATOM   10014  C4'   A B   5       2.900  87.646 -49.612  1.00 54.28           C
ATOM   10015  C3'   A B   5       1.593  88.294 -49.977  1.00 55.43           C
ATOM   10016  C2'   A B   5       1.090  87.424 -51.109  1.00 57.71           C
ATOM   10017  P     A B   5       2.705  87.473 -45.706  1.00 54.24           P
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ATOM   10018  OP1   A B  5     3.194   88.866  -45:472  1.00  52.69   O
ATOM   10019  OP2   A B  5     1,528   86.907  -45,002  1,00  63.86   O
ATOM   10020  C5'   A B  5     3..344  87,909  -48:204  1,00  57,18   C
ATOM   10021  04'   A B  5     2.643   86:233  -49:790  1.00  61.22   O
ATOM   10022  03'   A B  5     1,745   89.652  -50,329  1,00  64,76   O
ATOM   10023  02'   A B  5     1.786   87,740  -52 :298  1,00  55,38   O
ATOM   10024  CI'   A B  5     1.528   86,052  -50.637  1,00  56,95   c
ATOM   10025  N9    A B  5     0,487   85.362  -49,858  1,00  59,67   N
ATOM   10026  C8    A B  5     0.394   85:317  -48:492  1,00  62.93   C
ATOM   10027  N7    A B  5    -0.608   84,597  -48:045  1,00  63,39   N
ATOM   10028  C5    A B  5    -1,206   84.129  -49,197  1,00  59.75   C
ATOM   10029  C4    A B  5    -0.545   84.584  -50:324  1,00  62.69   C
ATOM   10030  N1.   A B  5    -2.667   83,022  -50.646  1,00  65,66   N
ATOM   10031  C2    A B  5    -1.932   83:532  -51:646  1.00  68.74   c
ATOM   10032  N3    A B  5    -0,861   84.319  -51,602  1,00  68.15   N
ATOM   10033  C6    A B  5    -2.322   83,311  -49:381  1,00  62,00   C
ATOM   10034  N6    A B  5    -3.037   82:813  -48:371  1.00  64.63   N
ATOM   10035  05'   U B  6    -0,589   90.234  -50,993  1,00  59,35   O
ATOM   10036  C4'   υ B  6    -1.595   89,718  -53:102  1,00  64.98   C
ATOM   10037  C3'   u B  6    -2.839   90,431  -52 .610  1,00  60,23   c
ATOM   10038  C2'   u B  6    -3,954   89.450  -52 ,928  1,00  66,24   C
ATOM   10039  P     u B  6     0.556   90:663  -49:984  1,00  55.38   P
ATOM   10040  OF1   u B  6     0.938   92,068  -50.306  1,00  54,32   0
ATOM   10041  OP2   u B  6     0,131   90.258  -48,617  1,00  49.83   0
ATOM   10042  C5'   u B  6    -0.347   90.158  -52 :391  1,00  62.16   C
ATOM   10043  04'   u B  6    -1.861   88,310  -52.848  1,00  55,15   0
ATOM   10044  03'   u B  6    -2,979   91.695  -53.214  1,00  67.22   0
ATOM   10045  02'   u B  6    -4,323   89.559  -54,294  1,00  62.60   0
ATOM   10046  CI'   u B  6    -3.253   88,102  -52.703  1,00  6.1,61   c
ATOM   10047  Nl    u B  6    -3.505   87:506  -51:362  1.00  65.73   N
ATOM   10048  C2    u B  6    -4,504   86.561  -51,292  1,00  66.85   c
ATOM   10049  N3    υ B  6    -4.708   85,979  -50:064  1,00  6.3,20   N
ATOM   10050  C4    u B  6    -4.015   86:238  -48:901  1.00  61.09   c
ATOM   10051  C5    u B  6    -2,985   87.226  -49,045  1,00  59,65   c
ATOM   10052  C6    υ B  6    -2.764   87,806  -50:236  1,00  61,95   c
ATOM   10053  02    u B  6    -5.161   86,263  -52 .268  1,00  68,11   0
ATOM   10054  04    u B  6    -4,316   85.623  -47,874  1,00  54,84   0
ATOM   10055  05'   u B  7    -5.360   92.373  -53:480  1,00  76.29   0
ATOM   10056  C4'   u B  7    -7.698   91,879  -53.059  1,00  79,80   c
ATOM   10057  C3'   u B  7    -8,723   92.092  -51,965  1,00  79.95   c
ATOM   10058  C2'   u B  7    -9,365   90.713  -51,861  1,00  79.33   c
ATOM   10059  P     u B  7    -4.052   92,740  -52.656  1,00  72,84   P
ATOM   10060  OP1   u B  7    -3.577   94:101  -53:003  1.00  62.69   0
ATOM   10061  OP2   u B  7    -4,370   92.373  -51,255  1,00  77.09   0
ATOM   10062  C5'   υ B  7    -6.606   92,915  -53:103  1,00  79,25   c
ATOM   10063  04'   u B  7    -7.168   90:553  -52 .769  1.00  77.09   0
ATOM   10064  03'   u B  7    -9,602   93.176  -52 ,219  1,00  77,67   0
ATOM   10065  02'   υ B  7   -10.238   90,477  -52 :956  1,00  75,95   0
ATOM   10066  CI'   u B  7    -8.130   89,815  -52 .027  1,00  79,17   c
ATOM   10067  N1    u B  7    -7,554   89.401  -50,716  1,00  75,54   N
ATOM   10068  C2    u B  7    -8.085   88:263  -50:131  1,00  75.26   c
ATOM   10069  N3    u B  7    -7.550   87,889  -48.911  1,00  72,02   N
ATOM   10070  C4    u B  7    -6,547   88:528  -48,199  1,00  68.13   c
ATOM   10071  C5    u B  7    -6.051   89:702  -48:860  1,00  64.68   c
ATOM   10072  C6    u B  7    -6.554   90,089  -50.051  1,00  72,54   c
ATOM   10073  02    u B  7    -8,967   87:619  -50,666  1,00  79.56   0
ATOM   10074  04    u B  7    -8,169   88:063  -47,106  1,00  58.82   0
ATOM   10075  P     G B  8    -9.328   94,592  -51.506  1,00  79,44   P
ATOM   10076  OP1   G B  8    -9:824   95:664  -52 .394  1.00  81.66   0
ATOM   10077  OP2   G B  8    -7,930   94.678  -51,026  1,00  89.34   0
ATOM   10078  05'   G B  8   -10.189   94,506  -50:170  1,00  88,57   0
ATOM   10079  C5'   G B  8   -11.602   94:603  -50.209  1.00  85.66   c
ATOM   10080  C4'   G B  8   -12,267   93.317  -49,792  1,00  81,14   c
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ATOM  10081  04'   G B   8    -11.322  92.219 -49.793  1.00 82.73   O
ATOM  10082  C3'   G B   8   --12.839  93.285 -48.392  1.00 83.07   C
ATOM  10083  03'   G B   8    -14.067  93.973 -48.299  1.00 85.34   O
ATOM  10084  C2'   G B   8    -12.964  91.793 -48.136  1.00 80.72   C
ATOM  10085  02'   G B   8    -14.082  91.268 -48.839  1.00 80.03   O
ATOM  10086  CI '  G B   8    -11.693  91.276 -48.805  1.00 78.69   C
ATOM  10087  N9    G B   8    -10.583  91.113 -47.841  1.00 77.46   N
ATOM  10088  C8    G B   8     -9.401  91.815 -47.753  1.00 78.66   C
ATOM  10089  N7    G B   8     -8.620  91.409 -46.782  1.00 73.05   N
ATOM  10090  C5    G B   8     -9.325  90.368 -46.188  1.00 70.61   C
ATOM  10091  C4    G B   8    -10.530  90.180 -46.838  1.00 72.78   C
ATOM  10092  Ml    G B   8    -10.016  88.616 -44.843  1.00 70.30   N
ATOM  10093  C2    G B   8    -11.187  88.515 -45.557  1.00 73.18   C
ATOM  10094  N3    G B   8    -11.498  89.287 -46.582  1.00 72.00   N
ATOM  10095  C6    G B   8     -9.003  89.524 -45.085  1.00 68.48   C
ATOM  10096  06    G B   8     -8.000  89.484 -44.357  1.00 67.50   O
ATOM  10097  N2    G B   8    -12.041  87.555 -45.156  1.00 73.46   N
ATOM  10098  05'   G B   9    -15.192  95.159 -46.433  1.00 85.84   O
ATOM  10099  C4'   G B   9    -15.664  93.088 -45.257  1.00 80.62   C
ATOM  10100  C3'   G B   9    -16.029  92.720 -43.829  1.00 78.37   C
ATOM  10101  C2'   G B   9    -15.938  91.200 -43.796  1.00 74.53   C
ATOM  10102  P     G B   9    -14.142  95.408 -47.590  1.00 81.91   P
ATOM  10103  OF1   G B   9    -14.744  96.324 -48.592  1.00 93.73   0
ATOM  10104  OP2   G B   9    -12.863  95.761 -46.919  1.00 82.41   0
ATOM  10105  C5'   G B   9    -14.839  94.348 -45.334  1.00 83.60   C
ATOM  10106  04'   G B   9    -14.875  91.971 -45.746  1.00 78.66   0
ATOM  10107  03'   G B   9    -17.273  93.273 -43.443  1.00 76.97   0
ATOM  10108  02'   G B   9    -17.108  90.602 -44.326  1.00 76.43   0
ATOM  10109  CI '  G B   9    -14.800  90.960 -44.774  1.00 74.42   C
ATOM  10110  N9    G B   9    -13.465  91.085 -44.145  1.00 69.35   N
ATOM  10111  C8    G B   9    -12.539  92.045 -44.499  1.00 69.15   C
ATOM  10112  N1    G B   9    -11.422  91.982 -43.834  1.00 69.86   N
ATOM  10113  C5    G B   9    -11.604  90.894 -42.991  1.00 62.65   C
ATOM  10114  C4    G B   9    -12.853  90.326 -43.164  1.00 63.93   C
ATOM  10115  Nl    G B   9    -11.262  89.252 -41.384  1.00 57.95   N
ATOM  10116  C2    G B   9    -12.521  88.754 -41.625  1.00 59.14   C
ATOM  10117  N3    G B   9    -13.369  89.261 -42.513  1.00 63.32   N
ATOM  10118  C6    G B   9    -10.710  90.342 -42.042  1.00 58.22   C
ATOM  10119  06    G B   9     -9.571  90.719 -41.765  1.00 57.81   0
ATOM  10120  N2    G B   9    -12.870  87.692 -40.888  1.00 54.99   N
ATOM  10121  05'   G B  10    -17.080  93.767 -41.015  1.00 73.95   O
ATOM  10122  C4'   G B  10    -17.159  91.628 -39.875  1.00 69.29   C
ATOM  10123  C3'   G B  10    -16.752  92.073 -38.484  1.00 70.01   C
ATOM  10124  C2'   G B  10    -15.736  90.998 -38.106  1.00 62.21   C
ATOM  10125  P     G B  10    -17.266  94.499 -42.416  1.00 83.96   P
ATOM  10126  OP1   G B  10    -18.613  95.119 -42.461  1.00 93.18   0
ATOM  10127  OP2   G B  10    -16.048  95.323 -42.635  1.00 83.38   0
ATOM  10128  C5'   G B  10    -17.872  92.630 -40.735  1.00 66.10   C
ATOM  10129  04'   G B  10    -15.904  91.214 -40.471  1.00 67.47   0
ATOM  10130  03'   G B  10    -17.853  92.171 -37.585  1.00 70.02   0
ATOM  10131  02'   G B  10    -16.396  89.802 -37.729  1.00 66.80   0
ATOM  10132  CI '  G B  10    -15.044  90.743 -39.450  1.00 63.03   C
ATOM  10133  N9    G B  10    -13.733  91.417 -39.530  1.00 59.06   N
ATOM  10134  C8    G B  10    -13.381  92.497 -40.289  1.00 56.40   C
ATOM  10135  N7    G B  10    -12.142  92.853 -40.115  1.00 54.34   N
ATOM  10136  C5    G B  10    -11.642  91.955 -39.173  1.00 55.95   C
ATOM  10137  C4    G B  10    -12.615  91.058 -38.802  1.00 55.01   C
ATOM  10138  K1    G B  10    -10.248  90.790 -37.694  1.00 51.54   N
ATOM  10139  C2    G B  10    -11.282  89.951 -37.390  1.00 55.86   C
ATOM  10140  N3    G B  10    -12.511  90.040 -37.920  1.00 50.91   N
ATOM  10141  C6    G B  10    -10.346  91.831 -38.593  1.00 47.58   C
ATOM  10142  06    G B  10     -9.352  92.513 -38.788  1.00 47.78   0
ATOM  10143  N2    G B  10    -10.964  89.013 -36.487  1.00 50.24   N
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ATOM	10144	05'	U	B	11	-16.774	92.475	-35.309	1.00	62.88	O
ATOM	10145	C4'	U	B	11	-15.921	90.642	-33.921	1.00	62.84	C
ATOM	10146	C3'	U	B	11	-15.360	91.505	-32.807	1.00	62.64	C
ATOM	10147	C2'	U	B	11	-13.974	90.912	-32.605	1.00	57.60	c
ATOM	10148	P	U	B	11	-17.808	93.161	-36.313	1.00	66.00	P
ATOM	10149	OP1	U	B	11	-19.148	93.099	-35.680	1.00	71.84	0
ATOM	10150	OF2	u	B	11	-17.264	94.474	-36.734	1.00	59.83	0
ATOM	10151	C5'	u	B	11	-17.074	91.217	-34.717	1.00	65.19	C
ATOM	10152	04'	u	B	11	-14.775	90.417	-34.777	1.00	57.33	0
ATOM	10153	03'	u	B	11	-16.143	91.504	-31.633	1.00	68.21	0
ATOM	10154	02'	u	B	11	-14.061	89.675	-31.913	1.00	62.96	0
ATOM	10155	CI'	u	B	11	-13.580	90.609	-34.040	1.00	56.69	c
ATOM	10156	N1.	u	B	11	-12.803	91.699	-34.671	1.00	52.71	N
ATOM	10157	C2	u	B	11	-11.452	91.850	-34.382	1.00	50.38	c
ATOM	10158	N3	u	B	11	-10.825	92.879	-35.058	1.00	46.06	N
ATOM	10159	C4	U	B	11	-11.390	93.733	-35.991	1.00	48.93	c
ATOM	10160	C5	u	B	11	-12.781	93.497	-36.235	1.00	55.41	c
ATOM	10161	C6	u	B	11	-13.419	92.519	-35.590	1.00	57.62	c
ATOM	10162	02	U	B	11	-10.860	91.147	-33.577	1.00	51.69	0
ATOM	10163	04	u	B	11	-10.722	94.618	-36.542	1.00	47.46	0
ATOM	10164	05'	G	B	12	-14.483	92.656	-30.100	1.00	56.50	0
ATOM	10165	C4'	G	B	12	-12.626	91.769	-28.881	1.00	50.88	c
ATOM	10166	C3'	G	B	12	-11.859	92.813	-28.099	1.00	48.01	c
ATOM	10167	C2'	G	B	12	-10.451	92.683	-28.666	1.00	44.43	c
ATOM	10168	P	G	B	12	-15.992	92.730	-30.609	1.00	71.91	P
ATOM	10169	OP1	G	B	12	-16.890	92.430	-29.463	1.00	74.94	0
ATOM	10170	OP2	G	B	12	-16.046	93.985	-31.408	1.00	56.20	0
ATOM	10171	C5'	G	B	12	-14.118	91.934	-28.944	1.00	45.20	c
ATOM	10172	04'	G	B	12	-12.057	91.858	-30.205	1.00	53.37	0
ATOM	10173	03'	G	B	12	-11.917	92.565	-26.709	1.00	50.58	0
ATOM	10174	02'	G	B	12	-9.824	91.531	-28.119	1.00	49.78	0
ATOM	10175	CI'	G	B	12	-10.742	92.365	-30.121	1.00	45.02	c
ATOM	10176	N9	G	B	12	-10.577	93.480	-31.067	1.00	42.31	N
ATOM	10177	C8	G	B	12	-11.557	94.018	-31.870	1.00	46.68	c
ATOM	10178	N1	G	B	12	-11.134	94.959	-32.661	1.00	47.61	N
ATOM	10179	C5	G	B	12	-9.766	95.016	-32.397	1.00	45.36	c
ATOM	10180	C4	G	B	12	-9.413	94.113	-31.419	1.00	40.83	c
ATOM	10181	Ml	G	B	12	-7.524	95.600	-32.396	1.00	45.80	N
ATOM	10182	C2	G	B	12	-7.286	94.668	-31.423	1.00	43.73	c
ATOM	10183	N3	G	B	12	-8.210	93.888	-30.886	1.00	43.05	N
ATOM	10184	C6	G	B	12	-8.766	95.844	-32.955	1.00	44.94	c
ATOM	10185	06	G	B	12	-8.881	96.698	-33.831	1.00	47.16	0
ATOM	10186	N2	G	B	12	-6.010	94.580	-31.011	1.00	43.52	N
ATOM	10187	05'	C	B	13	-10.371	94.266	-25.733	1.00	46.66	0
ATOM	10188	C4'	C	B	13	-8.005	94.089	-25.364	1.00	44.26	c
ATOM	10189	C3'	C	B	13	-7.895	95.551	-24.971	1.00	42.02	c
ATOM	10190	C2'	C	B	13	-6.695	96.012	-25.788	1.00	45.49	c
ATOM	10191	P	C	B	13	-11.879	93.782	-25.672	1.00	51.89	P
ATOM	10192	OF1	C	B	13	-12.151	93.113	-24.365	1.00	49.35	0
ATOM	10193	OP2	C	B	13	-12.730	94.893	-26.158	1.00	41.90	0
ATOM	10194	C5'	C	B	13	-y.352	93.463	-25.159	1.00	39.87	c
ATOM	10195	04'	C	B	13	-7.682	94.097	-26.777	1.00	44.32	0
ATOM	10196	03'	C	B	13	-7.758	95.743	-23.580	1.00	50.00	0
ATOM	10197	02'	C	B	13	-5.491	95.514	-25.220	1.00	46.79	0
ATOM	10198	CI'	C	B	13	-6.931	95.261	-27.089	1.00	41.74	c
ATOM	10199	Nl	C	B	13	-7.695	96.044	-28.077	1.00	38.96	N
ATOM	10200	C2	C	B	13	-6.995	96.870	-28.929	1.00	43.07	c
ATOM	10201	N3	C	B	13	-7.666	97.581	-29.865	1.00	45.16	N
ATOM	10202	C4	C	B	13	-8.987	97.461	-29.980	1.00	43.88	c
ATOM	10203	C5	C	B	13	-9.744	96.620	-29.133	1.00	38.86	c
ATOM	10204	C6	C	B	13	-9.058	95.932	-28.211	1.00	43.96	c
ATOM	10205	02	C	B	13	-5.771	96.940	-28.783	1.00	49.41	0
ATOM	10206	N4	C	B	13	-9.582	98.166	-30.934	1.00	45.65	N

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ATOM   10207   05'   G  B   14       --7.350   98..201  -23..591   1.00  41.68          O
ATOM   10208   C4'   G  B   14       -5.,310   99..349  -24,056    1,00  43..43         C
ATOM   10209   C3'   G  B   14       -5..823  100.,773  -24..012   1.00  39,.78         C
ATOM   10210   C2'   G  B   14       --5..234 101.,354  -25,282    1.00  45..86         c
ATOM   10211   P     G  B   14       -8.,275   97. 113  -22.,916   1,00  46..27         P
ATOM   10212   OP1   G  B   14       -7.978    97.,112  -21..465   1.00  47,67          0
ATOM   10213   OF2   G  B   14       --9..660  97.,332  -23..413   1,00  45,.67         0
ATOM   10214   C5'   G  B   14       -6.,017   98. 358  -23,173    1,00  37.10          C
ATOM   10215   04'   G  B   14       -5..460   98..994  -25,462    1,00  40..67         0
ATOM   10216   03'   G  B   14       --5..479 101.,479  —22.835    1,00  45,.94         0
ATOM   10217   02'   G  B   14       -.3.,850 101..607  -25,101    1,00  48..12         0
ATOM   10218   CI'   G  B   14       -5..391  100..170  -26..248   1,00  45..00         c
ATOM   10219   N9    G  B   14       -6. 611  100.,315  -27.065    1,00  43,11          N
ATOM   10220   C8    G  B   14       --7.839   99.730   -26..892   1.00  42.50          c
ATOM   10221   N7    G  B   14       -8.,697  100..088  -27,801    1,00  41.24          N
ATOM   10222   C5    G  B   14       -8..023  100.,977  -28.613    1.00  38,.78         C
ATOM   10223   C4    G  B   14       --6..728 101.,111  -28,165    1.00  40..43         c
ATOM   10224   N1    G  B   14       -7„419   102. 474  -30.,305   1,00  42.57          N
ATOM   10225   C2    G  B   14       -6..142  102.,523  -29..762   1.00  48,.09         C
ATOM   10226   N3    G  B   14       --5..754 101.,864  -28.685    1,00  45,.32         N
ATOM   10227   C6    G  B   14       -8.,448  101. 704  -29.,760   1,00  39..30         C
ATOM   10228   06    G  B   14       -9.547   101.,686  -30.,310   1,00  42.73          O
ATOM   10229   N2    G  B   14       --5..242 103.,302  -30..362   1,00  47,42          N
ATOM   10230   05'   C  B   15       -6,,088  .103..886 -2.3.,248   1,00  44.27          O
ATOM   10231   C4'   C  B   15       -4.570   105..329  -24,448    1,00  47.17          C
ATOM   10232   C3'   C  B   15       -5. 489  106,544   -24 .486    1,00  42,70          C
ATOM   10233   C2'   c  B   15       -5.,413  106.943   -25,943    1,00  44.90          C
ATOM   10234   P     c  B   15       9,455    102..660  -22.,318   1,00  43..30         P
ATOM   10235   OP1   c  B   15       -6. 165  102.,970  -20. 901    1,00  39,60          O
ATOM   10236   OP2   C  B   15       --7,787  102.,200  -22.,721   1.00  40..36         O
ATOM   10237   C5'   c  B   15       -4,763   104 .377  -23,296    1,00  46.71          C
ATOM   10238   04'   c  B   15       -4.8.14   104.,661  -25.7.19    1.00  44,94          0
ATOM   10239   03'   C  B   15       --5..034 107 .565   -23.637    1.00  43..90         0
ATOM   10240   02'   c  B   15       -4„169    .107.582  -26,166    1,00  42.30          0
ATOM   10241   CI'   c  B   15       -5...389  105.,572  -26.627    1.00  46,.02         c
ATOM   10242   Nl    c  B   15       --6..752 105.,104  -26.979    1,00  45,.18         N
ATOM   10243   C2    c  B   15       -7„285    .105. 533 -28,195    1,00  46..17         c
ATOM   10244   N3    c  B   15       -8.,524   105.,138  -28,562    1,00  42.45          N
ATOM   10245   C4    c  B   15       -9. 232   104.,346  -27.768    1,00  4.1,90          C
ATOM   10246   C5    c  B   15       -8,,725   .103..870 -26.,522   1,00  37.55          C
ATOM   10247   C6    c  B   15       -7„488    104 .272  -26,171    1,00  40..88         C
ATOM   10248   02    c  B   15       -6. 596   106,283   -28. 902    1,00  47,00          0
ATOM   10249   N4    C  B   15       -10.,455  103.,999  -28,186    1.00  36..91         N
ATOM   10250   05'   u  B   16       9,570    109..461  -24,045    1,00  46..28         0
ATOM   10251   C4'   υ  B   16       -6..2.17  110.,885  -25.976    1.00  4.3,.61         c
ATOM   10252   C3'   u  B   16       --7.514   Ill ,654  -25,782    1,00  48..85         c
ATOM   10253   C2'   u  B   16       -8.,029   111.730   -27,195    1,00  43..44         c
ATOM   10254   P     υ  B   16       -6..055   108.,524  -22.867    1.00  47,87          P
ATOM   10255   OF1   u  B   16       --5..246 109.,329  -21 .909    1,00  44,55          0
ATOM   10256   OP2   u  B   16       -7,145    .107.709  -22.,304   1,00  47.66          0
ATOM   10257   C5'   u  B   16       -5.,628   110.,228  -24,767    1,00  45..17         c
ATOM   10258   04'   u  B   16       --6..551 109.,898  -26.972    1,00  45,.22         0
ATOM   10259   03'   u  B   16       -7,312    112 .933  -25,218    1,00  50..60         0
ATOM   10260   02'   u  B   16       -7,229    112.,672  -27,880    1,00  46..59         0
ATOM   10261   CI'   u  B   16       -7.665    110.,336  -27.7.14   1,00  47,11          c
ATOM   10262   Nl    u  B   16       -8.,759   109..349  -27.,523   1,00  43..99         N
ATOM   10263   C2    u  B   16       -9.,770   109..275  -28,457    1,00  45..64         c
ATOM   10264   N3    u  B   16       ~10. 724  108.,322  -28. 172    1,00  43,90          N
ATOM   10265   C4    u  B   16       -10.,766  107 ,462  -27..095    1.00  44.87          c
ATOM   10266   C5    u  B   16       -9.,672   107..591  -26,203    1,00  40..01         C
ATOM   10267   C6    υ  B   16       -8..744   108.,505  -26.444    1.00  42,45          C
ATOM   10268   02    u  B   16       -9..836   110.,006  -29,443    1.00  49..51         O
ATOM   10269   04    u  B   16       -11,696   .106. 654 -26,982    1,00  44.52          0
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ATOM   10270  05 '  U B  17     --9.706  113.677  -25.142  1.00  37.80      O
ATOM   10271  C4 '  U B  17     --10.972 114.598  -26.979  1.00  43.98      C
ATOM   10272  C3 '  U B  17     -12.361  114.708  -26.360  1.00  40.48      C
ATOM   10273  C2 '  u B  17     -13.198  114.283  -27.549  1.00  41.36      c
ATOM   10274  P    u B  17      -8.407  113.559  -24.232  1.00  46.63      P
ATOM   10275  OP1   U B  17      -7.851  114.880  -23.900  1.00  47.33      0
ATOM   10276  OF2  u B  17     --8.804  112.632  -23.151  1.00  43.80      0
ATOM   10277  C5 '  u B  17      -9.757  114.682  -26.107  1.00  43.24      C
ATOM   10278  04 '  u B  17     --11.026 113.342  -27.705  1.00  47.42      0
ATOM   10279  03 '  u B  17     -12.670  116.025  -25.900  1.00  41.72      0
ATOM   10280  02 '  u B  17     -13.134  115.310  -28.520  1.00  44.97      0
ATOM   10281  CI '  u B  17     -12.369  113.107  -28.088  1.00  41.16      C
ATOM   10282  in.  u B  17     -12.846  111.830  -27.518  1.00  44.02      N
ATOM   10283  C2   u B  17     -14.079  111.413  -27.997  1.00  44.11      c
ATOM   10284  N3   u B  17     -14.560  110.262  -27.463  1.00  39.28      N
ATOM   10285  C4   U B  17     -13.972  109.536  -26.479  1.00  37.62      C
ATOM   10286  C5   u B  17     -12.707  110.025  -26.002  1.00  38.65      c
ATOM   10287  C6   u B  17     -12.195  111.135  -26.527  1.00  38.74      C
ATOM   10288  02   U B  17     -14.714  112.002  -28.845  1.00  42.26      0
ATOM   10289  04   u B  17     -14.570  108.540  -26.118  1.00  41.81      0
ATOM   10290  05 '  G B  18     -15.210  116.317  -25.856  1.00  38.06      0
ATOM   10291  C4 '  G B  18     -16.473  116.963  -27.848  1.00  43.01      C
ATOM   10292  C3 '  G B  18     -17.877  117.039  -27.231  1.00  35.62      C
ATOM   10293  C2 '  G B  18     -18.687  116.195  -28.191  1.00  39.68      C
ATOM   10294  P    G B  18     -13.925  116.360  -24.909  1.00  39.20      P
ATOM   10295  OP1  G B  18     -13.696  117.757  -24.570  1.00  48.09      0
ATOM   10296  OP2  G B  18     -14.169  115.424  -23.802  1.00  44.04      0
ATOM   10297  C5 '  G B  18     -15.303  117.234  -26.941  1.00  43.77      C
ATOM   10298  04 '  G B  18     -16.384  115.611  -28.365  1.00  42.88      0
ATOM   10299  03 '  G B  18     -18.367  118.360  -27.108  1.00  43.83      0
ATOM   10300  02 '  G B  18     -18.941  116.911  -29.391  1.00  44.16      0
ATOM   10301  CI '  G B  18     -17.688  115.081  -28.509  1.00  42.54      C
ATOM   10302  N9   G B  18     -17.838  113.974  -27.568  1.00  40.73      N
ATOM   10303  C8   G B  18     -17.018  113.609  -26.532  1.00  42.61      C
ATOM   10304  N1   G B  18     -17.468  112.561  -25.884  1.00  43.91      N
ATOM   10305  C5   G B  19     -18.666  112.264  -26.525  1.00  42.06      C
ATOM   10306  C4   G B  18     -18.917  113.141  -27.559  1.00  41.11      C
ATOM   10307  Ml   G B  18     -20.673  111.327  -27.165  1.00  38.66      N
ATOM   10308  C2   G B  18     -20.816  112.259  -28.164  1.00  36.59      C
ATOM   10309  N3   G B  18     -19.958  113.214  -28.413  1.00  36.57      N
ATOM   10310  C6   G B  18     -19.601  111.249  -26.285  1.00  39.85      C
ATOM   10311  06   G B  18     -19.560  110.375  -25.431  1.00  40.58      0
ATOM   10312  N2   G B  18     -21.905  112.158  -28.910  1.00  37.51      N
ATOM   10313  05 '  G B  19     -20.673  118.075  -26.096  1.00  41.91      0
ATOM   10314  C4 '  G B  19     -22.606  117.414  -27.372  1.00  38.90      C
ATOM   10315  C3 '  G B  19     -23.553  117.346  -26.181  1.00  33.34      C
ATOM   10316  C2 '  G B  19     -24.253  116.022  -26.419  1.00  39.07      C
ATOM   10317  P    G B  19     -19.276  118.795  -25.848  1.00  43.96      P
ATOM   10318  OF1  G B  19     -19.464  120.245  -25.895  1.00  42.48      0
ATOM   10319  OP2  G B  19     -18.717  118.213  -24.619  1.00  45.13      0
ATOM   10320  C5 '  G B  19     -21.415  118.326  -27.262  1.00  38.83      C
ATOM   10321  04 '  G B  19     -22.157  116.046  -27.546  1.00  40.69      0
ATOM   10322  03 '  G B  19     -24.431  118.466  -26.097  1.00  42.61      0
ATOM   10323  02 '  G B  19     -25.217  116.146  -27.453  1.00  39.48      0
ATOM   10324  C1 '  G B  19     -23.088  115.169  -26.957  1.00  39.22      C
ATOM   10325  N1   G B  19     -23.446  111.112  -24.200  1.00  40.32      N
ATOM   10326  N9   G B  19     -22.405  114.458  -25.870  1.00  36.58      N
ATOM   10327  C8   G B  19     -21.287  114.792  -25.152  1.00  34.76      C
ATOM   10328  N7   G B  19     -21.035  113.913  -24.248  1.00  37.01      N
ATOM   10329  C5   G B  19     -22.027  112.940  -24.387  1.00  38.19      C
ATOM   10330  C6   G B  19     -22.304  111.715  -23.712  1.00  41.28      C
ATOM   10331  06   G B  19     -21.704  111.163  -22.785  1.00  44.61      0
ATOM   10332  C2   G B  19     -24.221  111.594  -25.229  1.00  40.29      C
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ATOM   10333  N2   G B  19    -25..302  110..897  -25..608  1.00  40..10      N
ATOM   10334  N3   G B  19    --23,972  112..700  -25,854   1,00  42.39       N
ATOM   10335  C4   G B  19    -22..884  113.,301  -25...366 1.00  37,.86      C
ATOM   10336  05'  C B  20    -26..430  117.666   -24..845  1.00  33..29      O
ATOM   10337  C4'  C B  20    -27,560   115. 774  -23,959   1,00  39..00      C
ATOM   10338  C3'  C B  20    -28..305  115.,189  -22..793  1.00  42,.73      C
ATOM   10339  C2'  C B  20    -28..362  113.,712  -23..149  1,00  41,.78      C
ATOM   10340  P    C B  20    -25,305   118. 770  -24.,773   1,00  36..32      P
ATOM   10341  OP1  C B  20    -25..908  120.,110  -24..906  1,00  41.82       0
ATOM   10342  OF2  C B  20    -24.577   118.,537  -23..517  1,00  35,.32      0
ATOM   10343  C5'  C B  20    -26.,919  117.092   -23,666   1,00  33..65      C
ATOM   10344  04'  C B  20    -26..558  114.754   -24..287  1,00  37.05       0
ATOM   10345  03'  C B  20    -29. 560  115.,797  -22.603   1,00  45,95       0
ATOM   10346  02'  C B  20    -29..369  113..474  -24.,111   1.00  42.60       0
ATOM   10347  CI'  C B  20    -26,975   113..504  -23,781   1,00  37.36       C
ATOM   10348  Nl   C B  20    -26..004  113.,076  -22..749  1.00  38,.45      N
ATOM   10349  C2   C B  20    -26..146  Ill.824   -22..134  1.00  39..28      C
ATOM   10350  N3   C B  20    -25,286   111.489   -21.,167   1,00  40..34      N
ATOM   10351  C4   C B  20    -24..315  112.,312  -20..793  1.00  39,.55      C
ATOM   10352  C5   C B  20    -24.130   113.,589  -21 .371   1,00  36,.34      C
ATOM   10353  C6   C B  20    -25,008   113. 926  -22.,334   1,00  43..11      C
ATOM   10354  02   C B  20    -27..038  Ill,021   -22..461  1,00  40..72      0
ATOM   10355  N4   C B  20    -23..517  Ill,870   -19..831  1,00  43,.10      N
ATOM   10356  05'  G B  21    -30.,181  114.796   -20.,389   1,00  40..37      O
ATOM   10357  C4'  G B  21    -30..794  112..497  -20..132  1,00  45..93      C
ATOM   10358  C3'  G B  21    -30. 912  112.,616  -18. 625   1,00  45,42       C
ATOM   10359  C2'  G B  21    -30.,054  Ill.470   -18.,140   1,00  43..18      C
ATOM   10360  P    G B  21    -30.,048  116..195  -21.,129   1,00  46..13      P
ATOM   10361  OP1  G B  21    -31. 404  116,779   -21.265   1,00  52,92       0
ATOM   10362  OP2  G B  21    -28..975  116..968  -20,498   1.00  41.23       0
ATOM   10363  C5'  G B  21    -31.,012  113.. 772  -20,894   1,00  40..12      C
ATOM   10364  04'  G B  21    -29..439  112.,020  -20...346  1.00  44,04       0
ATOM   10365  03'  G B  21    -32..246  112..483  -18..196  1.00  48..64      0
ATOM   10366  02'  G B  21    -30.,768  110. 270  -18.,323   1,00  45..83      0
ATOM   10367  CI'  G B  21    -28..925  Ill,491   -19..153  1.00  39,.58      C
ATOM   10368  N9   G B  21    -27.800   112.,351  -18..735  1,00  45,.24      N
ATOM   10369  C8   G B  21    -27,487   113. 609  -19,207   1,00  36...33      C
ATOM   10370  N7   G B  21    -26..400  114,072   -18.,664   1,00  38..37      N
ATOM   10371  C5   G B  21    -25. 965  113.,078  -17 .788   1,00  39,24       C
ATOM   10372  C4   G B  21    -26.,823  112.012   -17,826   1,00  39..55      C
ATOM   10373  Nl   G B  21    -24,798   Ill.818   -16.,214   1,00  40..40      N
ATOM   10374  C2   G B  21    -25. 721  110.,814  -16. .329   1,00  45,49       C
ATOM   10375  N3   G B  21    -26..766  110..860  -17 .142   1.00  44.76       N
ATOM   10376  C6   G B  21    -24,845   113..015  -16.,921   1,00  39..99      C
ATOM   10377  06   G B  21    -23..962  113.,858  -16..737  1.00  4.1,94       O
ATOM   10378  N2   G B  21    -25..528  109..724  -15.,577   1,00  43..82      N
ATOM   10379  05'  U B  22    -32.,259  112.840   -15.,698   1,00  46...30      O
ATOM   10380  C4'  U B  22    -31..422  Ill,082   -14 .264   1.00  46,.05      C
ATOM   10381  C3'  U B  22    -31..438  112.,029  -13..068  1,00  49,.47      C
ATOM   10382  C2'  U B  22    -30.,057  111.841   -12.,461   1,00  50..75      C
ATOM   10383  P    U B  22    -32..841  113.,429  -17,058   1,00  40..51      P
ATOM   10384  OF1  U B  22    -34..318  113.,216  -17.086   1,00  56,.75      0
ATOM   10385  OP2  U B  22    -32.,267  114.762   -17,284   1,00  42.94       0
ATOM   10386  C5'  U B  22    -32.,349  Ill.454   -15.,395   1,00  44.07       C
ATOM   10387  04'  U B  22    -30. 036  111,084   -14.719   1,00  40,03       0
ATOM   10388  03'  U B  22    -32.,472  Ill.704   -12.,155   1,00  54.90       0
ATOM   10389  02'  U B  22    -30.,053  110..678  -11,645   1,00  50..96      0
ATOM   10390  CI'  U B  22    -29. 196  111,581   -13. 703   1,00  46,49       C
ATOM   10391  Nl   U B  22    -28..541  112..800  -14,227   1.00  48..41      N
ATOM   10392  C2   U B  22    -27,351   113.. 147  -13.,648   1,00  43..20      C
ATOM   10393  N3   U B  22    -26..742  114,236   -14.192   1.00  38,.43      N
ATOM   10394  C4   u B  22    -27,200   115.,019  -15..236  1.00  36..20      C
ATOM   10395  C5   u B  22    -28,445   114. 617  -15.,792   1,00  37.07       C
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ATOM   10396   C6    U B  22     -29..063  113.,537  -15..278   1,00  46..06           C
ATOM   10397   02    U B  22     --26,882  112..511  -12.,723   1,00  48..09           0
ATOM   10398   04    U B  22     -26..518  115.,980  -15..593   1.00  37,49            0
ATOM   10399   05'   U B  23     -32..233  113.,201  -10.,175   1,00  48..66           0
ATOM   10400   C4'   U B  23     -30.,732  112 .712   -8.,399   1,00  49.,57           C
ATOM   10401   C3'   U B  23     -30..846  114,084    -7.773   1.00  48,.24           C
ATOM   10402   C2'   u B  23     -29..392  114 ,512   -7.635   1,00  51,47            C
ATOM   10403   P     u B  23     -33.,239  112 .837  -11,331   1,00  50.,23           P
ATOM   10404   OP1   u B  23     -34..414  112.,208  -10..697   1,00  59..95           0
ATOM   10405   OF2   u B  23     -33..413  114 ,019  -12..193   1,00  52,04            0
ATOM   10406   C5'   u B  23     -31.,931  112 .261   -9.,173   1,00  45..15           C
ATOM   10407   04'   u B  23     -29..597  112.,824   -9.292   1,00  50..80           0
ATOM   10408   03'   u B  23     -31. 559  114 ,053   -6. 541   1,00  56,87            0
ATOM   10409   02'   u B  23     -28..826  113.,915   -6.,486   1,00  56..88           0
ATOM   10410   CI'   u B  23     -28,749   113..860   -8.,865   1,00  49..31           C
ATOM   10411   Nl    u B  23     -28..546  114,788    -9.997   1.00  43,.66           N
ATOM   10412   C2    u B  23     -27..362  115.,486  -10.,091   1,00  43..00           C
ATOM   10413   N3    u B  23     -27,238   116. 331  -11,160    1,00  38.,05           N
ATOM   10414   C4    u B  23     -28.185   116.,537  -12 .145   1.00  40,.27           C
ATOM   10415   C5    u B  23     -29.397   115.,803  -11 .990   1,00  39,.85           C
ATOM   10416   C6    u B  23     -29.,525  114. 968  -10.,948   1,00  45.,82           C
ATOM   10417   02    u B  23     -26,467   115.,382   -9.290   1,00  50..38           0
ATOM   10418   04    u B  23     -27..927  117 ,304  -13..066   1,00  41,05            0
ATOM   10419   05'   u B  24     -31.,713  116...369   -5.,657   1,00  60..45           0
ATOM   10420   C4'   u B  24     -30.,375  117 ,521   -4,049    1,00  55..81           C
ATOM   10421   C3'   u B  24     -30. 955  118.,909   -4.279    1,00  49,01            C
ATOM   10422   C2'   u B  24     -29.,703  119.729    -4,530    1,00  53..32           C
ATOM   10423   P     u B  24     -32.,638  115..203   -9,176    1,00  53..98           P
ATOM   10424   OP1   u B  24     -33. 444  114 ,866   -4.988    1,00  59,65            0
ATOM   10425   OP2   u B  24     -33.,382  115.,564   -7,391    1,00  48..46           0
ATOM   10426   C5'   u B  24     -31.,294  116..370   -4,309    1,00  56..83           C
ATOM   10427   04'   u B  24     -29..270  117,448    -4.975    1.00  49,.15           0
ATOM   10428   03'   u B  24     -31.,715  119.,359   -3.,172   1,00  61 .18           0
ATOM   10429   02'   u B  24     -29.,000  119. 922   -3.,314   1,00  54 ,84           0
ATOM   10430   CI'   u B  24     -28.874   118.,745   -5...345  1.00  56,.24           C
ATOM   10431   Nl    u B  24     -29.048   118.,878   -6..810   1,00  51,19            N
ATOM   10432   C2    u B  24     -28,379   119. 897   -7,440    1,00  49.,69           C
ATOM   10433   N3    u B  24     -28,529   119.,941   -8..799   1,00  50..89           N
ATOM   10434   C4    u B  24     -29. 251  119,062    -9. 583   1,00  46,92            C
ATOM   10435   C5    u B  24     -29.,909  118..032   -8.,857   1,00  43..91           C
ATOM   10436   C6    u B  24     -29,778   117 .969   -7,529    1,00  46..56           C
ATOM   10437   02    u B  24     -27.706   120,705    -6. 838   1,00  54,38            0
ATOM   10438   04    u B  24     -29,283   119.,228  -10.,800   1,00  46..17           0
ATOM   10439   05'   u B  25     -31.,784  121 .870   -3.,668   1,00  55..40           0
ATOM   10440   C4'   u B  25     -29..987  123,485    -3..438   1.00  58,.15           C
ATOM   10441   C3'   u B  25     -30.,736  124.,629   -4,117    1,00  54 .37           C
ATOM   10442   C2'   u B  25     -29.,702  125. 145   -5,109    1,00  57,03            C
ATOM   10443   P     u B  25     -32..702  120,634    -3..251   1.00  57,22            P
ATOM   10444   OF1   u B  25     -33.077   120,818    -1.843    1,00  64,10            0
ATOM   10445   OP2   u B  25     -33.,740  120. 456   -4,293    1,00  45.,26           0
ATOM   10446   C5'   u B  25     -30.,840  122.,428   -2.,769   1,00  55..12           C
ATOM   10447   04'   u B  25     -29.185   122.,908   -4.505    1,00  56,.13           0
ATOM   10448   03'   u B  25     -31.,181  125..603   -3.,196   1,00  56..34           0
ATOM   10449   02'   u B  25     -28,688   125.,880   -4,439    1,00  55..39           0
ATOM   10450   CI'   u B  25     -29. 072  123,835    -5. 576   1,00  56,10            C
ATOM   10451   Nl    u B  25     -29.,738  123..274   -6.,785   1,00  47 .32           N
ATOM   10452   C2    u B  25     -29,323   123..706   -8.,027   1,00  47 .52           C
ATOM   10453   N3    u B  25     -29. 969  123,147    -9. 088   1,00  44,01            N
ATOM   10454   C4    u B  25     -30.,953  122.,169   -9.,048   1,00  50..41           C
ATOM   10455   C5    u B  25     -31.,331  121 .770   -7,730    1,00  46..61           C
ATOM   10456   C6    u B  25     -30..727  122.,332   -6..685   1.00  49,.16           C
ATOM   10457   02    u B  25     -28,447   124.,535   -8.,183   1,00  48..91           0
ATOM   10458   04    u B  25     -31.,445  121 .707  -10.,093   1,00  49.,71           0
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ATOM	10459	05'	A	B	26	-31.774	127.596	-4.603	1.00	56.19	O
ATOM	10460	C4'	A	B	26	--30,270	129.252	-5,445	1,00	58.89	C
ATOM	10461	C3'	A	B	26	-31.418	129,817	-6:262	1,00	54,22	C
ATOM	10462	C2'	A	B	26	-30..752	130:067	-7:612	1.00	54.86	C
ATOM	10463	P	A	B	26	-32 ,394	126.607	-3,537	1,00	60,51	P
ATOM	10464	OP1	A	B	26	-32 .573	127,343	-2:276	1,00	64,51	0
ATOM	10465	OF2	A	B	26	-33.576	125,950	-4.152	1,00	55,02	0
ATOM	10466	C5'	A	B	26	-30,663	128.404	-4,269	1,00	58,77	C
ATOM	10467	04'	A	B	26	-29.526	128.446	-6:397	1,00	55.85	0
ATOM	10468	03'	A	B	26	-32 .017	130,958	-5.666	1,00	61,17	0
ATOM	10469	02'	A	B	26	-29,942	131:231	-7,586	1,00	59.88	0
ATOM	10470	CI'	A	B	26	-29.835	128.842	-7.711	1,00	54.69	C
ATOM	10471	N9	A	B	26	-30.563	127,746	-8..358	1,00	47,71	N
ATOM	10472	C8	A	B	26	-31.386	126:807	-7.794	1.00	48.29	C
ATOM	10473	N7	A	B	26	-31,947	126.014	-8,669	1,00	47.14	N
ATOM	10474	C5	A	B	26	-31.476	126,479	-9:895	1,00	47,56	C
ATOM	10475	C4	A	B	26	-30..633	127.558	-9.701	1.00	46.62	C
ATOM	10476	N1	A	B	26	-31,042	126.773	-12,190	1,00	50,38	N
ATOM	10477	C2	A	B	26	-30.259	127,799	-11:834	1,00	51,66	C
ATOM	10478	N3	A	B	26	-29.980	128,271	-10.623	1,00	46,77	N
ATOM	10479	C6	A	B	26	-31,682	126.077	-11,232	1,00	49,51	C
ATOM	10480	N6	A	B	26	-32 .462	125:068	-11:630	1,00	52.11	N
ATOM	10481	05'	G	B	27	-33.902	131,470	-7,252	1,00	48,96	O
ATOM	10482	C4'	G	B	27	-33,498	132:559	-9,365	1,00	54.33	C
ATOM	10483	C3'	G	B	27	-34.948	132.441	-9:813	1,00	56.48	C
ATOM	10484	C2'	G	B	27	-34.781	131,977	-11.249	1,00	59,49	C
ATOM	10485	P	G	B	27	-33,618	131:196	-5,715	1,00	65.71	P
ATOM	10486	OP1	G	B	27	-33,817	132.490	-5,001	1,00	70.68	0
ATOM	10487	OP2	G	B	27	-34.419	130,042	-5.242	1,00	55,14	0
ATOM	10488	C5'	G	B	27	-33:241	132:546	-7,891	1.00	55.08	C
ATOM	10489	04'	G	B	27	-32 ,864	131.404	-9,966	1,00	63.59	0
ATOM	10490	03'	G	B	27	-35.676	133,660	-9:691	1,00	70,30	0
ATOM	10491	02'	G	B	27	-34.397	133:064	-12,057	1.00	63.48	0
ATOM	10492	C1'	G	B	27	-33,575	131.030	-11,128	1,00	61,12	C
ATOM	10493	N9	G	B	27	-34.046	129,635	-11:033	1,00	53,63	N
ATOM	10494	C8	G	B	27	-34.429	128,946	-9.910	1,00	52,33	C
ATOM	10495	N7	G	B	27	-34,897	127.761	-10,187	1,00	57,72	N
ATOM	10496	C5	G	B	27	-34.827	127.679	-11:579	1,00	52.17	C
ATOM	10497	C4	G	B	27	-34..326	128,834	-12.122	1,00	51,98	C
ATOM	10498	Nl	G	B	27	-34,981	126:954	-13,798	1,00	51.58	N
ATOM	10499	C2	G	B	27	-34,452	128.139	-14,248	1,00	49.57	C
ATOM	10500	N3	G	B	27	-34.111	129,130	-13.433	1,00	51,82	N
ATOM	10501	C6	G	B	27	-35.198	126:634	-12.456	1.00	50.78	C
ATOM	10502	06	G	B	27	-35,662	125.527	-12,152	1,00	59.57	0
ATOM	10503	N2	G	B	27	-34.316	128,255	-15:584	1,00	47,68	N
ATOM	10504	P	A	B	28	-37:285	133:708	-9.470	1.00	65.10	P
ATOM	10505	OP1	A	B	28	-37,956	132.404	-9,625	1,00	66,63	0
ATOM	10506	OP2	A	B	28	-37.770	134,801	-10:.349	1,00	58,89	0
ATOM	10507	05'	A	B	28	-37.436	134,103	-7.941	1,00	63,97	0
ATOM	10508	C5'	A	B	28	-36,934	133.269	-6,897	1,00	64,82	C
ATOM	10509	C4'	A	B	28	-37.674	133.501	-5:597	1,00	75.43	C
ATOM	10510	04'	A	B	28	-37.317	134,808	-5.057	1,00	68,06	0
ATOM	10511	C3'	A	B	28	-39,197	133:499	-5,716	1,00	73.24	C
ATOM	10512	03'	A	B	28	-39:762	133.050	-4.490	1,00	71.09	0
ATOM	10513	C2'	A	B	28	-39.512	134,978	-5.894	1,00	77,51	C
ATOM	10514	02'	A	B	28	-40,837	135:.347	-5,560	1,00	85.63	0
ATOM	10515	CI'	A	B	28	-38,478	135.619	-4,966	1,00	80.59	C
ATOM	10516	N9	A	B	28	-38.105	136,988	-5..338	1,00	79,87	N
ATOM	10517	C8	A	B	28	-38.153	137:571	-6.583	1.00	77.10	C
ATOM	10518	N7	A	B	28	-37,733	138.813	--8,584	1,00	81.82	N
ATOM	10519	C5	A	B	28	-37..381	139,061	-5:259	1,00	80,23	C
ATOM	10520	C4	A	B	28	-37.607	137:942	-4.486	1.00	73.29	C
ATOM	10521	Nl	A	B	28	-36,635	140.102	-3,265	1,00	76,10	N

ATOM	10522	C2	A	B	28	-36.908	138.947	-2.655	1,00	75.75	C
ATOM	10523	N3	A	B	28	--37,396	137.819	-3,168	1,00	74.29	N
ATOM	10524	C6	A	B	28	-36.871	140,197	-4.592	1,00	80,92	C
ATOM	10525	N6	A	B	28	-36.601	141.361	-5.192	1,00	81.76	N
ATOM	10526	P	G	B	29	-40,143	131.507	-4,290	1,00	75,54	P
ATOM	10527	OP1	G	B	29	-40.780	131,324	-2.966	1,00	78,46	O
ATOM	10528	OF2	G	B	29	-38.893	130,749	-4.558	1,00	83,34	O
ATOM	10529	05'	G	B	29	-41,232	131.219	-5,423	1,00	74,95	O
ATOM	10530	C5'	G	B	29	-42.623	131.452	-5.204	1,00	77.00	C
ATOM	10531	C4'	G	B	29	-43.171	132,498	-6.147	1,00	77,75	C
ATOM	10532	04'	G	B	29	-43,678	131.891	-7,366	1,00	69.50	0
ATOM	10533	C3'	G	B	29	-44.352	133.323	-5.656	1,00	77.68	C
ATOM	10534	03'	G	B	29	-43.991	134,321	-4.716	1,00	80,54	0
ATOM	10535	C2'	G	B	29	-44.905	133.898	-6.956	1,00	78.24	C
ATOM	10536	02'	G	B	29	-44,140	135.020	-7,371	1,00	81.98	0
ATOM	10537	CI'	G	B	29	-44.652	132,749	-7.940	1,00	80,60	C
ATOM	10538	N9	G	B	29	-45.890	132.011	-8.286	1,00	83.08	N
ATOM	10539	C8	G	B	29	-46,900	132.453	-9,127	1,00	80,96	C
ATOM	10540	N1	G	B	29	-47.899	131,617	-9.258	1,00	77,82	N
ATOM	10541	C5	G	B	29	-47.523	130,557	-8.448	1,00	77.63	C
ATOM	10542	C4	G	B	29	-46,299	130.786	-7,841	1,00	80,06	C
ATOM	10543	Ml	G	B	29	-47.461	128.556	-7.305	1,00	82.52	N
ATOM	10544	C2	G	B	29	-46.247	128,889	-6.754	1,00	82,69	C
ATOM	10545	N3	G	B	29	-45,604	130.012	-6,992	1,00	76.71	N
ATOM	10546	C6	G	B	29	-48.193	129.342	-8.184	1,00	79.14	C
ATOM	10547	06	G	B	29	-49.281	128,941	-8.618	1,00	80,97	O
ATOM	10548	N2	G	B	29	-45,702	127.989	-5,923	1,00	94.34	N
ATOM	10549	P	C	B	30	-45,040	134.820	-3,596	1,00	86.47	P
ATOM	10550	OP1	C	B	30	-44.428	136,002	-2.936	1,00	84,04	O
ATOM	10551	OP2	C	B	30	-45.468	133.679	-2,750	1,00	77.69	O
ATOM	10552	05'	C	B	30	-46,318	135.285	-4,428	1,00	75.47	O
ATOM	10553	C5'	C	B	30	-46.340	136,531	-5.107	1,00	77,66	C
ATOM	10554	C4'	c	B	30	-47.625	136.714	-5.876	1,00	79.78	C
ATOM	10555	04'	C	B	30	-47,796	135.620	-6,812	1,00	72,66	0
ATOM	10556	C3'	c	B	30	-48.911	136,704	-5.062	1,00	80,94	C
ATOM	10557	03'	c	B	30	-49.170	137,941	-4.416	1,00	82,52	0
ATOM	10558	C2'	c	B	30	-49,955	136.316	-6,104	1,00	80,85	C
ATOM	10559	02'	c	B	30	-50.310	137.433	-6.905	1,00	81.73	0
ATOM	10560	CI'	c	B	30	-49.168	135,336	-6.975	1,00	75,03	C
ATOM	10561	Nl	c	B	30	-49,417	133.938	-6,580	1,00	71.66	N
ATOM	10562	C2	c	B	30	-50,463	133.279	-7,214	1,00	80.38	C
ATOM	10563	N3	c	B	30	-50.723	132,000	-6.882	1,00	81,13	N
ATOM	10564	C4	c	B	30	-49.994	131.402	-5.952	1,00	78.88	C
ATOM	10565	C5	c	B	30	-48.927	132.057	-5,277	1,00	74.92	C
ATOM	10566	C6	c	B	30	-48.675	133,319	-5.621	1,00	73,88	C
ATOM	10567	02	c	B	30	-51.124	133.876	-8,080	1,00	82.39	0
ATOM	10568	N4	c	B	30	-50,310	130.141	-5,675	1,00	82,70	N
ATOM	10569	P	u	B	31	-50.058	138,003	-3.071	1,00	90,29	P
ATOM	10570	OF1	u	B	31	-50.024	139,401	-2.571	1,00	84,29	O
ATOM	10571	OP2	u	B	31	-49,633	136.923	-2,146	1,00	86,60	O
ATOM	10572	05'	u	B	31	-51.536	137.687	-3.577	1,00	82.61	O
ATOM	10573	C5'	u	B	31	-52.155	138,480	-4.583	1,00	84,57	C
ATOM	10574	C4'	u	B	31	-53,561	138.014	-4,847	1,00	84.56	C
ATOM	10575	04'	u	B	31	-53.545	136.828	-5.682	1,00	87.72	0
ATOM	10576	C3'	u	B	31	-54.323	137,584	-3.610	1,00	86,88	C
ATOM	10577	03'	u	B	31	-54,863	138.677	-2,905	1,00	92.63	0
ATOM	10578	C2'	u	B	31	-55,358	136.613	-4,163	1,00	92.48	C
ATOM	10579	02'	u	B	31	-56.457	137,298	-4.749	1,00	94,00	0
ATOM	10580	CI'	u	B	31	-54.557	135.930	-5,271	1,00	89.00	C
ATOM	10581	Nl	u	B	31	-53,919	134.686	-4,781	1,00	88.47	N
ATOM	10582	C2	u	B	31	-54.608	133,509	-4.987	1,00	91,78	C
ATOM	10583	N3	u	B	31	-53.977	132.382	-4,510	1,00	90.28	N
ATOM	10584	C4	u	B	31	-52,761	132.322	-3,854	1,00	88,47	C

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ATOM   10585  C5    U B  31    -52 .109 133.581  -3.670  1,00 84.65   C
ATOM   10586  C6    U B  31    --52,700 134.686  -4,130  1,00 87.96   C
ATOM   10587  02    ʋ B  31    -55.686  133,473  -5.560  1.00 91,84   0
ATOM   10588  04    U B  31    -52 .331 131:233  -3.482  1,00 88.58   0
ATOM   10589  P     A B  32    -55,186  138.536  -1,346  1,00 89,96   P
ATOM   10590  OP1   A B  32    -54.981  139,871  -0.735  1.00 93,57   0
ATOM   10591  OF2   A B  32    -54.452  137,365  -0.801  1,00 95,61   0
ATOM   10592  05'   A B  32    -56,726  138.167  -1,354  1,00 92,45   0
ATOM   10593  C5'   A B  32    -57.241  137.226  -0:441  1,00 95.24   C
ATOM   10594  C4'   A B  32    -58.228  136,300  -1.098  1,00 96,76   C
ATOM   10595  04'   A B  32    -57,553  135.532  -2,128  1,00 95.55   0
ATOM   10596  CI'   A B  32    -57.973  134.187  -2:090  1,00 97.33   C
ATOM   10597  C2'   A B  32    -59.139  134,095  -1.113  1,00 98,87   C
ATOM   10598  02'   A B  32    -60.336  134:327  -1.837  1,00101.09   0
ATOM   10599  C3'   A B  32    -58,830  135.256  -0,170  1,00103.22   C
ATOM   10600  03'   A B  32    -59.959  135,748   0.538  1.00101,89   0
ATOM   10601  N9    A B  32    -56.829  133:375  -1.647  1,00 96.63   N
ATOM   10602  C8    A B  32    -55,659  133.826  -1,092  1,00 97,08   C
ATOM   10603  N1    A B  32    -54.813  132,874  -0.792  1.00 98,00   N
ATOM   10604  C5    A B  32    -55.480  131,720  -1.182  1,00101,10   C
ATOM   10605  C4    A B  32    -56,723  132.016  -1,709  1,00 97,38   C
ATOM   10606  Ml    A B  32    -56.010  129:456  -1:603  1,00 99.69   N
ATOM   10607  C2    A B  32    -57.180  129,898  -2.084  1,00 99,67   C
ATOM   10608  N3    A B  32    -57,631  131.147  -2,183  1,00 97.70   N
ATOM   10609  C6    A B  32    -55.122  130.362  -1:136  1,00102.25   C
ATOM   10610  N6    A B  32    -53.956  129,935  -0.653  1,00101,08   N
ATOM   10611  P     G B  33    -59,806  136.438   1,985  1,00 97.65   P
ATOM   10612  OP1   G B  33    -60,902  137.435   2,132  1,00103.94   0
ATOM   10613  OP2   G B  33    -58.390  136,800   2.261  1,00 83,50   0
ATOM   10614  05'   G B  33    -60.134  135:263   2,990  1,00103.19   0
ATOM   10615  C5'   G B  33    -59,125  134.339   3,317  1,00107.91   C
ATOM   10616  C4'   G B  33    -59.602  132,933   3.143  1.00111,70   C
ATOM   10617  04'   G B  33    -58.945  132:353   1.985  1,00114.73   0
ATOM   10618  C1'   G B  33    -58,515  131.043   2,279  1,00113,85   C
ATOM   10619  N9    G B  33    -57.043  131,076   2.390  1.00113,31   N
ATOM   10620  C8    G B  33    -56.269  132,200   2.597  1,00112,56   C
ATOM   10621  N7    G B  33    -54,991  131.948   2,673  1,00110,49   N
ATOM   10622  C5    G B  33    -54.915  130:569   2:508  1,00113.46   C
ATOM   10623  C4    G B  33    -56.167  130,010   2.335  1,00114,12   C
ATOM   10624  N3    G B  33    -56,487  128:706   2,143  1,00114.92   N
ATOM   10625  C2    G B  33    -55,417  127.919   2,135  1,00116.06   C
ATOM   10626  N2    G B  33    -55.549  126,593   1.959  1,00116,75   N
ATOM   10627  Nl    G B  33    -54.134  128:383   2:300  1,00113.60   N
ATOM   10628  C6    G B  33    -53,785  129.716   2,497  1,00111,20   C
ATOM   10629  06    G B  33    -52 .601 130,030   2.637  1.00108,42   O
ATOM   10630  C2'   G B  33    -59.160  130:651   3.605  1,00118.71   C
ATOM   10631  02'   G B  33    -60,464  130.158   3,336  1,00121,36   0
ATOM   10632  C3'   G B  33    -59.236  132,006   4.289  1.00119,25   C
ATOM   10633  03'   G B  33    -60.156  132,078   5.366  1,00125,37   0
ATOM   10634  P     A B  34    -59,839  132.989   6,658  1,00128,76   P
ATOM   10635  OP1   A B  34    -61.081  133:016   7:472  1,00127.85   0
ATOM   10636  OF2   A B  34    -59.210  134,274   6.267  1,00114,47   0
ATOM   10637  05'   A B  34    -58,733  132.167   7,455  1,00126.61   0
ATOM   10638  C5'   A B  34    -57.661  132.843   8:098  1,00126.62   C
ATOM   10639  C4'   A B  34    -56.737  131,891   8.817  1,00130,62   C
ATOM   10640  04'   A B  34    -57,399  131..376 10,008  1,00133.94   0
ATOM   10641  CI'   A B  34    -57,245  129.974  10,064  1,00133.69   C
ATOM   10642  N9    A B  34    -58.376  129,373  10.805  1,00136,92   N
ATOM   10643  C8    A B  34    -58:650  129:612  12.136  1,00132.04   C
ATOM   10644  N7    A B  34    -59,692  128.976  12,618  1,00132.06   N
ATOM   10645  C5    A B  34    -60.161  128,247  11.535  1.00135,56   C
ATOM   10646  C4    A B  34    -59.371  128:473  10.405  1,00137.36   C
ATOM   10647  N3    A B  34    -59,573  127.900   9,194  1,00130,72   N
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ATOM	10648	C2	A	B	34	-60.631	127.092	9.198	1.00132.26	C
ATOM	10649	N1	A	B	34	-61.467	126.793	10.204	1.00135.62	N
ATOM	10650	C6	A	B	34	-61.257	127.364	11.411	1.00133.04	C
ATOM	10651	N6	A	B	34	-62.095	127.062	12.408	1.00127.45	N
ATOM	10652	C2'	A	B	34	-57.087	129.522	8.616	I.00133.42	C
ATOM	10653	02'	A	B	34	-56.453	128.265	8.542	1.00133.84	O
ATOM	10654	C3'	A	B	34	-56.278	130.671	8.010	1.00133.18	C
ATOM	10655	03'	A	B	34	-54.883	130.434	8.214	I.00134.86	0
ATOM	10656	P	A	B	35	-53.929	130.079	6.964	1.00133.54	P
ATOM	10657	OF1	A	B	35	-54.396	130.858	5.785	1.00125.01	0
ATOM	10658	OP2	A	B	35	-52.525	130.232	7.428	I.00130.10	0
ATOM	10659	05'	A	B	35	-54.220	128.533	6.669	1.00131.41	0
ATOM	10660	C5'	A	B	35	-53.494	127.499	7.330	1.00132.74	C
ATOM	10661	C4'	A	B	35	-54.173	126.146	7.215	1.00133.35	C
ATOM	10662	04'	A	B	35	-55.545	126.234	7.675	1.00132.70	0
ATOM	10663	CI'	A	B	35	-56.352	125.310	6.975	1.00130.09	C
ATOM	10664	C2'	A	B	35	-55.472	124.587	5.953	1.00131.44	C
ATOM	10665	02'	A	B	35	-55.063	123.346	6.506	I.00132.85	0
ATOM	10666	C3'	A	B	35	-54.287	125.542	5.819	1.00132.32	C
ATOM	10667	03'	A	B	35	-53.096	124.893	5.397	1.00132.28	0
ATOM	10668	N9	A	B	35	-57.489	126.019	6.352	I.00131.23	N
ATOM	10669	C8	A	B	35	-57.644	127.363	6.112	1.00129.32	C
ATOM	10670	N7	A	B	35	-58.787	127.681	5.556	1.00128.27	N
ATOM	10671	C5	A	B	35	-59.433	126.460	5.413	I.00130.65	C
ATOM	10672	C4	A	B	35	-58.645	125.431	5.899	1.00131.41	C
ATOM	10673	Nl.	A	B	35	-61.025	124.795	4.891	1.00127.54	N
ATOM	10674	C2	A	B	35	-60.158	123.914	5.399	I.00128.89	C
ATOM	10675	N3	A	B	35	-58.952	124.124	5.920	1.00130.19	N
ATOM	10676	C6	A	B	35	-60.686	126.102	4.883	1.00129.55	C
ATOM	10677	N6	A	B	35	-61.553	126.980	4.375	1.00128.37	N
ATOM	10678	P	A	B	36	-52.920	124.416	3.868	1.00134.84	P
ATOM	10679	OP1	A	B	36	-53.563	125.424	2.977	1.00127.45	O
ATOM	10680	OP2	A	B	36	-51.502	124.021	3.664	1.00134.52	O
ATOM	10681	05'	A	B	36	-53.788	123.088	3.766	I.00131.04	O
ATOM	10682	C5'	A	B	36	-53.219	121.806	3.974	1.00129.77	C
ATOM	10683	C4'	A	B	36	-54.249	120.745	3.711	1.00129.22	C
ATOM	10684	04'	A	B	36	-55.490	121.141	4.355	I.00129.46	0
ATOM	10685	CI'	A	B	36	-56.585	120.861	3.512	1.00129.03	C
ATOM	10686	N9	A	B	36	-57.135	122.149	3.047	1.00129.22	N
ATOM	10687	C8	A	B	36	-56.450	123.310	2.778	I.00126.85	C
ATOM	10688	N7	A	B	36	-57.201	124.301	2.373	1.00127.02	N
ATOM	10689	C5	A	B	36	-58.478	123.753	2.372	1.00128.42	C
ATOM	10690	C4	A	B	36	-58.453	122.430	2.780	1.00130.95	C
ATOM	10691	N3	A	B	36	-59.508	121.601	2.896	1.00131.11	N
ATOM	10692	C2	A	B	36	-60.636	122.219	2.555	1.00127.22	C
ATOM	10693	N1	A	B	36	-60.814	123.481	2.145	1.00128.31	N
ATOM	10694	C6	A	B	36	-59.734	124.288	2.039	I.00127.60	C
ATOM	10695	N6	A	B	36	-59.910	125.545	1.627	1.00127.44	N
ATOM	10696	C2'	A	B	36	-56.056	120.032	2.348	1.00128.92	C
ATOM	10697	02'	A	B	36	-56.058	118.664	2.728	I.00128.12	0
ATOM	10698	C3'	A	B	36	-54.634	120.562	2.251	1.00128.69	C
ATOM	10699	03'	A	B	36	-53.744	119.724	1.538	1.00128.15	0
ATOM	10700	P	U	B	37	-54.023	119.361	-0.004	I.00134.51	P
ATOM	10701	OP1	U	B	37	-54.674	118.026	-0.048	1.00135.23	0
ATOM	10702	OP2	u	B	37	-52.768	119.609	-0.760	1.00130.64	0
ATOM	10703	05'	u	B	37	-55.115	120.416	-0.489	I.00128.00	0
ATOM	10704	C5'	u	B	37	-56.077	120.051	-1.468	1.00124.91	C
ATOM	10705	C4'	u	B	37	-57.221	121.031	-1.537	1.00122.41	C
ATOM	10706	04'	u	B	37	-57.030	122.099	-0.576	1.00125.03	0
ATOM	10707	CI'	u	B	37	-57.561	123.305	-1.082	1.00121.02	C
ATOM	10708	C2'	u	B	37	-58.145	123.017	-2.468	1.00116.56	C
ATOM	10709	02'	u	B	37	-59.536	122.770	-2.334	1.00114.55	0
ATOM	10710	C3'	u	B	37	-57.396	121.749	-2.864	I.00116.44	C

ATOM	10711	03'	U	B	37	-58.085	120.955	-3.811	1.00121.79	O
ATOM	10712	Nl	U	B	37	--56,476	124.309	-1,126	1,00118.46	N
ATOM	10713	C2	U	B	37	-56.815	125,623	-1.391	1.00113,71	C
ATOM	10714	N3	U	B	37	-55.753	126.489	-1.418	1.00109.36	N
ATOM	10715	C4	U	B	37	-54,428	126.182	-1,202	1,00110.50	C
ATOM	10716	C5	U	B	37	-54.162	124,804	-0.929	1.00116,70	C
ATOM	10717	C6	U	B	37	-55.174	123,935	-0.898	1,00118,44	C
ATOM	10718	02	U	B	37	-57,960	125.996	-1,599	1,00111.61	0
ATOM	10719	04	U	B	37	-53.590	127.077	-1.260	1,00109.25	0
ATOM	10720	P	A	B	38	-57.860	121,178	-5.387	1,00122,68	P
ATOM	10721	OP1	A	B	38	-59,189	121.104	-6,050	1,00117,09	0
ATOM	10722	OP2	A	B	38	-56.737	120.328	-5.857	1,00123.38	0
ATOM	10723	05'	A	B	38	-57.360	122,677	-5.491	1,00116,42	0
ATOM	10724	C5'	A	B	38	-57.486	123.376	-6.711	1.00114.24	C
ATOM	10725	C4'	A	B	38	-58,658	124.316	-8,675	1,00111.65	C
ATOM	10726	04'	A	B	38	-58.875	124,781	-5.308	1.00111,68	0
ATOM	10727	CI'	A	B	38	-59.006	126.187	-5.304	1.00106.43	C
ATOM	10728	C2'	A	B	38	-59,331	126.588	-6,729	1,00103.49	C
ATOM	10729	02'	A	B	38	-60.703	126,324	-6.969	1.00101,79	0
ATOM	10730	C3'	A	B	38	-58.448	125,596	-7.465	1,00108,16	C
ATOM	10731	03'	A	B	38	-58,652	125.488	-8,861	1,00107,86	0
ATOM	10732	N9	A	B	38	-57.669	126.696	-4.966	1,00101.98	N
ATOM	10733	C8	A	B	38	-56.627	125,933	-4.509	1,00102,37	C
ATOM	10734	N7	A	B	38	-55,527	126.606	-4,309	1,00103.57	N
ATOM	10735	C5	A	B	38	-55.859	127.895	-4.686	1,00101.48	C
ATOM	10736	C4	A	B	38	-57.177	127,971	-5.106	1,00100,58	C
ATOM	10737	Nl	A	B	38	-55,721	130.206	-5,132	1,00 92.71	N
ATOM	10738	C2	A	B	38	-57,003	130.128	-5,510	1,00 94.32	C
ATOM	10739	N.3	A	B	38	-57.816	129,074	-5.534	1,00 97,55	N
ATOM	10740	C6	A	B	38	-55.105	129.078	-4,705	1.00 97.88	C
ATOM	10741	N6	A	B	38	-53,828	129.123	-4,323	1,00 93.32	N
ATOM	10742	P	G	B	39	-59.946	124,777	-9.482	1.00110,70	P
ATOM	10743	OP1	G	B	39	-60.996	124.579	-8.445	1.00112.90	O
ATOM	10744	OP2	G	B	39	-59,444	123.619	-10,261	1,00105,37	O
ATOM	10745	05'	G	B	39	-60.482	125,879	-10.501	1.00106,20	O
ATOM	10746	C5'	G	B	39	-59.569	126,610	-11.304	1,00103,36	C
ATOM	10747	C4'	G	B	39	-59,487	128.065	-10,908	1,00 99.06	C
ATOM	10748	04'	G	B	39	-59.059	128.201	-9.528	1,00 99.04	0
ATOM	10749	C3'	G	B	39	-58.460	128,870	-11.676	1,00 95,56	C
ATOM	10750	03'	G	B	39	-58,902	129.238	-12,958	1,00 94.81	0
ATOM	10751	C2'	G	B	39	-58,181	130.035	-10,748	1,00 92.15	C
ATOM	10752	02'	G	B	39	-59.240	130,970	-10.800	1,00 97,40	0
ATOM	10753	CI'	G	B	39	-58.225	129.339	-9,394	1.00 97.05	C
ATOM	10754	N9	G	B	39	-56,881	128.905	-8,957	1,00 94.51	N
ATOM	10755	C8	G	B	39	-56.418	127,616	-8.862	1.00 93,56	C
ATOM	10756	N7	G	B	39	-55.192	127.527	-8.435	1.00 91.91	N
ATOM	10757	C5	G	B	39	-54,806	128.847	-8,245	1,00 91.48	C
ATOM	10758	C4	G	B	39	-55.837	129,710	-8.565	1.00 88,64	C
ATOM	10759	Nl	G	B	39	-53.608	130,774	-7.750	1,00 86,70	N
ATOM	10760	C2	G	B	39	-54,688	131.544	-8,093	1,00 87.08	C
ATOM	10761	N3	G	B	39	-55.845	131.056	-8.512	1,00 88.37	N
ATOM	10762	C6	G	B	39	-53.573	129,387	-7.792	1,00 88,76	C
ATOM	10763	06	G	B	39	-52 ,540	128.794	-7,465	1,00 88.49	0
ATOM	10764	N2	G	B	39	-54.514	132.867	-7,980	1,00 86.53	N
ATOM	10765	P	C	B	40	-58.137	128,614	-14.216	1,00101,64	P
ATOM	10766	OP1	C	B	40	-58,928	128.997	-15,415	1,00 94.51	0
ATOM	10767	OP2	C	B	40	-57,838	127.180	-13,919	1,00 89.16	0
ATOM	10768	05'	C	B	40	-56.735	129,381	-14.204	1,00 95,05	0
ATOM	10769	C5'	C	B	40	-56.650	130.724	-14,648	1.00 90.15	C
ATOM	10770	C4'	C	B	40	-55,559	131.512	-13,961	1,00 87.10	C
ATOM	10771	04'	C	B	40	-55.437	131,167	-12.557	1.00 86,57	0
ATOM	10772	C3'	C	B	40	-54.141	131.345	-14.464	1.00 84.03	C
ATOM	10773	03'	C	B	40	-53,903	131.906	-15,746	1,00 86.42	0

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ATOM  10774  C2'  C B  40    -53.353 131.996 -13.333  1.00 83.85          C
ATOM  10775  02'  C B  40    -53.497 133.409 -13.361  1.00 82.12          0
ATOM  10776  CI'  C B  40    -54.127 131.488 -12.117  1.00 83.67          c
ATOM  10777  Nl   C B  40    -53.479 130.297 -11.521  1.00 85.51          N
ATOM  10778  C2   C B  40    -52.318 130.483 -10.752  1.00 78.37          c
ATOM  10779  N3   C B  40    -51.707 129.417 -10.205  1.00 79.47          N
ATOM  10780  C4   c B  40    -52.198 128.190 -10.397  1.00 86.12          c
ATOM  10781  C5   C B  40    -53.378 127.966 -11.168  1.00 84.44          c
ATOM  10782  C6   c B  40    -53.979 129.036 -11.711  1.00 87.48          c
ATOM  10783  02   c B  40    -51.862 131.623 -10.584  1.00 79.09          0
ATOM  10784  N4   c B  40    -51.556 127.160  -9.828  1.00 86.86          N
ATOM  10785  P    A B  41    -52.730 131.307 -16.677  1.00 87.02          P
ATOM  10786  OP1  A B  41    -52.781 131.938 -18.018  1.00 81.23          O
ATOM  10787  OP2  A B  41    -52.754 129.826 -16.569  1.00 80.47          O
ATOM  10788  05'  A B  41    -51.403 131.854 -15.996  1.00 73.66          O
ATOM  10789  C5'  A B  41    -51.119 133.243 -15.988  1.00 71.55          C
ATOM  10790  C4'  A B  41    -49.902 133.538 -15.157  1.00 71.88          c
ATOM  10791  04'  A B  41    -50.041 132.909 -13.861  1.00 71.65          0
ATOM  10792  C3'  A B  41    -48.593 132.995 -15.701  1.00 65.23          c
ATOM  10793  03'  A B  41    -48.038 133.864 -16.671  1.00 68.74          0
ATOM  10794  C2'  A B  41    -47.739 132.830 -14.448  1.00 67.55          c
ATOM  10795  02'  A B  41    -47.134 134.054 -14.067  1.00 67.44          0
ATOM  10796  CI'  A B  41    -48.787 132.471 -13.395  1.00 73.00          c
ATOM  10797  N9   A B  41    -48.868 131.024 -13.138  1.00 69.92          N
ATOM  10798  C8   A B  41    -49.850 130.141 -13.519  1.00 75.34          C
ATOM  10799  N7   A B  41    -49.650 128.912 -13.115  1.00 73.89          N
ATOM  10800  C5   A B  41    -48.456 129.001 -12.421  1.00 73.07          C
ATOM  10801  C4   A B  41    -47.973 130.299 -12.418  1.00 70.44          c
ATOM  10802  Nl   A B  41    -46.552 128.468 -11.158  1.00 72.45          N
ATOM  10803  C2   A B  41    -46.207 129.761 -11.244  1.00 72.94          c
ATOM  10804  N3   A B  41    -46.848 130.760 -11.850  1.00 72.70          N
ATOM  10805  C6   A B  41    -47.690 128.042 -11.748  1.00 71.49          C
ATOM  10806  N6   A B  41    -48.031 126.754 -11.658  1.00 74.52          N
ATOM  10807  P    A B  42    -47.427 133.295 -18.044  1.00 69.77          P
ATOM  10808  OP1  A B  42    -47.321 134.381 -19.044  1.00 68.02          O
ATOM  10809  OF2  A B  42    -48.063 131.995 -18.410  1.00 66.50          O
ATOM  10810  05'  A B  42    -45.948 132.954 -17.617  1.00 68.20          O
ATOM  10811  C5'  A B  42    -45.591 131.612 -17.423  1.00 65.82          C
ATOM  10812  C4'  A B  42    -44.550 131.472 -16.358  1.00 68.78          c
ATOM  10813  04'  A B  42    -45.184 130.999 -15.146  1.00 62.35          0
ATOM  10814  C3'  A B  42    -43.474 130.449 -16.711  1.00 57.50          c
ATOM  10815  03'  A B  42    -42.328 131.113 -17.205  1.00 56.75          0
ATOM  10816  C2'  A B  42    -43.222 129.694 -15.414  1.00 58.30          c
ATOM  10817  02'  A B  42    -42.206 130.328 -14.658  1.00 60.63          0
ATOM  10818  CI'  A B  42    -44.561 129.837 -14.684  1.00 66.45          c
ATOM  10819  N9   A B  42    -45.494 128.738 -14.972  1.00 64.60          N
ATOM  10820  C8   A B  42    -46.567 128.835 -15.815  1.00 63.16          c
ATOM  10821  N1   A B  42    -47.256 127.736 -15.915  1.00 66.34          N
ATOM  10822  C5   A B  42    -46.586 126.860 -15.076  1.00 66.12          c
ATOM  10823  C4   A B  42    -45.491 127.456 -14.482  1.00 66.30          c
ATOM  10824  Ml   A B  42    -45.987 124.916 -13.884  1.00 66.55          N
ATOM  10825  C2   A B  42    -44.962 125.620 -13.381  1.00 64.13          c
ATOM  10826  N3   A B  42    -44.623 126.886 -13.619  1.00 67.59          N
ATOM  10827  C6   A B  42    -46.833 125.525 -14.751  1.00 66.82          C
ATOM  10828  N6   A B  42    -47.867 124.853 -15.265  1.00 67.82          N
ATOM  10829  P    G B  43    -41.751 130.834 -18.674  1.00 54.11          P
ATOM  10830  OP1  G B  43    -42.802 130.622 -19.693  1.00 56.94          O
ATOM  10831  OP2  G B  43    -40.778 131.900 -18.936  1.00 57.42          0
ATOM  10832  05'  G B  43    -40.927 129.494 -18.431  1.00 60.28          0
ATOM  10833  C5'  G B  43    -40.077 129.374 -17.287  1.00 54.15          c
ATOM  10834  C4'  G B  43    -39.871 127.938 -16.883  1.00 53.38          c
ATOM  10835  04'  G B  43    -41.147 127.343 -16.531  1.00 58.00          0
ATOM  10836  C3'  G B  43    -39.272 127.033 -17.953  1.00 53.20          c
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ATOM	10837	03'	G	B	43	-38.530	126.005	-17.298	1.00	60.85	O
ATOM	10838	C2'	G	B	43	-40.511	126.420	-18.582	1.00	55.65	C
ATOM	10839	02'	G	B	43	-40.309	125.214	-19.287	1.00	56.11	O
ATOM	10840	CI '	G	B	43	-41.392	126.223	-17.357	1.00	55.97	c
ATOM	10841	N9	G	B	43	-42.812	126.194	-17.694	1.00	64.93	N
ATOM	10842	C8	G	B	43	-43.486	127.138	-18.433	1.00	58.32	C
ATOM	10843	N7	G	B	43	-44.736	126.832	-18.595	1.00	61.44	N
ATOM	10844	C5	G	B	43	-44.893	125.625	-17.929	1.00	62.13	C
ATOM	10845	C4	G	B	43	-43.707	125.208	-17.368	1.00	65.99	C
ATOM	10846	N1	G	B	43	-45.764	123.657	-17.030	1.00	66.93	N
ATOM	10847	C2	G	B	43	-44.532	123.343	-16.506	1.00	67.00	C
ATOM	10848	N3	G	B	43	-43.448	124.096	-16.648	1.00	61.60	N
ATOM	10849	C6	G	B	43	-46.038	124.805	-17.776	1.00	64.96	C
ATOM	10850	06	G	B	43	-47.176	125.012	-18.206	1.00	67.60	O
ATOM	10851	N2	G	B	43	-44.469	122.196	-15.813	1.00	69.61	N
ATOM	10852	P	U	B	44	-36.930	126.007	-17.338	1.00	51.86	P
ATOM	10853	OP1	U	B	44	-36.349	127.309	-16.965	1.00	51.01	O
ATOM	10854	OP2	U	B	44	-36.516	124.828	-16.568	1.00	55.46	O
ATOM	10855	05'	U	B	44	-36.620	125.802	-18.886	1.00	51.68	0
ATOM	10856	C5'	u	B	44	-36.605	124.511	-19.473	1.00	46.83	c
ATOM	10857	C4'	u	B	44	-35.955	124.547	-20.825	1.00	48.54	c
ATOM	10858	04'	u	B	44	-36.890	125.125	-21.782	1.00	53.06	0
ATOM	10859	C3'	u	B	44	-34.692	125.398	-20.898	1.00	50.83	c
ATOM	10860	03'	u	B	44	-33.789	124.817	-21.839	1.00	48.13	0
ATOM	10861	C2'	u	B	44	-35.233	126.729	-21.432	1.00	50.62	c
ATOM	10862	02'	u	B	44	-34.298	127.609	-22.031	1.00	52.23	0
ATOM	10863	CI '	u	B	44	-36.299	126.247	-22.405	1.00	51.69	c
ATOM	10864	Nl	u	B	44	-37.334	127.260	-22.657	1.00	56.29	N
ATOM	10865	C2	u	B	44	-37.268	127.952	-23.853	1.00	59.00	c
ATOM	10866	N3	u	B	44	-38.243	128.913	-24.017	1.00	61.37	N
ATOM	10867	C4	u	B	44	-39.241	129.240	-23.111	1.00	61.71	C
ATOM	10868	C5	U	B	44	-39.235	128.480	-21.895	1.00	54.11	C
ATOM	10869	C6	u	B	44	-38.295	127.548	-21.717	1.00	55.65	c
ATOM	10870	02	u	B	44	-36.417	127.735	-24.706	1.00	55.74	0
ATOM	10871	04	U	B	44	-40.045	130.135	-23.392	1.00	63.85	0
ATOM	10872	05'	u	B	45	-31.594	125.164	-20.651	1.00	43.32	0
ATOM	10873	C4'	u	B	45	-30.466	127.280	-20.414	1.00	43.85	c
ATOM	10874	C3'	u	B	45	-29.387	126.697	-19.507	1.00	43.52	c
ATOM	10875	C2'	u	B	45	-29.362	127.703	-18.365	1.00	43.14	c
ATOM	10876	P	u	B	45	-32 .457	124.041	-21.365	1.00	49.45	P
ATOM	10877	OP1	u	B	45	-31.783	123.608	-22.623	1.00	47.61	0
ATOM	10878	OP2	u	B	45	-32.760	122.991	-20.357	1.00	43.77	0
ATOM	10879	C5'	u	B	45	-31.146	126.306	-21.353	1.00	44.52	c
ATOM	10880	04'	u	B	45	-31.449	127.816	-19.484	1.00	43.14	0
ATOM	10881	03'	U	B	45	-28.123	126.501	-20.142	1.00	47.98	0
ATOM	10882	02'	u	B	45	-28.696	128.892	-18.759	1.00	49.65	0
ATOM	10883	C1'	u	B	45	-30.860	128.007	-18.217	1.00	43.95	c
ATOM	10884	N1	U	B	45	-31.485	127.056	-17.274	1.00	41.06	N
ATOM	10885	C2	u	B	45	-31.165	127.201	-15.941	1.00	41.23	c
ATOM	10886	N3	u	B	45	-31.734	126.273	-15.129	1.00	41.71	N
ATOM	10887	C4	u	B	45	-32 .563	125.242	-15.497	1.00	46.86	c
ATOM	10888	C5	u	B	45	-32 .855	125.143	-16.896	1.00	41.24	c
ATOM	10889	C6	u	B	45	-32 .295	126.033	-17.719	1.00	44.48	c
ATOM	10890	02	u	B	45	-30.444	128.087	-15.502	1.00	43.06	0
ATOM	10891	04	u	B	45	-32.992	124.506	-14.610	1.00	50.82	0
ATOM	10892	05'	A	B	46	-26.391	125.820	-18.404	1.00	32.46	0
ATOM	10893	C4'	A	B	46	-25.533	127.570	-17.018	1.00	42.65	c
ATOM	10894	C3'	A	B	46	-24.715	126.641	-16.158	1.00	44.65	c
ATOM	10895	C2'	A	B	46	-25.177	126.993	-14.753	1.00	43.85	c
ATOM	10896	P	A	B	46	-27.116	125.299	-19.700	1.00	38.75	P
ATOM	10897	OP1	A	B	46	-26.057	125.231	-20.740	1.00	41.34	0
ATOM	10898	OP2	A	B	46	-27.917	124.124	-19.314	1.00	36.72	0
ATOM	10899	C5'	A	B	46	-25.734	127.069	-18.418	1.00	40.62	c

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ATOM   10900   04'   A B  46    -26..805  127 .678  -16..324   1,00  41.64   O
ATOM   10901   03'   A B  46    --23,340  126..866  -16.,375   1,00  43..89  O
ATOM   10902   02'   A B  46    -24..548  128,193   -14 ..351  1,00  47,57   O
ATOM   10903   CI'   A B  46    -26..657  127 .280  -14 .986   1,00  38..44  C
ATOM   10904   N9    A B  46    -27,542   126.111   -14 ,762   1,00  50.,49  N
ATOM   10905   C8    A B  46    -28..249  125,345   -15..680   1,00  41,35   C
ATOM   10906   N7    A B  46    -28..992  124.,396  -15..136   1,00  35,.65  N
ATOM   10907   C5    A B  46    -28,749   124 .529  -13.,774   1,00  38.,47  C
ATOM   10908   C4    A B  46    -27..872  125..585  -13.,535   1,00  46..04  C
ATOM   10909   Nl    A B  46    -28..793  124.,266  -11 .419   1,00  47,19   N
ATOM   10910   C2    A B  46    -27.,934  125..288  -11,368    1,00  45..35  C
ATOM   10911   N3    A B  46    -27..416  126.,014  -12.,349   1,00  42 .92  N
ATOM   10912   C6    A B  46    -29. 232  123,858   -12 .633   1,00  40,74   C
ATOM   10913   N6    A B  46    -30..088  122.,849  -12.,646   1,00  38..07  N
ATOM   10914   05'   A B  47    -22.,049  125..587  -14 ,696   1,00  43..51  O
ATOM   10915   C4'   A B  47    -21..723  126,487   -12 .479   1,00  43,.04  C
ATOM   10916   C3'   A B  47    -21..025  125,233   -12..005   1,00  41.65   C
ATOM   10917   C2'   A B  47    -21.,797  124 .844  -10.,758   1,00  48.,46  C
ATOM   10918   P     A B  47    -22..289  125,671   -16..258   1,00  44,46   P
ATOM   10919   OF1   A B  47    -21 .086  126.,102  -17.030    1,00  42,34   0
ATOM   10920   OP2   A B  47    -22.,922  124 .402  -16,677    1,00  44,03   0
ATOM   10921   C5'   A B  47    -21..628  126.,734  -13.,961   1,00  45..32  C
ATOM   10922   04'   A B  47    -23..104  126.,273  -12..127   1,00  40,.16  0
ATOM   10923   03'   A B  47    -19.,659  125..434  -11,774    1,00  47.51   0
ATOM   10924   02'   A B  47    -21..335  125..597   -9,654    1,00  47.53   0
ATOM   10925   CI'   A B  47    -23 .203  125,305   -11 .110   1,00  41,86   C
ATOM   10926   N9    A B  47    -24.,104  124..253  -11,608    1,00  42.50   N
ATOM   10927   C8    A B  47    -24,375   123..943  -12.,913   1,00  38..11  C
ATOM   10928   N7    A B  47    -25. .302  123,026   -13. 047   1,00  37,63   N
ATOM   10929   C5    A B  47    -25..661  122.,728  -11 ,758   1,00  35..93  C
ATOM   10930   C4    A B  47    -24,945   123..481  -10.,857   1,00  42 .72  C
ATOM   10931   Nl    A B  47    -26..726  121.,784   -9.899    1,00  42,49   N
ATOM   10932   C2    A B  47    -25..963  122.,576   -9.,138   1,00  42 .61  C
ATOM   10933   N3    A B  47    -25,044   123. 457   -9.,517   1,00  45.,54  N
ATOM   10934   C6    A B  47    -26..587  121.,847  -11 .240   1,00  38,.83  C
ATOM   10935   N6    A B  47    -27.329   121.,066  -11 .995   1,00  41,65   N
ATOM   10936   05'   A B  48    -18.,967  123. 095  -11,342    1,00  43.,9.3 O
ATOM   10937   C4'   A B  48    -19..337  122.,058   -9,192    1,00  41.15   C
ATOM   10938   C3'   A B  48    -19. 017  120,667    -9. 711   1,00  37,30   C
ATOM   10939   C2'   A B  48    -20.,130  119.834    -9.,104   1,00  36..85  C
ATOM   10940   P     A B  48    -18.,637  124 .316  -12.,305   1,00  47.55   P
ATOM   10941   OP1   A B  48    -17.237   124,799   -12 .137   1,00  43,92   0
ATOM   10942   OP2   A B  48    -19..056  124.,011  -13.,684   1,00  47.20   0
ATOM   10943   C5'   A B  48    -18.,772  123..224   -9.,949   1,00  43..27  C
ATOM   10944   04'   A B  48    -20..774  122.,109   -9.232    1,00  42,32   0
ATOM   10945   03'   A B  48    -17 .738  120,224    -9.,324   1,00  43..41  0
ATOM   10946   02'   A B  48    -19,867   119. 599   -7,731    1,00  36.,91  0
ATOM   10947   CI'   A B  48    -21..298  120,798    -9.188    1,00  44,26   C
ATOM   10948   N9    A B  48    —22.131   120,588   -10..384   1,00  47,02   N
ATOM   10949   C8    A B  48    -22.,061  121 .305  -11,542    1,00  39.,65  C
ATOM   10950   N7    A B  48    -22..937  120.,904  -12.,413   1,00  42 .74  N
ATOM   10951   C5    A B  48    -23..633  119.,878  -11 .770   1,00  39,.93  C
ATOM   10952   C4    A B  48    -23,150   119.660   -10.,516   1,00  42 .13  C
ATOM   10953   Nl    A B  48    -25..162  118..118  -11 ,301   1,00  48..07  N
ATOM   10954   C2    A B  48    -24 .588  118.,015  -10. 091   1,00  42,37   C
ATOM   10955   N3    A B  48    -23,581   118..741   -9.,615   1,00  43..98  N
ATOM   10956   C6    A B  48    -24,708   119..069  -12.,168   1,00  43..08  C
ATOM   10957   N6    A B  48    -25. 264  119,196   -13. 375   1,00  35,10   N
ATOM   10958   05'   A B  49    -17 .949  117 ,713   -9.,592   1,00  42.56   O
ATOM   10959   C4'   A B  49    -18.,838  116..040   -8.,130   1,00  43..13  C
ATOM   10960   C3'   A B  49    -18..636  114,912    -9.140    1,00  41,62   C
ATOM   10961   C2'   A B  49    -19..986  114 ,226   -9.,109   1,00  41.17   C
ATOM   10962   P     A B  49    -17 ,062  118. 948  -10.,043   1,00  45.,32  P
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ATOM   10963  OP1   A B  49     -15.708  118.856   -9.485  1.00 50.60         O
ATOM   10964  OP2   A B  49     -17.222  119.027  -11.513  1.00 44.26         O
ATOM   10965  C5'   A B  49     -17.921  117.221   -8.269  1.00 39.52         C
ATOM   10966  04'   A B  49     -20.205  116.455   -8.341  1.00 38.20         O
ATOM   10967  03'   A B  49     -17.576  114.060   -8.779  1.00 44.25         O
ATOM   10968  02'   A B  49     -20.094  113.475   -7.906  1.00 48.81         O
ATOM   10969  CI'   A B  49     -20.921  115.436   -9.002  1.00 43.85         c
ATOM   10970  N9    A B  49     -21.317  115.947  -10.334  1.00 39.98         N
ATOM   10971  C8    A B  49     -20.687  116.906  -11.078  1.00 41.32         C
ATOM   10972  N7    A B  49     -21.245  117.154  -12.242  1.00 40.13         N
ATOM   10973  C5    A B  49     -22.298  116.271  -12.267  1.00 36.11         C
ATOM   10974  C4    A B  49     -22.360  115.527  -11.122  1.00 37.97         C
ATOM   10975  N1.   A B  49     -24.215  115.111  -12.996  1.00 43.52         N
ATOM   10976  C2    A B  49     -24.148  114.450  -11.835  1.00 43.73         c
ATOM   10977  N3    A B  49     -23.267  114.575  -10.843  1.00 45.10         N
ATOM   10978  C6    A B  49     -23.281  116.055  -13.231  1.00 44.72         C
ATOM   10979  N6    A B  49     -23.319  116.758  -14.368  1.00 46.25         N
ATOM   10980  05'   U B  50     -17.391  112.380  -10.675  1.00 41.39         O
ATOM   10981  C4'   ʋ B  50     -19.078  110.691  -10.836  1.00 42.73         C
ATOM   10982  C3'   u B  50     -18.592  110.251  -12.214  1.00 40.12         c
ATOM   10983  C2'   u B  50     -19.879  110.258  -13.031  1.00 36.47         C
ATOM   10984  P     u B  50     -16.537  113.456   -y.873  1.00 47.48         P
ATOM   10985  OF1   u B  50     -15.539  112.753   -9.038  1.00 39.54         0
ATOM   10986  OP2   u B  50     -16.048  114.475  -10.818  1.00 47.0.1          0
ATOM   10987  C5'   u B  50     -18.069  111.365   -y.964  1.00 41.76         C
ATOM   10988  04'   u B  50     -20.130  111.625  -11.106  1.00 39.12         0
ATOM   10989  03'   u B  50     -18.022  108.966  -12.161  1.00 43.22         0
ATOM   10990  02'   u B  50     -20.636  109.095  -12.757  1.00 39.04         0
ATOM   10991  CI'   u B  50     -20.646  111.417  -12.394  1.00 41.52         c
ATOM   10992  Nl    u B  50     -20.564  112.668  -13.180  1.00 38.65         N
ATOM   10993  C2    u B  50     -21.598  112.790  -14.061  1.00 38.35         c
ATOM   10994  N3    ʋ B  50     -21.557  113.926  -14.827  1.00 37.61         N
ATOM   10995  C4    u B  50     -20.601  114.903  -14.784  1.00 43.31         c
ATOM   10996  C5    u B  50     -19.541  114.687  -13.826  1.00 41.18         c
ATOM   10997  C6    ʋ B  50     -19.556  113.585  -13.074  1.00 37.95         c
ATOM   10998  02    u B  50     —22.463  111.923  -14.119  1.00 35.47         0
ATOM   10999  04    u B  50     -20.702  115.857  -15.550  1.00 40.27         0
ATOM   11000  P     A B  51     -16.550  108.629  -12.719  1.00 43.43         P
ATOM   11001  OP1   A B  51     -16.735  107.933  -13.995  1.00 38.78         0
ATOM   11002  OP2   A B  51     -15.679  109.804  -12.777  1.00 43.78         0
ATOM   11003  05'   A B  51     -15.947  107.814  -11.491  1.00 41.50         0
ATOM   11004  C5'   A B  51     -16.432  106.537  -11.1.19  1.00 42.46         c
ATOM   11005  C4'   A B  51     -17.576  106.518  -10.129  1.00 40.90         c
ATOM   11006  04'   A B  51     -18.153  105.191  -10.228  1.00 41.67         0
ATOM   11007  C3'   A B  51     -17.228  106.711   -8.641  1.00 4.3.88          c
ATOM   11008  03'   A B  51     -17.501  108.020   -8.153  1.00 46.24         0
ATOM   11009  C2'   A B  51     -18.051  105.643   -7.924  1.00 44.24         c
ATOM   11010  02'   A B  51     -19.348  106.103   -7.643  1.00 48.93         0
ATOM   11011  CI'   A B  51     -18.148  104.555   -8.983  1.00 46.52         c
ATOM   11012  N9    A B  51     -16.954  103.675   -8.926  1.00 45.33         N
ATOM   11013  C8    A B  51     -15.640  104.062   -8.725  1.00 47.39         c
ATOM   11014  N7    A B  51     -14.734  103.136   -8.670  1.00 46.18         N
ATOM   11015  C5    A B  51     -15.535  102.041   -8.851  1.00 45.88         c
ATOM   11016  C4    A B  51     -16.883  102.342   -9.009  1.00 40.20         c
ATOM   11017  N1.   A B  51     -16.068   99.815   -9.062  1.00 45.76         N
ATOM   11018  C2    A B  51     -17.334  100.292   -9.186  1.00 49..32          c
ATOM   11019  N3    A B  51     -17.885  101.512   -9.188  1.00 40.80         N
ATOM   11020  C6    A B  51     -15.128  100.734   -8.892  1.00 41.89         C
ATOM   11021  N6    A B  51     -13.852  100.440   -8.765  1.00 53.36         N
ATOM   11022  P     A B  52     -16.678  108.680   -6.921  1.00 45.09         P
ATOM   11023  OP1   A B  52     -17.349  109.995   -6.658  1.00 52.51         O
ATOM   11024  OP2   A B  52     -15.219  108.709   -7.151  1.00 41.57         O
ATOM   11025  05'   A B  52     -17.004  107.775   -5.663  1.00 48.76         O
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ATOM	11026	C5'	A	B	52	-17.958	108.201	-4.708	1.00	53.11	C
ATOM	11027	C4'	A	B	52	-17.823	107.513	-3.372	1.00	55.17	C
ATOM	11028	04'	A	B	52	-17.754	106.082	-3.577	1.00	58.62	0
ATOM	11029	C3'	A	B	52	-16.591	107.826	-2.523	1.00	60.80	C
ATOM	11030	03'	A	B	52	-16.710	109.024	-1.756	1.00	56.75	0
ATOM	11031	C2'	A	B	52	-16.507	106.590	-1.639	1.00	56.53	C
ATOM	11032	02'	A	B	52	-17.527	106.639	-0.650	1.00	64.33	0
ATOM	11033	C1'	A	B	52	-16.887	105.499	-2.627	1.00	59.28	C
ATOM	11034	N9	A	B	52	-15.703	104.939	-3.324	1.00	57.23	N
ATOM	11035	C8	A	B	52	-15.150	105.345	-4.515	1.00	51.47	C
ATOM	11036	N7	A	B	52	-14.076	104.673	-4.876	1.00	49.87	N
ATOM	11037	C5	A	B	52	-13.904	103.753	-3.859	1.00	49.73	C
ATOM	11038	C4	A	B	52	-14.887	103.908	-2.887	1.00	54.53	C
ATOM	11039	Nl	A	B	52	-13.033	101.989	-2.558	1.00	48.72	N
ATOM	11040	C2	A	B	52	-14.037	102.256	-1.697	1.00	54.25	C
ATOM	11041	N3	A	B	52	-15.014	103.177	-1.757	1.00	57.25	N
ATOM	11042	C6	A	B	52	-12.934	102.730	-3.682	1.00	53.69	C
ATOM	11043	N6	A	B	52	-11.936	102.489	-4.554	1.00	45.60	N
ATOM	11044	05'	G	B	53	-14.210	109.650	-1.342	1.00	56.62	O
ATOM	11045	C4'	G	B	53	-13.162	107.547	-0.919	1.00	58.66	C
ATOM	11046	C3'	G	B	53	-11.668	107.828	-0.957	1.00	56.97	C
ATOM	11047	C2'	G	B	53	-11.186	106.797	-1.967	1.00	56.54	C
ATOM	11048	P	G	B	53	-15.622	110.222	-1.796	1.00	57.72	P
ATOM	11049	OP1	G	B	53	-16.182	111.172	-0.792	1.00	66.05	0
ATOM	11050	OP2	G	B	53	-15.241	110.711	-3.140	1.00	53.62	0
ATOM	11051	C5'	G	B	53	-14.054	108.634	-0.376	1.00	58.65	C
ATOM	11052	04'	G	B	53	-13.486	107.284	-2.313	1.00	52.62	0
ATOM	11053	03'	G	B	53	-11.035	107.698	0.309	1.00	61.60	0
ATOM	11054	02'	G	B	53	-11.132	105.509	-1.376	1.00	56.90	0
ATOM	11055	CI'	G	B	53	-12.330	106.808	-2.981	1.00	52.90	C
ATOM	11056	N9	G	B	53	-11.992	107.685	-4.111	1.00	46.29	N
ATOM	11057	C8	G	B	53	-12.553	108.872	-4.482	1.00	48.27	C
ATOM	11058	N7	G	B	53	-11.958	109.405	-5.520	1.00	51.03	N
ATOM	11059	C5	G	B	53	-10.952	108.516	-5.855	1.00	40.68	C
ATOM	11060	C4	G	B	53	-10.953	107.443	-4.991	1.00	46.27	C
ATOM	11061	Nl	G	B	53	-9.167	107.437	-6.891	1.00	48.04	N
ATOM	11062	C2	G	B	53	-9.244	106.425	-5.970	1.00	44.90	C
ATOM	11063	N3	G	B	53	-10.129	106.360	-4.985	1.00	44.44	N
ATOM	110 64	C6	G	B	53	-10.005	108.553	-6.906	1.00	47.99	C
ATOM	11065	06	G	B	53	-9.848	109.404	-7.784	1.00	49.46	O
ATOM	11066	N2	G	B	53	-8.348	105.456	-6.149	1.00	47.31	N
ATOM	11067	05'	G	B	54	-8.539	107.678	-0.225	1.00	57.14	O
ATOM	11068	C4'	G	B	54	-7.270	105.759	-1.004	1.00	57.68	C
ATOM	11069	C3'	G	B	54	-5.917	106.435	-0.916	1.00	57.96	C
ATOM	11070	C2'	G	B	54	-5.301	106.141	-2.281	1.00	59.38	C
ATOM	11071	P	G	B	54	-9.641	108.448	0.628	1.00	64.31	P
ATOM	11072	OP1	G	B	54	-9.404	108.213	2.079	1.00	69.71	0
ATOM	11073	OP2	G	B	54	-9.686	109.838	0.113	1.00	66.54	0
ATOM	11074	C5'	G	B	54	-8.329	106.279	-0.061	1.00	58.42	C
ATOM	11075	04'	G	B	54	-7.672	105.961	-2.380	1.00	59.39	0
ATOM	11076	03'	G	B	54	-5.154	105.959	0.178	1.00	69.97	0
ATOM	11077	02'	G	B	54	-4.738	104.840	-2.317	1.00	67.35	0
ATOM	11078	CI'	G	B	54	-6.531	106.160	-3.193	1.00	55.12	C
ATOM	11079	Nl	G	B	54	-5.156	108.900	-7.294	1.00	49.54	N
ATOM	11080	N9	G	B	54	-6.688	107.426	-3.946	1.00	52.44	N
ATOM	11081	C8	G	B	54	-7.520	108.481	-3.631	1.00	50.50	C
ATOM	11082	N7	G	B	54	-7.460	109.465	-4.501	1.00	50.80	N
ATOM	11083	C5	G	B	54	-6.545	109.047	-5.440	1.00	45.64	C
ATOM	11084	C6	G	B	54	-6.081	109.701	-6.610	1.00	50.12	C
ATOM	11085	06	G	B	54	-6.401	110.813	-7.056	1.00	48.85	0
ATOM	11086	C2	G	B	54	-4.745	107.649	-6.879	1.00	48.41	C
ATOM	11087	N2	G	B	54	-3.858	107.046	-7.670	1.00	47.71	N
ATOM	11088	N3	G	B	54	-5.165	107.033	-5.790	1.00	48.04	N

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ATOM  11089  C4    G B  54      -6.060 107.783  -5.120  1.00 47.36           C
ATOM  11090  05'   C B  55      -3.150 107.474   0.316  1.00 67.16           O
ATOM  11091  C4'   C B  55      -0.996 106.789  -0.373  1.00 72.96           C
ATOM  11092  C3'   C B  55      -0.007 107.795  -0.952  1.00 82.27           C
ATOM  11093  C2'   C B  55       0.140 107.288  -2.375  1.00 80.47           C
ATOM  11094  P     C B  55      -4.393 106.978   1.168  1.00 73.70           P
ATOM  11095  OF1   C B  55      -3.850 106.176   2.276  1.00 72.18           0
ATOM  11096  OP2   C B  55      -5.250 108.146   1.493  1.00 63.74           0
ATOM  11097  C5'   C B  55      -1.832 107.251   0.772  1.00 70.22           C
ATOM  11098  04'   C B  55      -1.910 106.553  -1.476  1.00 75.60           0
ATOM  11099  03'   C B  55       1.208 108.013  -0.200  1.00 92.57           0
ATOM  11100  02'   C B  55       0.814 106.046  -2.366  1.00 87.85           0
ATOM  11101  CI'   C B  55      -1.307 106.953  -2.693  1.00 74.34           C
ATOM  11102  N1    C B  55      -2.052 108.109  -3.256  1.00 66.41           N
ATOM  11103  C2    C B  55      -1.720 108.583  -4.532  1.00 62.67           C
ATOM  11104  N3    C B  55      -2.385 109.633  -5.058  1.00 54.48           N
ATOM  11105  C4    C B  55      -3.370 110.202  -4.369  1.00 56.73           C
ATOM  11106  C5    C B  55      -3.741 109.738  -3.070  1.00 56.98           C
ATOM  11107  C6    C B  55      -3.066 108.707  -2.556  1.00 59.13           C
ATOM  11108  02    C B  55      -0.805 108.043  -5.165  1.00 66.56           0
ATOM  11109  N4    C B  55      -4.016 111.234  -4.943  1.00 55.08           N
ATOM  11110  05'   u B  56       3.612 107.983  -1.118  1.00 88.51           0
ATOM  11111  C4'   u B  56       3.979 108.605  -3.453  1.00 87.22           C
ATOM  11112  C3'   u B  56       3.414 109.374  -4.635  1.00 84.66           C
ATOM  11113  C2'   u B  56       2.462 108.365  -5.252  1.00 81.09           C
ATOM  11114  P     u B  56       2.555 107.108  -0.304  1.00 95.07           P
ATOM  11115  OP1   u B  56       2.406 105.816  -1.018  1.00 87.31           0
ATOM  11116  OP2   u B  56       3.061 107.078   1.091  1.00100.78           0
ATOM  11117  C5'   u B  56       3.209 108.842  -2.173  1.00 87.40           C
ATOM  11118  04'   u B  56       3.924 107.197  -3.836  1.00 89.36           0
ATOM  11119  03'   u B  56       4.462 109.659  -5.553  1.00 82.04           0
ATOM  11120  02'   u B  56       2.129 108.635  -6.595  1.00 83.72           0
ATOM  11121  CI'   u B  56       3.263 107.073  -5.095  1.00 88.46           C
ATOM  11122  N1    u B  56       2.457 105.826  -5.090  1.00 92.38           N
ATOM  11123  C2    u B  56       1.496 105.547  -6.070  1.00 83.70           C
ATOM  11124  N3    u B  56       0.826 104.353  -5.930  1.00 86.79           N
ATOM  11125  C4    u B  56       1.007 103.397  -4.951  1.00 94.86           C
ATOM  11126  C5    u B  56       2.016 103.730  -3.989  1.00 99.56           C
ATOM  11127  C6    u B  56       2.690 104.886  -4.103  1.00 95.71           C
ATOM  11128  02    u B  56       1.218 106.272  -7.009  1.00 78.62           0
ATOM  11129  04    u B  56       0.325 102.368  -4.966  1.00 98.34           0
ATOM  11130  P     A B  57       4.726 111.184  -5.967  1.00 82.89           P
ATOM  11131  OP1   A B  57       4.885 111.948  -4.704  1.00 74.22           0
ATOM  11132  OP2   A B  57       5.753 111.228  -7.047  1.00 75.70           0
ATOM  11133  05'   A B  57       3.338 111.652  -6.591  1.00 78.39           0
ATOM  11134  C5'   A B  57       3.283 112.845  -7.349  1.00 71.94           C
ATOM  11135  C4'   A B  57       1.890 113.403  -7.463  1.00 73.39           C
ATOM  11136  04'   A B  57       0.932 112.655  -6.648  1.00 65.97           0
ATOM  11137  C3'   A B  57       1.763 114.865  -7.048  1.00 66.73           C
ATOM  11138  03'   A B  57       0.894 115.524  -7.959  1.00 64.00           0
ATOM  11139  C2'   A B  57       1.112 114.772  -5.671  1.00 64.49           C
ATOM  11140  02'   A B  57       0.396 115.924  -5.282  1.00 70.86           0
ATOM  11141  CI'   A B  57       0.201 113.564  -5.850  1.00 59.04           C
ATOM  11142  N9    A B  57      -0.174 112.902  -4.608  1.00 57.07           N
ATOM  11143  C8    A B  57       0.410 111.823  -4.010  1.00 60.52           C
ATOM  11144  N7    A B  57      -0.195 111.460  -2.903  1.00 61.18           N
ATOM  11145  C5    A B  57      -1.242 112.349  -2.771  1.00 49.57           C
ATOM  11146  C4    A B  57      -1.241 113.240  -3.823  1.00 52.75           C
ATOM  11147  N1    A B  57      -3.146 113.488  -1.998  1.00 52.05           N
ATOM  11148  C2    A B  57      -3.014 114.278  -3.068  1.00 51.09           C
ATOM  11149  N3    A B  57      -2.103 114.239  -4.034  1.00 50.90           N
ATOM  11150  C6    A B  57      -2.253 112.494  -1.819  1.00 52.23           C
ATOM  11151  N6    A B  57      -2.384 111.720  -0.747  1.00 58.22           N
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ATOM	11152	P	G	B	58	1.466	116.005	-9.379	1.00	75.95	P
ATOM	11153	OP1	G	B	58	2.887	116.397	-9.204	1.00	79.84	O
ATOM	11154	OP2	G	B	58	0.470	116.958	-9.957	1.00	76.14	O
ATOM	11155	05'	G	B	58	1.532	114.675	-10.255	1.00	68.92	O
ATOM	11156	C5'	G	B	58	2.758	114.200	-10.809	1.00	71.85	C
ATOM	11157	C4'	G	B	58	2.478	113.160	-11.863	1.00	67.87	C
ATOM	11158	04'	G	B	58	1.841	112.020	-11.215	1.00	66.30	O
ATOM	11159	C3'	G	B	58	1.489	113.632	-12.928	1.00	65.07	C
ATOM	11160	03'	G	B	58	2.132	114.165	-14.081	1.00	67.08	O
ATOM	11161	C2'	G	B	58	0.630	112.405	-13.209	1.00	59.54	C
ATOM	11162	02'	G	B	58	1.265	111.570	-14.159	1.00	59.78	0
ATOM	11163	CI'	G	B	58	0.630	111.701	-11.852	1.00	57.01	C
ATOM	11164	N9	G	B	58	-0.464	112.156	-10.958	1.00	52.72	N
ATOM	11165	C8	G	B	58	-1.234	113.276	-11.047	1.00	49.46	C
ATOM	11166	N7	G	B	58	-2.097	113.396	-10.070	1.00	52.99	N
ATOM	11167	C5	G	B	58	-1.894	112.293	-9.277	1.00	43.38	C
ATOM	11168	C4	G	B	58	-0.887	111.525	-9.806	1.00	50.65	C
ATOM	11169	N1	G	B	58	-1.989	110.688	-7.605	1.00	52.02	N
ATOM	11170	C2	G	B	58	-0.988	109.990	-8.205	1.00	52.40	C
ATOM	11171	N3	G	B	58	-0.394	110.371	-9.326	1.00	50.47	N
ATOM	11172	C6	G	B	58	-2.523	111.877	-8.078	1.00	50.97	C
ATOM	11173	06	G	B	58	-3.442	112.396	-7.423	1.00	53.97	O
ATOM	11174	N2	G	B	58	-0.625	108.861	-7.571	1.00	55.13	N
ATOM	11175	P	U	B	59	1.955	115.720	-14.467	1.00	63.66	P
ATOM	11176	OP1	U	B	59	2.617	116.027	-15.758	1.00	55.90	O
ATOM	11177	OP2	U	B	59	2.334	116.468	-13.239	1.00	69.29	O
ATOM	11178	05'	U	B	59	0.376	115.901	-14.661	1.00	69.39	O
ATOM	11179	C5'	U	B	59	-0.367	115.086	-15.567	1.00	60.60	C
ATOM	11180	C4'	U	B	59	-1.852	115.151	-15.285	1.00	56.08	C
ATOM	11181	04'	U	B	59	-2.314	116.509	-15.473	1.00	57.97	0
ATOM	11182	C3'	U	B	59	-2.742	114.312	-16.198	1.00	54.19	C
ATOM	11183	03'	U	B	59	-2.845	112.973	-15.759	1.00	49.67	0
ATOM	11184	C2'	U	B	59	-4.074	115.055	-16.175	1.00	56.83	C
ATOM	11185	02'	U	B	59	-4.864	114.667	-15.054	1.00	52.52	0
ATOM	11186	CI'	U	B	59	-3.620	116.511	-15.995	1.00	54.88	C
ATOM	11187	N1	U	B	59	-3.610	117.282	-17.255	1.00	59.08	N
ATOM	11188	C2	U	B	59	-4.845	117.707	-17.737	1.00	51.56	C
ATOM	11189	N3	U	B	59	-4.824	118.424	-18.890	1.00	45.19	N
ATOM	11190	C4	U	B	59	-3.720	118.793	-19.609	1.00	58.80	C
ATOM	11191	C5	U	B	59	-2.469	118.324	-19.049	1.00	56.73	C
ATOM	11192	C6	U	B	59	-2.445	117.608	-17.907	1.00	52.82	C
ATOM	11193	02	U	B	59	-5.887	117.443	-17.186	1.00	49.97	0
ATOM	11194	04	U	B	59	-3.890	119.466	-20.641	1.00	59.39	0
ATOM	11195	05'	C	B	60	-3.220	110.519	-16.027	1.00	53.93	0
ATOM	11196	C4'	C	B	60	-1.648	109.325	-14.678	1.00	52.91	C
ATOM	11197	C3'	C	B	60	-2.751	108.305	-14.484	1.00	52.89	C
ATOM	11198	C2'	C	B	60	-2.509	107.853	-13.043	1.00	55.43	C
ATOM	11199	P	C	B	60	-3.752	111.915	-16.553	1.00	46.43	P
ATOM	11200	OF1	C	B	60	-5.124	111.880	-16.007	1.00	50.80	0
ATOM	11201	OP2	C	B	60	-3.505	112.066	-17.995	1.00	44.96	0
ATOM	11202	C5'	C	B	60	-1.842	110.285	-15.815	1.00	52.57	C
ATOM	11203	04'	C	B	60	-1.618	110.027	-13.412	1.00	52.31	0
ATOM	11204	03'	C	B	60	-2.729	107.264	-15.456	1.00	55.20	0
ATOM	11205	02'	C	B	60	-1.400	106.962	-12.980	1.00	53.55	0
ATOM	11206	C1'	C	B	60	-2.084	109.171	-12.385	1.00	46.94	C
ATOM	11207	N1	C	B	60	-3.160	109.854	-11.626	1.00	43.93	N
ATOM	11208	C2	C	B	60	-3.588	109.315	-10.416	1.00	46.57	C
ATOM	11209	N3	C	B	60	-4.557	109.945	-9.701	1.00	48.64	N
ATOM	11210	C4	C	B	60	-5.092	111.101	-10.152	1.00	45.38	C
ATOM	11211	C5	C	B	60	-4.679	111.695	-11.377	1.00	36.63	C
ATOM	11212	C6	C	B	60	-3.726	111.042	-12.064	1.00	50.01	C
ATOM	11213	02	C	B	60	-3.084	108.260	-10.027	1.00	52.87	0
ATOM	11214	N4	C	B	60	-6.038	111.665	-9.397	1.00	38.99	N

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ATOM   11215   05'   C B  61     -4.284  105.638  -14.312  1.00  45..85     O
ATOM   11216   C4'   C B  61     -3.957  103.998  -12.570  1,00  38..01     C
ATOM   11217   C3'   C B  61     -5.4.13 10.3.580 -12.546  1.00  42,23      C
ATOM   11218   C2'   C B  61     --5.755 103.639  -11.065  1.00  46..20     C
ATOM   11219   P     C B  61     -4.032  .106.355 -15.707  1,00  48.,13     P
ATOM   11220   OP1   C B  61     -3.690  105.297  -16.666  1.00  44,89      0
ATOM   11221   OF2   C B  61     --5.184 107.252  -15.998  1,00  48,.03     0
ATOM   11222   C5'   C B  61     -3.466  .104.556 -13.878  1,00  45.,84     C
ATOM   11223   04'   C B  61     -3.885  105.026  -11.549  1,00  42.70      0
ATOM   11224   03'   C B  61     --5.624 102.319  -13.125  1,00  47,95      0
ATOM   11225   02'   C B  61     -5.279  102.490  -10.390  1,00  52.07      0
ATOM   11226   CI'   C B  61     -4.926  104.839  -10.607  1,00  41.52      C
ATOM   11227   N1.   C B  61     -5.748  106.058  -10.5.13 1,00  4.1,64     N
ATOM   11228   C2    C B  61     --6.588 106.170   -9.401  1.00  47.74      C
ATOM   11229   N3    C B  61     -7.373  107.253   -9.244  1,00  44.86      N
ATOM   112 30  C4    C B  61     -7..347  108.213  -10.164  1.00  46,.50     C
ATOM   11231   C5    C B  61     --6.500 108.124  -11.322  1.00  44.68      C
ATOM   11232   C6    C B  61     -5.725  .107.035 -1.1.468  1,00  44,46      C
ATOM   112 33  02    C B  61     -6.604  105.282   -8.545  1.00  47,79      0
ATOM   11234   N4    C B  61     --8.168 109.260   -9.952  1,00  41,02      N
ATOM   11235   05'   G B  62     -8.014  .101.970 -12.460  1,00  34,30      0
ATOM   11236   C4'   G B  62     -y.139   101.139  -10.509  1,00  43..69     C
ATOM   11237   C3'   G B  62    -10.574  101.365  -10.993  1,00  40,.49     C
ATOM   11238   C2'   G B  62    -11.167  102.186   -9.856  1,00  40..8.3    C
ATOM   11239   P     G B  62     -7.055  101.901  -13.711  1,00  40..42     P
ATOM   112 40  OP1   G B  62     -7.008  100.456  -14.1.18  1,00  50,53      0
ATOM   11241   OP2   G B  62     -7.366  102.821  -14.798  1,00  45..66     0
ATOM   11242   C5'   G B  62     -8.104  100.878  -11.562  1,00  37.79      C
ATOM   112 43  04'   G B  62     -8.800  102.389   -9.852  1,00  44,69      0
ATOM   11244   03'   G B  62    -11.324  100.174  -11.237  1.00  40..47     0
ATOM   11245   02'   G B  62    -11.566  101.366   -8.786  1,00  38..08     0
ATOM   112 46  CI'   G B  62     -9.973  10.3.018  -9..395  1.00  42,60      C
ATOM   11247   Nl    G B  62    -12.405  107.407   -8.934  1.00  34.53      N
ATOM   11248   N9    G B  62    -10.078  .104.372  -9.956  1,00  45.,27     N
ATOM   112 49  C8    G B  62     -9.442  104.931  -11.035  1.00  42,17      C
ATOM   11250   N7    G B  62     -9.826  106.161  -11.243  1,00  38,.50     N
ATOM   11251   C5    G B  62    -10.768  .106.398 -10.258  1,00  39.,07     C
ATOM   11252   C6    G B  62    -11.554  107.560  -10.018  1,00  41.26      C
ATOM   112 53  06    G B  62    -11.525  108.612  -10.667  1,00  4.1,19     O
ATOM   11254   C2    G B  62    -12.500  .106.267  -8.169  1,00  45..02     C
ATOM   11255   N2    G B  62    -13.397  106.341   -7.159  1,00  44.32      N
ATOM   112 56  N3    G B  62    -11.778  105.140   -8.392  1,00  38,47      N
ATOM   11257   C4    G B  62    -10.948  105.302   -9.455  1.00  38..96     C
ATOM   11258   P     U B  63    -11.019   99.208  -12.495  1,00  47.23      P
ATOM   11259   OP1   υ B  63     -9.874   98.331  -12.120  1.00  48,.28     0
ATOM   11260   OP2   U B  63    -10.850   99.953  -13.757  1.00  42.09      0
ATOM   112 61  05'   U B  63    -12.327   98.308  -12.598  1,00  40.,54     0
ATOM   11262   C5'   υ B  63    -12.5.15   97.150  -11.795  1.00  35,.70     C
ATOM   11263   C4'   u B  63    -13.828   96.473  -12.101  1,00  38,.97     C
ATOM   112 64  04'   u B  63    -14.926   97.344  -1.1.723  1,00  49.,28     0
ATOM   11265   C3'   u B  63    -14.060   96.129  -13.566  1,00  42.02      C
ATOM   11266   03'   u B  63    -14.928   95.004  -13.626  1,00  42,93      0
ATOM   112 67  C2'   u B  63    -14.831   97..347 -14.075  1,00  43..07     C
ATOM   11268   02'   u B  63    -15.616   97.097  -15.223  1,00  46..61     0
ATOM   112 69  C1'   u B  63    -15.709   97.660  -12.871  1,00  45,08      C
ATOM   11270   Nl    u B  63    -16.157   99.057  -12.755  1,00  39..84     N
ATOM   11271   C2    u B  63    -17.499   99.327  -12.932  1,00  44.03      C
ATOM   112 72  N3    u B  63    -17.883  100.661  -12.773  1,00  44,16      N
ATOM   11273   C4    u B  63    -17.018  101.693  -12.435  1.00  43..26     C
ATOM   11274   C5    u B  63    -15.646  101.294  -12.269  1,00  44.13      C
ATOM   11275   C6    υ B  63    -15.274  100.034  -12.425  1.00  42,01      C
ATOM   11276   02    u B  63    -18.264   98.424  -13.222  1.00  42.24      0
ATOM   11277   04    u B  63    -17.386  102.852  -12.324  1,00  41,44      0
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ATOM   11278   05'   U B  64     -13.764   93.171  -14.864   1.00  46.03        O
ATOM   112 79  C4'   U B  64     -13.812   92.511  -17.160   1.00  45.84        C
ATOM   112 80  C3'   υ B  64     -13.146   9.1.134 -17.007   1.00  4.1.70       C
ATOM   11281   C2'   u B  64     -11.989   91.225  -17.974   1.00  40.08        C
ATOM   11282   P     u B  64     -14.360   93.516  -13.434   1.00  42.47        P
ATOM   112 83  OP1   υ B  64     -15.5.19   92.649  -13.126   1.00  39.79        0
ATOM   11284   OF2   u B  64     -13.212   93.557  -12.506   1.00  46.68        0
ATOM   11285   C5'   u B  64     -14.612   92.981  -15.986   1.00  39.93        C
ATOM   11286   04'   u B  64     -12.693   93.416  -17.360   1.00  41.95        0
ATOM   11287   03'   u B  64     -14.002   90.042  -17.266   1.00  40.17        0
ATOM   11288   02'   u B  64     -12.434   91.065  -19.311   1.00  42.18        0
ATOM   11289   CI'   u B  64     -11.552   92.673  -17.767   1.00  45.99        C
ATOM   112 90  N1.   u B  64     -10.5.11   92.760  -16.7.13   1.00  48.98        N
ATOM   11291   C2    u B  64      -9.239   92.359  -17.061   1.00  45.16        C
ATOM   11292   N3    u B  64      -8.300   92.461  -16.081   1.00  47.10        N
ATOM   112 93  C4    υ B  64      -8.507   92.915  -14.792   1.00  5.3.00       C
ATOM   11294   C5    u B  64      -9.844   93.313  -14.499   1.00  48.83        C
ATOM   112 95  C6    u B  64     -10.781   93.222  -15.445   1.00  49.13        C
ATOM   11296   02    υ B  64      -8.964   9.1.969 -18.171   1.00  48.73        0
ATOM   11297   04    u B  64      -7.566   92.946  -14.004   1.00  58.33        0
ATOM   112 98  05'   A B  65     -12.645   88.068  -16.505   1.00  53.50        0
ATOM   11299   C4'   A B  65     -10.757   87.363  -17.862   1.00  42.07        C
ATOM   11300   C3'   A B  65     -10.309   86.298  -16.871   1.00  47.62        C
ATOM   11301   C2'   A B  65      -8.834   86.625  -16.668   1.00  48.09        C
ATOM   11302   P     A B  65     -14.043   88.802  -16.255   1.00  39.80        P
ATOM   11303   OP1   A B  65     -15.136   87.905  -16.686   1.00  47.19        0
ATOM   11304   OP2   A B  65     -14.057   89..308  -14.877   1.00  44.24        0
ATOM   11305   C5'   A B  65     -12.226   87.696  -17.819   1.00  43.98        C
ATOM   11306   04'   A B  65      -9.956   88.532  -17.530   1.00  51.11        0
ATOM   11307   03'   A B  65     -10.536   84.992  -17.379   1.00  48.60        0
ATOM   11308   02'   A B  65      -8.057   86.122  -17.745   1.00  53.59        0
ATOM   11309   CI'   A B  65      -8.834   88.150  -16.759   1.00  50.02        C
ATOM   11310   N9    A B  65      -8.957   88.757  -15.427   1.00  50.32        N
ATOM   11311   C8    A B  65     -10.074   89.374  -14.937   1.00  48.16        C
ATOM   11312   N1    A B  65      -9.932   89.799  -13.7.15   1.00  52.05        N
ATOM   11313   C5    A B  65      -8.649   89.442  -13.364   1.00  53.21        C
ATOM   11314   C4    A B  65      -8.033   88.787  -14.412   1.00  53.03        C
ATOM   11315   Ml    A B  65      -6.647   89.115  -12.141   1.00  57.74        N
ATOM   11316   C2    A B  65      -6.183   88.506  -13.240   1.00  54.25        C
ATOM   11317   N3    A B  65      -6.785   88.296  -14.408   1.00  57.13        N
ATOM   11318   C6    A B  65      -7.908   89.610  -12.179   1.00  57.73        C
ATOM   11319   N6    A B  65      -8.381   90.221  -11.096   1.00  56.86        N
ATOM   11320   P     U B  66     -11.345   83.884  -16.557   1.00  46.57        P
ATOM   11321   OP1   U B  66     -11.407   82.663  -17.400   1.00  48.70        0
ATOM   11322   OP2   υ B  66     -12.601   84.397  -15.998   1.00  55.18        0
ATOM   11323   05'   u B  66     -10.380   83.579  -15.331   1.00  55.81        0
ATOM   11324   C5'   u B  66      -9.026   83.220  -15.562   1.00  52.66        C
ATOM   11325   C4'   υ B  66      -8.2.11   8.3.260 -14.294   1.00  51.23        C
ATOM   11326   04'   u B  66      -7.904   84.635  -13.946   1.00  51.46        0
ATOM   11327   C3'   u B  66      -8.877   82.705  -13.051   1.00  46.2.1       C
ATOM   11328   03'   u B  66      -8.840   81.297  -12.976   1.00  46.35        0
ATOM   11329   C2'   u B  66      -8.104   83.400  -11.947   1.00  50.56        C
ATOM   11330   02'   u B  66      -6.820   82.832  -11.818   1.00  49.08        0
ATOM   11331   CI'   u B  66      -7.931   84.791  -12.548   1.00  54.19        C
ATOM   11332   N1.   u B  66      -9.059   85.681  -12.180   1.00  47.59        N
ATOM   11333   C2    u B  66      -8.929   86..390  -11.016   1.00  52.85        C
ATOM   11334   N3    u B  66      -9.977   87.197  -10.671   1.00  59.06        N
ATOM   11335   C4    u B  66     -11.153   87.347  -11.359   1.00  53.10        C
ATOM   11336   C5    u B  66     -11.237   86.551  -12.547   1.00  51.07        C
ATOM   11337   C6    u B  66     -10.217   85.767  -12.904   1.00  49.89        C
ATOM   11338   02    υ B  66      -7.932   86.348  -10..344   1.00  6.3.62       0
ATOM   11339   04    u B  66     -11.996   88.106  -10.918   1.00  47.36        0
ATOM   11340   05'   C B  67      -9.948   80.758  -10.762   1.00  49.69        0
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ATOM  11341  C4'  C B  67     --9.129  80.659  -8.518  1.00 45.18           C
ATOM  11342  C3'  C B  67    --10.398  79.982  -8.034  1.00 48.68           C
ATOM  11343  C2'  C B  67     -10.895  80.904  -6.926  1.00 46.73           C
ATOM  11344  P    C B  67     -10.035  80.454 -12.310  1.00 46.06           P
ATOM  11345  OP1  C B  67      -9.735  79.038 -12.583  1.00 47.51           0
ATOM  11346  OP2  C B  67     -11.362  80.949 -12.714  1.00 49.58           0
ATOM  11347  C5'  C B  67      -8.817  80.416  -9.972  1.00 47.70           C
ATOM  11348  04'  C B  67      -9.390  82.075  -8.331  1.00 49.10           0
ATOM  11349  03'  C B  67     -10.184  78.645  -7.624  1.00 47.07           0
ATOM  11350  02'  C B  67     -10.240  80.658  -5.701  1.00 57.85           0
ATOM  11351  CI'  C B  67     -10.440  82.265  -7.418  1.00 44.90           C
ATOM  11352  Ml   C B  67     -11.516  83.021  -8.091  1.00 47.51           N
ATOM  11353  C2   C B  67     -12.532  83.520  -7.295  1.00 40.01           C
ATOM  11354  N3   C B  67     -13.510  84.227  -7.875  1.00 48.74           N
ATOM  11355  C4   C B  67     -13.507  84.446  -9.172  1.00 44.97           C
ATOM  11356  C5   C B  67     -12.484  83.929 -10.025  1.00 41.90           C
ATOM  11357  C6   C B  67     -11.499  83.235  -9.445  1.00 46.97           C
ATOM  11358  02   C B  67     -12.543  83.314  -6.070  1.00 43.82           0
ATOM  11359  N4   C B  67     -14.542  85.154  -9.618  1.00 45.85           N
ATOM  11360  05'  A B  68     -12.165  78.205  -6.160  1.00 51.08           O
ATOM  11361  C4'  A B  68     -12.777  77.192  -4.066  1.00 52.43           C
ATOM  11362  C3'  A B  68     -12.380  76.771  -2.665  1.00 56.07           C
ATOM  11363  C2'  A B  68     -13.322  75.612  -2.376  1.00 52.41           C
ATOM  11364  P    A B  68     -11.434  77.665  -7.462  1.00 53.05           P
ATOM  11365  OP1  A B  68     -10.947  76.282  -7.245  1.00 54.53           0
ATOM  11366  OP2  A B  68     -12.376  77.954  -8.563  1.00 52.85           0
ATOM  11367  C5'  A B  68     -11.700  77.876  -4.865  1.00 52.19           C
ATOM  11368  04'  A B  68     -13.158  75.953  -4.715  1.00 45.89           0
ATOM  11369  03'  A B  68     -12.480  77.827  -1.729  1.00 60.33           0
ATOM  11370  02'  A B  68     -14.595  76.058  -1.965  1.00 52.49           0
ATOM  11371  CI'  A B  68     -13.447  74.969  -3.748  1.00 49.94           C
ATOM  11372  Nl   A B  68     -11.722  70.359  -2.112  1.00 55.43           N
ATOM  11373  N9   A B  68     -12.464  73.883  -3.897  1.00 55.21           N
ATOM  11374  C8   A B  68     -11.441  73.844  -4.804  1.00 52.97           C
ATOM  11375  N7   A B  68     -10.716  72.763  -4.730  1.00 51.64           N
ATOM  11376  C5   A B  68     -11.295  72.049  -3.697  1.00 50.56           C
ATOM  11377  C6   A B  68     -10.959  70.810  -3.133  1.00 53.87           C
ATOM  11378  N6   A B  68      -9.933  70.080  -3.581  1.00 48.07           N
ATOM  11379  C2   A B  68     -12.754  71.118  -1.694  1.00 50.83           C
ATOM  11380  N3   A B  68     -13.154  72.312  -2.150  1.00 51.45           N
ATOM  11381  C4   A B  68     -12.369  72.724  -3.162  1.00 51.03           C
ATOM  11382  P    A B  69     -11.238  78.188  -0.781  1.00 57.11           P
ATOM  11383  OP1  A B  69     -11.673  79.384  -0.015  1.00 55.73           O
ATOM  11384  OP2  A B  69      -9.980  78.227  -1.587  1.00 46.81           O
ATOM  11385  05'  A B  69     -11.136  76.940   0.202  1.00 52.25           O
ATOM  11386  C5'  A B  69     -12.242  76.514   0.980  1.00 52.90           C
ATOM  11387  C4'  A B  69     -11.953  75.192   1.639  1.00 58.61           C
ATOM  11388  04'  A B  69     -12.020  74.131   0.646  1.00 57.54           0
ATOM  11389  C3'  A B  69     -10.561  75.064   2.239  1.00 58.55           C
ATOM  11390  03'  A B  69     -10.498  75.579   3.551  1.00 58.17           0
ATOM  11391  C2'  A B  69     -10.287  73.563   2.170  1.00 60.14           C
ATOM  11392  02'  A B  69     -10.884  72.873   3.259  1.00 59.31           0
ATOM  11393  CI'  A B  69     -11.017  73.174   0.887  1.00 56.34           C
ATOM  11394  N9   A B  69     -10.107  73.162  -0.261  1.00 53.94           N
ATOM  11395  C8   A B  69      -9.939  74.113  -1.226  1.00 57.64           C
ATOM  11396  N7   A B  69      -9.030  73.783  -2.119  1.00 57.52           N
ATOM  11397  C5   A B  69      -8.577  72.534  -1.697  1.00 58.06           C
ATOM  11398  C4   A B  69      -9.240  72.155  -0.547  1.00 54.44           C
ATOM  11399  Nl   A B  69      -7.416  70.490  -1.512  1.00 55.32           N
ATOM  11400  C2   A B  69      -8.131  70.269  -0.412  1.00 56.19           C
ATOM  11401  N3   A B  69      -9.063  71.030   0.156  1.00 60.89           N
ATOM  11402  C6   A B  69      -7.608  71.631  -2.197  1.00 57.28           C
ATOM  11403  N6   A B  69      -6.876  71.829  -3.291  1.00 55.16           N
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ATOM   11404   P      C B   70      -9.167   76.287    4.079   1.00 58.49           P
ATOM   11405   OP1    C B   70      -9.544   76.793    5.416   1.00 62.42           O
ATOM   11406   OP2    C B   70      -8.609   77.154    3.007   I.00 56.53           O
ATOM   11407   05'    C B   70      -8.095   75.119    4.262   1.00 68.23           O
ATOM   11408   C5'    C B   70      -8.312   74.035    5.158   1.00 71.16           C
ATOM   11409   C4'    C B   70      -7.299   72.932    4.950   I.00 73.80           C
ATOM   11410   04'    C B   70      -7.453   72.358    3.628   1.00 69.38           O
ATOM   11411   C3'    C B   70      -5.844   73.361    4.990   1.00 84.21           C
ATOM   11412   03'    C B   70      -5.348   73.499    6.305   1.00 89.40           O
ATOM   11413   C2'    C B   70      -5.146   72.270    4.190   1.00 80.90           C
ATOM   11414   02'    C B   70      -4.959   71.115    4.995   1.00 84.86           0
ATOM   11415   CI'    C B   70      -6.195   71.961    3.122   1.00 74.08           C
ATOM   11416   N1.    C B   70      -5.933   72.676    1.848   1.00 72.86           N
ATOM   11417   C2     C B   70      -5.054   72.101    0.922   1.00 72.07           C
ATOM   11418   N3     C B   70      -4.799   72.727   -0.239   1.00 73.33           N
ATOM   11419   C4     C B   70      -5.373   73.888   -0.515   I.00 67.30           C
ATOM   11420   C5     C B   70      -6.274   74.511    0.399   1.00 64.65           C
ATOM   11421   C6     C B   70      -6.526   73.877    1.555   1.00 68.41           C
ATOM   11422   02     C B   70      -4.516   71.024    1.166   I.00 75.08           0
ATOM   11423   N4     C B   70      -5.063   74.441   -1.685   1.00 68.01           N
ATOM   11424   P      U B   71      -3.970   74.276    6.546   1.00 94.97           P
ATOM   11425   OP1    U B   71      -3.781   75.343    5.524   1.00 88.54           0
ATOM   11426   OF2    U B   71      -3.924   74.615    7.990   1.00105.74           0
ATOM   11427   05'    U B   71      -2.872   73.176    6.237   1.00 95.29           0
ATOM   11428   C5'    U B   71      -1.554   73.582    5.930   1.00102.48           C
ATOM   11429   C4'    U B   71      -0.767   72.486    5.270   1.00103.31           C
ATOM   11430   04'    U B   71      -1.472   72.008    4.094   1.00 96.02           0
ATOM   11431   CI'    U B   71      -0.549   71.737    3.060   1.00101.17           C
ATOM   11432   C2'    U B   71       0.851   71.905    3.644   1.00106.44           C
ATOM   11433   02'    U B   71       1.240   70.663    4.211   1.00110.70           0
ATOM   11434   C3'    U B   71       0.584   72.923    4.736   1.00106.53           C
ATOM   11435   03'    U B   71       1.584   72.993    5.735   I.00111.50           0
ATOM   11436   N1     U B   71      -0.819   72.674    1.942   1.00100.52           N
ATOM   11437   C2     U B   71      -0.121   72.543    0.744   1.00102.42           C
ATOM   11438   N3     U B   71      -0.467   73.451   -0.231   I.00 99.68           N
ATOM   11439   C4     U B   71      -1.420   74.445   -0.137   1.00 98.47           C
ATOM   11440   C5     U B   71      -2.095   74.514    1.123   1.00 92.30           C
ATOM   11441   C6     U B   71      -1.784   73.645    2.088   1.00 94.40           C
ATOM   11442   02     U B   71       0.740   71.700    0.544   1.00104.68           0
ATOM   11443   04     U B   71      -1.616   75.187   -1.100   1.00102.77           0
ATOM   11444   P      U B   72       2.480   74.318    5.855   1.00116.11           P
ATOM   11445   OP1    U B   72       3.840   73.907    6.304   1.00114.15           0
ATOM   11446   OP2    U B   72       1.699   75.331    6.619   1.00109.16           0
ATOM   11447   05'    U B   72       2.589   74.822    4.347   1.00111.13           0
ATOM   11448   C5'    U B   72       3.796   75.371    3.845   I.00116.67           C
ATOM   11449   C4'    U B   72       4.384   74.519    2.747   1.00118.61           C
ATOM   11450   04'    U B   72       3.317   73.936    1.948   1.00118.57           0
ATOM   11451   CI'    U B   72       3.670   73.958    0.579   I.00118.60           C
ATOM   11452   C2'    U B   72       5.129   74.397    0.493   1.00121.99           C
ATOM   11453   02'    U B   72       5.950   73.245    0.609   1.00121.03           0
ATOM   11454   C3'    U B   72       5.241   75.266    1.734   1.00122.39           C
ATOM   11455   03'    U B   72       6.570   75.482    2.166   1.00120.67           0
ATOM   11456   N1     U B   72       2.765   74.913   -0.107   1.00118.68           N
ATOM   11457   C2     U B   72       2.865   75.094   -1.480   1.00117.15           C
ATOM   11458   N3     U B   72       1.973   76.000   -2.009   1.00115.78           N
ATOM   11459   C4     U B   72       1.014   76.727   -1.326   1.00114.90           C
ATOM   11460   C5     U B   72       0.977   76.491    0.085   1.00114.28           C
ATOM   11461   C6     U B   72       1.827   75.612    0.625   1.00115.88           C
ATOM   11462   02     U B   72       3.671   74.508   -2.185   1.00119.13           0
ATOM   11463   04     U B   72       0.280   77.502   -1.941   1.00115.36           0
ATOM   11464   P      G B   73       7.145   76.979    2.238   I.00125.80           P
ATOM   11465   OP1    G B   73       8.529   76.888    2.779   1.00129.55           0
ATOM   11466   OP2    G B   73       6.132   77.823    2.933   1.00123.82           0
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ATOM   11467   05'   G B   73        7.197   77.459    0.713   1.00127.51          O
ATOM   11468   C5'   G B   73        8.185   76.964   -0.184   1.00126.25          C
ATOM   11469   C4'   G B   73        8.043   77.542   -1.576   1.00125.60          C
ATOM   11470   04'   G B   73        6.810   77.077   -2.188   1.00126.17          O
ATOM   11471   C1'   G B   73        6.279   78.087   -3.022   1.00123.46          C
ATOM   11472   N9    G B   73        4.993   78.534   -2.461   1.00122.72          N
ATOM   11473   C8    G B   73        4.592   78.565   --1.146  1.00122.59          c
ATOM   11474   N7    G B   73        3.387   79.050   -0.989   1.00123.08          N
ATOM   11475   C5    G B   73        2.970   79.365   -2.278   1.00121.76          C
ATOM   11476   C4    G B   73        3.961   79.055   --3.191  1.00122.44          c
ATOM   11477   N3    G B   73        3.968   79.204   -4.529   1.00121.82          N
ATOM   11478   C2    G B   73        2.832   79.724   -4.961   1.00122.58          C
ATOM   11479   N2    G B   73        2.674   79.938   -6.276   1.00121.00          N
ATOM   11480   Nl    G B   73        1.775   80.069   -4.142   1.00121.66          N
ATOM   11481   C6    G B   73        1.750   79.928   -2.755   1.00120.30          C
ATOM   11482   06    G B   73        0.742   80.272   -2.117   1.00115.31          O
ATOM   11483   C2'   G B   73        7.282   79.237   --3.043  1.00122.78          c
ATOM   11484   02'   G B   73        8.207   79.011   -4.098   1.00120.67          0
ATOM   11485   C3'   G B   73        7.951   79.058   -1.689   1.00124.16          c
ATOM   11486   03'   G B   73        9.198   79.720   --1.577  1.00125.65          0
ATOM   11487   P     A B   74        9.308   81.092   -0.743   1.00120.12          P
ATOM   11488   OP1   A B   74       10.547   81.783   -1.185   1.00119.16          0
ATOM   11489   OF2   A B   74        9.102   80.777    0.694   1.00121.19          0
ATOM   11490   05'   A B   74        8.061   81.949   -1.237   1.00118.17          0
ATOM   11491   C5'   A B   74        7.593   83.056   -0.484   1.00119.69          C
ATOM   11492   C4'   A B   74        7.429   84.276   -1.354   1.00121.94          C
ATOM   11493   04'   A B   74        8.717   84.646   -1.909   1.00120.82          0
ATOM   11494   CI'   A B   74        8.556   85.124   -3.229   1.00120.61          c
ATOM   11495   N9    A B   74        9.262   84.208   -4.146   1.00122.01          N
ATOM   11496   C8    A B   74        9.744   82.950   --3.870  1.00122.76          c
ATOM   11497   N7    A B   74       10.334   82.375   -4.887   1.00121.92          N
ATOM   11498   C5    A B   74       10.233   83.320   -5.902   1.00124.54          C
ATOM   11499   C4    A B   74        9.576   84.453   --5.462  1.00122.72          c
ATOM   11500   N3    A B   74        9.306   85.559   -6.182   1.00126.45          N
ATOM   11501   C2    A B   74        9.757   85.449   -7.430   1.00125.12          C
ATOM   11502   Nl    A B   74       10.404   84.423   -7.995   1.00126.79          N
ATOM   11503   C6    A B   74       10.662   83.325   -7.243   1.00128.55          C
ATOM   11504   N6    A B   74       11.309   82.301   -7.808   1.00130.91          N
ATOM   11505   C2'   A B   74        7.057   85.182   -3.517   1.00121.29          C
ATOM   11506   02'   A B   74        6.572   86.462   -3.133   1.00113.18          O
ATOM   11507   C3'   A B   74        6.537   84.107   -2.576   1.00123.03          C
ATOM   11508   03'   A B   74        5.156   84.225   -2.286   1.00122.04          O
ATOM   11509   P     G B   75        4.145   83.081   -2.780   1.00118.55          P
ATOM   11510   OP1   G B   75        4.757   81.780   -2.411   1.00124.29          O
ATOM   11511   OP2   G B   75        2.777   83.418   -2.312   1.00124.70          O
ATOM   11512   05'   G B   75        4.174   83.199   -4.366   1.00119.41          O
ATOM   11513   C5'   G B   75        3.807   84.407   -5.014   1.00124.20          C
ATOM   11514   C4'   G B   75        4.397   84.483   -6.399   1.00126.08          c
ATOM   11515   04'   G B   75        5.800   84.123   --6.349  1.00124.85          0
ATOM   11516   C1'   G B   75        6.186   83.505   -7.556   1.00124.35          c
ATOM   11517   N9    G B   75        6.863   82.220   -7.260   1.00125.28          N
ATOM   11518   C8    G B   75        6.755   81.435   --6.132  1.00123.67          c
ATOM   11519   N7    G B   75        7.510   80.368   -6.169   1.00121.44          N
ATOM   11520   C5    G B   75        8.171   80.451   -7.391   1.00124.86          c
ATOM   11521   C4    G B   75        7.786   81.590   -8.070   1.00124.15          c
ATOM   11522   N3    G B   75        8.200   82.027   -9.279   1.00124.43          N
ATOM   11523   C2    G B   75        9.084   81.215   -9.834   1.00125.56          C
ATOM   11524   N2    G B   75        9.598   81.501  -11.041   1.00125.99          N
ATOM   11525   Nl    G B   75        9.530   80.059   --9.246  1.00127.83          N
ATOM   11526   C6    G B   75        9.126   79.581   -8.001   1.00129.99          C
ATOM   11527   06    G B   75        9.607   78.514   -7.578   1.00131.84          O
ATOM   11528   C2'   G B   75        4.941   83.369   --8.442  1.00124.03          c
ATOM   11529   02'   G B   75        4.942   84.434   -9.381   1.00123.23          0
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ATOM	11530	C3'	G	B	75	3.802	83.536	--7.433	1.00126 .95	c
ATOM	11531	03'	G	B	75	2.604	84.056	-8.004	1.00128 .52	O
ATOM	11532	P	A	B	76	1.315	83.122	-8.280	1.00125 .59	P
ATOM	11533	OP1	A	B	76	1.226	82.085	--7.220	1.00121 .78	0
ATOM	11534	OP2	A	B	76	0.143	84.003	-8.516	1.00.129.28	0
ATOM	11535	05'	A	B	76	1.635	82.427	-9.679	1.0012.3.71	0
ATOM	11536	C5'	A	B	76	1.842	83.196	--10.860	1.00122 .14	c
ATOM	11537	C4'	A	B	76	2.691	82.451	-11.865	1.00.120.40	C
ATOM	11538	04'	A	B	76	4.015	82.221	--11.303	1.00121 .62	0
ATOM	11539	CI'	A	B	76	4.501	80.951	--11.691	1.00122 .34	c
ATOM	11540	N9	A	B	76	4.720	80.130	-10 .471	1.00122 .52	N
ATOM	11541	C8	A	B	76	4.079	80.260	-9.260	1.00121 .76	C
ATOM	11542	N7	A	B	76	4.455	79.398	-8.344	1.00122 .85	N
ATOM	11543	C5	A	B	76	5.417	78.628	-8.982	1.00124 .42	c
ATOM	11544	C4	A	B	76	5.592	79.066	-10.292	1.00123 .40	c
ATOM	11545	N3	A	B	76	6.452	78.541	-11 .187	1.0012.3.46	N
ATOM	11546	C2	A	B	76	7.134	77.521	-10 .658	1.00127 .66	c
ATOM	11547	N1	A	B	76	7.070	76.993	-9.425	1.00.128.20	N
ATOM	11548	C6	A	B	76	6.201	77.535	-8.540	1.00125 .76	C
ATOM	11549	N6	A	B	76	6.139	77.005	-7.311	1.00124 .02	N
ATOM	11550	C2'	A	B	76	3.472	80.329	-12.645	1.00.119.33	C
ATOM	11551	02'	A	B	76	3.841	80.628	-13.985	1.00111 .53	O
ATOM	11552	C3'	A	B	76	2.190	81.062	-12 .245	1.00120 .23	c
ATOM	11553	03'	A	B	76	1.183	81.075	-13 .255	1.00.114.99	0
ATOM	11554	P	A	B	77	-0.352	80.702	-12.908	1.00113 .09	P
ATOM	11555	OP1	A	B	77	-1.111	80.468	-14 .172	1.00100 .61	0
ATOM	11556	OP2	A	B	77	-0.856	81.697	-11.929	1.00.115.4.3	0
ATOM	11557	05'	A	B	77	-0.252	79.316	-12 .124	1.00120 .67	0
ATOM	11558	C5'	A	B	77	0.273	78.144	-12.735	1.00114 .95	c
ATOM	11559	C4'	A	B	77	1.352	77.520	-11 .883	1.00117 .43	c
ATOM	11560	04'	A	B	77	1.610	78.355	-10.723	1.00116 .19	0
ATOM	115 61	CI'	A	B	77	2.006	77.551	-9.631	1.00118 .10	c
ATOM	115 62	C2'	A	B	77	2.025	76.099	-10 .110	1.00117 .88	c
ATOM	11563	02'	A	B	77	3.341	75.802	-10 .562	1.00.116.99	0
ATOM	11564	C3'	A	B	77	1.052	76.156	-11 .284	1.00119 .01	c
ATOM	11565	03'	A	B	77	1.200	75.090	-12 .212	1.00116 .45	0
ATOM	11566	N9	A	B	77	1.080	77.766	-8.496	1.00.118.79	N
ATOM	11567	C8	A	B	77	-0.141	78.402	-8.481	1.00119 .91	c
ATOM	11568	N7	A	B	77	-0.721	78.430	-7.303	1.00118 .67	N
ATOM	11569	C5	A	B	77	0.179	77.770	-6.481	1.00.116.20	c
ATOM	11570	C4	A	B	77	1.291	77.356	-7.198	1.00118 .36	c
ATOM	11571	in.	A	B	77	1.214	76.794	-4.600	1.00118 .63	N
ATOM	11572	C2	A	B	77	2.225	76.457	-5.415	1.00118 .64	c
ATOM	11573	N3	A	B	77	2.360	76.690	-6.720	1.00118 .50	N
ATOM	11574	C6	A	B	77	0.156	77.464	-5.1.11	1.00114 .79	c
ATOM	11575	N6	A	B	77	--0.845	77.797	-4.296	1.00113 .88	N
ATOM	11576	P	A	B	78	0.362	73.726	-12 .034	1.00.107.67	P
ATOM	11577	OP1	A	B	78	0.376	73.008	-13 ..333	1.00107 .15	0
ATOM	11578	OF2	A	B	78	--0.956	74.041	-11 .434	1.00111 .43	0
ATOM	11579	05'	A	B	78	1.198	72.904	-10 .942	1.00.120.29	0
ATOM	11580	C5'	A	B	78	2.621	72.829	-10 .999	1.00116 .73	c
ATOM	11581	C4'	A	B	78	3.245	72.446	-9.672	1.00112 .83	c
ATOM	11582	04'	A	B	78	3.096	73.502	-8.686	1.00.114.18	0
ATOM	11583	CI'	A	B	78	3.014	72.937	-7.389	1.00112 .76	c
ATOM	11584	C2'	A	B	78	3.124	71.419	-7.536	1.00109 .70	c
ATOM	11585	02'	A	B	78	4.487	71.053	-7.366	1.00.107.82	0
ATOM	11586	C3'	A	B	78	2.669	71.226	-8.983	1.00111 .25	c
ATOM	11587	03'	A	B	78	3.102	70.016	-9.576	1.00116.24	0
ATOM	11588	N9	A	B	78	1.743	73.348	-6.752	1.00114 .67	N
ATOM	11589	C8	A	B	78	0.640	73.922	-7.341	1.00113 .06	c
ATOM	11590	N1	A	B	78	-0.340	74.175	-6.504	1.00109 .93	N
ATOM	11591	C5	A	B	78	0.141	73.747	-5.274	1.00110 .06	c
ATOM	11592	C4	A	B	78	1.423	73.234	-5.413	1.00112 .09	c

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ATOM  11593  N1    A B  78     0.330  73.242  -2.968  1.00106.38     N
ATOM  11594  C2    A B  78     1.549  72.775  -3.260  1.00107.25     C
ATOM  11595  N.3   A B  78     2.191  72.733  -4.428  1.00110.24     N
ATOM  11596  C6    A B  78    -0.415  73.746  -3.975  1.00108.22     c
ATOM  11597  N6    A B  78    -1.633  74.200  -3.674  1.00106.62     N
ATOM  11598  P     G B  79     2.273  68.661  -9.344  1.00107.23     P
ATOM  11599  OP1   G B  79     2.772  67.659 -10.320  1.00114.55     O
ATOM  11600  OP2   G B  79     0.819  68.964  -9.309  1.00110.60     O
ATOM  11601  05'   G B  79     2.710  68.233  -7.876  1.00104.29     O
ATOM  11602  C5'   G B  79     1.850  67.455  -7.071  1.00100.35     c
ATOM  11603  C4'   G B  79     2.154  67.618  -5.607  1.00 97.72     c
ATOM  11604  04'   G B  79     2.075  69.014  -5.225  1.00101.07     0
ATOM  11605  CI'   G B  79     1.420  69.144  -3.983  1.00 99.60     c
ATOM  11606  C2'   G B  79     1.193  67.741  -3.430  1.00 90.23     c
ATOM  11607  02'   G B  79     2.311  67.388  -2.638  1.00 92.89     0
ATOM  11608  C3'   G B  79     1.163  66.917  -4.706  1.00 87.88     c
ATOM  11609  03'   G B  79     1.519  65.571  -4.530  1.00 83.15     0
ATOM  11610  N9    G B  79     0.161  69.884  -4.218  1.00103.04     N
ATOM  11611  C8    G B  79    -0.241  70.363  -5.448  1.00103.07     c
ATOM  11612  N7    G B  79    -1.374  71.007  -5.412  1.00102.30     N
ATOM  11613  C5    G B  79    -1.755  70.961  -4.075  1.00 98.65     C
ATOM  11614  C4    G B  79    -0.816  70.280  -3.316  1.00 98.12     C
ATOM  11615  Nl    G B  79    -2.910  71.240  -2.080  1.00 86.86     N
ATOM  11616  C2    G B  79    -1.929  70.548  -1.411  1.00 92.68     C
ATOM  11617  N3    G B  79    -0.846  70.038  -1.985  1.00 94.93     N
ATOM  11618  C6    G B  79    -2.908  71.501  -3.442  1.00 88.42     C
ATOM  11619  06    G B  79    -3.838  72.136  -3.954  1.00 86.75     O
ATOM  11620  N2    G B  79    -2.123  70.402  -0.095  1.00 88.85     N
ATOM  11621  P     U B  80     0.529  64.422  -5.032  1.00 90.70     P
ATOM  11622  OP1   U B  80    -0.224  64.933  -6.203  1.00 92.05     O
ATOM  11623  OP2   U B  80     1.303  63.166  -5.185  1.00 95.14     O
ATOM  11624  05'   U B  80    -0.435  64.251  -3.782  1.00 82.56     O
ATOM  11625  C5'   U B  80     0.084  64.452  -2.481  1.00 79.08     c
ATOM  11626  C4'   U B  80    -1.006  64.620  -1.470  1.00 74.61     c
ATOM  11627  04'   U B  80    -1.376  66.013  -1.344  1.00 79.52     0
ATOM  11628  C3'   u B  80    -2.303  63.924  -1.802  1.00 73.78     c
ATOM  11629  03'   u B  80    -2.245  62.543  -1.521  1.00 69.56     0
ATOM  11630  C2'   u B  80    -3.314  64.688  -0.954  1.00 76.46     c
ATOM  11631  02'   u B  80    -3.279  64.233   0.388  1.00 79.00     0
ATOM  11632  CI'   u B  80    -2.744  66.112  -1.003  1.00 79.65     c
ATOM  11633  Nl    u B  80    -3.444  66.985  -1.986  1.00 79.51     N
ATOM  11634  C2    u B  80    -4.617  67.612  -1.584  1.00 75.38     c
ATOM  11635  N3    u B  80    -5.215  68.403  -2.538  1.00 78.24     N
ATOM  11636  C4    u B  80    -4.780  68.635  -3.828  1.00 83.57     C
ATOM  11637  C5    U B  80    -3.559  67.955  -4.173  1.00 82.57     C
ATOM  11638  C6    u B  80    -2.957  67.181  -3.264  1.00 82.64     c
ATOM  11639  02    u B  80    -5.109  67.489  -0.475  1.00 68.40     0
ATOM  11640  04    U B  80    -5.445  69.378  -4.563  1.00 78.87     0
ATOM  11641  P     G B  81    -2.950  61.492  -2.494  1.00 76.06     P
ATOM  11642  OP1   G B  81    -3.002  62.143  -3.821  1.00 80.96     0
ATOM  11643  OP2   G B  81    -2.267  60.167  -2.376  1.00 78.54     0
ATOM  11644  05'   G B  81    -4.417  61.359  -1.898  1.00 64.56     0
ATOM  11645  C5'   G B  81    -4.627  60.936  -0.558  1.00 67.83     c
ATOM  11646  C4'   G B  81    -6.038  60.454  -0.339  1.00 67.35     c
ATOM  11647  04'   G B  81    -6.922  61.600  -0.234  1.00 71.16     0
ATOM  11648  C3'   G B  81    -6.603  59.609  -1.460  1.00 68.29     c
ATOM  11649  03'   G B  81    -7.660  58.812  -0.922  1.00 76.34     0
ATOM  11650  C2'   G B  81    -7.205  60.665  -2.384  1.00 69.74     c
ATOM  11651  02'   G B  81    -8.184  60.153  -3.254  1.00 67.00     0
ATOM  11652  CI'   G B  81    -7.778  61.665  -1.370  1.00 62.84     c
ATOM  11653  N9    G B  81    -7.749  63.074  -1.781  1.00 59.19     N
ATOM  11654  C8    G B  81    -6.725  63.721  -2.419  1.00 63.97     c
ATOM  11655  N7    G B  81    -6.947  64.998  -2.587  1.00 57.59     N
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ATOM  11656  C5    G B  81      -8.183  65.225  -2.004  1.00 55.34     C
ATOM  11657  C4    G B  81      -8.677  64.059  -1.486  1.00 52.89     C
ATOM  11658  N1    G B  81     -10.147  66.237  -1.199  1.00 40.95     N
ATOM  11659  C2    G B  81     -10.548  65.021  -0.728  1.00 51.24     C
ATOM  11660  N3    G B  81      -9.852  63.900  -0.847  1.00 56.50     N
ATOM  11661  C6    G B  81      -8.959  66.434  -1.875  1.00 54.06     C
ATOM  11662  06    G B  81      -8.689  67.569  -2.273  1.00 51.32     O
ATOM  11663  N2    G B  81     -11.728  64.989  -0.108  1.00 52.29     N
ATOM  11664  P     G B  82      -7.373  57.339  -0.332  1.00 82.13     P
ATOM  11665  OF1   G B  82      -8.689  56.641  -0.185  1.00 67.39     O
ATOM  11666  OP2   G B  82      -6.481  57.505   0.842  1.00 72.31     O
ATOM  11667  05'   G B  82      -6.553  56.605  -1.488  1.00 73.92     O
ATOM  11668  C5'   G B  82      -7.215  56.159  -2.665  1.00 77.26     C
ATOM  11669  C4'   G B  82      -6.840  54.740  -3.033  1.00 81.92     C
ATOM  11670  04'   G B  82      -6.739  53.922  -1.834  1.00 80.43     0
ATOM  11671  C3'   G B  82      -7.836  53.986  -3.910  1.00 79.90     C
ATOM  11672  03'   G B  82      -7.732  54.316  -5.290  1.00 76.56     0
ATOM  11673  C2'   G B  82      -7.505  52.530  -3.601  1.00 85.63     C
ATOM  11674  02'   G B  82      -6.338  52.118  -4.304  1.00 85.66     0
ATOM  11675  CI'   G B  82      -7.166  52.606  -2.111  1.00 79.70     C
ATOM  11676  N9    G B  82      -8.328  52.284  -1.259  1.00 81.64     N
ATOM  11677  C8    G B  82      -9.047  53.118  -0.430  1.00 79.36     C
ATOM  11678  N7    G B  82     -10.029  52.513   0.194  1.00 77.49     N
ATOM  11679  C5    G B  82      -9.950  51.196  -0.248  1.00 87.33     C
ATOM  11680  C4    G B  82      -8.909  51.040  -1.140  1.00 87.11     C
ATOM  11681  N1.   G B  82     -10.313  48.922  -0.609  1.00 91.26     N
ATOM  11682  C2    G B  82      -9.257  48.876  -1.480  1.00 91.62     C
ATOM  11683  N3    G B  82      -8.512  49.921  -1.781  1.00 90.12     N
ATOM  11684  C6    G B  82     -10.741  50.060   0.066  1.00 90.56     C
ATOM  11685  06    G B  82     -11.709  49.984   0.830  1.00 92.67     O
ATOM  11686  N2    G B  82      -8.988  47.690  -2.042  1.00 95.42     N
ATOM  11687  05'   C B  83      -9.094  52.521  -6.481  1.00 90.21     O
ATOM  11688  C4'   C B  83      -8.482  50.318  -7.252  1.00 90.46     C
ATOM  11689  C3'   C B  83      -9.860  49.985  -7.802  1.00 93.16     C
ATOM  11690  C2'   C B  83     -10.157  48.640  -7.159  1.00 95.17     C
ATOM  11691  P     C B  83      -8.964  54.098  -6.307  1.00 84.78     P
ATOM  11692  OP1   C B  83      -8.500  54.647  -7.613  1.00 80.03     0
ATOM  11693  OP2   C B  83     -10.251  54.513  -5.680  1.00 80.39     0
ATOM  11694  C5'   C B  83      -8.132  51.782  -7.222  1.00 91.39     C
ATOM  11695  04'   C B  83      -8.516  49.806  -5.894  1.00 88.97     0
ATOM  11696  03'   C B  83      -9.918  49.961  -9.217  1.00 91.21     0
ATOM  11697  02'   C B  83      -9.482  47.594  -7.844  1.00 99.51     0
ATOM  11698  CI'   C B  83      -9.517  48.813  -5.782  1.00 93.95     C
ATOM  11699  N1    C B  83     -10.507  49.208  -4.751  1.00 90.78     N
ATOM  11700  C2    C B  83     -11.327  48.205  -4.235  1.00 92.75     C
ATOM  11701  N3    C B  83     -12.249  48.501  -3.300  1.00 94.90     N
ATOM  11702  C4    C B  83     -12.370  49.748  -2.868  1.00 90.28     C
ATOM  11703  C5    C B  83     -11.548  50.798  -3.374  1.00 86.28     C
ATOM  11704  C6    C B  83     -10.636  50.494  -4.307  1.00 87.58     C
ATOM  11705  02    C B  83     -11.197  47.047  -4.646  1.00100.25     0
ATOM  11706  N4    C B  83     -13.296  49.975  -1.938  1.00 89.21     N
ATOM  11707  05'   A B  84     -11.984  48.600  -9.778  1.00 97.93     0
ATOM  11708  C4'   A B  84     -11.912  46.166  -9.766  1.00 98.17     C
ATOM  11709  C3'   A B  84     -13.398  45.946  -9.988  1.00 99.73     C
ATOM  11710  C2'   A B  84     -13.779  45.015  -8.843  1.00 98.15     C
ATOM  11711  P     A B  84     -11.341  50.051  -9.959  1.00 95.76     P
ATOM  11712  OP1   A B  84     -11.071  50.272 -11.402  1.00110.11     0
ATOM  11713  OP2   A B  84     -12.181  51.030  -9.233  1.00 97.22     0
ATOM  11714  C5'   A B  84     -11.354  47.449 -10.333  1.00101.79     C
ATOM  11715  04'   A B  84     -11.754  46.142  -8.322  1.00 94.88     0
ATOM  11716  03'   A B  84     -13.666  45.411 -11.270  1.00 99.88     0
ATOM  11717  02'   A B  84     -13.428  43.672  -9.149  1.00101.77     0
ATOM  11718  C1'   A B  84     -12.870  45.518  -7.722  1.00 97.89     C
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ATOM   11719   N9     A B   84     -13.543   46.505    -6.851   1.00101.49          N
ATOM   11720   C8     A B   84    --13.272   47.847    -6.769   1.00 98.07          C
ATOM   11721   N1     A B   84     -14.016   48.497    -5.9.11  1.00100.26          N
ATOM   11722   C5     A B   84     -14.849   47.525    -5.386   1.00100.22          c
ATOM   11723   C4     A B   84     -14.567   46.292    -5.955   1.00 99.70          C
ATOM   11724   Nl     A B   84     -16.512   46.425    -4.130   1.00106.28          N
ATOM   11725   C2     A B   84     -16.131   45.306    -4.764   1.00100.98          c
ATOM   11726   N3     A B   84     -15.184   45.136    -5.684   1.00 98.32          N
ATOM   11727   C6     A B   84     -15.875   47.583    -4.422   1.00102.63          C
ATOM   11728   N6     A B   84     -16.257   48.697    -3.787   1.00 98.57          N
ATOM   11729   05'    C B   85     -16.124   44.869   -11.122   1.00 97.80          O
ATOM   11730   C4'    c B   85     -16.980   42.993    -9.909   1.00 96.64          C
ATOM   117 31  C3'    c B   85     -18.428   43.401   -10.113   1.00 97.23          c
ATOM   117 32  C2'    c B   85     -18.986   43.429    -8.697   1.00 97.97          c
ATOM   117 33  P      c B   85     -15.071   45.683   -11.993   1.00 99.35          P
ATOM   11734   OP1    c B   85     -15.025   45.062   -13..341   1.0010.3.11         0
ATOM   11735   OP2    c B   85     -15.387   47.124   -11.859   1.00102.01          0
ATOM   11736   C5'    c B   85     -16.043   43.460   -10.986   1.00 97.85          c
ATOM   11737   04'    c B   85     -16.611   43.612    -8.649   1.00 95.23          0
ATOM   11738   03'    c B   85     -19.130   42.534   -10.976   1.00 93.52          0
ATOM   11739   02'    c B   85     -19.373   42.132    -8.272   1.00 96.22          0
ATOM   11740   CI'    c B   85     -17.771   43.899    -7.890   1.00 98.29          c
ATOM   11741   Nl     c B   85     -17.825   45.357    -7.609   1.00 98.07          N
ATOM   11742   C2     c B   85     -18.718   45.839    -6.639   1.00.100.02         c
ATOM   11743   N3     c B   85     -18.781   47.167    -6.386   1.00100.81          N
ATOM   117 44  C4     c B   85     -17.996   48.012    -7.054   1.00103.47          C
ATOM   11745   C5     c B   85     -17.075   47.557    -8.047   1.00 98.66          C
ATOM   117 46  C6     c B   85     -17.030   46.240    -8.289   1.00 98.45          C
ATOM   11747   02     c B   85     -19.444   45.047    -6.023   1.00 99.82          0
ATOM   11748   N4     c B   85     -18.096   49.313    -6.763   1.00102.52          N
ATOM   11749   05'    c B   86     -21.567   43.180   -10.860   1.00 93.93          0
ATOM   11750   C4'    c B   86     -23.261   42.341    -9..354   1.00100.55          c
ATOM   11751   C3'    c B   86     -24.319   43.318    -9.832   1.00103.17          c
ATOM   11752   C2'    c B   86     -24.808   43.966    -8.540   1.00.100.23         c
ATOM   117 53  P      c B   86     -20.334   43.104   -11.866   1.00 94.09          P
ATOM   11754   OF1    c B   86     -20.677   42.112   -12.911   1.00111.45          0
ATOM   11755   OP2    c B   86     -19.945   44.470   -12.288   1.00.104.25         0
ATOM   11756   C5'    c B   86     -22.192   42.006   -10.364   1.00 98.40          c
ATOM   11757   04'    c B   86     -22.659   43.002    -8.2.10  1.00104.10          0
ATOM   11758   03'    c B   86     -25.341   42.699   -10.582   1.00.104.24         0
ATOM   117 59  02'    c B   86     -25.750   43.135    -7.874   1.00 96.61          0
ATOM   11760   C1'    c B   86     -23.520   44.013    -7.7.19  1.00102.51          c
ATOM   11761   Nl     c B   86     -22.823   45.321    -7.826   1.00 98.08          N
ATOM   11762   C2     c B   86     -23.301   46.436    -7.131   1.00 95.69          c
ATOM   11763   N3     c B   86     -22.642   47.619    -7.242   1.00 94.09          N
ATOM   11764   C4     c B   86     -21.543   47.712    -7.993   1.00 95.25          c
ATOM   117 65  C5     c B   86     -21.034   46.592    -8.703   1.00 96.86          c
ATOM   11766   C6     c B   86     -21.697   45.439    -8.588   1.00 97.60          c
ATOM   11767   02     c B   86     -24.329   46.322    -6.441   1.00 93.79          0
ATOM   117 68  N4     c B   86     -20.914   48.886    -8.076   1.00 93.16          N
ATOM   11769   05'    G B   87     -26.657   44.814   -10.893   1.00 97.77          O
ATOM   11770   C4'    G B   87     -28.463   45.796    -9.651   1.00 93.21          c
ATOM   11771   C3'    G B   87     -29.036   47.192    -9.783   1.00 89.28          c
ATOM   11772   C2'    G B   87     -28.796   47.775    -8.396   1.00 92.07          c
ATOM   117 73  P      G B   87     -26.115   43.556   -11.693   1.00108.98          P
ATOM   11774   OP1    G B   87     -27.325   42.804   -12.127   1.00.116.2.3        0
ATOM   117 75  OP2    G B   87     -25.100   44.030   -12.673   1.00 99.39          0
ATOM   117 76  C5'    G B   87     -28.031   45.149   -10.936   1.00 98.40          c
ATOM   11777   04'    G B   87     -27.311   45.967    -8.783   1.00 91.90          0
ATOM   117 78  03'    G B   87     -30.395   47.188   -10.185   1.00 92.52          0
ATOM   11779   02'    G B   87     -29.770   47.305    -7.473   1.00 89.40          0
ATOM   11780   CI'    G B   87     -27.443   47.157    -8.040   1.00 86.72          c
ATOM   11781   N9     G B   87     -26.313   48.046    -8.379   1.00 86.88          N
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ATOM	11782	C8	G	B	87	-25.220	47.739	-9.154	1.00	88.18	C
ATOM	11783	N7	G	B	87	--24.369	48.723	-9.281	1.00	83.17	N
ATOM	11784	C5	G	B	87	-24.934	49.759	-8.548	1.00	85.40	C
ATOM	11785	C4	G	B	87	-26.133	49.356	-7.982	1.00	85.93	C
ATOM	11786	N1	G	B	87	-25.359	51.795	-7.507	1.00	78.21	N
ATOM	11787	C2	G	B	87	-26.539	51.302	-6.998	1.00	80.76	C
ATOM	11788	N3	G	B	87	-26.979	50.074	-7.207	1.00	83.88	N
ATOM	11789	C6	G	B	87	-24.472	51.088	-8.315	1.00	79.62	C
ATOM	11790	06	G	B	87	-23.438	51.634	-8.728	1.00	75.38	O
ATOM	11791	N2	G	B	87	-27.268	52.126	-6.238	1.00	72.43	N
ATOM	11792	05'	A	B	88	-30.852	49.651	-10.110	1.00	86.63	O
ATOM	11793	C4'	A	B	88	-31.486	51.057	-8.237	1.00	80.16	C
ATOM	11794	C3'	A	B	88	-32.199	52.169	-8.977	1.00	78.36	C
ATOM	11795	C2'	A	B	88	-31.089	52.756	-9.833	1.00	78.26	C
ATOM	11796	P	A	B	88	-30.984	48.395	-11.071	1.00	95.11	P
ATOM	11797	OP1	A	B	88	-32.456	48.237	-11.272	1.00	80.48	0
ATOM	11798	OP2	A	B	88	-30.060	48.546	-12.229	1.00	94.90	0
ATOM	11799	C5'	A	B	88	-31.582	49.704	-8.889	1.00	87.81	C
ATOM	11800	04'	A	B	88	-30.094	51.467	-8.155	1.00	81.28	0
ATOM	11801	03'	A	B	88	-32.572	53.126	-8.010	1.00	81.47	0
ATOM	11802	02'	A	B	88	-31.332	54.072	-10.275	1.00	79.52	0
ATOM	11803	CI '	A	B	88	-29.912	52.673	-8.871	1.00	73.90	C
ATOM	11804	N9	A	B	88	-28.601	52.605	-9.511	1.00	76.65	N
ATOM	11805	C8	A	B	88	-28.032	51.516	-10.114	1.00	75.62	C
ATOM	11806	N7	A	B	88	-26.834	51.744	-10.582	1.00	75.52	N
ATOM	11807	C5	A	B	88	-26.589	53.066	-10.247	1.00	74.94	C
ATOM	11808	C4	A	B	88	-27.667	53.609	-9.572	1.00	77.84	C
ATOM	11809	Nl	A	B	88	-25.560	55.180	-9.991	1.00	72.33	N
ATOM	11810	C2	A	B	88	-26.669	55.567	-9.354	1.00	70.19	C
ATOM	11811	N3	A	B	88	-27.772	54.866	-9.097	1.00	71.60	N
ATOM	11812	C6	A	B	88	-25.483	53.911	-10.457	1.00	72.48	C
ATOM	11813	N6	A	B	88	-24.365	53.525	-11.088	1.00	74.85	N
ATOM	11814	P	G	B	89	-33.936	53.941	-8.156	1.00	95.88	P
ATOM	11815	OP1	G	B	89	-35.017	53.068	-7.629	1.00	94.36	O
ATOM	11816	OP2	G	B	89	-34.027	54.498	-9.538	1.00	90.88	O
ATOM	11817	05'	G	B	89	-33.722	55.147	-7.138	1.00	92.92	O
ATOM	11818	C5'	G	B	89	-32.425	55.706	-6.921	1.00	88.26	C
ATOM	11819	C4'	G	B	89	-32.517	57.168	-6.567	1.00	83.67	C
ATOM	11820	04'	G	B	89	-33.371	57.809	-7.551	1.00	81.37	0
ATOM	11821	C3'	G	B	89	-33.146	57.460	-5.205	1.00	83.75	C
ATOM	11822	03'	G	B	89	-32.629	58.685	-4.679	1.00	88.54	0
ATOM	11823	C2'	G	B	89	-34.615	57.660	-5.561	1.00	84.69	C
ATOM	11824	02'	G	B	89	-35.338	58.433	-4.629	1.00	92.64	0
ATOM	11825	CI '	G	B	89	-34.510	58.361	-6.915	1.00	87.38	C
ATOM	11826	N9	G	B	89	-35.666	58.159	-7.802	1.00	89.64	N
ATOM	11827	C8	G	B	89	-36.127	56.943	-8.247	1.00	92.59	C
ATOM	11828	N7	G	B	89	-37.158	57.030	-9.040	1.00	93.72	N
ATOM	11829	C5	G	B	89	-37.404	58.390	-9.133	1.00	91.23	C
ATOM	11830	C4	G	B	89	-36.492	59.106	-8.383	1.00	89.64	C
ATOM	11831	Nl	G	B	89	-38.312	60.455	-9.686	1.00	89.03	N
ATOM	11832	C2	G	B	89	-37.368	61.082	-8.918	1.00	87.69	C
ATOM	11833	N3	G	B	89	-36.423	60.449	-8.235	1.00	90.17	N
ATOM	11834	C6	G	B	89	-38.410	59.083	-9.856	1.00	92.38	C
ATOM	11835	06	G	B	89	-39.304	58.622	-10.577	1.00	92.84	O
ATOM	11836	N2	G	B	89	-37.450	62.419	-8.888	1.00	85.47	N
ATOM	11837	P	U	B	90	-31.246	58.748	-3.854	1.00	83.23	P
ATOM	11838	OP1	U	B	90	-31.462	59.806	-2.835	1.00	73.70	O
ATOM	11839	OP2	U	B	90	-30.761	57.397	-3.485	1.00	81.85	O
ATOM	11840	05'	U	B	90	-30.218	59.321	-4.918	1.00	79.52	O
ATOM	11841	C5'	U	B	90	-28.826	59.360	-4.663	1.00	74.23	C
ATOM	11842	C4'	U	B	90	-28.192	60.466	-5.463	1.00	75.93	C
ATOM	11843	04'	U	B	90	-29.073	60.791	-6.576	1.00	72.03	0
ATOM	11844	C3'	U	B	90	-27.977	61.774	-4.702	1.00	67.48	C

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ATOM  11845  03'   U B  90    -26.858  62.448  -5.277  1.00 71.37           O
ATOM  11846  C2'   U B  90   --29.249  62.543  -5.042  1.00 69.61           C
ATOM  11847  02'   u B  90    -29.174  63.947  -4.878  1.00 71.80           O
ATOM  11848  CI '  u B  90    -29.431  62.155  -6.501  1.00 71.95           c
ATOM  11849  N1    u B  90    -30.791  62.339  -7.019  1.00 71.53           N
ATOM  11850  C2    u B  90    -30.971  63.504  -7.711  1.00 64.79           C
ATOM  11851  N3    u B  90    -32 .222  63.719  -8.212  1.00 70.92           N
ATOM  11852  C4    u B  90    -33.309  62.876  -8.084  1.00 75.17           C
ATOM  11853  C5    u B  90    -33.040  61.678  -7.345  1.00 74.28           C
ATOM  11854  C6    u B  90    -31.816  61.445  -6.851  1.00 74.56           c
ATOM  11855  02    u B  90    -30.064  64.284  -7.860  1.00 65.64           0
ATOM  11856  04    u B  90    -34.390  63.201  -8.590  1.00 76.55           0
ATOM  11857  P     C B  91    -25.490  62.703  -4.471  1.00 74.09           P
ATOM  11858  OP1   c B  91    -24.319  62.425  -5.330  1.00 72.34           0
ATOM  11859  OP2   c B  91    -25.608  63.941  -3.679  1.00 77.35           0
ATOM  11860  05'   c B  91    -25.331  61.493  -3.482  1.00 76.96           0
ATOM  11861  C5'   c B  91    -24.524  60.393  -3.839  1.00 68.40           c
ATOM  11862  C4'   c B  91    -25.353  59.153  -3.720  1.00 72.16           c
ATOM  11863  04'   c B  91    -25.758  58.673  -5.023  1.00 73.59           0
ATOM  11864  C3'   c B  91    -24.723  57.945  -3.074  1.00 72.26           c
ATOM  11865  03'   c B  91    -24.620  58.093  -1.669  1.00 71.43           0
ATOM  11866  C2'   c B  91    -25.680  56.856  -3.527  1.00 72.18           c
ATOM  11867  02'   c B  91    -26.922  57.001  -2.857  1.00 72.22           0
ATOM  11868  CI '  c B  91    -25.920  57.277  -4.973  1.00 72.23           c
ATOM  11869  Ml    c B  91    -24.952  56.652  -5.897  1.00 69.17           N
ATOM  11870  C2    c B  91    -25.164  55.313  -6.204  1.00 70.82           c
ATOM  11871  N3    c B  91    -24.310  54.667  -7.031  1.00 70.77           N
ATOM  11872  C4    c B  91    -23.273  55.317  -7.551  1.00 68.94           c
ATOM  11873  C5    c B  91    -23.033  56.697  -7.253  1.00 71.55           c
ATOM  11874  C6    c B  91    -23.890  57.326  -6.427  1.00 66.53           c
ATOM  11875  02    c B  91    -26.149  54.764  -5.695  1.00 71.88           0
ATOM  11876  N4    c B  91    -22.465  54.642  -8.366  1.00 56.94           N
ATOM  11877  05'   G B  92    -24.443  55.784  -0.748  1.00 75.67           0
ATOM  11878  C4'   G B  92    -26.440  54.436  -0.419  1.00 81.34           c
ATOM  11879  C3'   G B  92    -25.674  53.220   0.061  1.00 87.06           c
ATOM  11880  C2'   G B  92    -26.388  52.107  -0.685  1.00 89.06           c
ATOM  11881  P     G B  92    -23.653  57.163  -0.786  1.00 70.44           P
ATOM  11882  OP1   G B  92    -23.732  57.729   0.580  1.00 67.36           0
ATOM  11883  OP2   G B  92    -22.303  56.951  -1.387  1.00 69.07           0
ATOM  11884  C5'   G B  92    -25.767  55.769  -0.238  1.00 78.14           c
ATOM  11885  04'   G B  92    -26.658  54.156  -1.829  1.00 81.14           0
ATOM  11886  03'   G B  92    -25.642  53.072   1.466  1.00 88.91           0
ATOM  11887  02'   G B  92    -27.696  51.911  -0.157  1.00 86.56           0
ATOM  11888  CI '  G B  92    -26.525  52.766  -2.056  1.00 87.16           c
ATOM  11889  N9    G B  92    -25.301  52.528  -2.842  1.00 81.20           N
ATOM  11890  C8    G B  92    -24.167  53.298  -2.956  1.00 80.98           c
ATOM  11891  N7    G B  92    -23.244  52.751  -3.707  1.00 83.30           N
ATOM  11892  C5    G B  92    -23.808  51.546  -4.094  1.00 87.51           c
ATOM  11893  C4    G B  92    -25.066  51.395  -3.562  1.00 87.66           c
ATOM  11894  Nl    G B  92    -24.210  49.465  -5.037  1.00 87.39           N
ATOM  11895  C2    G B  92    -25.455  49.411  -4.455  1.00 89.49           c
ATOM  11896  N3    G B  92    -25.936  50.375  -3.693  1.00 90.85           N
ATOM  11897  C6    G B  92    -23.303  50.515  -4.914  1.00 89.52           c
ATOM  11898  06    G B  92    -22.205  50.468  -5.481  1.00 94.04           0
ATOM  11899  N2    G B  92    -26.208  48.321  -4.689  1.00 87.59           N
ATOM  11900  05'   G B  93    -25.266  50.711   2.170  1.00 99.08           0
ATOM  11901  C4'   G B  93    -25.035  48.479   1.253  1.00102.13           c
ATOM  11902  C3'   G B  93    -24.130  47.270   1.078  1.00106.11           c
ATOM  11903  C2'   G B  93    -24.458  46.794  -0.333  1.00103.62           c
ATOM  11904  P     G B  93    -24.537  52.125   2.144  1.00 93.99           P
ATOM  11905  OP1   G B  93    -24.338  52.597   3.538  1.00 97.54           0
ATOM  11906  OP2   G B  93    -23.345  51.994   1.263  1.00 92.60           0
ATOM  11907  C5'   G B  93    -24.514  49.512   2.218  1.00102.55           c
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ATOM   11908   04'   G B  93      -25.143   49.050   -0.081   1.00 98.98            O
ATOM   11909   03'   G B  93      --24.326  46.300    2.092   1.00110.71            O
ATOM   11910   02'   G B  93      -25.666   46.046   -0.366   1.00 99.86            O
ATOM   11911   CI'   G B  93      -24.688   48.126   -1.045   1.00 99.71            c
ATOM   11912   N9    G B  93      -23.435   48.661   -1.601   1.00 98.39            N
ATOM   11913   C8    G B  93      -22.886   49.882   -1.296   1.00 97.07            C
ATOM   11914   N7    G B  93      -21.767   50.107   -1.923   1.00101.15            N
ATOM   11915   C5    G B  93      -21.566   48.961   -2.685   1.00 99.86            C
ATOM   11916   C4    G B  93      -22.588   48.055   -2.498   1.00100.31            C
ATOM   11917   Nl    G B  93      -20.702   47.369   -4.131   1.00101.51            N
ATOM   11918   C2    G B  93      -21.763   46.539   -3.875   1.00 98.37            C
ATOM   11919   N3    G B  93      -22.751   46.836   -3.054   1.00 98.32            N
ATOM   11920   C6    G B  93      -20.514   48.629   -3.574   1.00 99.74            C
ATOM   11921   06    G B  93      -19.516   49.296   -3.874   1.00100.72            O
ATOM   11922   N2    G B  93      -21.761   45.364   -4.519   1.00100.26            N
ATOM   11923   05'   ʋ B  94      -22.377   44.780    2.512   1.00111.21            O
ATOM   11924   C4'   U B  94      -22.243   43.043    0.835   1.00106.87            c
ATOM   11925   C3'   U B  94      -20.775   42.860    1.180   1.00109.95            c
ATOM   11926   C2'   ʋ B  94      -20.121   42.767   -0.191   1.00111.58            c
ATOM   11927   P     u B  94      -23.167   45.999    3.165   1.00110.22            P
ATOM   11928   OP1   u B  94      -22.246   47.161    3.253   1.00103.92            0
ATOM   11929   OP2   u B  94      -23.837   45.514    4.394   1.00104.61            0
ATOM   11930   C5'   u B  94      -23.080   43.711    1.893   1.00107.86            c
ATOM   11931   04'   u B  94      -22.220   43.860   -0.366   1.00105.49            0
ATOM   11932   03'   u B  94      -20.531   41.739    2.007   1.00115.96            0
ATOM   11933   02'   u B  94      -20.328   41.484   -0.767   1.00108.86            0
ATOM   11934   CI'   u B  94      -20.942   43.792   -0.971   1.00106.63            c
ATOM   11935   Nl    u B  94      -20.323   45.136   -0.902   1.00109.96            N
ATOM   11936   C2    u B  94      -19.149   45.375   -1.607   1.00108.74            c
ATOM   11937   N3    u B  94      -18.642   46.646   -1.467   1.00106.71            N
ATOM   11938   C4    u B  94      -19.186   47.675   -0.720   1.00107.11            C
ATOM   11939   C5    ʋ B  94      -20.398   47.353   -0.028   1.00105.80            C
ATOM   11940   C6    u B  94      -20.909   46.127   -0.142   1.00107.53            c
ATOM   11941   02    u B  94      -18.578   44.540   -2.291   1.00107.90            0
ATOM   11942   04    ʋ B  94      -18.621   48.768   -0.694   1.00109.72            0
ATOM   11943   05'   G B  95      -18.040   41.613    2.416   1.00105.25            0
ATOM   11944   C4'   G B  95      -16.605   40.467    0.850   1.00104.11            c
ATOM   11945   C3'   G B  95      -15.255   40.984    1.317   1.00103.14            c
ATOM   11946   C2'   G B  95      -14.646   41.531    0.034   1.00105.44            c
ATOM   11947   P     G B  95      -19.430   41.832    3.171   1.00112.13            P
ATOM   11948   OP1   G B  95      -19.674   40.703    4.099   1.00114.16            0
ATOM   11949   OP2   G B  95      -19.450   43.214    3.705   1.00107.31            0
ATOM   11950   C5'   G B  95      -17.676   40.344    1.901   1.00103.56            c
ATOM   11951   04'   G B  95      -17.016   41.434   -0.146   1.00110.96            0
ATOM   11952   03'   G B  95      -14.458   39.987    1.926   1.00103.34            0
ATOM   11953   02'   G B  95      -14.106   40.486   -0.758   1.00103.27            0
ATOM   11954   Cl'   G B  95      -15.878   42.083   -0.679   1.00111.81            c
ATOM   11955   N9    G B  95      -16.004   43.547   -0.517   1.00110.18            N
ATOM   11956   C8    G B  95      -16.912   44.263    0.226   1.00107.36            c
ATOM   11957   N7    G B  95      -16.731   45.555    0.132   1.00106.46            N
ATOM   11958   C5    G B  95      -15.640   45.702   -0.719   1.00107.40            c
ATOM   11959   C4    G B  95      -15.183   44.469   -1.128   1.00106.67            c
ATOM   11960   Nl    G B  95      -13.909   46.537   -2.043   1.00104.37            N
ATOM   11961   C2    G B  95      -13.533   45.259   -2.391   1.00103.03            c
ATOM   11962   N3    G B  95      -14.150   44.179   -1.951   1.00106.47            N
ATOM   11963   C6    G B  95      -14.975   46.867   -1.198   1.00106.09            c
ATOM   11964   06    G B  95      -15.233   48.059   -0.956   1.00 99.57            0
ATOM   11965   N2    G B  95      -12.485   45.125   -3.219   1.00100.46            N
ATOM   11966   05'   C B  96      -12.091   40.841    1.642   1.00106.17            0
ATOM   11967   C4'   C B  96      -10.388   40.528   -0.040   1.00105.41            c
ATOM   11968   C3'   C B  96       -9.381   41.349    0.746   1.00105.95            c
ATOM   11969   C2'   C B  96       -8.832   42.298   -0.306   1.00107.44            c
ATOM   11970   P     C B  96      -13.147   40.400    2.752   1.00103.48            P
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ATOM   11971   OP1    C  B   96      -12.612   39.206     3.450   1.00110.64          O
ATOM   11972   OP2    C  B   96      -13.509   41.599     3.545   1.00109.88          O
ATOM   11973   C5'    C  B   96      -11.484   39.894     0.777   1.00103.34          C
ATOM   11974   04'    C  B   96      -10.956   41.482    -0.978   1.00104.90          O
ATOM   11975   03'    C  B   96       -8.394   40.572     1.384   1.00.107.77         O
ATOM   11976   02'    c  B   96       -7.906   4.1.634    -1.154   1.00111.68          O
ATOM   11977   CI'    c  B   96      -10.098   42.601    -1.105   1.00107.54          c
ATOM   11978   N1     c  B   96      -10.796   43.795    -0.567   1.00.108.13         N
ATOM   11979   C2     c  B   96      -10.276   45.075    -0.814   1.00106.16          C
ATOM   11980   N3     c  B   96      -10.917   46.161    -0.313   1.00104.74          N
ATOM   11981   C4     c  B   96      -12.027   46.0.12     0.416   1.00.104.15         C
ATOM   11982   C5     c  B   96      -12.570   44.725     0.692   1.00106.56          C
ATOM   11983   C6     c  B   96      -11.931   43.661     0.186   1.00107.38          c
ATOM   11984   02     c  B   96       -9.242   45.195    -1.489   1.00106.35          0
ATOM   11985   N4     c  B   96      -12.625   47.107     0.892   1.00102.09          N
ATOM   11986   P      υ  B   97       -8.069   40.850     2.926   1.00113.85          P
ATOM   11987   OP1    u  B   97       -7.294   39.691     3.439   1.00124.18          O
ATOM   11988   OP2    u  B   97       -9.358   41.2.18     3.575   1.00.107.97         O
ATOM   11989   05'    υ  B   97       -7.101   42.121     2.899   1.00111.65          0
ATOM   11990   C5'    u  B   97       -5.814   42.050     2.297   1.00110.91          c
ATOM   11991   C4'    u  B   97       -5.235   43.4.19     2.018   1.00.110.33         c
ATOM   11992   04'    u  B   97       -6.162   44.195     1.211   1.00106.78          0
ATOM   11993   C3'    u  B   97       -4.959   44.310     3.225   1.00108.74          c
ATOM   11994   03'    u  B   97       -3.742   44.003     3.892   1.00.100.18         0
ATOM   11995   C2'    u  B   97       -4.982   45.706     2.615   1.00107.24          c
ATOM   11996   02'    u  B   97       -3.761   45.981     1.943   1.00108.85          0
ATOM   11997   CI'    u  B   97       -6.088   45.560     1.568   1.00.105.58         c
ATOM   11998   Nl     u  B   97       -7.406   45.973     2.100   1.00107.04          N
ATOM   11999   C2     u  B   97       -7.657   47.325     2.275   1.00105.19          c
ATOM   12000   N3     u  B   97       -8.901   47.622     2.782   1.00 99.50          N
ATOM   12001   C4     u  B   97       -9.897   46.731     3.128   1.00100.25          C
ATOM   12002   C5     υ  B   97       -9.562   45.357     2.9.19   1.00105.71          C
ATOM   12003   C6     u  B   97       -8.360   45.035     2.424   1.00107.83          c
ATOM   12004   02     u  B   97       -6.848   48.198     2.008   1.00.103.39         0
ATOM   12005   04     υ  B   97      -10.963   47.153     3.576   1.00 99.89          0
TER
ATOM   12006   06    DG  C    1      -23.729  .109.460   -18.317   1.00 44.35          0
ATOM   12007   C6    DG  c    1      -24.617  108.681   -18.661   1.00 43.85          c
ATOM   12008   Nl    DG  C    1      -25.526  109.043   -19.665   1.00 44.12          N
ATOM   12009   C2    DG  C    1      -26.573  .108.257   -20.096   1.00 39.95          C
ATOM   12010   N2    DG  c    1      -27.364  108.764   -21.054   1.00 42.69          N
ATOM   12011   N3    DG  c    1      -26.820  107.058   -19.633   1.00 43.03          N
ATOM   12012   C4    DG  c    1      -25.938  106.690   -18.684   1.00 45.32          c
ATOM   12013   C5    DG  c    1      -24.882  107.390   -18.167   1.00 46.28          C
ATOM   12014   N7    DG  c    1      -24.230  106.640   -17.200   1.00 50.06          N
ATOM   12015   C8    DG  c    1      -24.898  105.532   -17.156   1.00 48.39          c
ATOM   12016   N9    DG  c    1      -25.966  .105.5.19  -18.011   1.00 48.71          N
ATOM   12017   CI'   DG  c    1      -26.875  104.442   -18.270   1.00 53.26          C
ATOM   12018   04'   DG  c    1      -26.882  103.551   -17.187   1.00 56.91          O
ATOM   12019   C2'   DG  c    1      -26.423  .103.654   -19.490   1.00 56.35          C
ATOM   12020   C3'   DG  c    1      -25.825  102.397   -18.890   1.00 55.21          C
ATOM   12021   03'   DG  c    1      -25.943  101.315   -19.832   1.00 56.22          O
ATOM   12022   C4'   DG  c    1      -26.772  .102.222   -17.708   1.00 63.92          C
ATOM   12023   C5'   DG  c    1      -26.373  101.298   -16.570   1.00 67.39          c
ATOM   12024   05'   DG  c    1      -27.277  101.544   -15.450   1.00 76.41          0
ATOM   12025   P     DG  c    1      -27.806  .100..348   -14.527   1.00.105.45         P
ATOM   12026   OP1   DG  c    1      -26.583   99.797   -13.897   1.00 75.08          0
ATOM   12027   OP2   DG  c    1      -28.698   99.490   -15.349   1.00 86.30          0
ATOM   12028   OP3   DG  c    1      -28.655  100.902   -13.442   1.00 70.28          0
ATOM   12029   05'   DC  c    2      -25.888  102.514   -22.097   1.00 55.48          0
ATOM   12030   C4'   DC  c    2      -27.573  103.607   -23.322   1.00 47.78          c
ATOM   12031   C3'   DC  c    2      -26.755  103.903   -24.558   1.00 43.76          c
ATOM   12032   C2'   DC  c    2      -27.030  .105.382   -24.724   1.00 55.80          c
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ATOM	12033	P	DC	C	2	-25.188	101.367	-21.258	1.00	57.19	P
ATOM	12034	OP1	DC	C	2	-25.590	100.129	-21.958	1.00	59.14	O
ATOM	12035	OP2	DC	C	2	-23.789	101.817	-21.092	1.00	53.41	O
ATOM	12036	C5'	DC	C	2	-27.187	102.358	-22.588	1.00	48.22	C
ATOM	12037	O4'	DC	C	2	-27.299	104.739	-22.463	1.00	53.50	O
ATOM	12038	O3'	DC	C	2	-27.253	103.176	-25.664	1.00	57.50	O
ATOM	12039	C1'	DC	C	2	-27.066	105.872	-23.268	1.00	52.27	C
ATOM	12040	N1	DC	C	2	-25.805	106.512	-22.847	1.00	46.39	N
ATOM	12041	C2	DC	C	2	-25.486	107.771	-23.367	1.00	43.48	C
ATOM	12042	N3	DC	C	2	-24.321	108.361	-22.999	1.00	43.72	N
ATOM	12043	C4	DC	C	2	-23.495	107.739	-22.143	1.00	45.23	C
ATOM	12044	C5	DC	C	2	-23.806	106.441	-21.601	1.00	45.19	C
ATOM	12045	C6	DC	C	2	-24.959	105.868	-21.987	1.00	42.90	C
ATOM	12046	O2	DC	C	2	-26.272	108.309	-24.161	1.00	43.90	O
ATOM	12047	N4	DC	C	2	-22.358	108.377	-21.800	1.00	38.83	N
ATOM	12048	P	DC	C	3	-26.279	102.722	-26.870	1.00	63.08	P
ATOM	12049	OP1	DC	C	3	-27.031	101.694	-27.616	1.00	60.75	O
ATOM	12050	OP2	DC	C	3	-24.945	102.332	-26.366	1.00	48.15	O
ATOM	12051	O5'	DC	C	3	-26.066	104.067	-27.726	1.00	56.26	O
ATOM	12052	C5'	DC	C	3	-27.138	104.660	-28.438	1.00	45.79	C
ATOM	12053	C4'	DC	C	3	-26.743	106.014	-28.995	1.00	42.76	C
ATOM	12054	O4'	DC	C	3	-26.489	106.926	-27.904	1.00	48.50	O
ATOM	12055	C3'	DC	C	3	-25.454	106.044	-29.784	1.00	47.12	C
ATOM	12056	O3'	DC	C	3	-25.636	105.577	-31.117	1.00	52.57	O
ATOM	12057	C2'	DC	C	3	-25.141	107.526	-29.755	1.00	41.21	C
ATOM	12058	C1'	DC	C	3	-25.510	107.879	-28.317	1.00	43.87	C
ATOM	12059	N1	DC	C	3	-24.328	107.845	-27.383	1.00	40.67	N
ATOM	12060	C2	DC	C	3	-23.475	108.936	-27.357	1.00	40.44	C
ATOM	12061	N3	DC	C	3	-22.402	108.909	-26.541	1.00	38.67	N
ATOM	12062	C4	DC	C	3	-22.163	107.847	-25.772	1.00	40.73	C
ATOM	12063	C5	DC	C	3	-23.010	106.693	-25.783	1.00	34.06	C
ATOM	12064	C6	DC	C	3	-24.069	106.729	-26.610	1.00	41.16	C
ATOM	12065	O2	DC	C	3	-23.720	109.911	-28.084	1.00	41.62	O
ATOM	12066	N4	DC	C	3	-21.088	107.900	-24.983	1.00	42.56	N
ATOM	12067	O5'	DA	C	4	-23.430	106.138	-32.233	1.00	52.48	O
ATOM	12068	C4'	DA	C	4	-22.916	108.433	-32.797	1.00	54.65	C
ATOM	12069	C3'	DA	C	4	-21.511	108.108	-33.237	1.00	51.83	C
ATOM	12070	C2'	DA	C	4	-20.786	109.322	-32.691	1.00	49.26	C
ATOM	12071	P	DA	C	4	-24.398	104.924	-31.908	1.00	56.29	P
ATOM	12072	OP1	DA	C	4	-24.923	104.335	-33.156	1.00	73.82	O
ATOM	12073	OP2	DA	C	4	-23.648	104.072	-30.957	1.00	62.81	O
ATOM	12074	C5'	DA	C	4	-23.920	107.291	-32.884	1.00	57.61	C
ATOM	12075	O4'	DA	C	4	-22.722	108.836	-31.426	1.00	49.72	O
ATOM	12076	O3'	DA	C	4	-21.421	108.030	-34.664	1.00	63.30	O
ATOM	12077	C1'	DA	C	4	-21.458	109.477	-31.327	1.00	46.08	C
ATOM	12078	N9	DA	C	4	-20.699	108.856	-30.254	1.00	45.11	N
ATOM	12079	C8	DA	C	4	-21.016	107.716	-29.588	1.00	44.37	C
ATOM	12080	N7	DA	C	4	-20.136	107.377	-28.665	1.00	43.46	N
ATOM	12081	C5	DA	C	4	-19.180	108.371	-28.740	1.00	41.31	C
ATOM	12082	C4	DA	C	4	-19.505	109.291	-29.714	1.00	38.57	C
ATOM	12083	N1	DA	C	4	-17.265	109.691	-28.340	1.00	42.83	N
ATOM	12084	C2	DA	C	4	-17.710	110.489	-29.319	1.00	41.58	C
ATOM	12085	N3	DA	C	4	-18.802	110.369	-30.062	1.00	38.24	N
ATOM	12086	C6	DA	C	4	-17.987	108.590	-28.023	1.00	42.28	C
ATOM	12087	N6	DA	C	4	-17.548	107.769	-27.051	1.00	42.02	N
ATOM	12088	O5'	DA	C	5	-18.939	108.177	-35.211	1.00	51.78	O
ATOM	12089	C4'	DA	C	5	-17.678	110.205	-35.447	1.00	53.18	C
ATOM	12090	C3'	DA	C	5	-16.411	109.459	-35.841	1.00	51.30	C
ATOM	12091	C2'	DA	C	5	-15.375	110.136	-34.946	1.00	46.93	C
ATOM	12092	P	DA	C	5	-20.215	107.218	-35.367	1.00	60.70	P
ATOM	12093	OP1	DA	C	5	-20.584	107.156	-36.788	1.00	57.52	O
ATOM	12094	OP2	DA	C	5	-19.908	105.995	-34.597	1.00	56.31	O
ATOM	12095	C5'	DA	C	5	-18.969	109.483	-35.747	1.00	47.38	C

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ATOM  12096  04'  DA C  5   -17.553   110.385   -34.017   1.00  43.98   O
ATOM  12097  03'  DA C  5   -16.115   109.648   -37.246   1.00  57.26   O
ATOM  12098  CI'  DA C  5   -16.177   110.411   -33.663   1.00  44.67   C
ATOM  12099  N9   DA C  5   -15.941   109.428   -32.596   1.00  42.91   N
ATOM  12100  C8   DA C  5   -16.757   .108.399  -32.224   1.00  45.49   C
ATOM  12101  Nl   DA C  5   -16.291   107.674   -31.230   1.00  4.1.42  N
ATOM  12102  C5   DA C  5   -15.065   108.265   -30.945   1.00  42.64   C
ATOM  12103  C4   DA C  5   -14.840   .109.340  -3.1.775  1.00  44.53   C
ATOM  12104  Ml   DA C  5   -12.972   108.767   -29.973   1.00  44.71   N
ATOM  12105  C2   DA C  5   -12.893   109.761   -30.838   1.00  43.82   C
ATOM  12106  N3   DA C  5   -13.766   110.133   -31.774   1.00  47..38   N
ATOM  12107  C6   DA C  5   -14.058   107.974   -29.995   1.00  46.14   C
ATOM  12108  N6   DA C  5   -14.127   106.952   -29.124   1.00  46.70   N
ATOM  12109  05'  DG C  6   -13.777   108.651   -37.454   1.00  56.20   O
ATOM  12110  C4'  DG C  6   -11.666   109.705   -36.905   1.00  57.33   C
ATOM  12111  C3'  DG C  6   -10.764   108.510   -37.040   1.00  56.64   C
ATOM  12112  C2'  DG C  6    -9.937   108.655   -35.773   1.00  59.18   C
ATOM  12113  P    DG C  6   -15.250   .108.548  -38.073   1.00  61.57   P
ATOM  12114  OP1  DG C  6   -15.283   108.986   -39.480   1.00  61.43   0
ATOM  12115  OF2  DG C  6   -15.670   107.182   -37.723   1.00  49.96   0
ATOM  12116  C5'  DG C  6   -12.900   .109.7.19  -37.797   1.00  57.95   C
ATOM  12117  04'  DG C  6   -12.072   109.609   -35.530   1.00  55.70   0
ATOM  12118  03'  DG C  6    -9.954   108.617   -38.177   1.00  69.13   0
ATOM  12119  CI'  DG C  6   -10.993   109.113   -.34.777   1.00  54.9.3  C
ATOM  12120  N9   DG C  6   -11.454   108.039   -33.899   1.00  52.16   N
ATOM  12121  C8   DG C  6   -12.616   107.305   -33.994   1.00  46.37   C
ATOM  12122  N7   DG C  6   -12.732   106.405   -.3.3.052  1.00  48.69   N
ATOM  12123  C5   DG C  6   -11.565   106.555   -32.293   1.00  45.68   C
ATOM  12124  C4   DG C  6   -10.776   107.550   -32.8.12   1.00  46.15   C
ATOM  12125  Nl   DG C  6    -9.889   106.352   -30.688   1.00  48.06   N
ATOM  12126  C2   DG C  6    -9.182   107.361   -31.292   1.00  48.24   C
ATOM  12127  N3   DG C  6    -9.579   107.996   -32.372   1.00  47.18   N
ATOM  12128  C6   DG C  6   -11.120   105.868   -31.133   1.00  45.95   C
ATOM  12129  06   DG C  6   -11.675   .104.948  -30.519   1.00  43.32   0
ATOM  12130  N2   DG C  6    -8.022   107.688   -30.741   1.00  48.26   N
ATOM  12131  05'  DC C  7    -7.967   107.064   -37.809   1.00  65.24   0
ATOM  12132  C4'  DC C  7    -5.905   107.473   -36.716   1.00  55.43   C
ATOM  12133  C3'  DC C  7    -5.447   106.051   -36.962   1.00  56.85   C
ATOM  12134  C2'  DC C  7    -5.003   105.614   -35.569   1.00  55.00   C
ATOM  12135  P    DC C  7    -9.220   .107..309  -.38.777   1.00  67..30   P
ATOM  12136  OP1  DC C  7    -8.814   107.741   -40.133   1.00  70.76   0
ATOM  12137  OP2  DC C  7    -9.996   106.064   -38.561   1.00  62.07   0
ATOM  12138  C5'  DC C  7    -6.906   107.994   -37.718   1.00  55.71   C
ATOM  12139  04'  DC C  7    -6.545   107.405   -35.425   1.00  56.99   0
ATOM  12140  03'  DC C  7    -4..377   106.012   -37.908   1.00  59.06   0
ATOM  12141  CI'  DC C  7    -6.008   106.341   -34.668   1.00  52.92   C
ATOM  12142  N1   DC C  7    -7.140   .105.474  -34.192   1.00  49.2.1  N
ATOM  12143  C2   DC C  7    -7.009   104.752   -33.004   1.00  49.59   C
ATOM  12144  N3   DC C  7    -8.030   103.983   -32.586   1.00  49.72   N
ATOM  12145  C4   DC C  7    -9.147   .103.9.12  -33.292   1.00  47.52   C
ATOM  12146  C5   DC C  7    -ÿ.315    104.635   -34.506   1.00  49.46   C
ATOM  12147  C6   DC C  7    -8.294   105.406   -34.911   1.00  52.23   C
ATOM  12148  02   DC C  7    -5.963   .104.834  -.32.360   1.00  50.59   0
ATOM  12149  N4   DC C  7   -10.118   103.121   -32.828   1.00  47.59   N
ATOM  12150  05'  DG C  8    -3.385   103.708   -37.668   1.00  54.77   O
ATOM  12151  C4'  DG C  8    -.1.881  .103.225  -.35.874   1.00  51.22   C
ATOM  12152  C3'  DG C  8    -1.826   101.751   -36.216   1.00  56.57   C
ATOM  12153  C2'  DG C  8    -1.949   10.1.128  -34.819   1.00  54.54   C
ATOM  12154  P    DG C  8    -4.077   104.650   -38.734   1.00  64.79   P
ATOM  12155  OP1  DG C  8    -3.122   105.012   -39.798   1.00  69.25   0
ATOM  12156  OP2  DG C  8    -5..327  10.3.970  -39.123   1.00  61.45   0
ATOM  12157  C5'  DG C  8    -2.226   104.143   -37.022   1.00  53.71   C
ATOM  12158  04'  DG C  8    -2.874   .103.328  -34.827   1.00  59.16   0
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ATOM	12159	03'	DG	C	8	-0.554	101.479	-36.813	1.00	59.38	O
ATOM	12160	CI '	DG	C	8	-2.894	102.119	-34.087	1.00	56.90	C
ATOM	12161	N9	DG	C	8	-4.280	101.641	-33.986	1.00	52.04	N
ATOM	12162	C8	DG	C	8	-5.298	101.848	-34.886	1.00	50.34	C
ATOM	12163	N7	DG	C	8	-6.422	101.267	-34.547	1.00	48.75	N
ATOM	12164	C5	DG	C	8	-6.123	100.623	-33.355	1.00	49.66	C
ATOM	12165	C4	DG	C	8	-4.809	100.836	-32.999	1.00	48.98	C
ATOM	12166	N1	DG	C	8	-6.245	99.367	-31.400	1.00	47.12	N
ATOM	12167	C2	DG	C	8	-4.915	99.629	-31.144	1.00	46.34	C
ATOM	12168	N3	DG	C	8	-4.152	100.382	-31.912	1.00	46.70	N
ATOM	12169	C6	DG	C	8	-6.944	99.837	-32.512	1.00	49.17	C
ATOM	12170	06	DG	C	8	-8.134	99.544	-32.665	1.00	53.66	O
ATOM	12171	N2	DC-	C	8	-4.398	99.093	-30.025	1.00	44.24	N
ATOM	12172	05'	DC	C	9	-0.316	98.953	-36.554	1.00	55.66	O
ATOM	12173	C4'	DC	C	9	0.234	97.732	-34.521	1.00	46.82	C
ATOM	12174	C3'	DC	C	9	-0.171	96.370	-35.104	1.00	52.92	C
ATOM	12175	C2'	DC	C	9	-1.157	95.848	-34.054	1.00	49.75	C
ATOM	12176	P	DC	C	9	-0.236	100.137	-37.644	1.00	59.25	P
ATOM	12177	OP1	DC	C	9	1.154	100.413	-38.094	1.00	65.81	0
ATOM	12178	OF2	DC	C	9	-1.241	99.768	-38.675	1.00	50.20	0
ATOM	12179	C5'	DC	C	9	0.686	98.778	-35.537	1.00	53.30	C
ATOM	12180	04'	DC	C	9	-0.962	98.213	-33.845	1.00	59.14	0
ATOM	12181	03'	DC	C	9	1.003	95.457	-35.245	1.00	50.09	0
ATOM	12182	CI '	DC	C	9	-1.813	97.130	-33.515	1.00	52.84	C
ATOM	12183	Ml	DC	C	9	-3.155	97.361	-34.092	1.00	49.22	N
ATOM	12184	C2	DC	C	9	-4.273	96.795	-33.479	1.00	50.85	C
ATOM	12185	N3	DC	C	9	-5.505	96.991	-34.037	1.00	47.82	N
ATOM	12186	C4	DC	C	9	-5.605	97.697	-35.170	1.00	50.78	C
ATOM	12187	C5	DC	C	9	-4.469	98.264	-35.809	1.00	50.03	C
ATOM	12188	C6	DC	C	9	-3.281	98.067	-35.243	1.00	52.84	C
ATOM	12189	02	DC	C	9	-4.117	96.152	-32.433	1.00	48.46	0
ATOM	12190	N4	DC	C	9	-6.812	97.878	-35.695	1.00	51.68	N
ATOM	12191	05'	DA	C	10	-0.052	93.117	-35.261	1.00	45.05	0
ATOM	12192	C4'	DA	C	10	-0.836	91.877	-33.309	1.00	43.80	C
ATOM	12193	C3'	DA	C	10	-1.462	90.754	-34.136	1.00	49.34	C
ATOM	12194	C2'	DA	C	10	-2.877	90.674	-33.577	1.00	47.67	C
ATOM	12195	P	DA	C	10	0.899	94.082	-36.104	1.00	51.21	P
ATOM	12196	OP1	DA	C	10	2.257	93.520	-36.107	1.00	52.71	0
ATOM	12197	OP2	DA	C	10	0.231	94.333	-37.417	1.00	44.91	0
ATOM	12198	C5'	DA	C	10	0.331	92.618	-33.966	1.00	43.72	C
ATOM	12199	04'	DA	C	10	-1.919	92.797	-33.048	1.00	48.86	0
ATOM	12200	03'	DA	C	10	-0.763	89.538	-33.890	1.00	53.33	0
ATOM	12201	CI '	DA	C	10	-3.162	92.119	-33.125	1.00	49.09	C
ATOM	12202	N9	DA	C	10	-4.039	92.829	-34.046	1.00	41.22	N
ATOM	12203	C8	DA	C	10	-3.671	93.660	-35.060	1.00	43.88	C
ATOM	12204	N7	DA	C	10	-4.683	94.121	-35.760	1.00	49.17	N
ATOM	12205	C5	DA	C	10	-5.791	93.541	-35.160	1.00	49.15	C
ATOM	12206	C4	DA	C	10	-5.402	92.725	-34.113	1.00	48.52	C
ATOM	12207	Nl	DA	C	10	-8.014	92.918	-34.629	1.00	42.58	N
ATOM	12208	C2	DA	C	10	-7.495	92.171	-33.649	1.00	47.56	C
ATOM	12209	N3	DA	C	10	-6.206	92.007	-33.308	1.00	52.45	N
ATOM	12210	C6	DA	C	10	-7.181	93.631	-35.416	1.00	45.31	C
ATOM	12211	N6	DA	C	10	-7.702	94.357	-36.406	1.00	46.51	N
ATOM	12212	05'	DC	C	11.	-2.482	87.793	-34.639	1.00	57.34	O
ATOM	12213	C4'	DC	C	11	-4.398	86.886	-33.614	1.00	57.70	C
ATOM	12214	C3'	DC	C	11	-4.925	85.942	-34.688	1.00	53.86	C
ATOM	12215	C2'	DC	C	11	-6.228	86.600	-35.153	1.00	54.76	C
ATOM	12216	P	DC	C	11	-0.982	88.257	-34.835	1.00	56.18	P
ATOM	12217	OP1	DC	C	11	-0.095	87.201	-34.312	1.00	61.83	0
ATOM	12218	OP2	DC	C	11	-0.987	88.783	-36.224	1.00	52.86	0
ATOM	12219	C5'	DC	C	11	-2.883	87.011	-33.564	1.00	49.85	C
ATOM	12220	04'	DC	C	11	-4.955	88.173	-33.943	1.00	50.15	0
ATOM	12221	03'	DC	C	11	-5.192	84.718	-34.091	1.00	59.34	0

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ATOM   12222   CI '  DC  C   11      --6..195   88..003  -34..575   1 .00  48..78            C
ATOM   12223   N1    DC  C   11       -9,328    89..036  -35.,601   1 ,00  50..37            N
ATOM   12224   C2    DC  C   11       -7 .600   89.,533  -35..923   1 ,00  52 ,.31           C
ATOM   12225   N3    DC  C   11      --7 .712   90.,471  -36 ..881   1 .00  48..32            N
ATOM   12226   C4    DC  C   11       -6,,622   90. 929  -.37.,490   1 ,00  50..79            C
ATOM   12227   C5    DC  C   11       -5...3.15 90.,436  -37..176   1 ,00  48,.15            C
ATOM   12228   C6    DC  C   11      --5..216   89.,499  -36 ..234   1 ,00  48,.21            C
ATOM   12229   02    DC  C   11       -8.,591   89. 082  -.35.,341   1 ,00  56..89            0
ATOM   12230   N4    DC  C   11       -6 .785   91.,873  -38..427   1 ,00  50..68            N
ATOM   12231   05 '  DC  C   12       -7 .071   83.,810  -35..555   1 ,00  67 ,.11           0
ATOM   12232   C4 '  DC  C   12       -9,,493   83..891  -35.,516   1 ,00  63..52            C
ATOM   12233   C3 '  DC  C   12       -9 .561   82..905  -36 ,688   1 ,00  65..30            C
ATOM   12234   C2 '  DC  C   12       -9. 481   83.,794  -37. 928   1 ,00  62 ,60            C
ATOM   12235   P     DC  C   12      --5..641   83.,431  -34.,934   1 .00  73..82            P
ATOM   12236   OP1   DC  C   12       -5.,902   82..431  -33.,854   1 ,00  62 .91            0
ATOM   12237   OP2   DC  C   12       -4 .689   8.3.,206  -36 ..048   1 ,00  62 ,.77           0
ATOM   12238   C5 '  DC  C   12      --8..224   83.,804  -34. .705   1 .00  63..24            C
ATOM   12239   04 '  DC  C   12       -9.,606   85. 221  -.36 ,077   1 ,00  58..94            0
ATOM   12240   03 '  DC  C   12      -10..783   82.,164  -36 ..643   1 .00  7.3,.75            0
ATOM   12241   CI '  DC  C   12      --9..996   85.,136  -37 .418   1 ,00  59,.10            C
ATOM   12242   N1    DC  C   12       -9.,405   86. 271  -.38.,133   1 ,00  52 .17            N
ATOM   12243   C2    DC  C   12      -10..198   87.,018  -38.,989   1 ,00  53..23            C
ATOM   12244   N3    DC  C   12      --9..652   88.,050  -39 ..657   1 ,00  54 ,.54           N
ATOM   12245   C4    DC  C   12       -8.,368   88...341  -.39 ,491   1 ,00  55..98            C
ATOM   12246   C5    DC  C   12       -7 .530   87..577  -38..619   1 ,00  54 .12            C
ATOM   12247   C6    DC  C   12       -8. 092   86.,563  -37. 965   1 ,00  50 ,77            C
ATOM   12248   02    DC  C   12      -11 ,388   86..727  -.39 ,101   1 ,00  57 ,.76           0
ATOM   12249   N4    DC  C   12       -7 ,874   89..377  -40 ,173   1 ,00  53..41            N
ATOM   12250   05 '  DC  C   13      -11 .793   8.1.,390  -38. 815   1 ,00  67 ,.38           0
ATOM   12251   C4 '  DC  C   13      -13..436   82.,631  -39 ..953   1 .00  66..94            C
ATOM   12252   C3 '  DC  C   13      -13.,295   81..641  -41 ,111   1 ,00  62 .98            C
ATOM   12253   C2 '  DC  C   13      -12 .228   82.,266  -42 .016   1 .00  66,.99            C
ATOM   12254   P     DC  C   13      -10.,978   80.,851  -37..560   1 .00  75..86            P
ATOM   12255   OP1   DC  C   13      -11 ,855   79 .918  -.36 ,810   1 ,00  66..48            0
ATOM   12256   OP2   DC  C   13       -9 .652   80.,433  -38..090   1 .00  67 ,.95           0
ATOM   12257   C5 '  DC  C   13      -12..980   82.,091  -38..629   1 ,00  63,.50            C
ATOM   12258   04 '  DC  C   13      -12.,634   83. 790  -40.,300   1 ,00  70..50            0
ATOM   12259   03 '  DC  C   13      -14 ,536   81.,507  -41 ,780   1 ,00  73..68            0
ATOM   12260   CI '  DC  C   13      -12 ..329   83.,747  -41 .671   1 ,00  64 ,17            C
ATOM   122 61  N1    DC  C   13      -11 ,067   84..488  -4.1 ,889   1 ,00  53..97            N
ATOM   12262   C2    DC  C   13      -11 ,035   85..546  -42.,792   1 ,00  57 .44            C
ATOM   12263   02    DC  C   13      -12 .070   85.,852  -43. .398   1 ,00  60 ,29            0
ATOM   12264   N3    DC  C   13       -9.,867   86.,210  -42..982   1 .00  56..72            N
ATOM   12265   C4    DC  C   13       -8.,774   85..842  -42.,310   1 ,00  58..46            C
ATOM   12266   N4    DC  C   13       -7 .646   86.,527  -42 .524   1 .00  61 ,.41           N
ATOM   12267   C5    DC  C   13       -8..789   84.,759  -41 .381   1 .00  55..54            C
ATOM   12268   C6    DC  C   13       -9.,947   84. 120  -41 ,205   1 ,00  56..93            C
ATOM   12269   05 '  DA  C   14      -14 .407   80.,701  -44 .164   1 .00  75,.98            0
ATOM   12270   C4 '  DA  C   14      -14 .362   82.,104  -46 ..079   1 ,00  77 ,.19           C
ATOM   12271   C3 '  DA  C   14      -13.,736   80. 861  -46 ,728   1 ,00  84 .51            C
ATOM   12272   C2 '  DA  C   14      -12.,235   81.,155  -46 ,710   1 ,00  78..49            C
ATOM   12273   P     DA  C   14      -14 .836   80.,226  -42..707   1 ,00  83,.46            P
ATOM   12274   OP1   DA  C   14      -16.,304   80..020  -42.,696   1 ,00  75..58            0
ATOM   12275   OP2   DA  C   14      -13.,896   79..136  -42.,358   1 ,00  75..30            0
ATOM   12276   C5 '  DA  C   14      -14 .996   81.,836  -44 .741   1 ,00  74 ,.03           C
ATOM   12277   04 '  DA  C   14      -13.,284   83..063  -45 ,921   1 ,00  71 .91            0
ATOM   12278   03 '  DA  C   14      -14 ,222   80..693  -48 ,052   1 ,00  90..01            0
ATOM   12279   CI '  DA  C   14      -12. 223   82.,673  -46. 751   1 ,00  74 ,.33           C
ATOM   12280   N9    DA  C   14      -10.,994   83.,242  -46.,237   1 .00  65..22            N
ATOM   12281   C8    DA  C   14      -10.,230   82..750  -45 ,226   1 ,00  59..46            C
ATOM   12282   N1    DA  C   14       -9 .162   8.3.,466  -44 .983   1 .00  62 ,.78           N
ATOM   12283   C5    DA  C   14       -9..236   84.,499  -45..903   1 .00  59..62            C
ATOM   12284   C4    DA  C   14      -10.,353   84. 365  -46 ,689   1 ,00  61 .46            C
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ATOM  12285  N1   DA C 14    -8.758  86.438 -47.159  1.00 65.27   N
ATOM  12286  C2   DA C 14    -9.882  86.184 -47.831  1.00 69.26   C
ATOM  12287  N3   DA C 14   -10.739  85.173 -47.678  1.00 71.05   N
ATOM  12288  C6   DA C 14    -8.398  85.599 -46.166  1.00 64.18   C
ATOM  12289  N6   DA C 14    -7.265  85.840 -45.490  1.00 66.61   N
ATOM  12290  05'  DA C 15   -12.794  78.810 -48.985  1.00 90.63   O
ATOM  12291  C4'  DA C 15   -12.347  79.556 -51.285  1.00 89.20   C
ATOM  12292  C3'  DA C 15   -11.159  79.569 -52 .237 1.00 89.88   C
ATOM  12293  C2'  DA C 15   -10.905  81.059 -52 .466 1.00 88.31   C
ATOM  12294  P    DA C 15   -14.335  79.219 -48.692  1.00 94.40   P
ATOM  12295  OP1  DA C 15   -15.119  79.435 -49.932  1.00 92.99   0
ATOM  12296  OP2  DA C 15   -14.880  78.293 -47.662  1.00 79.21   0
ATOM  12297  C5'  DA C 15   -12.364  78.394 -50.294  1.00 87.27   C
ATOM  12298  04'  DA C 15   -12.316  80.826 -50.581  1.00 90.53   0
ATOM  12299  03'  DA C 15   -11.516  78.925 -53.441  1.00 90.78   0
ATOM  12300  CI'  DA C 15   -11.318  81.670 -51.132  1.00 85.83   C
ATOM  12301  N9   DA C 15   -10.228  81.782 -50.162  1.00 79.86   N
ATOM  12302  C8   DA C 15   -10.040  81.004 -49.053  1.00 78.32   C
ATOM  12303  N7   DA C 15    -8.991  81.338 -48.341  1.00 75.11   N
ATOM  12304  C5   DA C 15    -8.443  82.405 -49.036  1.00 71.41   C
ATOM  12305  C4   DA C 15    -9.194  82.697 -50.159  1.00 70.43   C
ATOM  12306  Ml   DA C 15    -7.038  84.189 -49.687  1.00 65.52   N
ATOM  12307  C2   DA C 15    -7.864  84.359 -50.727  1.00 71.68   C
ATOM  12308  N3   DA C 15    -8.960  83.668 -51.051  1.00 73.35   N
ATOM  12309  C6   DA C 15    -7.305  83.209 -48.798  1.00 68.05   C
ATOM  12310  N6   DA C 15    -6.489  83.042 -47.741  1.00 60.50   N
ATOM  12311  05'  DT C 16    -9.268  78.405 -54.473  1.00 90.13   0
ATOM  12312  C4'  DT C 16    -7.961  79.779 -55.996  1.00 93.11   C
ATOM  12313  C3'  DT C 16    -6.583  79.148 -55.888  1.00 89.24   C
ATOM  12314  C2'  DT C 16    -5.730  80.389 -55.659  1.00 89.86   C
ATOM  12315  P    DT C 16   -10.632  77.709 -53.997  1.00 98.91   P
ATOM  12316  OP1  DT C 16   -11.384  77.197 -55.170  1.00 95.27   0
ATOM  12317  OP2  DT C 16   -10.283  76.815 -52 .864 1.00 97.14   0
ATOM  12318  C5'  DT C 16    -9.144  78.842 -55.816  1.00 93.25   C
ATOM  12319  04'  DT C 16    -7.962  80.786 -54.953  1.00 91.01   0
ATOM  12320  03'  DT C 16    -6.229  78.495 -57.103  1.00 90.42   0
ATOM  12321  C1'  DT C 16    -6.629  81.213 -54.729  1.00 84.87   C
ATOM  12322  Ml   DT C 16    -6.300  81.012 -53.317  1.00 78.59   N
ATOM  12323  C2   DT C 16    -5.337  81.800 -52.757  1.00 76.53   C
ATOM  12324  N3   DT C 16    -5.080  81.542 -51.434  1.00 70.12   N
ATOM  12325  C4   DT C 16    -5.680  80.580 -50.641  1.00 74.94   C
ATOM  12326  C5   DT C 16    -6.684  79.772 -51.304  1.00 79.03   C
ATOM  12327  C6   DT C 16    -6.940  80.024 -52 .596 1.00 80.62   C
ATOM  12328  02   DT C 16    -4.756  82.674 -53.380  1.00 75.99   0
ATOM  12329  04   DT C 16    -5.375  80.417 -49.459  1.00 73.83   0
ATOM  12330  C7   DT C 16    -7.406  78.691 -50.549  1.00 82.08   C
ATOM  12331  P    DT C 17    -5.147  77.298 -57.109  1.00 96.67   P
ATOM  12332  OP1  DT C 17    -5.316  76.419 -55.923  1.00 86.35   0
ATOM  12333  OF2  DT C 17    -5.223  76.732 -58.473  1.00 97.42   0
ATOM  12334  05'  DT C 17    -3.736  78.037 -56.977  1.00 87.15   0
ATOM  12335  03'  DT C 17    -0.292  77.652 -58.133  1.00 75.39   0
ATOM  12336  CI'  DT C 17    -0.923  80.392 -55.804  1.00 79.36   C
ATOM  12337  C2'  DT C 17     0.024  79.329 -56.364  1.00 77.18   C
ATOM  12338  C3'  DT C 17    -0.946  78.412 -57.097  1.00 80.55   C
ATOM  12339  C4'  DT C 17    -1.907  79.436 -57.706  1.00 84.38   C
ATOM  12340  C5'  DT C 17    -3.291  78.903 -58.016  1.00 87.16   C
ATOM  12341  04'  DT C 17    -2.009  80.492 -56.712  1.00 78.68   0
ATOM  12342  Nl   DT C 17    -1.424  80.053 -54.405  1.00 79.36   N
ATOM  12343  C2   DT C 17    -0.753  80.576 -53.327  1.00 70.59   C
ATOM  12344  N3   DT C 17    -1.235  80.203 -52 .108 1.00 69.07   N
ATOM  12345  C4   DT C 17    -2.300  79.364 -51.850  1.00 76.19   C
ATOM  12346  C5   DT C 17    -2.959  78.827 -53.017  1.00 77.98   C
ATOM  12347  C6   DT C 17    -2.493  79.188 -54.230  1.00 79.15   C
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ATOM   12348  02    DT  C  17      0..189   81..329  -53..440  1,00  71.96     O
ATOM   12349  04    DT  C  17     -2.,662   79.092   --50.,704 1,00  76..12    O
ATOM   12350  C7    DT  C  17     -4.128    77,,900  -52..856  1,00  81,32     C
ATOM   12351  P     DT  C  18      0..273   76.,169  -57.,858  1,00  73..29    P
ATOM   12352  OP1   DT  C  18      0,,847   75.763   -59.,161  1,00  80.,02    O
ATOM   12353  OP2   DT  C  18     -0..694   75.,298  -57..148  1,00  65,.06    O
ATOM   12354  05'   DT  C  19      1.463    76,377   -56..816  1,00  71,30     O
ATOM   12355  C5'   DT  C  18      2,,611   77.118   -57 ,193  1,00  69.,60    C
ATOM   12356  C4'   DT  C  18      3..492   77.381   -55.,988  1,00  67.48     C
ATOM   12357  04'   DT  C  18      2.767    78,170   -55..012  1,00  69,,22    O
ATOM   12358  C3'   DT  C  18      3,,905   76..146  -55.,211  1,00  64.97     C
ATOM   12359  03'   DT  C  18      5..001   75..474  -55.,864  1,00  60..15    O
ATOM   12360  C2'   DT  C  18      4..319   76,763   -53. 878  1,00  59,47     C
ATOM   12361  CI'   DT  C  18      3..297   77,905   -53.,724  1,00  68..57    C
ATOM   12362  Nl    DT  C  18      2,192    77.549   -52.,795  1,00  71.83     N
ATOM   12363  C2    DT  C  18      2..304   77,892   -51..468  1,00  65,.58    C
ATOM   12364  N3    DT  C  18      1.268    77,479   -50.,683  1,00  71.02     N
ATOM   12365  C4    DT  C  18      0,,148   76.768   -51 ,077  1,00  74,66     C
ATOM   12366  C5    DT  C  18      0..101   76.,414  -52..482  1,00  76,.04    C
ATOM   12367  C6    DT  C  18      1.117    76,815   -53.263   1,00  73,.29    C
ATOM   12368  02    DT  C  18      3,,242   78.520   -51 ,019  1,00  62,51     0
ATOM   12369  04    DT  C  18     -0..731   76.,438  -50.,284  1,00  74.99     0
ATOM   12370  C7    DT  C  18     --1.061   75,627   -53.031   1,00  74,04     C
ATOM   12371  P     DC  C  19      5,372    73..966  -55.,468  1,00  61.86     P
ATOM   12372  OP1   DC  C  19      6,289    73.,463  -56,515   1,00  73..37    0
ATOM   12373  OP2   DC  C  19      4.154    73,187   -55. 176  1,00  62,95     0
ATOM   12374  05'   DC  C  19      6,,177   74.127   -54.,104  1,00  59..13    0
ATOM   12375  C5'   DC  C  19      5,,940   73.242   -53.,033  1,00  56..20    C
ATOM   12376  C4'   DC  C  19      6.469    73,826   -51. 742  1,00  57,19     C
ATOM   12377  04'   DC  C  19      5,652    74,974   -51.,355  1,00  66..25    0
ATOM   12378  C3'   DC  C  19      6,413    72.888   -50.,562  1,00  59..36    C
ATOM   12379  03'   DC  C  19      7.591    72.,111  -50..500  1,00  63,.29    0
ATOM   12380  C2'   DC  C  19      6..303   73.,845  -49,381   1,00  62.35     C
ATOM   12381  C1'   DC  C  19      5,,404   74.937   -49.,960  1,00  62,10     C
ATOM   12382  Nl    DC  C  19      3..949   74,700   -49.754   1,00  62,69     N
ATOM   12383  C2    DC  C  19      3..405   74,821   -48.475   1,00  61,30     C
ATOM   12384  N3    DC  C  19      2,,077   74.612   -48,300   1,00  66.,25    N
ATOM   12385  C4    DC  C  19      1,304    74,307   -49,350   1,00  72.23     C
ATOM   12386  C5    DC  C  19      1.845    74,178   -50. 670  1,00  66,55     C
ATOM   12387  C6    DC  C  19      3,,154   74..387  -50.,825  1,00  62.4.1    C
ATOM   12388  02    DC  C  19      4,143    75.110   -47,540   1,00  62.35     0
ATOM   12389  N4    DC  C  19     -0. 008   74,119   -49. 133  1,00  69,57     N
ATOM   12390  05'   DC  C  20      7,475    71,138   -48,179   1,00  71.10     0
ATOM   12391  C4'   DC  C  20      8,,314   71.796   -46,016   1,00  65..58    C
ATOM   12392  C3'   DC  C  20      7.955    70.,553  -45.222   1,00  63,.03    C
ATOM   12393  C2'   DC  C  20      7.088    71,122   -44,107   1,00  57.58     C
ATOM   12394  P     DC  C  20      7,541    70.713   -49.,726  1,00  62,96     P
ATOM   12395  OP1   DC  C  20      8..779   69.,936  -49.979   1,00  69,.30    0
ATOM   12396  OF2   DC  C  20      6..210   70,165   -50..036  1,00  65,.86    0
ATOM   12397  C5'   DC  C  20      8,,643   71.552   -47,480   1,00  63.,00    C
ATOM   12398  04'   DC  C  20      7,133    72.,640  -45,932   1,00  65..35    0
ATOM   12399  03'   DC  C  20      9.127    69.,943  -44.704   1,00  66,.38    0
ATOM   12400  CI'   DC  C  20      6,,351   72.258   -44 ,818  1,00  65..38    C
ATOM   12401  Nl    DC  C  20      4,983    71,892   -45,298   1,00  63..58    N
ATOM   124 02  C2    DC  C  20      3.942    71,750   -44 .371  1,00  65,23     C
ATOM   12403  N3    DC  C  20      2,,704   71.422   -44 ,820  1,00  65..31    N
ATOM   12404  C4    DC  C  20      2,491    71.251   -46,124   1,00  63..56    C
ATOM   12405  C5    DC  C  20      3.537    71,402   -47.086   1,00  62,19     C
ATOM   12406  C6    DC  C  20      4,755    71,723   -46,631   1,00  63..80    C
ATOM   12407  02    DC  C  20      4,179    71.915   -43,165   1,00  68..05    0
ATOM   12408  N4    DC  C  20      1.258    70.,928  -46..513  1,00  59,.23    N
TER
ATOM   12409  0     LYS D   3     26,,996   70.297    39,675   1,00  84,46     0
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ATOM	12410	N	LYS	D	3	27.400	73.484	38.276	1.00	89.12	N
ATOM	12411	CA	LYS	D	3	27.508	72.633	39.452	1.00	86.99	C
ATOM	12412	C	LYS	D	3	26.582	71.415	39.348	1.00	87.92	C
ATOM	12413	CB	LYS	D	3	27.201	73.433	40.723	1.00	85.45	C
ATOM	12414	O	LYS	D	4	24.295	70.371	36.419	I.00	73.23	0
ATOM	12415	N	LYS	D	4	25.346	71.618	38.884	1.00	77.37	N
ATOM	12416	CA	LYS	D	4	24.350	70.529	38.857	1.00	80.26	C
ATOM	12417	C	LYS	D	4	24.232	69.771	37.505	I.00	80.19	C
ATOM	12418	CB	LYS	D	4	22.972	71.074	39.255	1.00	66.31	C
ATOM	12419	O	TYR	D	5	22.957	65.936	37.810	1.00	60.10	0
ATOM	12420	N	TYR	D	5	24.053	68.449	37.585	I.00	71.86	N
ATOM	12421	CA	TYR	D	5	23.944	67.601	36.388	1.00	64.06	C
ATOM	12422	C	TYR	D	5	23.169	66.329	36.660	1.00	61.25	C
ATOM	12423	CB	TYR	D	5	25.324	67.221	35.839	1.00	55.67	C
ATOM	12424	CG	TYR	D	5	26.036	66.194	36.686	1.00	61.45	C
ATOM	12425	CD1	TYR	D	5	26.656	66.565	37.869	1.00	59.48	C
ATOM	12426	CD2	TYR	D	5	26.080	64.850	36.309	1.00	60.01	C
ATOM	12427	CE1	TYR	D	5	27.285	65.659	38.656	I.00	63.85	C
ATOM	12428	CE2	TYR	D	5	26.727	63.918	37.100	1.00	61.51	C
ATOM	12429	CZ	TYR	D	5	27.329	64.331	38.271	1.00	65.05	C
ATOM	12430	OH	TYR	D	5	27.986	63.430	39.071	I.00	60.13	0
ATOM	12431	N	SEP.	D	6	22.773	65.673	35.578	1.00	53.95	N
ATOM	12432	CA	SER	D	6	22.052	64.417	35.671	1.00	57.51	C
ATOM	12433	C	SER	D	6	22.724	63.313	34.844	I.00	52.45	C
ATOM	12434	O	SER	D	6	23.411	63.594	33.850	1.00	54.02	0
ATOM	12435	CB	SER	D	6	20.603	64.614	35.217	1.00	52.76	C
ATOM	12436	OG	SER	D	6	19.703	64.294	36.264	I.00	61.19	0
ATOM	12437	N	ILE	D	7	22.497	62.066	35.232	1.00	46.32	N
ATOM	12438	CA	ILE	D	7	23.034	60.923	34.474	1.00	42.14	C
ATOM	12439	C	ILE	D	7	21.929	59.987	33.977	1.00	42.53	C
ATOM	12440	O	ILE	D	7	21.105	59.510	34.766	1.00	40.60	0
ATOM	12441	CB	ILE	D	7	24.041	60.132	35.320	1.00	46.84	C
ATOM	12442	CGI	ILE	D	7	25.345	60.919	35.461	1.00	50.64	C
ATOM	12443	CG2	ILE	D	7	24.383	58.789	34.662	I.00	48.80	C
ATOM	12444	CD1	ILE	D	7	26.172	60.509	36.668	1.00	55.49	C
ATOM	12445	N	GLY	D	8	21.886	59.764	32.661	1.00	42.85	N
ATOM	12446	CA.	GLY	D	8	21.041	58.719	32.087	I.00	44.12	C
ATOM	12447	C	GLY	D	8	21.771	57.404	31.721	1.00	52.36	C
ATOM	12448	O	GLY	D	8	22.876	57.390	31.137	1.00	47.43	0
ATOM	12449	N	LEU	D	9	21.126	56.286	32.031	I.00	47.15	N
ATOM	12450	CA	LEU	D	9	21.734	54.961	31.871	1.00	42.60	C
ATOM	12451	C	LEU	D	9	20.863	54.039	31.043	1.00	47.59	C
ATOM	12452	O	LEU	D	9	19.701	53.854	31.373	1.00	50.41	0
ATOM	12453	CB	LEU	D	9	21.972	54.300	33.243	1.00	43.92	C
ATOM	12454	CG	LEU	D	9	23.026	54.849	34.218	1.00	39.71	C
ATOM	12455	CD1	LEU	D	9	22.984	54.105	35.539	1.00	32.79	C
ATOM	12456	CD2	LEU	D	9	24.408	54.866	33.618	I.00	38.19	C
ATOM	12457	N	ALA	D	10	21.427	53.438	29.993	1.00	46.25	N
ATOM	12458	CA	ALA	D	10	20.693	52.462	29.191	1.00	47.44	C
ATOM	12459	C	ALA	D	10	21.419	51.105	29.176	I.00	43.68	C
ATOM	12460	O	ALA	D	10	22.393	50.898	28.463	1.00	44.49	0
ATOM	12461	CB	ALA	D	10	20.484	52.986	27.764	1.00	43.53	C
ATOM	12462	N	ILE	D	11	20.935	50.180	29.980	I.00	48.74	N
ATOM	12463	CA	ILE	D	11	21.664	48.939	30.192	1.00	52.66	C
ATOM	12464	C	ILE	D	11	21.079	47.777	29.395	1.00	52.04	C
ATOM	12465	O	ILE	D	11	19.892	47.463	29.501	I.00	49.68	0
ATOM	12466	CB	ILE	D	11	21.681	48.567	31.683	1.00	50.01	C
ATOM	12467	CGI	ILE	D	11	22.359	49.656	32.505	1.00	41.36	C
ATOM	12468	CG2	ILE	D	11	22.385	47.247	31.896	1.00	49.13	C
ATOM	12469	CD1	ILE	D	11	22.004	49.575	33.970	1.00	46.65	C
ATOM	12470	N	GLY	D	12	21.923	47.153	28.582	1.00	50.28	N
ATOM	12471	CA	GLY	D	12	21.558	45.924	27.883	1.00	55.74	C
ATOM	12472	C	GLY	D	12	22.480	44.780	28.278	I.00	53.71	C

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ATOM   12473   O    GLY  D   12        23..334   44 .933   29..166   1 .00  55..91            O
ATOM   12474   O    THR  D   13        25,,526   42..084   28.,099   1 ,00  56..49            O
ATOM   12475   N    THR  D   13        22..336   43.,637   27..616   1 .00  61 ,55            N
ATOM   12476   CA   THR  D   13        23..154   42..457   27.,955   1 .00  61 .17            C
ATOM   12477   C    THR  D   13        24.,599   42 .648   27.,513   1 ,00  56..85            C
ATOM   12478   CB   THR  D   13        22..596   41 ,182   27 .320   1 ,00  57 ,.20           C
ATOM   12479   OG1  THR  D   13        22..177   41 ,464   25.. 975  1 ,00  60,.05            O
ATOM   12480   CG2  THR  D   13        21.,402   40. 702   28.,117   1 ,00  63..00            C
ATOM   12481   O    ASN  D   14        27..403   45..504   25..076   1 ,00  41 .75            O
ATOM   12482   N    ASN  D   14        24 .787   43.,491   26.. 505  1 ,00  53,.73            N
ATOM   12483   CA   ASM  D   14        26.,104   43..705   25.,962   1 ,00  43..96            C
ATOM   12484   C    ASN  D   14        26..502   45..166   25.,835   1 ,00  41 .92            C
ATOM   12485   CB   ASN  D   14        26. 183   42.,993   24 .621   1 ,00  43 ,85            C
ATOM   12486   CG   ASN  D   14        26..140   41 .491   24.,788   1 ,00  49..94            C
ATOM   12487   OD1  ASN  D   14        25.,073   40..871   24.,771   1 ,00  51 .37            0
ATOM   12488   ND2  ASN  D   14        27 ..309  40.,899   25 .021   1 .00  46,.48            N
ATOM   12489   O    SER  D   15        24..742   47 .941   28.,421   1 .00  49..52            O
ATOM   12490   N    SER  D   15        25 ,838   46. 038   26.,591   1 ,00  50..0.1           N
ATOM   12491   CA   SER  D   15        26..168   47 ,465   26..542   1 ,00  46,.56            C
ATOM   12492   C    SER  D   15        25..718   48.,270   27 .745   1 ,00  46,.42            C
ATOM   12493   CB   SER  D   15        25 ,591   48. 109   25 ,286   1 ,00  41 .97            C
ATOM   124 94  OG   SER  D   15        24..299   47 ,642   25.,047   1 ,00  43..38            0
ATOM   12495   O    VAL  D   16        27 .202   52.,223   27 .977   1 ,00  43,.03            0
ATOM   12496   N    VAL  D   16        26.,478   49 .320   28.,014   1 ,00  44 .48            N
ATOM   12497   CA   VAL  D   16        26..080   50.,348   28.,955   1 ,00  44 .61            C
ATOM   12498   C    VAL  D   16        26. 119   51 ,677   28. 217   1 ,00  41 ,95            C
ATOM   12499   CB   VAL  D   16        27.,002   50..415   .30.,187  1 ,00  45..39            C
ATOM   12500   CGI  VAL  D   16        26.,625   51..598   31.,051   1 ,00  48..75            C
ATOM   12501   CG2  VAL  D   16        26. 938   49.,121   30. 993   1 ,00  40 ,13            C
ATOM   12502   N    GLY  D   17        24..943   52.,169   27.,824   1 ,00  44 .45            N
ATOM   12503   CA   GLY  D   17        24.,818   53.. 494  27.,215   1 ,00  42 .07            C
ATOM   12504   C    GLY  D   17        24..672   54.,513   28.. .335  1 .00  42 ,.90           C
ATOM   12505   O    GLY  D   17        23..926   54.,265   29..296   1 .00  44 .34            O
ATOM   12506   N    TRP  D   18        25 ,390   55. 630   28.,250   1 ,00  39..47            N
ATOM   12507   CA   TP.P D   18        25 .332   56.,632   29.. 326  1 ,00  43,.64            C
ATOM   12508   C    TRP  D   18        25..317   58.,063   28.. 795  1 ,00  45,.15            C
ATOM   12509   0    TRP  D   18        25 ,828   58. 349   27.,703   1 ,00  42 .13            0
ATOM   12510   CB   TRP  D   18        26..512   56.,472   30.,304   1 ,00  42 .54            C
ATOM   12511   CG   TP.P D   18        27 .816   56.,442   29. 609   1 ,00  41 ,96            C
ATOM   12512   CD1  TRP  D   18        28.,457   55.. .336  29.,134   1 ,00  46..5.3           C
ATOM   12513   CD2  TRP  D   18        28.,629   57..567   29.,245   1 ,00  47 .89            C
ATOM   12514   NE1  TP.P D   18        29. 624   55.,694   28. 509   1 ,00  49 ,35            N
ATOM   12515   CE2  TRP  D   18        29..765   57.,056   28.,566   1 ,00  45..95            C
ATOM   12516   CE3  TRP  D   18        28.,514   58.. 959  29.,429   1 ,00  47 .89            C
ATOM   12517   Ca2  TP.P D   18        30..783   57.,879   28.. 074  1 .00  45,.18            C
ATOM   12518   CZ3  TRP  D   18        29..528   59.,787   28.,944   1 .00  45..23            C
ATOM   12519   CH2  TRP  D   18        30.,648   59. 240   28.,270   1 ,00  55..05            C
ATOM   12520   N    ALA  D   19        24..741   58.,969   29.. 579  1 ,00  48,.08            N
ATOM   12521   CA   ALA  D   19        24 .829   60.,397   29..227   1 ,00  51 ,98            C
ATOM   12522   C    ALA  D   19        24.,821   61. 320   30.,445   1 ,00  46..18            C
ATOM   12523   0    ALA  D   19        24..192   61.,028   31.,477   1 ,00  49..64            0
ATOM   12524   CB   ALA  D   19        23..718   60.,776   28.. 269  1 ,00  43,.13            C
ATOM   12525   N    VAL  D   20        25.,575   62.. 409  .30.,328  1 ,00  44 .44            N
ATOM   12526   CA   VAL  D   20        25..465   63.,505   31.,293   1 ,00  56..37            C
ATOM   12527   C    VAL  D   20        24 .529   64.,610   30. 745   1 ,00  52 ,01            C
ATOM   12528   O    VAL  D   20        24.,749   65..103   29.,638   1 ,00  53..46            0
ATOM   12529   CB   VAL  D   20        26.,843   64..125   31.,613   1 ,00  56..60            C
ATOM   12530   CGI  VAL  D   20        26. 732   65.,084   32. 800   1 ,00  57 ,.90           C
ATOM   12531   CG2  VAL  D   20        27..870   63.,042   31.,889   1 ,00  53..10            C
ATOM   12532   N    ILE  D   21        23.,480   64.. 976  31.,472   1 ,00  50..63            N
ATOM   12533   CA   ILE  D   21        22..728   66.,182   31.. 065  1 .00  56,.59            C
ATOM   12534   C    ILE  D   21        22..695   67.,279   32.,131   1 .00  57 .53            C
ATOM   12535   0    ILE  D   21        22.,615   67. 004   33.,331   1 ,00  56..80            0
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ATOM   12536   CB    ILE  D   21      21..953    65..894    30..676    1.00   53..71         C
ATOM   12537   CGI   ILE  D   21      20,,484    65..316    31.,854    1,00   55..02         C
ATOM   12538   CG2   ILE  D   21      21..167    65.,004    29..457    1,00   52,77          C
ATOM   12539   GDI   ILE  D   21      18..996    65..550    31..782    1.00   60..04         C
ATOM   12540   N     TH.R D   22      22.,763    68. 524    31.,658    1,00   64.72          N
ATOM   12541   CA    THR  D   22      22..436    69.,731    32..438    1,00   63,.82         C
ATOM   12542   C     THR  D   22      20..930    69.,823    32..733    1,00   69,.19         C
ATOM   12543   0     TH.R D   22      20.,177    68. 911    .32.,413   1,00   69..08         0
ATOM   12544   CB    THR  D   22      22..853    70..977    31..677    1,00   57.97          C
ATOM   12545   OG1   THR  D   22      21.901     71,205     30..635    1,00   67,71          0
ATOM   12546   CG2   THR  D   22      24.,221    70..775    31.,032    I,00   56..07         C
ATOM   12547   N     ASP  D   23      20..470    70..928    33..319    1,00   79..39         N
ATOM   12548   CA    ASP  D   23      19. 020    71,097     33.529     1,00   78,39          C
ATOM   12549   C     ASP  D   23      18..374    71.883     32..368    1.00   74.08          C
ATOM   12550   O     ASP  D   23      17,145     72.067     32.,320    1,00   66..82         0
ATOM   12551   CB    ASP  D   23      18.727     71,763     34..885    1,00   78,.35         C
ATOM   12552   CG    ASP  D   23      19..486    73..075    35..085    1.00   87.28          C
ATOM   12553   OD1   ASP  D   23      20.,061    73.601     .34.,098   1,00   81.11          0
ATOM   12554   OD2   ASP  D   23      19.492     73.,584    36..236    1,00   83,.37         0
ATOM   12555   N     GLU  D   24      19..219    72..327    31..439    1,00   64,85          N
ATOM   12556   CA.   GLU  D   24      18.,764    72.748     30.,124    1,00   64.67          C
ATOM   12557   C     GLU  D   24      18..538    71.558     29..195    1,00   71.64          C
ATOM   12558   O     GLU  D   24      18..094    71,737     28..067    1,00   72,87          0
ATOM   12559   CB    GLU  D   24      19.,775    73..689    29.,487    I,00   69..29         C
ATOM   12560   N     TYR  D   25      18..861    70..356    29..684    1,00   73..44         N
ATOM   12561   CA    TYR  D   25      18. 843    69.,098    28. 922    1,00   63,40          C
ATOM   12562   C     TYR  D   25      19.,867    69..092    27.,802    I,00   67.86          C
ATOM   12563   O     TYR  D   25      19.,646    68..485    26.,752    1,00   65..09         0
ATOM   12564   CB    TYR  D   25      17.465     68.,800    28. .327   1,00   56,59          C
ATOM   12565   CG    TYR  D   25      16..330    68..908    29..303    1.00   66..93         C
ATOM   12566   CD1   TYR  D   25      16.,161    67..956    30.,289    1,00   59..42         C
ATOM   12567   CD2   TYR  D   25      15.413     69.,973    29..237    1,00   65,.54         C
ATOM   12568   CE1   TYR  D   25      15..123    68..037    31..192    1.00   58..70         C
ATOM   12569   CE2   TYR  D   25      14,364     70.059     30.,135    1,00   59..73         C
ATOM   12570   CZ    TYR  D   25      14.230     69.,087    31..112    1,00   63,.97         C
ATOM   12571   OH    TYR  D   25      13..205    69.,140    32..020    1,00   67,68          0
ATOM   12572   O     LYS  D   26      23.,482    68. 562    28.,676    1,00   58..16         0
ATOM   12573   N     LYS  D   26      20..997    69..750    28..012    1,00   66..46         N
ATOM   12574   CA    LYS  D   26      22.060     69.,659    27.016     1,00   66,21          C
ATOM   12575   C     LYS  D   26      23.,274    68..815    27.,484    I,00   61.28          C
ATOM   12576   CB    LYS  D   26      22.,492    71.067     26.,602    1,00   67.10          C
ATOM   12577   CG    LYS  D   26      22.295     72.,115    27.681     1,00   72,09          C
ATOM   12578   CD    LYS  D   26      22..596    73..520    27..167    1.00   70..24         C
ATOM   12579   CE    LYS  D   26      21.,753    73.840     25.,944    1,00   70..30         C
ATOM   12580   NZ    LYS  D   26      22..221    75.,064    25.262     1,00   62,08          N
ATOM   12581   N     VAL  D   27      24..062    68..366    26..517    1.00   61.00          N
ATOM   12582   CA.   VAL  D   27      25,210     67. 526    26.,798    1,00   52.06          C
ATOM   12583   C     VAL  D   27      26..498    68.,343    26..760    1,00   47,50          C
ATOM   12584   O     VAL  D   27      26..922    68.,808    25..711    1,00   46,.00         0
ATOM   12585   CB    VAL  D   27      25,304     66. .328   25,795     1,00   54.90          C
ATOM   12586   CGI   VAL  D   27      26..642    65..548    25..953    1,00   48..85         C
ATOM   12587   CG2   VAL  D   27      24.130     65.,394    25..971    1,00   51,54          C
ATOM   12588   N     PRO  D   28      27.,150    68..481    27.,912    I,00   44.72          N
ATOM   12589   CA    PRO  D   28      28..421    69..203    27..994    1,00   37.58          C
ATOM   12590   C     PRO  D   28      29. 530    68.,540    27.235     1,00   55,22          C
ATOM   12591   O     PRO  D   28      29.,589    67..312    27.,143    I,00   65..32         0
ATOM   12592   CB    FRO  D   28      28.,747    69..199    29.,480    1,00   44.40          C
ATOM   12593   CG    PRO  D   28      27.851     68.,205    30. 105    1,00   46,81          C
ATOM   12594   CD    PRO  D   28      26..685    67..978    29..214    1.00   47.32          C
ATOM   12595   N     SEP. D   29      30.,410    69..362    26.,687    1,00   59..36         N
ATOM   12596   CA    SEP. D   29      31..683    68.,906    26..174    1,00   54,05          C
ATOM   12597   C     SER  D   29      32..724    69..331    27..183    1.00   60..59         C
ATOM   12598   O     SER  D   29      .32.,439   70.172     28.,029    1,00   67.28          0
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ATOM	12599	CB	SER	D	29	31.977	69.512	24.815	1.00	60.44	C
ATOM	12600	OG	SEP.	D	29	32,273	70.888	24,965	1,00	63.40	O
ATOM	12601	N	LYS	D	30	33.918	68,750	27.118	1,00	62,00	N
ATOM	12602	CA	LYS	D	30	35.015	69.208	27.955	1.00	60.45	C
ATOM	12603	C	LYS	D	30	36,311	69.022	27,212	1,00	62,65	C
ATOM	12604	O	LYS	D	30	36.317	68,525	26.089	1,00	68,76	0
ATOM	12605	CE	LYS	D	30	35.035	68,479	29.287	1,00	57,98	C
ATOM	12606	CG	LYS	D	30	34,108	69.123	30,293	1,00	60.74	C
ATOM	12607	CD	LYS	D	30	33.587	68.167	31.346	1,00	58.98	C
ATOM	12608	CE	LYS	D	30	34.334	68,311	32.651	1,00	64.48	C
ATOM	12609	NZ	LYS	D	30	33,718	69.326	33,561	1,00	61.60	N
ATOM	12610	N	LYS	D	31	37.407	69.473	27.803	1,00	65.68	N
ATOM	12611	CA	LYS	D	31	38.712	69,217	27.214	1,00	68,25	C
ATOM	12612	C	LYS	D	31	39.489	68.261	28.105	1.00	65.51	C
ATOM	12613	O	LYS	D	31	39,661	68.493	29,303	1,00	67.47	0
ATOM	12614	CB	LYS	D	31	39.483	70,513	26.988	1,00	76,66	C
ATOM	12615	CG	LYS	D	31	39.491	70.959	25.537	1.00	74.40	C
ATOM	12616	CD	LYS	D	31	40,206	72.289	25,379	1,00	80,61	C
ATOM	12617	CE	LYS	D	31	39.595	73,102	24.255	1,00	82,51	C
ATOM	12618	NZ	LYS	D	31	40.484	74,225	23.856	1,00	87,68	N
ATOM	12619	N	PHE	D	32	39,927	67.160	27,516	1,00	66.60	N
ATOM	12620	CA	PHE	D	32	40.479	66.067	28.299	1,00	64.69	C
ATOM	12621	C	PHE	D	32	41.936	65,867	27.962	1,00	66,96	C
ATOM	12622	0	PHE	D	32	42,308	65.851	26,791	1,00	64.61	0
ATOM	12623	CB	PHE	D	32	39.691	64.781	28.041	1,00	60.42	C
ATOM	12624	CG	PHE	D	32	38.284	64,807	28.592	1,00	57,59	C
ATOM	12625	CD1	PHE	D	32	38,036	64.450	29.905	1,00	56.92	C
ATOM	12626	CD2	PHE	D	32	37,216	65.175	27,790	1,00	55.46	C
ATOM	12627	CE1	PHE	D	32	36.759	64,467	30.410	1,00	53,29	C
ATOM	12628	CE2	PHE	D	32	35.931	65.193	28.290	1.00	55.95	C
ATOM	12629	CZ	PHE	D	32	35,702	64.845	29,603	1,00	56.37	C
ATOM	12630	N	LYS	D	33	42.762	65,738	28.994	1,00	68,91	N
ATOM	12631	CA	LYS	D	33	44.175	65.454	28.793	1.00	64.56	C
ATOM	12632	C	LYS	D	33	44,354	64.175	27,969	1,00	70.38	C
ATOM	12633	O	LYS	D	33	43.608	63,202	28.122	1,00	70,14	0
ATOM	12634	CB	LYS	D	33	44.900	65,328	30.140	1,00	61,42	C
ATOM	12635	CG	LYS	D	33	46,397	65.068	30,020	1,00	64.25	C
ATOM	12636	CD	LYS	D	33	47.264	66.278	30.382	1,00	70.79	C
ATOM	12637	CE	LYS	D	33	48.521	66,345	29.498	1,00	78,25	C
ATOM	12638	NZ	LYS	D	33	49,815	66.375	30,252	1,00	81.32	N
ATOM	12639	N	VAL	D	34	45,331	64.197	27,072	1,00	66.20	N
ATOM	12640	CA	VAL	D	34	45.727	63,004	26.349	1,00	64,83	C
ATOM	12641	C	VAL	D	34	47.174	62.649	26.679	1.00	64.23	C
ATOM	12642	O	VAL	D	34	48,086	63.433	26,429	1,00	63.89	0
ATOM	12643	CB	VAL	D	34	45.587	63,184	24.837	1,00	64,32	C
ATOM	12644	CGI	VAL	D	34	46.131	61.965	24.117	1.00	65.67	C
ATOM	12645	CG2	VAL	D	34	44,139	63.429	24,474	1,00	61.48	C
ATOM	12646	N	LEU	D	35	47.376	61,460	27.230	1,00	63,72	N
ATOM	12647	CA	LEU	D	35	48.706	61,002	27.599	1,00	56,83	C
ATOM	12648	C	LEU	D	35	49,436	60.353	26,445	1,00	58.12	C
ATOM	12649	O	LEU	D	35	49.046	60.491	25.286	1,00	61.61	0
ATOM	12650	CB	LEU	D	35	48.618	60,033	28.765	1,00	53,37	C
ATOM	12651	CG	LEU	D	35	48,018	60.772	29,949	1,00	55.68	C
ATOM	12652	CD1	LEU	D	35	48.209	59.979	31.203	1,00	52.95	C
ATOM	12653	CD2	LEU	D	35	48.671	62,134	30.073	1,00	59,28	C
ATOM	12654	O	GLY	D	36	52,909	60.663	25,882	1,00	61.27	0
ATOM	12655	N	GLY	D	36	50,522	59.660	26,765	1,00	62.39	N
ATOM	12656	CA	GLY	D	36	51.262	58,936	25.752	1,00	56,25	C
ATOM	12657	C	GLY	D	36	52.431	59.734	25.221	1.00	65.24	C
ATOM	12658	O	ASM	D	37	54,923	60.664	21,356	1,00	70.19	0
ATOM	12659	N	ASN	D	37	52.865	59,383	24.011	1,00	66,26	N
ATOM	12660	CA	ASN	D	37	54.114	59.866	23.452	1.00	61.12	C
ATOM	12661	C	ASM	D	37	53,988	60.648	22,152	1,00	67.25	C

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ATOM   12662   CB   ASN  D   37      55.056  58.677  23.225  1.00 68.73           C
ATOM   12663   CG   ASM  D   37      54.714  57.876  21.975  1.00 63.13           C
ATOM   12664   OD1  ASN  D   37      53.555  57.624  21.671  1.00 62.50           0
ATOM   12665   ND2  ASN  D   37      55.739  57.481  21.240  1.00 70.49           N
ATOM   12666   O    TH.R D   38      52.677  64.009  22.140  I.00 78.48           O
ATOM   12667   N    THR  D   38      52.845  61.289  21.923  1.00 67.43           N
ATOM   12668   CA   THR  D   38      52.657  62.079  20.703  1.00 70.61           C
ATOM   12669   C    TH.R D   38      52.485  63.571  21.006  I.00 74.67           C
ATOM   12670   CB   THR  D   38      51.437  61.595  19.904  1.00 74.38           C
ATOM   12671   OG1  THR  D   38      50.366  61.320  20.811  1.00 77.37           0
ATOM   12672   CG2  THR  D   38      51.761  60.331  19.155  I.00 70.23           C
ATOM   12673   O    ASP  D   39      50.357  67.038  21.508  1.00 76.69           0
ATOM   12674   N    ASP  D   39      52.113  64.342  19.988  1.00 76.60           N
ATOM   12675   CA   ASP  D   39      51.867  65.781  20.134  1.00 79.76           C
ATOM   12676   C    ASP  D   39      50.490  66.120  20.705  1.00 79.15           C
ATOM   12677   CB   ASP  D   39      52.010  66.476  18.784  1.00 83.99           C
ATOM   12678   CG   ASP  D   39      53.318  66.169  18.117  1.00 86.86           C
ATOM   12679   OD2  ASP  D   39      53.316  66.012  16.877  I.00 88.57           0
ATOM   12680   OD1  ASP  D   39      54.342  66.081  18.835  1.00 85.00           0
ATOM   12681   O    ARG  D   40      48.242  64.307  22.735  1.00 71.77           0
ATOM   12682   N    ARG  D   40      49.468  65.404  20.240  I.00 79.48           N
ATOM   12683   CA   ARG  D   40      48.108  65.580  20.723  1.00 72.69           C
ATOM   12684   C    ARG  D   40      48.101  65.420  22.224  1.00 72.50           C
ATOM   12685   CB   ARG  D   40      47.170  64.572  20.068  I.00 71.25           C
ATOM   12686   CG   ARG  D   40      45.696  64.900  20.182  1.00 73.01           C
ATOM   12687   CD   ARG  D   40      44.876  63.904  19.361  1.00 75.64           C
ATOM   12688   NE   ARG  D   40      43.662  64.491  18.795  I.00 76.72           N
ATOM   12689   CZ   ARG  D   40      42.865  63.872  17.925  1.00 73.73           C
ATOM   12690   NH1  ARG  D   40      43.132  62.640  17.504  1.00 67.45           N
ATOM   12691   NH2  ARG  D   40      41.792  64.492  17.468  1.00 77.55           N
ATOM   12692   O    HIS  D   41      46.562  66.584  26.252  1.00 64.20           O
ATOM   12693   N    HIS  D   41      47.963  66.543  22.924  1.00 68.49           N
ATOM   12694   CA   HIS  D   41      48.044  66.573  24.383  1.00 69.48           C
ATOM   12695   C    HIS  D   41      46.692  66.775  25.040  I.00 67.56           C
ATOM   12696   CB   HIS  D   41      48.995  67.675  24.850  1.00 75.64           C
ATOM   12697   CG   HIS  D   41      50.436  67.293  24.777  1.00 77.07           C
ATOM   12698   ND1  HIS  D   41      51.134  67.247  23.589  I.00 77.68           N
ATOM   12699   CD2  HIS  D   41      51.309  66.928  25.743  1.00 80.19           C
ATOM   127 00  CE1  HIS  D   41      52.379  66.875  23.827  1.00 80.87           C
ATOM   127 01  NE2  HIS  D   41      52.511  66.676  25.126  I.00 84.97           N
ATOM   12702   O    SEP. D   42      43.739  67.128  22.394  1.00 63.31           O
ATOM   127 03  N    SER  D   42      45.702  67.184  24.244  1.00 65.72           N
ATOM   12704   CA   SER  D   42      44.325  67.279  24.713  1.00 66.54           C
ATOM   12705   C    SER  D   42      43.365  67.038  23.560  1.00 61.94           C
ATOM   12706   CB   SER  D   42      44.049  68.645  25.363  1.00 71.60           C
ATOM   12707   OG   SER  D   42      43.286  69.479  24.504  1.00 73.78           0
ATOM   127 08  O    ILE  D   43      39.554  66.842  24.662  I.00 60.90           0
ATOM   12709   N    ILE  D   43      42.120  66.745  23.894  1.00 62.66           N
ATOM   12710   CA   ILE  D   43      41.118  66.449  22.888  1.00 61.40           C
ATOM   12711   C    ILE  D   43      39.750  66.851  23.446  I.00 57.70           C
ATOM   12712   CB   ILE  D   43      41.163  64.946  22.506  1.00 62.43           C
ATOM   12713   CGI  ILE  D   43      40.745  64.715  21.056  1.00 63.87           C
ATOM   12714   CG2  ILE  D   43      40.338  64.112  23.468  I.00 59.46           C
ATOM   12715   CD1  ILE  D   43      40.784  63.258  20.657  1.00 65.89           C
ATOM   12716   O    LYS  D   44      36.535  65.757  21.782  1.00 56.24           0
ATOM   12717   N    LYS  D   44      38.812  67.235  22.585  I.00 57.65           N
ATOM   12718   CA   LYS  D   44      37.471  67.549  23.084  1.00 60.97           C
ATOM   12719   C    LYS  D   44      36.518  66.391  22.839  1.00 56.50           C
ATOM   12720   CB   LYS  D   44      36.912  68.828  22.446  1.00 61.92           C
ATOM   12721   CG   LYS  D   44      35.648  69.347  23.130  1.00 59.13           C
ATOM   12722   CD   LYS  D   44      35.322  70.782  22.710  1.00 67.51           C
ATOM   12723   CE   LYS  D   44      36.389  71.776  23.141  1.00 65.40           C
ATOM   12724   NZ   LYS  D   44      36.340  72.000  24.613  I.00 69.48           N
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ATOM   12725   O    LYS  D   45       33..422   66.,109   25.,368   1,00  55..59         O
ATOM   12726   N    LYS  D   45       35,,680   66.. 110  23.,822   1,00  53..61         N
ATOM   12727   CA   LYS  D   45       34..727   65.,033   23.. 675  1 .00  54,.35        C
ATOM   12728   C    LYS  D   45       33..417   65.,416   24.,354   1,00  58..16         C
ATOM   12729   CB   LYS  D   45       35,301    63. 728   24.,261   1,00  58..60         C
ATOM   12730   CG   LYS  D   45       36..570   63.,242   23.. 549  1 .00  52,.31        C
ATOM   12731   CD   LYS  D   45       37.010    61.,860   23.. 949  1,00  63,.20        C
ATOM   127 32  CE   LYS  D   45       38.,139   61. 360   23.,029   1,00  60..30         C
ATOM   12733   NZ   LYS  D   45       39..281   60.,805   23.,813   1,00  61 .21         N
ATOM   12734   O    ASN  D   46       31..419   62.,960   25.. 432  1,00  60,.31         O
ATOM   12735   N    ASM  D   46       32.,296   64.. 972  23.,792   I,00  53..27         N
ATOM   12736   CA   ASN  D   46       31.,032   65.,121   24.,476   1,00  46..44         C
ATOM   12737   C    ASN  D   46       30. 890   64.,065   25. 546   1,00  50,.80         C
ATOM   12738   CB   ASN  D   46       29.,863   65.,042   23.,499   1,00  53..64         C
ATOM   12739   CG   ASN  D   46       29.,950   66.. 080  22.,409   1,00  56..15         C
ATOM   12740   OD1  ASN  D   46       30.. 209  67.,259   22.677    1.00  65,.82         0
ATOM   12741   ND2  ASN  D   46       29.,766   65.,650   21.,164   1,00  57.66          N
ATOM   12742   O    LEU  D   47       27.,816   62. 495   28.,249   1,00  46.,37         O
ATOM   12743   N    LEU  D   47       30.. 177  64.,415   26.. 597  1.00  51,.84         N
ATOM   12744   CA   LEU  D   47       29.. 938  63.,527   27.709    1,00  50,.14         C
ATOM   12745   C    LEU  D   47       28.,737   62. 645   27.,427   1,00  49..74         C
ATOM   12746   CB   LEU  D   47       29.,737   64.,332   28.,983   1,00  58..35         C
ATOM   12747   CG   LEU  D   47       31.. 014  64.,769   29.. 702  1,00  62,.88         C
ATOM   12748   CD1  LEU  D   47       32.,194   65.. 065  28.,771   I,00  59..47         C
ATOM   12749   CD2  LEU  D   47       30.,662   65.,981   30.,494   1,00  57.83          C
ATOM   12750   O    ILE  D   48       29. 484   59.,950   24.537    1,00  48,.88         0
ATOM   12751   N    ILE  D   48       28.,755   62.. 075  26.,234   I,00  48..32         N
ATOM   12752   CA   ILE  D   48       27.,785   61.. 067  25.,860   1,00  53..35         C
ATOM   12753   C    ILE  D   48       28. 504   59.,823   25. 286   1,00  50,.09         C
ATOM   12754   CB   ILE  D   48       26.,781   61.,633   24.,845   1,00  46..99         C
ATOM   12755   CGI  ILE  D   48       25.,709   60.. 601  24.,530   1,00  51 .19         C
ATOM   12756   CG2  ILE  D   48       27.488    62.,088   23.. 576  1.00  47,.03         C
ATOM   12757   CD1  ILE  D   48       24.,304   61.,172   24.,553   1,00  48..79         C
ATOM   12758   O    GLY  D   49       26.,919   55. 974   25,943    1,00  42.75          0
ATOM   12759   N    GLY  D   49       28.. 035  58.,626   25.638    1.00  47,.28         N
ATOM   12760   CA   GLY  D   49       28.. 595  57.,433   25.. 015  1,00  49,,22         C
ATOM   127 61  C    GLY  D   49       28.,000   56. 081   25,352    1,00  43..09         C
ATOM   12762   O    ALA  D   50       30.,389   52.,617   24.,448   1,00  44.58          0
ATOM   12763   N    ALA  D   50       28. 735   55.,034   24.979    1,00  46,.17         N
ATOM   12764   CA   ALA  D   50       28.,338   53.. 653  25.,280   I,00  48..45         C
ATOM   12765   C    ALA  D   50       29.,524   52.. 661  25.,338   1,00  45..63         C
ATOM   12766   CB   ALA  D   50       27.306    53.,178   24.259    1,00  45,.79         C
ATOM   12767   O    LEU  D   51       28.,781   49.,083   26.,366   1,00  41.79          0
ATOM   12768   N    LEU  D   51       29.,550   51.. 869  26.,399   1,00  40..70         N
ATOM   12769   CA   LEU  D   51       30.. 489  50.,763   26.. 497  1.00  45,.03         C
ATOM   12770   C    LEU  D   51       29.,845   49.,496   25.,911   1,00  42.02          C
ATOM   127 71  CB   LEU  D   51       30.,906   50. 565   27.,958   1,00  38..76         C
ATOM   12772   CG   LEU  D   51       31.. 853  49.,463   28.. .394 1.00  4.3,.77        C
ATOM   12773   CD1  LEU  D   51       33.. 312  49.,769   28.. 004  1,00  43,.97         C
ATOM   127 74  CD2  LEU  D   51       31.,697   49. 233   29.,896   1,00  40..54         C
ATOM   12775   O    LEU  D   52       32.,208   46.,491   24..608   1,00  49..19         0
ATOM   12776   N    LEU  D   52       30.. 471  48.,919   24.886    1,00  42,.04         N
ATOM   127 77  CA   LEU  D   52       30.,055   47.613    24.,330   I,00  44.00          C
ATOM   12778   C    LEU  D   52       30.,977   46.,440   24.,766   1,00  48..27         C
ATOM   12779   CB   LEU  D   52       30. 014   47,684    22.802    1,00  42,.42         C
ATOM   12780   CG   LEU  D   52       29.,292   48.. 895  22.,175   I,00  38..86         C
ATOM   12781   CD1  LEU  D   52       29.,312   48.. 808  20.,669   1,00  37.95          C
ATOM   12782   CD2  LEU  D   52       27.887    48.,899   22.623    1,00  39,.43         C
ATOM   12783   O    PHE  D   53       29.,412   42.,733   25.,342   1,00  38..65         0
ATOM   12784   N    PHE  D   53       30.,395   45.. 381  25.,316   1,00  44.63          N
ATOM   12785   CA   PHE  D   53       31.. 213  44,284    25.819    1.00  44,.19         C
ATOM   12786   C    PHE  D   53       30.,640   42.,905   25.,498   1,00  46..52         C
ATOM   127 87  CB   PHE  D   53       31.,391   44.399    27.,329   1,00  44.52          C
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ATOM	12788	CG	PHE	D	53	30.094	44.424	28.080	1.00	45.62	C
ATOM	12789	GDI	PHE	D	53	29,481	45.629	28,387	1,00	49.12	C
ATOM	12790	CD2	PHE	D	53	29.475	43,250	28.457	1,00	45,14	C
ATOM	12791	CE1	PHE	D	53	28.263	45,655	29.081	1.00	49.48	C
ATOM	12792	CE2	PHE	D	53	28,265	43.269	29,145	1,00	49.58	C
ATOM	12793	CZ	PHE	D	53	27.667	44,469	29.460	1,00	45,93	C
ATOM	12794	O	ASP	D	54	31.051	40,253	27.564	1,00	43,76	0
ATOM	12795	N	ASP	D	54	31,546	41.929	25,413	1,00	44.85	N
ATOM	12796	CA	ASP	D	54	31.180	40,519	25,188	1,00	41.89	C
ATOM	12797	C	ASP	D	54	30.585	39,940	26.463	1,00	46,07	C
ATOM	12798	CB	ASP	D	54	.32,387	39.710	24,753	1,00	39.05	C
ATOM	12799	CG	ASP	D	54	32.900	40.098	23,389	1,00	47.82	C
ATOM	12800	OD1	ASP	D	54	32.145	40,660	22.554	1,00	51,50	0
ATOM	12801	OD2	ASP	D	54	34.087	39,845	23,147	1.00	50.65	0
ATOM	12802	O	SEP.	D	55	30,664	37.148	28,116	1,00	48.48	0
ATOM	12803	N	SEP.	D	55	29.545	39,126	26.295	1,00	43,71	N
ATOM	12804	CA	SER	D	55	28.805	38,496	27.393	1.00	45.85	C
ATOM	12805	C	SER	D	55	29,633	37.741	28.433	1,00	49.62	C
ATOM	12806	CB	SER	D	55	27.790	37,515	26.815	1,00	42,86	C
ATOM	12807	OG	SER	D	55	27.022	38,138	25.789	1,00	50,57	0
ATOM	12808	O	GLY	D	56	28,313	35.200	29,825	1,00	50.68	0
ATOM	12809	N	GLY	D	56	29.168	37,758	29,681	1,00	50.02	N
ATOM	12810	CA	GLY	D	56	29.745	36,910	30.705	1,00	50,32	C
ATOM	12811	C	GLY	D	56	29,315	35.462	30,492	1,00	53.09	C
ATOM	12812	O	GLU	D	57	29.701	33.071	33,416	1,00	36.75	0
ATOM	12813	N	GUI	D	57	30.057	34,510	31.057	1,00	49,33	N
ATOM	12814	CA	GLU	D	57	29,597	33.125	31,037	1,00	42.37	C
ATOM	12815	C	GLU	D	57	29,216	32.615	32,413	1,00	37.19	C
ATOM	12816	CB	GLU	D	57	30.664	32,233	30.423	1,00	41,93	C
ATOM	12817	CG	GLU	D	57	31,192	32,822	29,179	1.00	47.32	C
ATOM	12818	CD	GLU	D	57	32,290	32.016	28,582	1,00	56.26	C
ATOM	12819	OE1	GLU	D	57	31.967	31,035	27.884	1.00	64,74	0
ATOM	12820	OE2	GLU	D	57	33.469	32,367	28.804	1,00	59.82	0
ATOM	12821	O	TH.R	D	58	30,242	29.939	33,394	1,00	37.94	0
ATOM	12822	N	THR	D	58	28..349	31,626	32.433	1.00	41.55	N
ATOM	12823	CA	THR	D	58	28.042	30,902	33.646	1,00	41,49	C
ATOM	12824	C	TH.R	D	58	29,234	30.034	34,101	1,00	42.87	C
ATOM	12825	CB	THR	D	58	26,794	30,037	33.436	1,00	50.51	C
ATOM	12826	OG1	THR	D	58	27.067	29,030	32.455	1,00	41,67	0
ATOM	12827	CG2	THR	D	58	25,605	30.931	.32,965	1,00	33.17	C
ATOM	12828	O	ALA	D	59	30,983	26.465	36,068	1,00	41.83	0
ATOM	12829	N	ALA	D	59	29.102	29,451	35.295	1,00	40,01	N
ATOM	12830	CA	ALA	D	59	30.165	28.722	35,973	1.00	34.60	C
ATOM	12831	C	ALA	D	59	30,069	27.213	35,721	1,00	43.94	C
ATOM	12832	CB	ALA	D	59	30.124	28,994	37.456	1.00	34,71	C
ATOM	12833	O	GLU	D	60	30.026	23,503	34.746	1.00	45.13	0
ATOM	12834	N	GLU	D	60	28,957	26.804	35,105	1,00	44.88	N
ATOM	12835	CA	GLU	D	60	28.588	25,419	34.892	1.00	40,58	C
ATOM	12836	C	GLU	D	60	29.664	24,565	34.229	1,00	43,23	C
ATOM	12837	CB	GLU	D	60	27,319	25.339	34,054	1,00	40.99	C
ATOM	12838	CG	GLU	D	60	27,035	23.929	33,597	1,00	45.07	C
ATOM	12839	CD	GLU	D	60	25.588	23,660	33.284	1,00	57,51	C
ATOM	12840	OE1	GLU	D	60	25,334	22.712	.32,509	1,00	67.87	0
ATOM	12841	OE2	GLU	D	60	24,702	24.368	33,814	1,00	68.15	0
ATOM	12842	N	ALA	D	61	30.150	25,024	33.081	1,00	41,46	N
ATOM	12843	CA	ALA	D	61	31,171	24.326	.32,332	1,00	38.07	C
ATOM	12844	C	ALA	D	61	32,439	24.161	33,187	1,00	41.43	C
ATOM	12845	O	ALA	D	61	33.067	23,104	33.196	1,00	46,25	0
ATOM	12846	CB	ALA	D	61	31,481	25,064	31.042	1.00	28.44	C
ATOM	12847	N	THR	D	62	32,790	25.208	33,925	1,00	48.39	N
ATOM	12848	CA	THR	D	62	33.954	25,186	34.781	1.00	39,59	C
ATOM	12849	C	THR	D	62	33.748	24,102	35.832	1.00	40.96	C
ATOM	12850	O	TH.R	D	62	34,688	23.364	36,156	1,00	43.87	0

ATOM	12851	CB	THR	D	62	34.199	26.587	35.391	1.00	41.46	C
ATOM	12852	OG1	THR	D	62	34,582	27.473	34,342	1,00	37.74	O
ATOM	12853	CG2	THR	D	62	35.302	26,598	36.444	1.00	34,22	C
ATOM	12854	N	ARG	D	63	32.496	23.933	36,261	1.00	39.53	N
ATOM	12855	CA.	ARG	D	63	32,105	22.990	37,314	1,00	39.73	C
ATOM	12856	C	ARG	D	63	32.167	21,504	36.866	1.00	45,30	C
ATOM	12857	O	ARG	D	63	32.654	20,643	37.610	1,00	45,60	O
ATOM	12858	CB	ARG	D	63	30,678	23.281	37,831	1,00	35.94	C
ATOM	12859	CG	ARG	D	63	30.313	22,505	39.101	1,00	38.96	C
ATOM	12860	CD	ARG	D	63	28.904	22,745	39.672	1,00	41,56	C
ATOM	12861	NE	ARG	D	63	27,826	22.437	38,733	1,00	41.03	N
ATOM	12862	CZ	ARG	D	63	27.069	23.367	38.135	1,00	47.70	C
ATOM	12863	NH1	ARG	D	63	26.127	22,995	37.279	1,00	49,29	N
ATOM	12864	NH2	ARG	D	63	27.249	24.666	38,383	1.00	34.95	N
ATOM	12865	N	LEU	D	64	31,615	21.210	35,692	1,00	40.47	N
ATOM	12866	CA	LEU	D	64	31.530	19,846	35.228	1.00	38,25	C
ATOM	12867	C	LEU	D	64	32.946	19.351	34.977	1,00	40.32	C
ATOM	12868	O	LEU	D	64	33,256	18.220	35,302	1,00	44.41	O
ATOM	12869	CB	LEU	D	64	30.684	19,732	33.959	1.00	40,90	C
ATOM	12870	CG	LEU	D	64	29.191	20,020	34.074	1,00	49,60	C
ATOM	12871	CD1	LEU	D	64	28,542	19.931	32,707	1,00	48.62	C
ATOM	12872	CD2	LEU	D	64	28.506	19,087	35.070	1,00	36.18	C
ATOM	12873	N	LYS	D	65	33.801	20,213	34.433	1,00	38,10	N
ATOM	12874	CA	LYS	D	65	35,214	19.878	34,308	1,00	38.64	C
ATOM	12875	C	LYS	D	65	35.893	19.753	35.650	1,00	41.01	C
ATOM	12876	O	LYS	D	65	36.729	18,875	35.824	1,00	53,02	O
ATOM	12877	CB	LYS	D	65	35,958	20.889	33,444	1,00	32.94	C
ATOM	12878	CG	LYS	D	65	35,460	20.801	32,038	1,00	38.82	C
ATOM	12879	CD	LYS	D	65	35.935	21,896	31.151	1,00	48,34	C
ATOM	12880	CE	LYS	D	65	35,213	21.792	29.807	1.00	46.80	C
ATOM	12881	NZ	LYS	D	65	35,745	22.798	28,869	1,00	55.82	N
ATOM	12882	N	ARG	D	66	35.509	20,561	36.625	1.00	42,22	N
ATOM	12883	CA	ARG	D	66	36.201	20.495	37,905	1,00	41.55	C
ATOM	12884	C	ARG	D	66	35,944	19.160	38,556	1,00	40.82	C
ATOM	12885	O	ARG	D	66	36.856	18,564	39.128	1.00	46,13	O
ATOM	12886	CB	ARG	D	66	35.778	21,631	38.841	1,00	36,06	C
ATOM	12887	CG	ARG	D	66	36,087	21.454	40,341	1,00	33.23	C
ATOM	12888	CD	ARG	D	66	35.176	22,431	41.196	1,00	43.84	C
ATOM	12889	NE	ARG	D	66	35.059	23,728	40.541	1,00	44,44	N
ATOM	12890	CZ	ARG	D	66	33,932	24.383	40,313	1,00	41.28	C
ATOM	12891	NH1	ARG	D	66	34,004	25.527	39,680	1,00	52.65	N
ATOM	12892	NH2	ARG	D	66	32.752	23,931	40.735	1,00	45,67	N
ATOM	12893	N	THR	D	67	34,707	18.697	38,477	1.00	38.33	N
ATOM	12894	CA	THR	D	67	34,345	17.482	39,170	1,00	41.57	C
ATOM	12895	C	THR	D	67	34.857	16,277	38.363	1.00	43,79	C
ATOM	12896	O	THR	D	67	35.186	15,249	38.933	1.00	39.76	O
ATOM	12897	CB	THR	D	67	32,826	17.333	39,387	1,00	38.35	C
ATOM	12898	OG1	THR	D	67	32.182	17,350	38.127	1,00	42,68	O
ATOM	12899	CG2	THR	D	67	32.263	18,431	40.315	1,00	35,95	C
ATOM	12900	N	ALA	D	68	34,928	16.420	37,046	1,00	40.45	N
ATOM	12901	CA	ALA	D	68	35.493	15,358	36.210	1,00	43.29	C
ATOM	12902	C	ALA	D	68	36.984	15,206	36.522	1,00	41,61	C
ATOM	12903	0	ALA	D	68	37,483	14.103	36,616	1,00	48.81	0
ATOM	12904	CB	ALA	D	68	35.268	15.652	34.704	1,00	39.51	C
ATOM	12905	N	ARG	D	69	37.684	16,319	36.726	1,00	47,02	N
ATOM	12906	CA	ARG	D	69	39,074	16.267	37,160	1,00	39.78	C
ATOM	12907	C	ARG	D	69	39,202	15.486	38,424	1,00	42.39	C
ATOM	12908	O	ARG	D	69	40.088	14,620	38.551	1,00	44,90	O
ATOM	12909	CB	ARG	D	69	39,623	17.630	37,420	1.00	38.21	C
ATOM	12910	CG	ARG	D	69	40,235	18.261	36,281	1,00	37.85	C
ATOM	12911	CD	ARG	D	69	40.930	19,453	36.818	1.00	40,98	C
ATOM	12912	NE	ARG	D	69	40.554	20.564	35.987	1.00	58.52	N
ATOM	12913	CZ	ARG	D	69	39,824	21.604	36,369	1,00	42.23	C

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ATOM   12914  NH1  ARG  D  69     39.427  21.744  37.625  1.00  47.75      N
ATOM   12915  NH2  ARG  D  69     39,554  22.514  35,473  1,00  40.34      N
ATOM   12916  N    ARG  D  70     38.299  15,768  39.360  1,00  37,78      N
ATOM   12917  CA   ARG  D  70     38.384  15,073  40.626  1.00  41.42      C
ATOM   12918  C    ARG  D  70     38,267  13.576  40,401  1,00  44.22      C
ATOM   12919  O    ARG  D  70     38.902  12,768  41.086  1,00  38,40      O
ATOM   12920  CB   ARG  D  70     37.322  15.530  41.613  1,00  34,40      C
ATOM   12921  CG   ARG  D  70     37,693  16.856  42,222  1,00  40.20      C
ATOM   12922  CD   ARG  D  70     36.752  17,275  43,347  1,00  42.67      C
ATOM   12923  NE   ARG  D  70     36.961  18,686  43.659  1,00  39,51      N
ATOM   12924  CZ   ARG  D  70     36,003  19.618  43,642  1,00  38.15      C
ATOM   12925  NH1  ARG  D  70     34.746  19.307  43,357  1,00  36.22      N
ATOM   12926  NH2  ARG  D  70     36.321  20,870  43.915  1,00  42,35      N
ATOM   12927  N    ARG  D  71     37.436  13.216  39,440  1.00  42.28      N
ATOM   12928  CA   ARG  D  71     37,030  11.847  39,361  1,00  43.26      C
ATOM   12929  C    ARG  D  71     38.054  10,993  38.586  1,00  43,58      C
ATOM   12930  O    ARG  D  71     38.238   9.850  38,921  1.00  48.91      0
ATOM   12931  CB   ARG  D  71     35,631  11.776  38,785  1,00  41.78      C
ATOM   12932  CG   ARG  D  71     34.607  11,945  39.874  1,00  38,08      C
ATOM   12933  CD   ARG  D  71     33.249  11,517  39.406  1,00  40,42      C
ATOM   12934  NE   ARG  D  71     32,842  12.318  38,264  1,00  44.16      N
ATOM   12935  CZ   ARG  D  71     32.221  11.822  37,201  1,00  54.38      C
ATOM   12936  NH1  ARG  D  71     31.885  12,631  36.197  1,00  49,01      N
ATOM   12937  NH2  ARG  D  71     31,941  10.513  37,144  1,00  49.02      N
ATOM   12938  N    TYR  D  72     38.744  11.562  37,603  1,00  44.09      N
ATOM   12939  CA   TYR  D  72     39.906  10,907  37.031  1,00  40,50      C
ATOM   12940  C    TYR  D  72     40,992  10.709  38,089  1,00  48.20      C
ATOM   12941  O    TYR  D  72     41,729   9.718  38,070  1,00  55.99      O
ATOM   12942  CB   TYR  D  72     40.466  11,698  35.863  1,00  37,94      C
ATOM   12943  CG   TYR  D  72     39.645  11.549  34,611  1.00  44.67      C
ATOM   12944  CD1  TYR  D  72     39,188  10.304  34,202  1,00  41.77      C
ATOM   12945  CD2  TYR  D  72     39.306  12,660  33.839  1,00  44,51      C
ATOM   12946  CE1  TYR  D  72     38.413  10.174  33,071  1.00  37.92      C
ATOM   12947  CE2  TYR  D  72     38,555  12.529  32,700  1,00  43.72      C
ATOM   12948  CZ   TYR  D  72     38.117  11,283  32.318  1,00  38,96      C
ATOM   12949  OH   TYR  D  72     37.361  11,177  31.188  1,00  42,06      0
ATOM   12950  N    TH.R D  73     41,091  11.642  39,023  1,00  49.57      N
ATOM   12951  CA   THR  D  73     42.121  11,552  40,035  1,00  44.24      C
ATOM   12952  C    THR  D  73     41.821  10,378  40.971  1,00  45,96      C
ATOM   12953  O    THR  D  73     42,715   9.618  41,359  1,00  46.51      0
ATOM   12954  CB   THR  D  73     42,240  12.879  40,819  1,00  44.70      C
ATOM   12955  OG1  THR  D  73     43.290  13,664  40.252  1,00  41,85      0
ATOM   12956  CG2  THR  D  73     42,570  12.637  42,307  1.00  47.95      C
ATOM   12957  N    ARG  D  74     40,552  10.227  41,313  1,00  39.82      N
ATOM   12958  C    ARG  D  74     40.096   7,811  41.612  1,00  45,53      C
ATOM   12959  CA   ARG  D  74     40.144   9,215  42,256  1.00  41.66      C
ATOM   12960  O    ARG  D  74     40,358   6.829  42,289  1,00  49.25      0
ATOM   12961  CB   ARG  D  74     38.783   9,594  42.878  1,00  36,61      C
ATOM   12962  CG   ARG  D  74     38.881  10,821  43.854  1,00  45,99      C
ATOM   12963  CD   ARG  D  74     37,510  11.524  44,177  1,00  43.49      C
ATOM   12964  ME   ARG  D  74     37.625  12,743  44,995  1,00  38.74      N
ATOM   12965  CZ   ARG  D  74     36.636  13,633  45.148  1,00  44,12      C
ATOM   12966  NH1  ARG  D  74     35,457  13.440  44,574  1,00  38.10      N
ATOM   12967  NH2  ARG  D  74     36.813  14.720  45,883  1,00  41.17      N
ATOM   12968  N    ARG  D  75     39.745   7,716  40.332  1,00  40,27      N
ATOM   12969  C    ARG  D  75     41,148   5.888  39,614  1,00  49.20      C
ATOM   12970  CA   ARG  D  75     39,708   6.433  39,659  1,00  45.23      C
ATOM   12971  O    ARG  D  75     41.403   4,740  39.965  1,00  46,69      0
ATOM   12972  CB   ARG  D  75     39,125   6,552  38,249  1.00  41.55      C
ATOM   12973  CG   ARG  D  75     38,952   5.222  37,562  1,00  37.06      C
ATOM   12974  CD   ARG  D  75     38.546   5,344  36.102  1.00  37,57      C
ATOM   12975  NE   ARG  D  75     39.609   5,862  35.253  1.00  31.75      N
ATOM   12976  CZ   ARG  D  75     39,456   6.097  33,958  1,00  39.38      C
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ATOM	12977	NH1	ARG	D	75	38.266	5.874	33.389	1.00	32.17	N
ATOM	12978	NH2	ARG	D	75	40.481	6.567	33.245	1.00	28.95	N
ATOM	12979	N	LYS	D	76	42.071	6.756	39.213	1.00	46.52	K
ATOM	12980	C	LYS	D	76	43.933	6.011	40.603	1.00	49.62	C
ATOM	12981	CA.	LYS	D	76	43.492	6.472	39.218	I.00	47.21	C
ATOM	12982	O	LYS	D	76	44.737	5.110	40.718	1.00	56.56	O
ATOM	12983	CB	LYS	D	76	44.281	7.709	38.756	1.00	45.09	C
ATOM	12984	CG	LYS	D	76	45.775	7.648	38.980	I.00	46.29	C
ATOM	12985	CD	LYS	D	76	46.571	8.208	37.787	1.00	46.70	C
ATOM	12986	CE	LYS	D	76	46.137	9.631	37.361	1.00	54.55	C
ATOM	12987	NZ	LYS	D	76	46.962	10.245	36.218	I.00	48.81	N
ATOM	12988	N	ASN	D	77	43.371	6.582	41.657	1.00	51.34	K
ATOM	12989	C	ASN	D	77	43.255	4.845	43.467	1.00	50.64	C
ATOM	12990	CA	ASN	D	77	43.777	6.216	43.017	1.00	50.27	C
ATOM	12991	O	ASM	D	77	43.897	4.163	44.263	1.00	50.90	0
ATOM	12992	CB	ASN	D	77	43.330	7.282	44.026	1.00	39.75	C
ATOM	12993	CG	ASN	D	77	44.215	8.522	44.002	1.00	49.42	C
ATOM	12994	OD1	ASN	D	77	45.354	8.475	43.522	I.00	53.72	0
ATOM	12995	KD2	ASK	D	77	43.693	9.648	44.517	1.00	43.77	K
ATOM	12996	N	ARG	D	78	42.075	4.473	42.995	1.00	48.35	N
ATOM	12997	C	ARG	D	78	42.524	2.063	42.740	I.00	47.63	C
ATOM	12998	CA	ARG	D	78	41.542	3.137	43.224	1.00	50.85	C
ATOM	12999	O	ARG	D	78	42.745	1.041	43.389	1.00	50.20	0
ATOM	13000	CB	ARG	D	78	40.218	2.963	42.489	I.00	48.49	C
ATOM	13001	CG	ARG	D	78	38.996	3.581	43.137	1.00	42.68	C
ATOM	13002	CD	ARG	D	78	37.725	2.953	42.529	1.00	44.10	C
ATOM	13003	NE	ARG	D	78	36.744	3.978	42.233	I.00	58.52	N
ATOM	13004	CZ	ARG	D	78	36.342	4.336	41.017	1.00	55.48	C
ATOM	13005	NH1	ARG	D	78	36.800	3.726	39.935	1.00	48.60	N
ATOM	13006	NH2	ARG	D	78	35.441	5.308	40.897	1.00	57.45	N
ATOM	13007	N	ILE	D	79	43.102	2.332	41.583	1.00	43.71	N
ATOM	13008	C	ILE	D	79	45.311	1.345	41.646	1.00	57.33	C
ATOM	13009	CA	ILE	D	79	43.980	1.414	40.892	1.00	51.35	C
ATOM	13010	O	ILE	D	79	45.914	0.266	41.795	I.00	53.08	0
ATOM	13011	CB	ILE	D	79	44.166	1.861	39.418	1.00	51.59	C
ATOM	13012	CGI	ILE	D	79	42.899	1.547	38.630	1.00	51.10	C
ATOM	13013	CG2	ILE	D	79	45.362	1.210	38.755	I.00	46.93	C
ATOM	13014	CD1	ILE	D	79	42.437	0.105	38.789	1.00	55.91	C
ATOM	13015	N	LEU	D	80	45.740	2.498	42.147	1.00	51.17	N
ATOM	13016	C	LEU	D	80	46.693	1.807	44.268	I.00	55.54	C
ATOM	13017	CA	LEU	D	80	46.926	2.566	42.961	1.00	49.16	C
ATOM	13018	O	LEU	D	80	47.590	1.128	44.759	1.00	52.61	0
ATOM	13019	CB	LEU	D	80	47.313	4.011	43.238	1.00	47.75	C
ATOM	13020	CG	LEU	D	80	47.856	4.847	42.075	1.00	51.22	C
ATOM	13021	CD1	LEU	D	80	48.091	6.315	42.511	1.00	50.92	C
ATOM	13022	CD2	LEU	D	80	49.122	4.254	41.503	1.00	48.52	C
ATOM	13023	N	TYR	D	81	45.495	1.902	44.836	I.00	53.84	N
ATOM	13024	C	TYR	D	81	45.373	-0.326	45.862	1.00	58.62	C
ATOM	13025	CA	TYR	D	81	45.252	1.190	46.083	1.00	55.78	C
ATOM	13026	O	TYR	D	81	45.967	-1.034	46.664	I.00	59.40	0
ATOM	13027	CB	TYR	D	81	43.887	1.501	46.645	1.00	56.85	C
ATOM	13028	CG	TYR	D	81	43.673	2.905	47.167	1.00	61.72	C
ATOM	13029	CD1	TYR	D	81	44.678	3.600	47.835	I.00	64.68	C
ATOM	13030	CD2	TYR	D	81	42.443	3.528	47.003	1.00	55.02	C
ATOM	13031	CE1	TYR	D	81	44.455	4.897	48.314	1.00	60.75	C
ATOM	13032	CE2	TYR	D	81	42.216	4.801	47.463	I.00	57.97	C
ATOM	13033	CZ	TYR	D	81	43.206	5.486	48.113	1.00	60.45	C
ATOM	13034	OH	TYR	D	81	42.913	6.754	48.563	1.00	58.50	0
ATOM	13035	N	LEU	D	82	44.796	-0.803	44.767	1.00	54.05	N
ATOM	13036	C	LEU	D	82	46.358	--2.611	44.069	1.00	56.89	C
ATOM	13037	CA	LEU	D	82	44.905	-2.193	44.367	1.00	56.17	C
ATOM	13038	O	LEU	D	82	46.812	-3.642	44.538	1.00	58.35	0
ATOM	13039	CB	LEU	D	82	44.039	-2.447	43.149	I.00	50.58	C

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ATOM  13040  CG   LEU  D  82    43.890   -3.896   42.728   1.00  53.60   c
ATOM  13041  GDI  LEU  D  82    43.147   -4.651   43.821   1.00  48.41   c
ATOM  13042  CD2  LEU  D  82    43.169   -3.976   41..380  1.00  49.69   c
ATOM  13043  N    GLN  D  83    47.082   -1.805   43.300   1.00  57.39   N
ATOM  13044  C    GLN  D  83    49.321   -2.088   44.291   I.00  61.56   C
ATOM  13045  CA   GLN  D  83    48.475   -2.089   43.016   1.00  51.96   C
ATOM  13046  O    GLN  D  83    50.380   -2.717   44.343   1.00  62.34   O
ATOM  13047  CB   GLN  D  83    49.035   -1.088   42.015   I.00  48.08   c
ATOM  13048  CG   GLN  D  83    48.457   -1.263   40.623   1.00  50.58   c
ATOM  13049  CD   GLN  D  83    49.193   -0.458   39.586   1.00  52.48   c
ATOM  13050  OE1  GLN  D  83    50.220    0.144   39.885   I.00  57.79   0
ATOM  13051  ME 2 GLN  D  83    48.682   -0.444   38.354   1.00  50.32   N
ATOM  13052  N    GLU  D  84    48.851   -1.392   45.323   1.00  62.86   N
ATOM  13053  c    GLU  D  84    49.428   -2.690   47.330   1.00  63.21   c
ATOM  13054  CA   GLU  D  84    49.569   -1.354   46.598   1.00  63.80   C
ATOM  13055  O    GLU  D  84    50.400   -3.230   47.866   1.00  57.02   O
ATOM  13056  CB   GLU  D  84    49.065   -0.212   47.489   1.00  58.09   c
ATOM  13057  CG   GLU  D  84    49.984    0.101   48.671   I.00  68.93   c
ATOM  13058  CD   GLU  D  84    49.300    0.893   49.791   1.00  84.61   c
ATOM  13059  OE1  GLU  D  84    48.157    1.377   49.584   1.00  86.87   0
ATOM  13060  OE2  GLU  D  84    49.912    1.027   50.882   I.00  80.22   0
ATOM  13061  N    ILE  D  85    48.196   -3.188   47.355   1.00  58.31   N
ATOM  13062  c    ILE  D  85    48.578   -5.612   47.093   1.00  60.13   c
ATOM  13063  CA   ILE  D  85    47.879   -4.493   47.894   I.00  58.87   C
ATOM  13064  O    ILE  D  85    48.831   -6.681   47.618   1.00  64.28   O
ATOM  13065  CB   ILE  D  85    46.349   -4.699   47.908   1.00  58.25   C
ATOM  13066  CGI  ILE  D  85    45.716   -3.771   48.940   I.00  54.86   c
ATOM  13067  CG2  ILE  D  85    45.962   -6.147   48.184   1.00  53.01   c
ATOM  13068  CD1  ILE  D  85    44.252   -4.062   49.227   1.00  59.29   c
ATOM  13069  O    PHE  D  86    51.672   -7.436   44.754   1.00  66.98   0
ATOM  13070  N    PHE  D  86    48.937   -5.351   45.841   1.00  62.45   N
ATOM  13071  CA   PHE  D  86    49.543   -6.402   45.017   1.00  64.33   C
ATOM  13072  c    PHE  D  86    51.072   -6.391   44.961   1.00  58.05   c
ATOM  13073  CB   PHE  D  86    48.987   -6.339   43.581   I.00  54.45   c
ATOM  13074  CG   PHE  D  86    47.850   -7.284   43..349  1.00  59.50   c
ATOM  13075  CD2  PHE  D  86    47.975   -8.339   42.451   1.00  55.67   c
ATOM  13076  CD1  PHE  D  86    46.654   -7.137   44.044   I.00  54.85   c
ATOM  13077  CE2  PHE  D  86    46.919   -9.223   42.249   1.00  52.34   c
ATOM  13078  CE1  PHE  D  86    45.606   -8.025   43.843   1.00  54.31   c
ATOM  13079  CZ   PHE  D  86    45.742   -9.067   42.950   I.00  51.50   c
ATOM  13080  O    SEP. D  87    55.109   -6.307   44.656   1.00  65.20   0
ATOM  13081  N    SER  D  87    51.691   -5.232   45.168   1.00  53.89   N
ATOM  13082  CA   SER  D  87    53.095   -4.998   44.799   1.00  58.51   c
ATOM  13083  C    SER  D  87    54.150   -5.981   45.356   1.00  68.31   c
ATOM  13084  CB   SER  D  87    53.511   -3.587   45.209   1.00  59.59   c
ATOM  13085  OG   SER  D  87    53.293   -3.390   46.594   1.00  67.63   0
ATOM  13086  O    ASN  D  88    55.751   -9.039   45.635   I.00  66.13   0
ATOM  13087  N    ASN  D  88    53.997   -6.421   46.602   1.00  61.20   N
ATOM  13088  CA   ASN  D  88    54.951   -7.353   47.176   1.00  69.69   c
ATOM  13089  C    ASN  D  88    54.869   -8.704   46.456   I.00  70.08   c
ATOM  13090  CB   ASN  D  88    54.711   -7.521   48.678   1.00  74.70   c
ATOM  13091  O    GLU  D  89    54.359  --11.590   44.023   1.00  72.63   0
ATOM  13092  N    GLU  D  89    53.798   -9.449   46.741   I.00  66.07   N
ATOM  13093  CA   GLU  D  89    53.545  -10.730   46.094   1.00  64.33   c
ATOM  13094  C    GLU  D  89    53.791  -10.665   44.595   1.00  67.05   c
ATOM  13095  CB   GLU  D  89    52.123  -11.206   46.379   I.00  59.49   c
ATOM  13096  CG   GLU  D  89    51.958  -11.897   47.731   1.00  69.36   c
ATOM  13097  CD   GLU  D  89    52.474  -13.357   47.743   1.00  75.89   c
ATOM  13098  OE1  GLU  D  89    53.663  -13.574   47.408   1.00  67.93   0
ATOM  13099  OE2  GLU  D  89    51.684  -14.285   48.079   1.00  69.21   0
ATOM  13100  O    MET  D  90    55.341  -10.174   41.139   1.00  66.32   0
ATOM  13101  N    MET  D  90    53.418   -y.551   43.970   1.00  73.74   N
ATOM  13102  CA.  MET  D  90    53.582   -9.406   42.521   I.00  71.10   C
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ATOM   13103  c    MET D  90      55.026  -9.472  42.091  1.00 63.39           c
ATOM   13104  CB   MET D  90      52.986  -8.090  42.013  1.00 66.27           c
ATOM   13105  CG   MET D  90      53.004  -7.971  40.486  1.00 60.26           c
ATOM   13106  SD   MET D  90      51.855  -9.143  39.717  1.00 70.43           s
ATOM   13107  CE   MET D  90      52.938  -9.833  38.512  1.00 64.04           c
ATOM   13108  O    ALA D  91      58.921 -10.299  41.664  1.00 64.24           0
ATOM   13109  N    ALA D  91      55.886  -8.739  42.793  1.00 58.61           N
ATOM   13110  CA.  ALA D  91      57.315  -8.668  42.474  1.00 66.75           C
ATOM   13111  C    ALA D  91      57.994 -10.063  42.443  1.00 67.73           C
ATOM   13112  CB   ALA D  91      58.015  -7.763  43.469  1.00 59.32           c
ATOM   13113  O    LYS D  92      58.640 -13.612  41.391  1.00 66.20           0
ATOM   13114  N    LYS D  92      57.513 -10.967  43.293  1.00 63.57           N
ATOM   13115  CA   LYS D  92      57.969 -12.353  43.320  1.00 68.74           c
ATOM   13116  c    LYS D  92      57.723 -13.029  41.974  1.00 69.66           c
ATOM   13117  CB   LYS D  92      57.261 -13.121  44.443  1.00 67.25           c
ATOM   13118  CG   LYS D  92      57.531 -12.569  45.851  1.00 68.97           c
ATOM   13119  CD   LYS D  92      56.758 -13.357  46.919  1.00 68.81           c
ATOM   13120  CE   LYS D  92      57.244 -13.044  48.339  1.00 60.89           c
ATOM   13121  NZ   LYS D  92      56.444 -13.761  49.382  1.00 62.75           N
ATOM   13122  O    VAL D  93      57.416 -13.187  38.236  1.00 66.27           0
ATOM   13123  N    VAL D  93      56.480 -12.922  41.495  1.00 70.88           N
ATOM   13124  CA   VAL D  93      56.043 -13.445  40.193  1.00 62.27           c
ATOM   13125  c    VAL D  93      56.634 -12.664  39.017  1.00 63.39           c
ATOM   13126  CB   VAL D  93      54.514 -13.406  40.080  1.00 61.14           c
ATOM   13127  CGI  VAL D  93      54.053 -14.051  38.778  1.00 59.90           c
ATOM   13128  CG2  VAL D  93      53.868 -14.057  41.294  1.00 60.03           c
ATOM   13129  O    ASP D  94      56.500  -8.725  39.484  1.00 60.82           0
ATOM   13130  N    ASP D  94      56.238 -11.402  38.882  1.00 70.96           N
ATOM   13131  CA   ASP D  94      56.869 -10.505  37.926  1.00 62.93           c
ATOM   13132  c    ASP D  94      57.250  -9.223  38.658  1.00 68.07           c
ATOM   13133  CB   ASP D  94      55.943 -10.219  36.752  1.00 58.64           c
ATOM   13134  CG   ASP D  94      56.665  -9.602  35.566  1.00 62.89           c
ATOM   13135  OD1  ASP D  94      57.605  -8.799  35.764  1.00 60.40           0
ATOM   13136  OD2  ASP D  94      56.284  -9.927  34.419  1.00 63.66           0
ATOM   13137  O    ASP D  95      58.876  -5.198  38.907  1.00 65.67           0
ATOM   13138  N    ASP D  95      58.432  -8.698  38.369  1.00 69.12           N
ATOM   13139  CA.  ASP D  95      58.929  -7.573  39.141  1.00 70.73           c
ATOM   13140  C    ASP D  95      58.832  -6.279  38.340  1.00 65.32           c
ATOM   13141  CB   ASP D  95      60.372  -7.834  39.582  1.00 69.28           c
ATOM   13142  CG   ASP D  95      61.351  -7.746  38.436  1.00 73.86           c
ATOM   13143  OD1  ASP D  95      61.039  -8.245  37.331  1.00 73.24           0
ATOM   13144  OD2  ASP D  95      62.433  -7.159  38.638  1.00 84.76           0
ATOM   13145  O    SER D  96      57.132  -4.783  34.255  1.00 60.83           0
ATOM   13146  N    SEP. D  96      58.718  -6.407  37.022  1.00 64.57           N
ATOM   13147  CA   SER D  96      58.569  -5.265  36.139  1.00 58.97           c
ATOM   13148  c    SER D  96      57.229  -5.294  35.368  1.00 58.79           c
ATOM   13149  CB   SER D  96      59.745  -5.200  35.162  1.00 61.44           c
ATOM   13150  OG   SER D  96      59.582  -6.086  34.064  1.00 58.25           0
ATOM   13151  O    PHE D  97      53.830  -4.108  34.224  1.00 50.98           0
ATOM   13152  N    PHE D  97      56.205  -5.885  35.973  1.00 54.33           N
ATOM   13153  CA   PHE D  97      54.875  -5.990  35.367  1.00 56.28           c
ATOM   13154  c    PHE D  97      54.169  -4.626  35.304  1.00 56.39           c
ATOM   13155  CB   PHE D  97      54.047  -6.989  36.174  1.00 56.92           c
ATOM   13156  CG   PHE D  97      52.597  -7.054  35.795  1.00 58.44           c
ATOM   13157  GDI  PHE D  97      52.215  -7.268  34.482  1.00 54.34           c
ATOM   13158  CD2  PHE D  97      51.612  -6.948  36.772  1.00 59.27           c
ATOM   13159  CEl  PHE D  97      50.887  -7.355  34.142  1.00 54.98           c
ATOM   13160  CE2  PHE D  97      50.281  -7.026  36.437  1.00 57.88           c
ATOM   13161  CZ   PHE D  97      49.918  -7.230  35.115  1.00 56.03           c
ATOM   13162  N    PHE D  98      53.977  -4.059  36.487  1.00 55.68           N
ATOM   13163  CA   PHE D  98      53.444  -2.717  36.658  1.00 52.07           c
ATOM   13164  c    PHE D  98      54.216  -1.684  35.872  1.00 57.81           c
ATOM   13165  O    PHE D  98      53.627  -0.738  35.355  1.00 61.09           0
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ATOM   13166  CB   PHE  D   98      53.429  -2.367  38.127  1.00 41.37           C
ATOM   13167  CG   PHE  D   98      52.445  -3.165  38.899  1.00 45.59           C
ATOM   13168  CD1  PHE  D   98      51.236  -3.516  38.330  1.00 49.29           C
ATOM   13169  CD2  PHE  D   98      52.719  -3.582  40.175  1.00 44.52           C
ATOM   13170  CE1  PHE  D   98      50.304  -4.252  39.039  1.00 48.61           C
ATOM   13171  CE2  PHE  D   98      51.794  -4.330  40.883  1.00 49.88           C
ATOM   13172  CZ   PHE  D   98      50.586  -4.663  40.314  1.00 48.95           C
ATOM   13173  N    HIS  D   99      55.522  -1.881  35.744  1.00 60.17           N
ATOM   13174  CA   HIS  D   99      56.341  -1.003  34.909  1.00 64.76           C
ATOM   13175  C    HIS  D   99      55.902  -1.067  33.458  1.00 62.55           C
ATOM   13176  0    HIS  D   99      55.923  -0.060  32.751  1.00 62.02           0
ATOM   13177  CB   HIS  D   99      57.823  -1.374  35.007  1.00 69.04           C
ATOM   13178  CG   HIS  D   99      58.452  -0.992  36.307  1.00 75.42           C
ATOM   13179  ND1  HIS  D   99      58.742   0.315  36.635  1.00 76.58           N
ATOM   13180  CD2  HIS  D   99      58.834  -1.743  37.368  1.00 77.18           C
ATOM   13181  CE1  HIS  D   99      59.279   0.353  37.842  1.00 81.87           C
ATOM   13182  NE2  HIS  D   99      59.348  -0.882  38.309  1.00 83.27           N
ATOM   13183  N    ARG  D  100      55.517  -2.265  33.017  1.00 62.04           N
ATOM   13184  CA   ARG  D  100      55.088  -2.460  31.641  1.00 62.66           C
ATOM   13185  C    ARG  D  100      53.681  -1.899  31.462  1.00 57.11           C
ATOM   13186  0    ARG  D  100      53.314  -1.412  30.392  1.00 51.62           0
ATOM   13187  CB   ARG  D  100      55.151  -3.941  31.260  1.00 58.97           C
ATOM   13188  CG   ARG  D  100      56.548  -4.389  30.814  1.00 63.38           C
ATOM   13189  CD   ARG  D  100      56.596  -5.868  30.420  1.00 56.49           C
ATOM   13190  NE   ARG  D  100      56.608  -6.736  31.595  1.00 62.35           N
ATOM   13191  CZ   ARG  D  100      55.721  -7.698  31.823  1.00 62.69           C
ATOM   13192  NH1  ARG  D  100      54.762  -7.924  30.952  1.00 66.30           N
ATOM   13193  NH2  ARG  D  100      55.787  -8.441  32.911  1.00 58.57           N
ATOM   13194  N    LEU  D  101      52.902  -1.981  32.529  1.00 55.62           N
ATOM   13195  CA   LEU  D  101      51.582  -1.408  32.546  1.00 53.06           C
ATOM   13196  C    LEU  D  101      51.668   0.107  32.352  1.00 58.77           C
ATOM   13197  O    LEU  D  101      51.090   0.666  31.407  1.00 57.05           O
ATOM   13198  CB   LEU  D  101      50.869  -1.738  33.855  1.00 49.22           C
ATOM   13199  CG   LEU  D  101      50.056  -3.021  33.787  1.00 50.73           C
ATOM   13200  CD1  LEU  D  101      48.895  -2.996  34.760  1.00 47.32           C
ATOM   13201  CD2  LEU  D  101      49.585  -3.292  32.383  1.00 47.14           C
ATOM   13202  N    GLU  D  102      52.435   0.762  33.218  1.00 55.29           N
ATOM   13203  CA   GLU  D  102      52.455   2.210  33.245  1.00 58.40           C
ATOM   13204  C    GLU  D  102      53.283   2.742  32.075  1.00 62.44           C
ATOM   13205  O    GLU  D  102      53.547   3.934  31.967  1.00 66.31           0
ATOM   13206  CB   GLU  D  102      52.974   2.711  34.599  1.00 58.82           C
ATOM   13207  CG   GLU  D  102      52.305   2.014  35.838  1.00 63.84           C
ATOM   13208  CD   GLU  D  102      50.769   2.224  35.969  1.00 67.10           C
ATOM   13209  OE1  GLU  D  102      50.363   3.338  36.406  1.00 67.53           0
ATOM   13210  OE2  GLU  D  102      49.970   1.281  35.664  1.00 52.95           0
ATOM   13211  N    GLU  D  103      53.621   1.855  31.149  1.00 52.23           N
ATOM   13212  CA   GLU  D  103      54.444   2.231  30.014  1.00 51.27           C
ATOM   13213  C    GLU  D  103      53.779   1.878  28.707  1.00 47.02           C
ATOM   13214  O    GLU  D  103      54.293   2.198  27.632  1.00 55.73           0
ATOM   13215  CB   GLU  D  103      55.798   1.520  30.123  1.00 64.52           C
ATOM   13216  CG   GLU  D  103      56.922   2.140  29.347  1.00 67.42           C
ATOM   13217  CD   GLU  D  103      58.211   1.348  29.514  1.00 70.10           C
ATOM   13218  OE1  GLU  D  103      58.150   0.239  30.086  1.00 72.64           0
ATOM   13219  OE2  GLU  D  103      59.269   1.823  29.046  1.00 69.84           0
ATOM   13220  N    SER  D  104      52.637   1.204  28.808  1.00 48.59           N
ATOM   13221  CA   SER  D  104      51.957   0.620  27.638  1.00 40.91           C
ATOM   13222  C    SER  D  104      51.820   1.587  26.495  1.00 47.15           C
ATOM   13223  O    SER  D  104      51.862   1.181  25.344  1.00 44.76           0
ATOM   13224  CB   SER  D  104      50.585   0.100  28.037  1.00 45.99           C
ATOM   13225  OG   SER  D  104      49.783   1.108  28.673  1.00 51.51           0
ATOM   13226  O    PHE  D  105      52.324   4.756  23.814  1.00 41.99           0
ATOM   13227  N    PHE  D  105      51.672   2.879  26.821  1.00 48.49           N
ATOM   13228  CA   PHE  D  105      51.311   3.927  25.851  1.00 43.46           C
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ATOM   13229   C    PHE  D  105     52.488   4.325   24.973  1.00  47.90       C
ATOM   13230   CB   PHE  D  105     50.778   5.150   26.622  1.00  48.95       C
ATOM   132 31  CG   PHE  D  105     50.373   6.301   25.761  1.00  49.27       C
ATOM   132 32  CD2  PHE  D  105     51.293   7.262   25.392  1.00  48.47       C
ATOM   13233   GDI  PHE  D  105     49.038   6.448   25.354  1.00  50.71       C
ATOM   132 34  CE2  PHE  D  105     50.888   8.345   24.601  1.00  53.16       C
ATOM   13235   CE1  PHE  D  105     48.636   7.515   24.565  1.00  50.63       C
ATOM   13236   CZ   PHE  D  105     49.560   8.464   24.183  1.00  49.30       C
ATOM   132 37  O    LEU  D  106     54.938   2.513   23.627  1.00  52.62       0
ATOM   13238   N    LEU  D  106     53.681   4.196   25.559  1.00  47.60       N
ATOM   13239   CA   LEU  D  106     54.926   4.559   24.892  1.00  50.30       C
ATOM   13240   C    LEU  D  106     55.199   3.727   23.643  1.00  55.57       C
ATOM   13241   CB   LEU  D  106     56.098   4.391   25.845  1.00  57.39       C
ATOM   13242   CG   LEU  D  106     56.157   5.376   26.995  1.00  60.35       C
ATOM   13243   CD1  LEU  D  106     57.518   5.278   27.662  1.00  61.49       C
ATOM   13244   CD2  LEU  D  106     55.904   6.762   26.473  1.00  50.37       C
ATOM   13245   O    VAL  D  107     57.942   2.770   22.932  1.00  55.90       0
ATOM   13246   N    VAL  D  107     55.730   4.399   22.620  1.00  53.98       N
ATOM   13247   CA   VAL  D  107     56.298   3.780   21.433  1.00  55.72       C
ATOM   13248   C    VAL  D  107     57.411   2.762   21.810  1.00  59.60       C
ATOM   13249   CB   VAL  D  107     56.826   4.892   20.483  1.00  60.05       C
ATOM   13250   CGI  VAL  D  107     57.748   4.364   19.378  1.00  69.12       C
ATOM   13251   CG2  VAL  D  107     55.662   5.620   19.859  1.00  54.92       C
ATOM   132 52  O    GLU  D  108     60.633   1.145   22.578  1.00  55.16       0
ATOM   132 53  N    GLU  D  108     57.723   1.849   20.894  1.00  62.95       N
ATOM   13254   CA   GLU  D  108     58.753   0.832   21.144  1.00  66.42       C
ATOM   13255   C    GLU  D  108     60.087   1.463   21.527  1.00  56.45       C
ATOM   13256   CB   GLU  D  108     58.922  --0.061   19.920  1.00  63.78       C
ATOM   13257   CG   GLU  D  108     59.609  -.1.367   20.196  1.00  72.61       C
ATOM   13258   CD   GLU  D  108     59.513  -2.323   19.015  1.00  80.49       C
ATOM   13259   OE1  GLU  D  108     59.033  --1.901   17.930  1.00  65.73       0
ATOM   132 60  OE2  GLU  D  108     59.921  -3.498   19.178  1.00  85.31       0
ATOM   13261   O    GLU  D  109     62.533   3.101   23.290  1.00  73.94       0
ATOM   13262   N    GLU  D  109     60.593   2.359   20.686  1.00  53.23       N
ATOM   132 63  CA   GLU  D  109     61.797   3.106   21.023  1.00  56.91       C
ATOM   13264   C    GLU  D  109     61.770   3.584   22.454  1.00  65.23       C
ATOM   13265   CB   GLU  D  109     61.972   4.316   20.128  1.00  66.36       C
ATOM   13266   CG   GLU  D  109     61.414   4.176   18.743  1.00  71.72       C
ATOM   132 67  CD   GLU  D  109     61.353   5.522   18.050  1.00  83.21       C
ATOM   13268   OE1  GLU  D  109     60.522   5.688   17.123  1.00  90.76       0
ATOM   13269   OE2  GLU  D  109     62.136   6.417   18.450  1.00  79.63       0
ATOM   13270   O    ASP  D  110     60.638   4.603   26.348  1.00  70.68       0
ATOM   13271   N    ASP  D  110     60.854   4.503   22.742  1.00  60.63       N
ATOM   13272   CA   ASP  D  110     60.811   5.170   24.035  1.00  61.83       C
ATOM   13273   C    ASP  D  110     60.498   4.227   25.182  1.00  64.61       C
ATOM   13274   CB   ASP  D  110     59.783   6.306   24.016  1.00  60.81       C
ATOM   13275   CG   ASP  D  110     59.946   7.215   22.820  1.00  64.51       C
ATOM   13276   OD1  ASP  D  110     60.612   6.815   21.837  1.00  66.95       0
ATOM   13277   OD2  ASP  D  110     59.394   8.334   22.853  1.00  74.37       0
ATOM   13278   O    LYS  D  111     62.183   1.531   25.825  1.00  64.85       0
ATOM   13279   N    LYS  D  111     60.078   3.007   24.875  1.00  60.46       N
ATOM   13280   CA   LYS  D  111     59.821   2.046   25.940  1.00  63.04       C
ATOM   132 81  C    LYS  D  111     61.152   1.526   26.501  1.00  68.46       C
ATOM   13282   CB   LYS  D  111     58.935   0.894   25.446  1.00  62.10       C
ATOM   132 83  CG   LYS  D  111     58.179   0.192   26.574  1.00  60.91       C
ATOM   13284   CD   LYS  D  111     57.091  -0.796   26.098  1.00  57.57       C
ATOM   13285   CE   LYS  D  111     56.190  --0.244   24.999  1.00  54.50       C
ATOM   13286   NZ   LYS  D  111     54.744  -0.621   25.210  1.00  56.00       N
ATOM   13287   O    LYS  D  112     63.124  -1.411   29.378  1.00  72.62       0
ATOM   13288   N    LYS  D  112     61.116   1.097   27.753  1.00  67.23       N
ATOM   13289   CA   LYS  D  112     62.299   0.652   28.458  1.00  65.56       C
ATOM   132 90  C    LYS  D  112     62.178  -0.819   28.856  1.00  71.58       C
ATOM   132 91  CB   LYS  D  112     62.533   1.506   29.701  1.00  64.05       C
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ATOM   13292  O    HIS  D 113     59.966  -2.836  26.627  1.00 59.85          O
ATOM   13293  N    HIS  D 113     61.004  --1.395 28.624  1.00 68.61          N
ATOM   13294  CA   HIS  D 113     60.772  -2.808  28.877  1.00 61.38          C
ATOM   13295  C    HIS  D 113     60.229  -3.491  27.645  1.00 60.55          C
ATOM   13296  CB   HIS  D 113     59.808  -3.014  30.037  I.00 64.60          C
ATOM   13297  CG   HIS  D 113     60.332  -2.537  31.350  1.00 65.60          C
ATOM   13298  ND1  HIS  D 113     60.828  -1.265  31.534  1.00 70.48          N
ATOM   13299  CD2  HIS  D 113     60.432  -3.160  32.547  I.00 68.07          C
ATOM   13300  CE1  HIS  D 113     61.208  --1.123 32.792  1.00 72.82          C
ATOM   13301  NE2  HIS  D 113     60.982  -2.260  33.428  1.00 74.06          N
ATOM   13302  O    GLU  D 114     57.349  -4.862  27.145  I.00 56.38          O
ATOM   13303  N    GLU  D 114     60.094  -4.815  27.745  1.00 67.99          N
ATOM   13304  CA   GLU  D 114     59.555  -5.637  26.664  1.00 63.50          C
ATOM   13305  C    GLU  D 114     58.187  -5.100  26.277  1.00 57.50          C
ATOM   13306  CB   GLU  D 114     59.460  -7.108  27.084  1.00 60.11          C
ATOM   13307  O    AP.G D 115     54.414  -4.262  24.567  1.00 54.62          0
ATOM   13308  N    ARG  D 115     57.967  -4.924  24.980  1.00 55.07          N
ATOM   13309  CA.  ARG  D 115     56.828  -4.153  24.509  I.00 57.67          C
ATOM   13310  C    ARG  D 115     55.482  -4.868  24.728  1.00 63.16          C
ATOM   13311  CB   ARG  D 115     57.016  -3.795  23.035  1.00 51.73          C
ATOM   13312  CG   ARG  D 115     56.629  -4.880  22.043  I.00 54.52          C
ATOM   13313  CD   ARG  D 115     57.003  -4.418  20.634  1.00 61.62          C
ATOM   13314  NE   ARG  D 115     56.576  -5.326  19.572  1.00 61.78          N
ATOM   13315  CZ   ARG  D 115     57.159  -6.496  19.320  I.00 69.98          C
ATOM   13316  NH1  ARG  D 115     58.175  --6.907 20.073  1.00 65.61          N
ATOM   13317  NH2  ARG  D 115     56.716  -7.264  18.328  1.00 64.68          N
ATOM   13318  O    HIS  D 116     54.793  -6.983  27.731  I.00 61.15          O
ATOM   13319  N    HIS  D 116     55.533  --6.140 25.116  1.00 55.67          N
ATOM   13320  CA   HIS  D 116     54.324  -6.905  25.402  1.00 54.69          C
ATOM   13321  C    HIS  D 116     53.994  -6.688  26.864  1.00 60.24          C
ATOM   13322  CB   HIS  D 116     54.517  --8.392 25.013  1.00 58.85          C
ATOM   13323  CG   HIS  D 116     54.798  -8.569  23.552  1.00 52.18          C
ATOM   13324  ND1  HIS  D 116     56.066  -8.481  23.022  1.00 53.92          N
ATOM   13325  CD2  HIS  D 116     53.961  -8.700  22.496  I.00 55.86          C
ATOM   13326  CE1  HIS  D 116     56.002  -8.577  21.705  1.00 54.80          C
ATOM   13327  NE2  HIS  D 116     54.734  -8.710  21.359  1.00 49.21          N
ATOM   13328  O    PRO  D 117     52.815  -6.722  30.650  I.00 64.82          O
ATOM   13329  N    FRO  D 117     52.833  --6.081 27.143  1.00 62.73          N
ATOM   13330  CA   PRO  D 117     52.681  -5.642  28.532  1.00 60.93          C
ATOM   13331  C    PRO  D 117     52.353  -6.758  29.505  I.00 60.83          C
ATOM   13332  CB   FRO  D 117     51.529  -4.616  28.458  1.00 58.00          C
ATOM   13333  CG   PRO  D 117     50.818  -4.908  27.201  1.00 55.19          C
ATOM   13334  CD   PRO  D 117     51.862  -5.435  26.244  1.00 59.21          C
ATOM   13335  O    ILE  D 118     52.385  --9.852 31.715  1.00 66.53          0
ATOM   13336  N    ILE  D 118     51.554  -7.727  29.093  1.00 57.46          N
ATOM   13337  CA   ILE  D 118     51.073  -8.694  30.073  1.00 59.69          C
ATOM   13338  C    ILE  D 118     52.159  -9.647  30.514  I.00 64.06          C
ATOM   13339  CB   ILE  D 118     49.926  -9.507  29.533  1.00 62.16          C
ATOM   13340  CGI  ILE  D 118     48.829  -8.562  29.035  1.00 53.95          C
ATOM   13341  CG2  ILE  D 118     49.432  ~10.482  30.610  I.00 57.36          C
ATOM   13342  CD1  ILE  D 118     47.527  --9.250 28.753  1.00 49.75          C
ATOM   13343  O    PHE  D 119     55.121  -9.408  28.498  1.00 71.26          0
ATOM   13344  N    PHE  D 119     52.814 -10.247  29.525  I.00 63.48          N
ATOM   13345  CA   PHE  D 119     53.974 -11.095  29.767  1.00 64.74          C
ATOM   13346  C    PHE  D 119     55.203 -10.464  29.113  1.00 67.88          C
ATOM   13347  CB   PHE  D 119     53.733 -12.496  29.222  I.00 62.49          C
ATOM   13348  CG   PHE  D 119     52.456 -13.120  29.700  1.00 56.31          C
ATOM   13349  GDI  PHE  D 119     52.355 -13.621  30.982  1.00 56.52          C
ATOM   13350  CD2  PHE  D 119     51.358 -13.210  28.862  1.00 58.79          C
ATOM   13351  CEl  PHE  D 119     51.188 -14.197  31.418  1.00 56.87          C
ATOM   13352  CE2  PHE  D 119     50.185 -13.786  29.295  1.00 51.26          C
ATOM   13353  CZ   PHE  D 119     50.100 -14.280  30.574  1.00 50.29          C
ATOM   13354  O    GLY  D 120     57.902  -9.971  26.306  I.00 73.19          0
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ATOM   13355  N    GLY D 120      56.346 --11.101  29.219  1.00 60.78           N
ATOM   13356  CA   GLY D 120      57.517 --10.518  28.604  1.00 68.22           C
ATOM   13357  C    GLY D 120      57.554  -10.823  27.130  1.00 64.73           C
ATOM   13358  O    ASN D 121      55.022 --12.574  25.041  1.00 58.74           0
ATOM   13359  N    ASM D 121      57.174  -12.049  26.797  I.00 70.01           N
ATOM   13360  CA   ASN D 121      57.384  -12.561  25.454  1.00 67.60           c
ATOM   13361  c    ASN D 121      56.154  -12.447  24.577  1.00 56.10           c
ATOM   13362  CB   ASN D 121      57.835  -14.022  25.513  I.00 55.15           c
ATOM   13363  N    1LE D 122      56.406  -12.233  23.299  1.00 52.98           N
ATOM   13364  CA   ILE D 122      55.375  -12.273  22.292  1.00 52.07           c
ATOM   13365  C    ILE D 122      54.626  -13.604  22.225  I.00 58.47           c
ATOM   13366  O    ILE D 122      53.486  -13.638  21.780  1.00 59.30           0
ATOM   13367  CB   ILE D 122      55.960  -11.984  20.918  1.00 52.86           c
ATOM   13368  CGI  ILE D 122      54.833  -11.704  19.924  1.00 50.86           c
ATOM   13369  CG2  ILE D 122      56.845  -13.159  20.469  1.00 57.60           c
ATOM   13370  CD1  ILE D 122      55.291  -11.144  18.604  1.00 56.35           c
ATOM   13371  N    VAL D 123      55.239  -14.704  22.655  1.00 59.70           N
ATOM   13372  CA.  VAL D 123      54.576  -16.006  22.518  I.00 56.40           C
ATOM   13373  C    VAL D 123      53.460  -16.153  23.546  1.00 56.83           C
ATOM   13374  O    VAL D 123      52.369  -16.641  23.247  1.00 57.55           O
ATOM   13375  CB   VAL D 123      55.571  -17.217  22.674  I.00 62.62           c
ATOM   13376  CGI  VAL D 123      54.799  -18.521  22.896  1.00 53.88           c
ATOM   13377  CG2  VAL D 123      56.486  -17.337  21.458  1.00 55.90           c
ATOM   13378  N    ASP D 124      53.755  -15.769  24.774  I.00 56.32           N
ATOM   13379  CA   ASP D 124      52.760  -15.797  25.828  1.00 63.04           c
ATOM   13380  C    ASP D 124      51.622  -14.784  25.538  1.00 63.67           c
ATOM   13381  O    ASP D 124      50.445  -15.084  25.745  I.00 62.15           0
ATOM   13382  CB   ASP D 124      53.427  -15.503  27.171  1.00 64.15           c
ATOM   13383  CG   ASP D 124      54.802  -16.156  27.296  1.00 70.04           c
ATOM   13384  OD1  ASP D 124      54.825  -17.350  27.644  1.00 77.65           0
ATOM   13385  OD2  ASP D 124      55.847  -15.487  27.054  1.00 61.08           0
ATOM   13386  N    GLU D 125      51.995  -13.606  25.035  1.00 60.03           N
ATOM   13387  CA   GLU D 125      51.059  -12.528  24.729  1.00 60.97           c
ATOM   13388  C    GLU D 125      49.985  -12.983  23.747  I.00 61.73           C
ATOM   13389  O    GLU D 125      48.783  -12.919  24.033  1.00 59.43           O
ATOM   13390  CB   GLU D 125      51.808  -11.318  24.148  1.00 59.57           c
ATOM   13391  CG   GLU D 125      51.210   -9.950  24.521  I.00 52.85           c
ATOM   13392  CD   GLU D 125      51.496   -9.558  25.961  1.00 60.60           c
ATOM   13393  OE1  GLU D 125      52.381  -10.186  26.585  1.00 67.47           0
ATOM   13394  OE2  GLU D 125      50.848   -8.619  26.481  I.00 64.78           0
ATOM   13395  N    VAL D 126      50.444  -13.445  22.590  1.00 63.56           N
ATOM   13396  CA   VAL D 126      49.577  -13.947  21.535  1.00 58.18           C
ATOM   13397  c    VAL D 126      48.707  -15.106  22.031  1.00 58.11           c
ATOM   13398  O    VAL D 126      47.555  -15.238  21.626  1.00 59.79           0
ATOM   13399  CB   VAL D 126      50.405  -14.380  20.320  1.00 54.03           c
ATOM   13400  CGI  VAL D 126      49.546  -15.085  19.301  1.00 51.44           c
ATOM   13401  CG2  VAL D 126      51.093  -13.165  19.691  I.00 52.58           c
ATOM   13402  N    ALA D 127      49.225  -15.906  22.955  1.00 54.06           N
ATOM   13403  CA   ALA D 127      48.458  -17.049  23.436  1.00 56.46           c
ATOM   13404  C    ALA D 127      47.385  -16.599  24.412  I.00 56.63           c
ATOM   13405  O    ALA D 127      46.324  -17.221  24.518  1.00 57.06           0
ATOM   13406  CB   ALA D 127      49.375  -18.098  24.088  1.00 52.22           c
ATOM   13407  N    TYR D 128      47.661  -15.523  25.138  I.00 53.73           N
ATOM   13408  CA   TYR D 128      46.640  -14.909  25.976  1.00 54.56           c
ATOM   13409  C    TYR D 128      45.446  -14.397  25.156  1.00 49.77           c
ATOM   13410  O    TYR D 128      44.286  -14.664  25.461  I.00 49.10           0
ATOM   13411  CB   TYR D 128      47.237  -13.752  26.778  1.00 59.28           c
ATOM   13412  CG   TYR D 128      46.190  -12.982  27.564  1.00 55.47           c
ATOM   13413  CD1  TYR D 128      45.689  -13.481  28.764  1.00 55.61           c
ATOM   13414  CD2  TYR D 128      45.691  -11.775  27.096  1.00 53.98           c
ATOM   13415  CE1  TYR D 128      44.715  -12.784  29.478  1.00 55.91           c
ATOM   13416  CE2  TYR D 128      44.722  -11.075  27.806  1.00 53.21           c
ATOM   13417  CZ   TYR D 128      44.252  -11.583  28.997  I.00 54.45           c
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ATOM	13418	OH	TYR	D	128	43.291	-10.894	29.705	1.00	65.71	O
ATOM	13419	N	HIS	D	129	45.752	-13.661	24.105	1.00	48.75	N
ATOM	13420	CA	HIS	D	129	44.721	-13.002	23.338	1.00	51.55	C
ATOM	13421	C	HIS	D	129	43.857	-13.977	22.583	1.00	54.74	C
ATOM	13422	O	HIS	D	129	42.745	-13.625	22.163	I.00	49.24	0
ATOM	13423	CB	HIS	D	129	45.340	-11.999	22.374	1.00	46.66	C
ATOM	13424	CG	HIS	D	129	45.560	-10.654	22.987	1.00	59.31	C
ATOM	13425	ND1	HIS	D	129	46.792	-10.033	23.008	I.00	61.99	N
ATOM	13426	CD2	HIS	D	129	44.703	-9.810	23.612	1.00	55.87	C
ATOM	13427	CE1	HIS	D	129	46.683	-8.865	23.617	1.00	53.11	C
ATOM	13428	NE2	HIS	D	129	45.423	-8.703	23.984	I.00	55.74	N
ATOM	13429	N	GLU	D	130	44.365	-15.202	22.420	1.00	54.13	N
ATOM	13430	CA	GUI	D	130	43.679	-16.216	21.634	1.00	48.86	C
ATOM	13431	C	GLU	D	130	42.774	-17.042	22.526	1.00	47.71	C
ATOM	13432	O	GLU	D	130	41.649	-17.355	22.157	1.00	48.97	0
ATOM	13433	CB	GLU	D	130	44.679	-17.101	20.908	1.00	57.96	C
ATOM	13434	CG	GLU	D	130	44.222	-17.571	19.538	1.00	61.05	C
ATOM	13435	CD	GLU	D	130	44.821	-16.743	18.427	I.00	71.18	C
ATOM	13436	OE1	GLU	D	130	45.966	-17.032	17.996	1.00	72.45	0
ATOM	13437	OE2	GLU	D	130	44.143	-15.795	17.975	1.00	79.39	0
ATOM	13438	N	LYS	D	131	43.246	-17.395	23.711	I.00	49.98	N
ATOM	13439	CA	LYS	D	131	42.358	-18.050	24.669	1.00	48.46	C
ATOM	13440	C	LYS	D	131	41.340	-17.031	25.193	1.00	49.75	C
ATOM	13441	0	LYS	D	131	40.193	-17.392	25.449	I.00	51.32	0
ATOM	13442	CB	LYS	D	131	43.146	-18.666	25.839	1.00	43.26	C
ATOM	13443	N	TYR	D	132	41.779	-15.772	25.367	1.00	45.81	N
ATOM	13444	CA	TYR	D	132	40.942	-14.705	25.975	I.00	53.58	C
ATOM	13445	C	TYR	D	132	40.809	-13.459	25.117	1.00	50.13	C
ATOM	13446	O	TYR	D	132	41.414	-12.432	25.429	1.00	52.17	0
ATOM	13447	CB	TYR	D	132	41.508	-14.261	27.327	1.00	51.71	C
ATOM	13448	CG	TYR	D	132	41.731	-15.375	28.326	1.00	52.03	C
ATOM	13449	CD1	TYR	D	132	40.670	-15.894	29.045	1.00	49.05	C
ATOM	13450	CD2	TYR	D	132	43.015	-15.893	28.560	1.00	53.83	C
ATOM	13451	CE1	TYR	D	132	40.864	-16.893	29.969	I.00	56.11	C
ATOM	13452	CE2	TYR	D	132	43.221	-16.892	29.484	1.00	47.65	C
ATOM	13453	CZ	TYR	D	132	42.142	-17.397	30.183	1.00	55.99	C
ATOM	13454	OH	TYR	D	132	42.309	-18.401	31.108	I.00	56.90	0
ATOM	13455	O	FRO	D	133	39.686	-9.987	23.464	1.00	47.88	0
ATOM	13456	N	PRO	D	133	40.031	-13.535	24.032	1.00	49.15	N
ATOM	13457	CA	PRO	D	133	39.917	-12.360	23.149	I.00	45.20	C
ATOM	13458	C	FRO	D	133	39.330	-11.105	23.849	1.00	47.05	C
ATOM	13459	CB	PRO	D	133	38.993	-12.849	22.018	1.00	47.48	C
ATOM	13460	CG	PRO	D	133	38.946	-14.357	22.161	1.00	46.01	C
ATOM	13461	CD	FRO	D	133	39.154	-14.644	23.619	1.00	45.13	C
ATOM	13462	O	THR	D	134	38.534	-11.479	27.502	1.00	45.61	0
ATOM	13463	N	THR	D	134	38.482	-11.264	24.859	1.00	38.47	N
ATOM	13464	CA.	THR	D	134	38.095	-10.097	25.642	I.00	45.68	C
ATOM	13465	C	THR	D	134	38.385	-10.342	27.103	1.00	48.15	C
ATOM	13466	CB	THR	D	134	36.591	-9.719	25.495	1.00	45.37	C
ATOM	13467	OG1	THR	D	134	35.784	-10.570	26.325	I.00	47.57	0
ATOM	13468	CG2	THR	D	134	36.133	-9.760	24.022	1.00	38.41	C
ATOM	13469	O	ILE	D	135	37.747	-10.562	31.090	1.00	44.04	0
ATOM	13470	N	ILE	D	135	38.439	-9.268	27.895	I.00	41.84	N
ATOM	13471	CA	ILE	D	135	38.740	-9.357	29.321	1.00	37.03	C
ATOM	13472	C	ILE	D	135	37.611	-10.085	29.996	1.00	39.25	C
ATOM	13473	CB	ILE	D	135	38.936	-7.922	29.941	I.00	46.86	C
ATOM	13474	CGI	ILE	D	135	39.395	-7.965	31.409	1.00	46.13	C
ATOM	13475	CG2	ILE	D	135	37.663	-7.080	29.797	1.00	41.62	C
ATOM	13476	CD1	ILE	D	135	40.837	-8.362	31.598	1.00	42.58	C
ATOM	13477	N	TYR	D	136	36.468	-10.158	29.330	1.00	43.76	N
ATOM	13478	CA	TYR	D	136	35.298	-10.793	29.916	1.00	48.22	C
ATOM	13479	C	TYR	D	136	35.437	-12.337	29.878	1.00	44.46	C
ATOM	13480	O	TYR	D	136	34.963	-13.051	30.788	I.00	42.21	0

ATOM	13481	CB	TYR	D	136	34.018	-10.304	29.196	1.00	44.19	C
ATOM	13482	CG	TYR	D	136	33.793	-8.806	29.389	1.00	47.14	C
ATOM	13483	GD1	TYR	D	136	33.370	-8.309	30.614	1.00	42.69	C
ATOM	13484	CD2	TYR	D	136	34.040	-7.897	28.361	1.00	43.07	C
ATOM	13485	CE1	TYR	D	136	33.200	-6.974	30.819	1.00	42.88	C
ATOM	13486	CE2	TYR	D	136	33.856	-6.541	28.552	1.00	43.55	C
ATOM	13487	CZ	TYR	D	136	33.439	-6.085	29.796	1.00	46.32	C
ATOM	13488	OH	TYR	D	136	33.253	-4.739	30.036	1.00	45.40	0
ATOM	13489	N	HIS	D	137	36.095	-12.832	28.834	1.00	44.68	N
ATOM	13490	CA	HIS	D	137	36.498	-14.255	28.791	1.00	48.25	C
ATOM	13491	C	HIS	D	137	37.339	-14.559	30.025	1.00	43.48	C
ATOM	13492	O	HIS	D	137	36.990	-15.425	30.791	1.00	46.15	0
ATOM	13493	CB	HIS	D	137	37.262	-14.583	27.514	1.00	40.91	C
ATOM	13494	CG	HIS	D	137	36.415	-14.571	26.283	1.00	43.70	C
ATOM	13495	ND1	HIS	D	137	36.199	-13.430	25.535	1.00	44.84	N
ATOM	13496	CD2	HIS	D	137	35.736	-15.562	25.663	1.00	40.74	C
ATOM	13497	CE1	HIS	D	137	35.417	-13.719	24.513	1.00	42.91	C
ATOM	13498	NE2	HIS	D	137	35.120	-15.005	24.570	1.00	52.42	N
ATOM	13499	N	LEU	D	138	38.399	-13.785	30.250	1.00	46.04	N
ATOM	13500	CA	LEU	D	138	39.242	-13.961	31.437	1.00	48.66	C
ATOM	13501	C	LEU	D	138	38.443	-13.929	32.716	1.00	47.79	C
ATOM	13502	O	LEU	D	138	38.606	-14.777	33.592	1.00	53.02	0
ATOM	13503	CB	LEU	D	138	40.328	-12.896	31.501	1.00	43.77	C
ATOM	13504	CG	LEU	D	138	41.284	-13.002	32.686	1.00	51.41	C
ATOM	13505	CD1	LEU	D	138	41.743	-14.453	32.877	1.00	50.45	C
ATOM	13506	CD2	LEU	D	138	42.504	-12.072	32.501	1.00	45.72	C
ATOM	13507	N	ARG	D	139	37.558	-12.955	32.804	1.00	50.00	N
ATOM	13508	CA	ARG	D	139	36.825	-12.714	34.025	1.00	50.68	C
ATOM	13509	C	ARG	D	139	35.922	-13.882	34.370	1.00	46.43	C
ATOM	13510	O	ARG	D	139	35.951	-14.363	35.500	1.00	51.44	O
ATOM	13511	CB	ARG	D	139	36.010	-11.413	33.918	1.00	45.16	C
ATOM	13512	CG	ARG	D	139	36.852	-10.140	34.004	1.00	48.78	C
ATOM	13513	CD	ARG	D	139	36.060	-8.850	33.636	1.00	39.41	C
ATOM	13514	NE	ARG	D	139	34.798	-8.725	34.358	1.00	43.57	N
ATOM	13515	CZ	ARG	D	139	34.201	-7.556	34.642	1.00	53.52	C
ATOM	13516	NH1	ARG	D	139	34.762	-6.410	34.261	1.00	40.25	N
ATOM	13517	NH2	ARG	D	139	33.044	-7.527	35.311	1.00	45.96	N
ATOM	13518	N	LYS	D	140	35.100	-14.327	33.431	1.00	46.44	N
ATOM	13519	CA	LYS	D	140	34.251	-15.478	33.736	1.00	52.01	C
ATOM	13520	C	LYS	D	140	35.090	-16.716	34.096	1.00	51.10	C
ATOM	13521	O	LYS	D	140	34.742	-17.456	35.015	1.00	50.88	O
ATOM	13522	CB	LYS	D	140	33.330	-15.801	32.570	1.00	49.66	C
ATOM	13523	CG	LYS	D	140	32.257	-16.779	32.924	1.00	47.31	C
ATOM	13524	CD	LYS	D	140	31.911	-17.636	31.725	1.00	52.33	C
ATOM	13525	CE	LYS	D	140	30.462	-18.107	31.794	1.00	55.46	C
ATOM	13526	NZ	LYS	D	140	30.119	-18.708	33.119	1.00	60.76	N
ATOM	13527	N	LYS	D	141	36.206	-16.916	33.387	1.00	52.57	N
ATOM	13528	CA	LYS	D	141	37.110	-18.034	33.671	1.00	52.98	C
ATOM	13529	C	LYS	D	141	37.593	-17.996	35.117	1.00	57.68	C
ATOM	13530	0	LYS	D	141	37.631	-19.025	35.783	1.00	56.81	0
ATOM	13531	CB	LYS	D	141	38.306	-18.035	32.722	1.00	52.49	C
ATOM	13532	N	LEU	D	142	37.937	-16.809	35.617	1.00	53.15	N
ATOM	13533	CA	LEU	D	142	38.436	-16.709	36.986	1.00	51.70	C
ATOM	13534	C	LEU	D	142	37.311	-16.795	37.999	1.00	53.54	C
ATOM	13535	O	LEU	D	142	37.554	-16.849	39.193	1.00	52.05	O
ATOM	13536	CB	LEU	D	142	39.221	-15.421	37.189	1.00	47.74	C
ATOM	13537	CG	LEU	D	142	40.381	-15.257	36.210	1.00	50.77	C
ATOM	13538	GDI	LEU	D	142	41.025	-13.885	36.350	1.00	44.39	C
ATOM	13539	*CD2*	LEU	D	142	41.427	-16.397	36.383	1.00	46.58	C
ATOM	13540	N	VAL	D	143	36.075	-16.822	37.527	1.00	51.41	N
ATOM	13541	CA	VAL	D	143	34.957	-17.026	38.439	1.00	54.78	C
ATOM	13542	C	VAL	D	143	34.602	-18.506	38.468	1.00	60.14	C
ATOM	13543	0	VAL	D	143	34.089	-19.024	39.464	1.00	59.31	0

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ATOM   13544   CB   VAL  D 143      33.706  --16.182  38.028  1.00 59.68          C
ATOM   13545   CGI  VAL  D 143      32.551  --16.355  39.037  1.00 51.22          C
ATOM   13546   CG2  VAL  D 143      34.074  -14.706   37.899  1.00 57.14          C
ATOM   13547   N    ASP  D 144      34.901  --19.183  37.365  1.00 59.12          N
ATOM   13548   CA.  ASP  D 144      34.515  -20.576   37.172  1.00 58.11          C
ATOM   13549   C    ASP  D 144      35.542  -21.578   37.707  1.00 59.82          C
ATOM   13550   O    ASP  D 144      35.242  -22.332   38.619  1.00 57.27          O
ATOM   13551   CB   ASP  D 144      34.263  -20.826   35.695  1.00 57.23          C
ATOM   13552   CG   ASP  D 144      32.924  -20.298   35.256  1.00 59.76          C
ATOM   13553   OD1  ASP  D 144      32.084  -20.083   36.147  1.00 59.74          0
ATOM   13554   OD2  ASP  D 144      .32.707  -20.111   .34.037 1.00 63.47          0
ATOM   135 55  N    SEP. D 145      36.744  -21.557   37.134  1.00 58.64          N
ATOM   13556   CA   SER  D 145      37.852  -22.404   37.542  1.00 55.55          C
ATOM   13557   C    SER  D 145      38.051  -22.517   39.048  1.00 60.83          C
ATOM   13558   0    SER  D 145      37.775  -21.576   39.791  1.00 63.28          0
ATOM   13559   CB   SER  D 145      39.150  -21.897   36.922  1.00 59.24          C
ATOM   135 60  OG   SER  D 145      38.934  -21.505   35.585  1.00 60.09          0
ATOM   135 61  O    TH.R D 146      41.230  -23.938   41.780  1.00 57.64          0
ATOM   13562   N    THR  D 146      38.517  -23.695   39.474  1.00 66.82          N
ATOM   13563   CA   THR  D 146      39.030  -23.916   40.822  1.00 62.79          C
ATOM   13564   C    TH.R D 146      40.550  -23.960   40.755  1.00 58.54          C
ATOM   135 65  CB   THR  D 146      38.499  -25.209   41.449  1.00 56.89          C
ATOM   13566   OG1  THR  D 146      38.557  -26.259   40.480  1.00 70.16          0
ATOM   13567   CG2  THR  D 146      .37.062  -25.041   41.884  1.00 60..32          C
ATOM   135 68  O    ASP  D 147      42.537  -21.866   40.469  1.00 71.61          0
ATOM   13569   N    ASP  D 147      41.071  -23.986   39.533  1.00 51.39          N
ATOM   13570   CA   ASP  D 147      42.513  -23.958   3 9.305  1.00 54.09          C
ATOM   13571   C    ASP  D 147      43.197  -22.732   39.915  1.00 61.42          C
ATOM   13572   CB   ASP  D 147      42.796  -24.018   37.802  1.00 59.73          C
ATOM   13573   CG   ASP  D 147      42.585  -25.419   37.215  1.00 68.68          C
ATOM   13574   OD2  ASP  D 147      42.934  -25.620   36.027  1.00 66.80          0
ATOM   13575   OD1  ASP  D 147      42.064  -26.312   37.935  1.00 65.97          0
ATOM   13576   O    LYS  D 148      46.278  -21.148   38.174  1.00 52.73          0
ATOM   13577   N    LYS  D 148      44.518  -22.652   39.802  1.00 60.72          N
ATOM   13578   CA   LYS  D 148      45.272  -21.507   40..303  1.00 58.92          C
ATOM   13579   C    LYS  D 148      45.704  -20.635   39.137  1.00 58.98          C
ATOM   13580   CB   LYS  D 148      46.496  -21.969   41.105  1.00 61.19          C
ATOM   13581   CG   LYS  D 148      47.572  -20.913   41.333  1.00 62.28          C
ATOM   13582   CD   LYS  D 148      48.652  -21.407   42.307  1.00 67.81          C
ATOM   13583   CE   LYS  D 148      49.777  -20..386   42.501  1.00 64..38          C
ATOM   13584   NZ   LYS  D 148      50.728  -20.775   43.595  1.00 63.24          N
ATOM   13585   O    ALA  D 149      47.507  -17.590   39.261  1.00 44.41          0
ATOM   13586   N    ALA  D 149      45.447  -19.320   39.210  1.00 56.65          N
ATOM   13587   CA   ALA  D 149      45.697  -18.477   38.039  1.00 48.25          C
ATOM   13588   C    ALA  D 149      47.011  -17.792   38.161  1.00 42.08          C
ATOM   13589   CB   ALA  D 149      44.590  -17.452   37.854  1.00 53.98          C
ATOM   13590   N    ASP  D 150      47.577  -17.420   37.027  1.00 36.71          N
ATOM   135 91  CA   ASP  D 150      48.695  -16.503   37.064  1.00 41.85          C
ATOM   13592   C    ASP  D 150      48.204  -15.227   37.744  1.00 51.56          C
ATOM   13593   0    ASP  D 150      47.037  -14.838   37.610  1.00 50.82          0
ATOM   135 94  CB   ASP  D 150      49.239  -16.217   35.672  1.00 41.14          C
ATOM   13595   CG   ASP  D 150      50.474  -15.331   35.704  1.00 59.66          C
ATOM   13596   OD2  ASP  D 150      51.472  -15.691   .35.036  1.00 71..32          0
ATOM   13597   OD1  ASP  D 150      50.470  -14.294   36.417  1.00 57.76          0
ATOM   13598   N    LEU  D 151      49.094  -14.599   38.499  1.00 51.69          N
ATOM   13599   CA   LEU  D 151      48.692  -13.559   3 9.413  1.00 49.56          C
ATOM   13600   C    LEU  D 151      48.460  -12.289   38.601  1.00 57.83          C
ATOM   13601   O    LEU  D 151      47.569  -11.504   38.904  1.00 52.24          0
ATOM   13602   CB   LEU  D 151      49.738  -13.342   40.494  1.00 47.74          C
ATOM   13603   CG   LEU  D 151      49.324  -12.409   41.632  1.00 53.59          C
ATOM   13604   CD1  LEU  D 151      48.197  -13.007   42.447  1.00 55.51          C
ATOM   13605   CD2  LEU  D 151      50.507  -12.124   42.520  1.00 60.74          C
ATOM   13606   N    ARG  D 152      49.259  -12.128   37.553  1.00 54.36          N
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ATOM   13607   CA   ARG  D  152       49.095  --11.045  36.611   1.00  51.25            C
ATOM   13608   C    ARG  D  152       47.667  --10.965  36.069   1.00  59.40            C
ATOM   13609   O    ARG  D  152       47.107    -9.878  35.933   1.00  59.57            O
ATOM   13610   CB   ARG  D  152       50.067  --11.202  35.460   1.00  52.42            C
ATOM   13611   CG   ARG  D  152       51.349  -10.468   35.697   I.00  61.0.1           C
ATOM   13612   CD   ARG  D  152       52.459  -10.931   34.799   1.00  61.04            C
ATOM   13613   NE   ARG  D  152       52.757  --12.338  35.074   1.00  71.59            N
ATOM   13614   CZ   ARG  D  152       53.714  -13.042   34.475   I.00  60.10            C
ATOM   13615   NH1  ARG  D  152       54.489  -12.486   33.545   1.00  57.40            N
ATOM   13616   NH2  ARG  D  152       53.877  -14.310   34.807   1.00  65.82            N
ATOM   13617   N    LEU  D  153       47.079  -12.1.14   35.764   I.00  56.68            N
ATOM   13618   CA   LEU  D  153       45.727  -12.128   35.248   1.00  49.26            C
ATOM   13619   C    LEU  D  153       44.755  -11.987   36.388   1.00  5.3.90           C
ATOM   13620   O    LEU  D  153       43.621  -11.536   36.181   1.00  58.63            O
ATOM   13621   CB   LEU  D  153       45.436  -13.408   34.466   1.00  46.15            C
ATOM   13622   CG   LEU  D  153       46.524  -13.729   33.443   1.00  50.99            C
ATOM   13623   CD1  LEU  D  153       46.232  -15.032   32.672   1.00  42.47            C
ATOM   13624   CD2  LEU  D  153       46.760  -12.564   32.494   I.00  43.89            C
ATOM   13625   N    ILE  D  154       45.159  -12.371   37.590   1.00  40.22            N
ATOM   13626   CA   ILE  D  154       44.263  -12.124   38.699   1.00  47.72            C
ATOM   13627   C    ILE  D  154       44.178  -10.579   38.883   I.00  55.70            C
ATOM   13628   O    ILE  D  154       43.122  -10.021   39.132   1.00  51.10            0
ATOM   13629   CB   ILE  D  154       44.720  -12.813   39.970   1.00  49.08            C
ATOM   13630   CGI  ILE  D  154       44.467  -14..3.19  39.853   I.00  58.62            C
ATOM   13631   CG2  ILE  D  154       43.977  -12.264   41.183   1.00  50.40            C
ATOM   13632   GDI  ILE  D  154       44.994  -15.135   41.021   1.00  56.43            C
ATOM   13633   N    TYR  D  155       45.306    -9.909  .38.697   I.00  53.06            N
ATOM   13634   CA   TYR  D  155       45.366    -8.491  38.850   1.00  53.59            C
ATOM   13635   C    TYR  D  155       44.436    -7.821  37.829   1.00  54.94            C
ATOM   13636   O    TYR  D  155       43.507    -7.098  38.208   1.00  55.37            0
ATOM   13637   CB   TYR  D  155       46.795    -7.971  38.682   1.00  50.04            C
ATOM   13638   CG   TYR  D  155       46.775    -6.466  38.588   1.00  56.31            C
ATOM   13639   GDI  TYR  D  155       46.331    -5.693  39.660   1.00  53.66            C
ATOM   13640   CD2  TYR  D  155       47.127    -5.8.12 37.406   I.00  58.29            C
ATOM   13641   CE1  TYR  D  155       46.262    -4.323  39.565   1.00  49.05            C
ATOM   13642   CE2  TYR  D  155       47.068    -4.430  37.313   1.00  48.69            C
ATOM   13643   CZ   TYR  D  155       46.633    -3.703  38.406   I.00  46.58            C
ATOM   13644   OH   TYR  D  155       46.577    -2.343  38.338   1.00  57.57            0
ATOM   13645   N    LEU  D  156       44.684    -8.078  36.548   1.00  46.29            N
ATOM   13646   CA   LEU  D  156       43.936    -7.447  35.488   I.00  46.50            C
ATOM   13647   C    LEU  D  156       42.412    -7.561  35.652   1.00  51.23            C
ATOM   13648   O    LEU  D  156       41.693    -6.557  35.529   1.00  52.07            0
ATOM   13649   CB   LEU  D  156       44.373    -8.012  34.158   1.00  41.79            C
ATOM   13650   CG   LEU  D  156       45.777    -7.477  33.875   1.00  44.21            C
ATOM   13651   GD1  LEU  D  156       46.337    -8.010  32.547   1.00  49.00            C
ATOM   13652   CD2  LEU  D  156       45.789    -5.967  33.879   1.00  45.11            C
ATOM   13653   N    ALA  D  157       41.924    -8.753  35.967   I.00  49.19            N
ATOM   13654   CA   ALA  D  157       40.496    -8.941  36.156   1.00  50.69            C
ATOM   13655   C    ALA  D  157       39.969    -8.084  37.302   1.00  54.09            C
ATOM   13656   0    ALA  D  157       38.841    -7.564  37.242   I.00  53.88            0
ATOM   13657   CB   ALA  D  157       40.163  -10.388   36.408   1.00  38.14            C
ATOM   13658   N    LEU  D  158       40.761    -7.956  38.356   1.00  48.85            N
ATOM   13659   CA   LEU  D  158       40.317    -7.180  39.502   I.00  52.85            C
ATOM   13660   C    LEU  D  158       40.413    -5.652  39.235   1.00  51.98            C
ATOM   13661   O    LEU  D  158       39.645    -4.880  39.770   1.00  49.52            0
ATOM   13662   CB   LEU  D  158       41.121    -7.570  40.747   I.00  54.62            C
ATOM   13663   CG   LEU  D  158       40.948    -9.016  41.240   1.00  57.62            C
ATOM   13664   GDI  LEU  D  158       41.944    -9.330  42.339   1.00  6.1.05           C
ATOM   13665   CD2  LEU  D  158       39.536    -y.325  41.714   1.00  54.36            C
ATOM   13666   N    ALA  D  159       41.360    -5.250  38.397   1.00  47.26            N
ATOM   13667   CA   ALA  D  159       41.617    -.3.864 38.105   1.00  45.57            C
ATOM   13668   C    ALA  D  159       40.505    -3.333  37.211   1.00  53.04            C
ATOM   13669   0    ALA  D  159       40.004    -2.222  37.380   I.00  48.44            0
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ATOM	13670	CB	ALA	D	159	42.960	-3.703	37.425	1.00	46.21	C
ATOM	13671	N	HIS	D	160	40.127	-4.163	36.259	1.00	48.21	N
ATOM	13672	CA	HIS	D	160	39.125	-3.823	35.295	1.00	43.62	C
ATOM	13673	C	HIS	D	160	37.816	-3.568	36.008	1.00	44.93	C
ATOM	13674	0	HIS	D	160	37.085	-2.645	35.658	I.00	45.36	0
ATOM	13675	CB	HIS	D	160	38.978	-4.941	34.296	1.00	37.50	C
ATOM	13676	CG	HIS	D	160	38.154	-4.593	33.106	1.00	37.20	C
ATOM	13677	ND1	HIS	D	160	36.842	-4.981	32.980	I.00	31.88	N
ATOM	13678	CD2	HIS	D	160	38.464	--3.924	31.970	1.00	39.64	C
ATOM	13679	CE1	HIS	D	160	36.382	-4.580	31.811	1.00	38.52	C
ATOM	13680	NE2	HIS	D	160	.37.345	-3.934	31.180	I.00	39..30	N
ATOM	13681	N	MET	D	161	37.534	-4.392	37.010	1.00	45.35	N
ATOM	13682	CA	MET	D	161.	36.322	-4.254	37.803	1.00	41..79	C
ATOM	13683	C	MET	D	161	36.373	-3.001	38.688	1.00	46.70	C
ATOM	13684	O	MET	D	161	35.353	--2.343	38.894	1.00	45.27	0
ATOM	13685	CB	MET	D	161	36.099	-5.487	38.668	1.00	43.19	C
ATOM	13686	CG	MET	D	161	35.797	-6.745	37.887	1.00	50.88	C
ATOM	13687	SD	MET	D	161	36.016	-8.244	38.887	I.00	52.21.	S
ATOM	13688	CE	MET	D	161	35.563	-9.503	37.697	1.00	49.83	C
ATOM	13689	N	ILE	D	162	37.558	-2.676	39.199	1.00	42.02	N
ATOM	13690	CA.	ILE	D	162	37.721	-1.487	40.018	I.00	46.61.	C
ATOM	13691	C	ILE	D	162	37.740	--0.194	39.185	1.00	39.24	C
ATOM	13692	O	ILE	D	162	37.231	0.809	39.608	1.00	48.50	O
ATOM	13693	CB	ILE	D	162	39.024	-1.569	40.856	I.00	45.51	C
ATOM	13694	CGI	ILE	D	162	38.941	-2.696	41.876	1.00	49.16	C
ATOM	13695	CG2	ILE	D	162	39.269	-0.289	41.584	1.00	47.86	C
ATOM	13696	CD1	ILE	D	162	.37.654	-2.745	42.595	I.00	54.08	C
ATOM	13697	N	LYS	D	163	38.347	--0.231	38.008	1.00	46.16	N
ATOM	13698	CA	LYS	D	163	38.512	0.946	37.184	1.00	42.32	C
ATOM	13699	C	LYS	D	163	37.178	1.349	36.528	1.00	45.47	C
ATOM	13700	O	LYS	D	163	36.943	2.525	36.246	1.00	47.05	0
ATOM	137 01	CB	LYS	D	163	39.589	0.722	36.107	1.00	37.41	C
ATOM	137 02	CG	LYS	D	163	40.303	2.031	35.682	1.00	41.24	C
ATOM	13703	CD	LYS	D	163	40.980	1.957	34.312	I.00	37.31	C
ATOM	13704	CE	LYS	D	163	41.892	3.150	34.086	1.00	33.95	C
ATOM	13705	NZ	LYS	D	163	42.623	3.216	32.778	1.00	39.46	N
ATOM	137 06	N	PHE	D	164	36.318	0.363	36.309	I.00	42.17	N
ATOM	13707	CA	PHE	D	164	35.055	0.541	35.626	1.00	40.65	C
ATOM	137 08	C	PHE	D	164	33.990	-0.125	36.457	1.00	42.21	C
ATOM	13709	O	PHE	D	164	.33.481	-1.186	36.111	I.00	45.21	O
ATOM	13710	CB	PHE	D	164	35.108	--0.044	34.214	1.00	38.56	C
ATOM	13711	CG	PHE	D	164	36.257	0.492	33.384	1.00	42.77	C
ATOM	13712	CD1	PHE	D	164	36.260	1.814	32.958	1.00	33.21	C
ATOM	13713	CD2	PHE	D	164	37.339	--0.330	33.041	1.00	33.22	C
ATOM	13714	CE1	PHE	D	164	37..324	2.311	32.218	1.00	34.16	C
ATOM	13715	CE2	PHE	D	164	38.394	0.149	32.315	1.00	29.57	C
ATOM	13716	CZ	PHE	D	164	38.397	1.451	31.878	I.00	38.90	C
ATOM	13717	O	AP.G	D	165	30.833	-0.897	39.409	1.00	45.43	0
ATOM	13718	N	ARG	D	165	33.630	0.516	37.558	1.00	37.44	N
ATOM	13719	CA.	ARG	D	165	32.961	-0.210	38.608	I.00	37.71	C
ATOM	13720	C	ARG	D	165	31.433	--0.248	38.563	1.00	44.94	C
ATOM	13721	CB	ARG	D	165	33.419	0.342	39.943	1.00	39.10	C
ATOM	13722	CG	ARG	D	165	.33.158	1.802	40.165	I.00	46.89	C
ATOM	13723	CD	ARG	D	165	33.459	2.152	41.604	1.00	45.78	C
ATOM	13724	NE	ARG	D	165	33.447	3.591	41.814	1.00	51..52	N
ATOM	13725	CZ	ARG	D	165	.33.562	4.173	42.999	I.00	49..38	C
ATOM	13726	NH1	ARG	D	165	33.696	3.441	44.096	1.00	50.86	N
ATOM	13727	NH2	ARG	D	165	33.523	5.485	43.081	1.00	46.16	N
ATOM	13728	O	GLY	D	166	29.405	1.962	39.396	1.00	46.42	0
ATOM	13729	N	GLY	D	166	30.800	0.401	37.586	1.00	39.21	N
ATOM	137 30	CA	GLY	D	166	29..344	0.424	37.545	1.00	45.98	C
ATOM	137 31	C	GLY	D	166	28.712	1.387	38.557	1.00	46.08	C
ATOM	137 32	O	HIS	D	167	26.100	1.248	41..053	I.00	55.75	0

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ATOM   13733  N    HIS  D 167      27.390   1.536   38.517  1.00 50.39          N
ATOM   13734  CA   HIS  D 167      26.744   2.663   39.223  1.00 46.10          C
ATOM   137 35 C    HIS  D 167      26.200   2.390   40.6.17 1.00 47.56          C
ATOM   13736  CB   HIS  D 167      25.619   3.226   38.373  1.00 42.67          C
ATOM   137 37 CG   HIS  D 167      24.460   2.302   38.204  I.00 44.61          C
ATOM   13738  ND1  HIS  D 167      23.671   1.900   39.255  1.00 48.35          N
ATOM   13739  CD2  HIS  D 167      23.936   1.725   37.099  1.00 46.86          C
ATOM   13740  CE1  HIS  D 167      22.718   1.104   38.809  I.00 47.45          C
ATOM   13741  ME2  HIS  D 167      22.861   0.973   37.505  1.00 45.53          N
ATOM   13742  O    PHE  D 168      23.613   4.620   43.773  1.00 52.02          0
ATOM   13743  N    PHE  D 168      25.847   3.470   4.1.306 I.00 48.3 6          N
ATOM   13744  CA   PHE  D 168      25.385   3.427   42.684  1.00 44.73          C
ATOM   13745  C    PHE  D 168      23.948   3.914   42.8.19 1.00 50.08          C
ATOM   13746  CB   PHE  D 168      26.303   4.268   43.559  1.00 46.05          C
ATOM   13747  CG   PHE  D 168      27.666   3.721   43.664  1.00 47.71          C
ATOM   13748  CD2  PHE  D 168      28.011   2.917   44.735  1.00 46.73          C
ATOM   13749  CD1  PHE  D 168      28.600   3.953   42.662  1.00 50.23          C
ATOM   137 50 CE2  PHE  D 168      29.268   2.371   44.818  I.00 47.57          C
ATOM   137 51 CE1  PHE  D 168      29.875   3.403   42.732  1.00 49.49          C
ATOM   13752  CZ   PHE  D 168      30.210   2.616   43.820  1.00 50.99          C
ATOM   13753  O    LEU  D 169      19.676   3.102   42.874  I.00 59.3.3           0
ATOM   137 54 N    LEU  D 169      23.111   3.550   41.855  1.00 49.25          N
ATOM   13755  CA   LEU  D 169      21.702   3.922   41.881  1.00 53.85          C
ATOM   13756  C    LEU  D 169      20.877   2.905   42.662  I.00 58.98          C
ATOM   13757  CB   LEU  D 169      21.147   4.060   40.461  1.00 47.96          C
ATOM   137 58 CG   LEU  D 169      21.915   5.028   39.559  1.00 49.52          C
ATOM   13759  CD1  LEU  D 169      21.357   5.032   .38.148 I.00 46.24          C
ATOM   13760  CD2  LEU  D 169      21.902   6.437   40.148  1.00 46.15          C
ATOM   137 61 O    ILE  D 170      22.791   0.361   45.231  1.00 55.75          0
ATOM   137 62 N    ILE  D 170      21.519   1.819   43.088  1.00 55.34          N
ATOM   13763  CA   ILE  D 170      20.851   0.798   43.888  1.00 54.55          C
ATOM   13764  C    ILE  D 170      21.587   0.632   45.207  1.00 56.47          C
ATOM   137 65 CB   ILE  D 170      20.772  -0.570   43.165  1.00 59.20          C
ATOM   13766  CGI  ILE  D 170      19.826  -0.5.10   4.1.981 I.00 53.67          C
ATOM   13767  CG2  ILE  D 170      20.233  -1.650   44.089  1.00 60.09          C
ATOM   13768  CD1  ILE  D 170      19.916  -1.738   41.116  1.00 43.75          C
ATOM   13769  O    GLU  D 171      19.839  -1.246   47.831  I.00 75.70          0
ATOM   13770  N    GLU  D 171      20.858   0.833   46.300  1.00 62.33          N
ATOM   13771  CA   GLU  D 171      21.373   0.573   47.638  1.00 64.94          C
ATOM   137 72 C    GLU  D 171      20.982  -0.840   48.026  I.00 65.90          C
ATOM   137 73 CB   GLU  D 171      20.824   1.576   48.657  1.00 59.96          C
ATOM   13774  O    GLY  D 172      23.220  -3.779   47.556  1.00 7.3.01           0
ATOM   13775  N    GLY  D 172      21.917  -1.599   48.566  1.00 58.81          N
ATOM   137 76 CA   GLY  D 172      21.567  --2.917   49.053  1.00 67.68          C
ATOM   13777  C    GLY  D 172      22.350  -4.030   48..390  1.00 72.04          C
ATOM   13778  O    ASP  D 173      20.714  -7.394   47.544  1.00 78.40          0
ATOM   13779  N    ASP  D 173      22.041  -5.265   48.765  I.00 73.15          N
ATOM   13780  CA   ASP  D 173      22.785  -6.415   48.278  1.00 70.93          C
ATOM   13781  C    ASP  D 173      21.933  -7.288   47.375  1.00 76.93          C
ATOM   137 82 CB   ASP  D 173      23.318  -7.229   49.450  I.00 74.09          C
ATOM   137 83 CG   ASP  D 173      24.435  --6.515   50.185  1.00 80.02          C
ATOM   13784  OD2  ASP  D 173      24.675  -6.820   51.375  1.00 75.98          0
ATOM   137 85 OD1  ASP  D 173      25.079  -5.646   49.558  I.00 80.4.1           0
ATOM   13786  O    LEU  D 174      23.605 -10.543   45.613  1.00 77.58          0
ATOM   137 87 N    LEU  D 174      22.587  -7.905   46.403  1.00 77.95          N
ATOM   137 88 CA   LEU  D 174      21.918  -8.833   45.510  I.00 79.51          C
ATOM   13789  C    LEU  D 174      22.411 --10.257   45.753  1.00 78.66          C
ATOM   137 90 CB   LEU  D 174      22.152  -8.433   44.055  1.00 75.15          C
ATOM   13791  CG   LEU  D 174      21.618  -y.457   43.060  1.00 77.62          C
ATOM   13792  CD1  LEU  D 174      20.416  --8.894   42.343  1.00 77.74          C
ATOM   137 93 CD2  LEU  D 174      22.708  -9.867   42.083  1.00 76.45          C
ATOM   137 94 O    ASN  D 175      21.083 --13.067   44.005  1.00 72.15          0
ATOM   137 95 N    ASM  D 175      21.496 -11.145   46.129  I.00 78.51          N
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ATOM   13796   CA   ASN  D  175        21.826 --12.559   46.203   1.00 77.72              C
ATOM   137 97  C    ASM  D  175        22.002 --13.134   44.814   1.00 74.58              C
ATOM   137 98  CB   ASN  D  175        20.745  -13.358   46.934   1.00 80.97              C
ATOM   13799   CG   ASN  D  175        20.431 --12.808   48.298   1.00 87.41              C
ATOM   13800   OD1  ASN  D  175        21.187  -12.001   48.850   1.00 92.12              0
ATOM   13801   ND2  ASN  D  175        19.304  -13.247   48.864   1.00 83.49              N
ATOM   13802   O    PRO  D  176        22.268  -16.378   42.333   1.00 85.14              O
ATOM   13803   N    PRO  D  176        23.178  -13.725   44.538   1.00 79.57              N
ATOM   13804   CA   PRO  D  176        23.337  -14.474   43.291   1.00 74.31              C
ATOM   13805   C    PRO  D  176        22.505  -15.744   43.358   1.00 76.79              C
ATOM   13806   CB   PRO  D  176        24.823  -14.784   43.255   1.00 77.23              C
ATOM   13807   CG   PRO  D  176        25.193  -14.872   44.696   1.00 77.36              C
ATOM   13808   CD   PRO  D  176        24.359  -13.859   45.409   1.00 77.86              C
ATOM   13809   O    ASP  D  177        19.608  -17.676   42.949   1.00 83.23              0
ATOM   13810   N    ASP  D  177        22.079  -16.105   44.566   1.00 73.18              N
ATOM   13811   CA   ASP  D  177        21.067  -17.134   44.782   1.00 80.67              C
ATOM   13812   C    ASP  D  177        19.860  -16.907   43.881   1.00 81.00              C
ATOM   13813   CB   ASP  D  177        20.599  -17.139   46.242   1.00 88.38              C
ATOM   13814   CG   ASP  D  177        21.384  -18.101   47.123   1.00 93.69              C
ATOM   13815   OD1  ASP  D  177        22.515  -18.481   46.747   1.00 92.69              0
ATOM   13816   OD2  ASP  D  177        20.861  -18.459   48.206   1.00 94.31              0
ATOM   13817   O    ASN  D  178        18.270  -14.057   41.616   1.00 76.53              0
ATOM   13818   N    ASN  D  178        19.119  -15.843   44.183   1.00 78.87              N
ATOM   13819   CA   ASN  D  178        17.894  -15.498   43.477   1.00 75.77              C
ATOM   13820   C    ASN  D  178        18.154  -15.215   42.016   1.00 72.72              C
ATOM   13821   CB   ASN  D  178        17.232  -14.282   44.123   1.00 76.33              C
ATOM   13822   CG   ASN  D  178        17.150  -14.400   45.624   1.00 78.23              C
ATOM   13823   OD1  ASN  D  178        17.049  -15.502   46.160   1.00 79.40              0
ATOM   13824   ND2  ASN  D  178        17.190  -13.261   46.317   1.00 77.58              N
ATOM   13825   O    SER  D  179        18.051  -17.017   37.693   1.00 69.87              O
ATOM   13826   N    SEP. D  179        18.227  -16.276   41.223   1.00 74.81              N
ATOM   13827   CA   SER  D  179        18.667  -16.172   39.837   1.00 74.88              C
ATOM   13828   C    SER  D  179        17.742  -16.893   38.873   1.00 72.21              C
ATOM   13829   CB   SER  D  179        20.079  -16.734   39.702   1.00 72.32              C
ATOM   13830   OG   SER  D  179        20.105  -18.092   40.101   1.00 75.65              0
ATOM   13831   N    ASP  D  180        16.619  -17.381   39.380   1.00 75.30              N
ATOM   13832   CA.  ASP  D  180        15.715  -18.179   38.563   1.00 78.25              C
ATOM   13833   C    ASP  D  180        14.323  -17.571   38.606   1.00 74.51              C
ATOM   13834   O    ASP  D  180        13.559  -17.861   39.518   1.00 73.54              O
ATOM   13835   CB   ASP  D  180        15.700  -19.633   39.056   1.00 74.71              C
ATOM   13836   CG   ASP  D  180        14.987  -20.574   38.104   1.00 77.39              C
ATOM   13837   OD1  ASP  D  180        13.861  -20.259   37.670   1.00 78.18              0
ATOM   13838   OD2  ASP  D  180        15.557  -21.639   37.788   1.00 84.71              0
ATOM   13839   N    VAL  D  181        14.002  -16.745   37.610   1.00 72.66              N
ATOM   13840   CA   VAL  D  181        12.769  -15.966   37.627   1.00 68.61              C
ATOM   13841   C    VAL  D  181        11.526  -16.836   37.712   1.00 71.58              C
ATOM   13842   O    VAL  D  181        10.616  -16.516   38.460   1.00 69.52              0
ATOM   13843   CB   VAL  D  181        12.647  -15.060   36.380   1.00 71.94              C
ATOM   13844   CGI  VAL  D  181        11.340  -14.257   36.424   1.00 70.83              C
ATOM   13845   CG2  VAL  D  181        13.832  -14.117   36.294   1.00 67.89              C
ATOM   13846   N    ASP  D  182        11.490  -17.932   36.952   1.00 76.70              N
ATOM   13847   CA   ASP  D  182        10.328  -18.836   36.941   1.00 74.74              C
ATOM   13848   C    ASP  D  182         9.961  -19.382   38.337   1.00 77.57              C
ATOM   13849   O    ASP  D  182         8.800  -19.313   38.754   1.00 75.89              O
ATOM   13850   CB   ASP  D  182        10.564  -20.013   35.985   1.00 71.84              C
ATOM   13851   CG   ASP  D  182        10.179  -19.697   34.534   1.00 79.52              C
ATOM   13852   OD1  ASP  D  182         9.461  -18.702   34.297   1.00 80.33              0
ATOM   13853   OD2  ASP  D  182        10.578  -20.462   33.622   1.00 84.11              0
ATOM   13854   N    LYS  D  183        10.947  -19.915   39.058   1.00 74.29              N
ATOM   13855   CA   LYS  D  183        10.707  -20.473   40.392   1.00 74.22              C
ATOM   13856   C    LYS  D  183        10.334  -19.371   41.383   1.00 76.33              C
ATOM   13857   O    LYS  D  183         9.357  -19.481   42.135   1.00 75.52              0
ATOM   13858   CB   LYS  D  183        11.939  -21.248   40.883   1.00 79.08              C
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ATOM   13859   N    LEU  D  184      11.107  --18.292   41.351   1.00  75.58            N
ATOM   13860   CA   LEU  D  184      10.864  --17.134   42.200   1.00  72.78            C
ATOM   138 61  C    LEU  D  184       9.569  -16.375   41.854   1.00  71.71            C
ATOM   138 62  O    LEU  D  184       9.107  --15.559   42.642   1.00  75.00            0
ATOM   13863   CB   LEU  D  184      12.067  -16.191   42.131   I.00  66.14            C
ATOM   13864   CG   LEU  D  184      13..340  -16.761   42.765   1.00  70.88            C
ATOM   13865   CD1  LEU  D  184      14.547  -15.936   42.407   1.00  68.97            C
ATOM   13866   CD2  LEU  D  184      13.189  -16.836   44.271   I.00  70.32            C
ATOM   13867   N    PHE  D  185       8.976  -16.641   40.695   1.00  69.35            N
ATOM   13868   CA   PHE  D  185       7.703  -16.002   40.363   1.00  73.75            C
ATOM   13869   C    PHE  D  185       6.574  -16.854   40.912   I.00  75.47            C
ATOM   13870   O    PHE  D  185       5.527  -16.342   41.312   1.00  75.96            O
ATOM   13871   CB   PHE  D  185       7.545  -15.804   38.848   1.00  72.01            C
ATOM   13872   CG   PHE  D  185       6.147  -15.439   38.419   1.00  68.52            C
ATOM   13873   CD1  PHE  D  185       5.701  -14.132   38.498   1.00  68.69            C
ATOM   13874   CD2  PHE  D  185       5.285  -16.399   37.920   1.00  68.27            C
ATOM   13875   CE1  PHE  D  185       4.415  -13.788   38.094   1.00  66.71            C
ATOM   13876   CE2  PHE  D  185       4.006  -16.064   37.516   I.00  69.99            C
ATOM   13877   CZ   PHE  D  185       3.570  -14.752   37.608   1.00  63.84            C
ATOM   13878   N    ILE  D  186       6.805  -18.161   40.920   1.00  74.86            N
ATOM   13879   CA.  ILE  D  186       5.864  -19.114   41.489   I.00  78.18            C
ATOM   13880   C    ILE  D  186       5.766  -18.892   42.987   1.00  78.22            C
ATOM   13881   O    ILE  D  186       4.680  -18.946   43.560   1.00  82.89            0
ATOM   13882   CB   ILE  D  186       6.291  -20.578   41.219   I.00  81.90            C
ATOM   13883   CGI  ILE  D  186       6.267  -20.889   39.724   1.00  80.54            C
ATOM   13884   CG2  ILE  D  186       5.387  -21.555   41.945   1.00  83.97            C
ATOM   13885   CDI  ILE  D  186       6.631  -22..331   39.412   I.00  80.23            C
ATOM   13886   N    GLN  D  187       6.908  -18.638   43.617   1.00  74.89            N
ATOM   13887   CA   GLN  D  187       6.945  -18.420   45.054   1.00  75.70            C
ATOM   13888   C    GLN  D  187       6.149  -17.180   45.444   1.00  79.77            C
ATOM   13889   O    GLN  D  187       5.530  -17.155   46.504   1.00  83.73            0
ATOM   13890   CB   GLN  D  187       8..388  -18.301   45.551   1.00  80.35            C
ATOM   13891   N    LEU  D  188       6.150  -16.156   44.593   1.00  79.02            N
ATOM   138 92  CA.  LEU  D  188       5.362  -14.954   44.862   I.00  74.50            C
ATOM   138 93  C    LEU  D  188       3.905  -15.223   44.566   1.00  80.06            C
ATOM   13894   O    LEU  D  188       3.020  -14.541   45.081   1.00  81.75            O
ATOM   13895   CB   LEU  D  188       5.848  -13.772   44.028   I.00  75.92            C
ATOM   13896   CG   LEU  D  188       4.955  -12.521   43.968   1.00  69.29            C
ATOM   138 97  GDI  LEU  D  188       4.861  -11.816   45.312   1.00  67.28            C
ATOM   13898   CD2  LEU  D  188       5.456  -11.568   42.907   I.00  66.61            C
ATOM   13899   N    VAL  D  189       3.659  -16.213   43.714   1.00  80.89            N
ATOM   13900   CA   VAL  D  189       2.290  -16.569   43.355   1.00  86.40            C
ATOM   13901   C    VAL  D  189       1.657  -17.302   44.532   1.00  83.45            C
ATOM   13902   O    VAL  D  189       0.654  -16.855   45.097   1.00  79.51            0
ATOM   13903   CB   VAL  D  189       2.235  -17.435   42.055   1.00  85.12            C
ATOM   13904   CGI  VAL  D  189       0.924  -18.227   41.953   1.00  81.81            C
ATOM   13905   CG2  VAL  D  189       2.421  -16.553   40.821   I.00  80.08            C
ATOM   13906   N    GLN  D  190       2.279  -18.411   44.913   1.00  81.10            N
ATOM   13907   CA   GLN  D  190       1.806  -19.224   46.018   1.00  81.54            C
ATOM   13908   C    GLN  D  190       1.725  -18.410   47.324   I.00  84.72            C
ATOM   13909   O    GLN  D  190       0.773  -18.560   48.091   1.00  86.62            0
ATOM   13910   CB   GLN  D  190       2.708  -20.459   46.159   1.00  77.92            C
ATOM   13911   CG   GLN  D  190       2.512  -21.471   45.002   I.00  78.64            C
ATOM   13912   CD   GLN  D  190       3.626  -22.506   44.872   1.00  83.17            C
ATOM   13913   OE1  GLN  D  190       4.633  -22.457   45.582   1.00  84.41            0
ATOM   13914   NE2  GLN  D  190       3.449  -23.448   43.947   I.00  84.14            N
ATOM   13915   N    THR  D  191       2.691  -17.522   47.551   1.00  82.12            N
ATOM   13916   CA   THR  D  191       2.638  -16.601   48.693   1.00  79.84            C
ATOM   13917   C    THR  D  191       1.394  -15.720   48.666   1.00  81.98            C
ATOM   13918   O    THR  D  191       0.711  -15.578   49.676   1.00  90.41            0
ATOM   13919   CB   THR  D  191       3.879  -15.686   48.750   1.00  79.42            C
ATOM   13920   OG1  THR  D  191       5.027  -16.456   49.120   1.00  73.04            0
ATOM   13921   CG2  THR  D  191       3.686  -14.571   49.763   I.00  77.89            C
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ATOM  13922  N    TYR D 192     1.103 -15.127  47.514  1.00 80.34     N
ATOM  13923  CA   TYR D 192    -0.064 -14.267  47.370  1.00 79.17     C
ATOM  13924  C    TYR D 192    -1.379 -15.028  47.524  1.00 82.29     C
ATOM  13925  O    TYR D 192    -2.380 -14.474  48.002  1.00 79.10     0
ATOM  13926  CB   TYR D 192    -0.049 -13.572  46.008  1.00 79.85     c
ATOM  13927  CG   TYR D 192    -1.279 -12.718  45.727  1.00 71.85     c
ATOM  13928  CD2  TYR D 192    -2.448 -13.282  45.220  1.00 73.45     c
ATOM  13929  GDI  TYR D 192    -1.262 -11.356  45.960  1.00 63.66     c
ATOM  13930  CE2  TYR D 192    -3.559 -12.516  44.972  1.00 72.10     c
ATOM  13931  CE1  TYR D 192    -2.369 -10.577  45.702  1.00 70.57     c
ATOM  13932  CZ   TYR D 192    -3.511 -11.163  45.210  1.00 70.20     c
ATOM  13933  OH   TYR D 192    -4.611 -10.389  44.951  1.00 75.70     0
ATOM  13934  N    ASN D 193    -1.388 -16.284  47.089  1.00 81.07     N
ATOM  13935  CA   ASN D 193    -2.628 -17.053  47.045  1.00 84.45     c
ATOM  13936  C    ASM D 193    -3.134 -17.413  48.443  1.00 87.31     c
ATOM  13937  O    ASN D 193    -4.334 -17.357  48.712  1.00 87.52     0
ATOM  13938  CB   ASN D 193    -2.445 -18.324  46.203  1.00 82.40     c
ATOM  13939  CG   ASN D 193    -2.508 -18.051  44.699  1.00 80.00     c
ATOM  13940  OD1  ASN D 193    -3.032 -17.033  44.258  1.00 76.28     0
ATOM  13941  ND2  ASN D 193    -1.980 -18.977  43.912  1.00 83.59     N
ATOM  13942  N    GLN D 194    -2.218 -17.767  49.337  1.00 88.02     N
ATOM  13943  CA   GLN D 194    -2.602 -18.123  50.693  1.00 86.42     C
ATOM  13944  c    GLN D 194    -3.285 -16.933  51.376  1.00 88.04     c
ATOM  13945  0    GLN D 194    -4.341 -17.087  51.991  1.00 91.44     0
ATOM  13946  CB   GLN D 194    -1.385 -18.594  51.495  1.00 89.57     c
ATOM  13947  CG   GLN D 194    -0.519 -19.649  50.784  1.00 93.39     c
ATOM  13948  CD   GLN D 194    -1.329 -20.801  50.182  1.00 98.41     c
ATOM  13949  OE1  GLN D 194    -2.199 -21.376  50.840  1.00 98.52     0
ATOM  13950  NE2  GLN D 194    -1.040 -21.139  48.924  1.00 91.35     N
ATOM  13951  N    LEU D 195    -2.699 -15.747  51.241  1.00 83.05     N
ATOM  13952  CA   LEU D 195    -3.256 -14.543  51.856  1.00 85.18     C
ATOM  13953  C    LEU D 195    -4.683 -14.274  51.392  1.00 84.39     C
ATOM  13954  O    LEU D 195    -5.547 -13.897  52.188  1.00 81.66     O
ATOM  13955  CB   LEU D 195    -2.382 -13.323  51.552  1.00 84.32     C
ATOM  13956  CG   LEU D 195    -1.126 -13.056  52.385  1.00 84.53     C
ATOM  13957  CD1  LEU D 195    -0.285 -11.982  51.710  1.00 82.63     c
ATOM  13958  CD2  LEU D 195    -1.481 -12.629  53.806  1.00 77.00     c
ATOM  13959  N    PHE D 196    -4.917 -14.469  50.098  1.00 85.79     N
ATOM  13960  CA   PHE D 196    -6.225 -14.235  49.499  1.00 81.09     C
ATOM  13961  C    PHE D 196    -6.773 -15.531  48.901  1.00 86.48     C
ATOM  13962  O    PHE D 196    -6.941 -15.635  47.689  1.00 87.90     0
ATOM  13963  CB   PHE D 196    -6.136 -13.160  48.421  1.00 77.71     c
ATOM  13964  CG   PHE D 196    -5.512 -11.877  48.882  1.00 71.69     c
ATOM  13965  CD1  PHE D 196    -6.292 -10.858  49.400  1.00 77.12     c
ATOM  13966  CD2  PHE D 196    -4.149 -11.678  48.776  1.00 75.02     c
ATOM  13967  CE1  PHE D 196    -5.721  -9.656  49.820  1.00 78.78     c
ATOM  13968  CE2  PHE D 196    -3.564 -10.485  49.198  1.00 76.50     c
ATOM  13969  CZ   PHE D 196    -4.354  -9.472  49.718  1.00 75.24     c
ATOM  13970  O    GLU D 197    -9.257 -18.545  47.808  1.00 89.42     0
ATOM  13971  N    GLU D 197    -7.043 -16.520  49.750  1.00 89.53     N
ATOM  13972  CA   GLU D 197    -7.521 -17.819  49.290  1.00 85.42     c
ATOM  13973  c    GLU D 197    -8.857 -17.674  48.575  1.00 86.55     c
ATOM  13974  CB   GLU D 197    -7.641 -18.797  50.462  1.00 85.00     c
ATOM  13975  O    GLU D 198   --11.242 -16.778  45.886  1.00 94.48     0
ATOM  13976  N    GLU D 198    -9.537 -16.560  48.827  1.00 88.46     N
ATOM  13977  CA   GLU D 198   -10.814 -16.271  48.185  1.00 88.07     C
ATOM  13978  C    GLU D 198   --10.633 -16.067  46.689  1.00 92.43     C
ATOM  13979  CB   GLU D 198   -11.468 -15.042  48.812  1.00 82.96     C
ATOM  13980  O    ASN D 199    -7.300 -14.125  44.283  1.00 93.80     O
ATOM  13981  N    ASN D 199    -9.786 -15.105  46.320  1.00 94.27     N
ATOM  13982  CA   ASK D 199    -9.494 -14.820  44.913  1.00 91.32     C
ATOM  13983  c    ASN D 199    -8.041 -15.072  44.520  1.00 89.76     c
ATOM  13984  CB   ASN D 199    -9.828 -13.363  44.575  1.00 91.13     c
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ATOM  13985  CG   ASN  D 199   -11.233  --12.973  44.970  1.00  92.38   C
ATOM  13986  OD1  ASM  D 199   --11.434  --12.319  45.988  1.00  99.29   O
ATOM  13987  ND2  ASN  D 199   -12.213  -13.358  44.159  1.00  91.48   N
ATOM  13988  O    PRO  D 200   --6.874  -15.691  41.837  1.00  94.29   O
ATOM  13989  N    PRO  D 200   -7.625  -16.344  44.432  I.00  87.72   N
ATOM  13990  CA   PRO  D 200   -6.255  -16.619  43.976  1.00  88.77   C
ATOM  13991  C    PRO  D 200   --5.993  -16.222  42.515  1.00  91.95   C
ATOM  13992  CB   PRO  D 200   -6.136  -18.138  44.140  I.00  86.24   C
ATOM  13993  CG   PRO  D 200   -7.542  -18.632  44.028  1.00  90.00   C
ATOM  13994  CD   PRO  D 200   --8.368  -17.583  44.713  1.00  89.09   C
ATOM  13995  N    ILE  D 201   -4.771  -16.458  42.049  I.00  89.91   N
ATOM  13996  CA   1LE  D 201   -4.468  -16.382  40.623  1.00  87.95   C
ATOM  13997  C    ILE  D 201   -3.613  -17.583  40.250  1.00  86.06   C
ATOM  13998  O    ILE  D 201   -2.958  -18.180  41.106  1.00  80.20   0
ATOM  13999  CB   ILE  D 201   -3.734  -15.084  40.226  1.00  87.54   C
ATOM  14000  CGI  ILE  D 201   -3.644  -14.117  41.408  1.00  84.36   C
ATOM  14001  CG2  ILE  D 201   -4.423  -14.440  39.017  1.00  86.64   C
ATOM  14002  CD1  ILE  D 201   -2.788  -12.906  41.133  I.00  79.17   C
ATOM  14003  N    ASN  D 202   -3.624  -17.946  38.976  1.00  85.75   N
ATOM  14004  CA   ASN  D 202   --2.891  -19.130  38.566  1.00  91.85   C
ATOM  14005  C    ASN  D 202   -1.954  -18.908  37.380  I.00  92.15   C
ATOM  14006  O    ASN  D 202   -2.226  -18.116  36.471  1.00  92.20   0
ATOM  14007  CB   ASN  D 202   --3.869  -20.266  38.256  1.00  89.16   C
ATOM  14008  CG   ASN  D 202   -4.855  -19.906  37.168  I.00  88.68   C
ATOM  14009  OD1  ASN  D 202   -5.044  -18.731  36.840  1.00  88.80   0
ATOM  14010  ND2  ASN  D 202   -5.501  -20.919  36.606  1.00  82.20   N
ATOM  14011  N    ALA  D 203   -0.835  -19.617  37.424  I.00  90.05   N
ATOM  14012  CA   ALA  D 203    0.131  -19.630  36.339  1.00  95.66   C
ATOM  14013  C    ALA  D 203    0.201  -21.030  35.741  1.00  95.01   C
ATOM  14014  O    ALA  D 203    0.870  -21.913  36.277  1.00  94.35   0
ATOM  14015  CB   ALA  D 203    1.502  -19.186  36.831  1.00  91.05   C
ATOM  14016  O    SEP. D 204    1.581  -22.868  32.778  1.00  92.37   0
ATOM  14017  N    SER  D 204   --0.517  -21.234  34.642  1.00  97.38   N
ATOM  14018  CA.  SER  D 204   -0.485  -22.507  33.936  I.00  96.71   C
ATOM  14019  C    SER  D 204    0.447  -22.391  32.743  1.00  92.79   C
ATOM  14020  CB   SER  D 204   --1.890  -22.927  33.485  1.00100.97   C
ATOM  14021  OG   SER  D 204   -2.441  -22.008  .32.554  I.00104.92   0
ATOM  14022  O    GLY  D 205    3.007  -20.804  30.213  1.00  94.21   0
ATOM  14023  N    GLY  D 205   -0.029  -21.740  31.693  1.00  88.38   N
ATOM  14024  CA   GLY  D 205    0.774  -21.565  30.506  I.00  85.82   C
ATOM  14025  C    GLY  D 205    1.900  -20.572  30.704  1.00  89.65   C
ATOM  14026  O    VAL  D 206    4..345  -19.369  32.591  1.00  82.47   O
ATOM  14027  N    VAL  D 206    1.629  -19.495  31.446  1.00  87.76   N
ATOM  14028  CA   VAL  D 206    2.483  -18.305  31.441  1.00  82.61   C
ATOM  14029  C    VAL  D 206    3.969  -18.626  31.683  1.00  81.08   C
ATOM  14030  CB   VAL  D 206    1.969  -17.242  32.461  1.00  77.10   C
ATOM  14031  CGI  VAL  D 206    0.465  -17..320  .32.571  I.00  83.40   C
ATOM  14032  CG2  VAL  D 206    2.563  -17.422  33.830  1.00  78.67   C
ATOM  14033  N    ASP  D 207    4.796  -18.096  30.790  1.00  79.52   N
ATOM  14034  CA.  ASP  D 207    6.237  -18.261  30.838  I.00  76.45   C
ATOM  14035  C    ASP  D 207    6.818  -16.951  31.323  1.00  76.83   C
ATOM  14036  O    ASP  D 207    7.165  -16.075  30.524  1.00  74.09   O
ATOM  14037  CB   ASP  D 207    6.791  -18.644  29.460  I.00  77.52   C
ATOM  14038  CG   ASP  D 207    8.313  -18.741  29.426  1.00  76.06   C
ATOM  14039  OD2  ASP  D 207    8.875  -18.625  28..320  1.00  75.29   0
ATOM  14040  OD1  ASP  D 207    8.949  -18.958  30.480  I.00  78.65   0
ATOM  14041  N    ALA  D 208    6.902  -16.831  32.645  1.00  73.39   N
ATOM  14042  CA   ALA  D 208    7.289  -15.596  33.298  1.00  72.61   C
ATOM  14043  C    ALA  D 208    8.723  -15.238  32.989  1.00  69.80   C
ATOM  14044  O    ALA  D 208    9.066  -14.063  32.889  1.00  70.76   0
ATOM  14045  CB   ALA  D 208    7.088  -15.712  34.801  1.00  76.52   C
ATOM  14046  N    LYS  D 209    9.560  -16.259  32.851  1.00  74.18   N
ATOM  14047  CA.  LYS  D 209   10.952  -16.048  .32.483  I.00  72.75   C
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ATOM   14048  c    LYS D 209       11.025 --15.219  31.206  1.00 76.07          c
ATOM   14049  O    LYS D 209       11.694  -14.194  31.174  1.00 73.59          0
ATOM   14050  CB   LYS D 209       11.682  -17.380  32.301  1.00 70.06          c
ATOM   14051  CG   LYS D 209       13.161 --17.208  32.014  1.00 68.59          c
ATOM   14052  CD   LYS D 209       13.807  -16.224  32.988  I.00 70.64          c
ATOM   14053  CE   LYS D 209       15.142  -15.730  32.463  1.00 70.39          c
ATOM   14054  NZ   LYS D 209       15.876  -16.836  31.785  1.00 63.29          N
ATOM   14055  N    ALA D 210       10.308  -15.656  30.171  I.00 74.91          N
ATOM   14056  CA   ALA D 210       10.243  -14.920  28.914  1.00 73.06          C
ATOM   14057  c    ALA D 210        9.651  -13.524  29.081  1.00 74.16          c
ATOM   14058  0    ALA D 210       10.306  -12.540  28.752  I.00 78.98          0
ATOM   14059  CB   ALA D 210        9.449  -15.695  27.896  1.00 75.01          c
ATOM   14060  N    ILE D 211        8.423  -13.436  29.590  1.00 73.57          N
ATOM   14061  CA   ILE D 211        7.713  -12.151  29.683  1.00 67.61          c
ATOM   14062  C    ILE D 211        8.477  -11.093  30.459  1.00 67.16          c
ATOM   14063  O    ILE D 211        8.622   -9.967  30.023  1.00 68.35          0
ATOM   14064  CB   ILE D 211        6.349  -12.308  30.361  1.00 68.54          c
ATOM   14065  CGI  ILE D 211        5.513  -13.380  29.666  I.00 62.54          c
ATOM   14066  CG2  ILE D 211        5.616  -10.986  30.354  1.00 69.77          c
ATOM   14067  CD1  ILE D 211        4.629  -14.151  30.607  1.00 69.89          c
ATOM   14068  N    LEU D 212        8.973  -11.487  31.622  I.00 74.98          N
ATOM   14069  CA   LEU D 212        9.578  -10.555  32.561  1.00 75.31          c
ATOM   14070  c    LEU D 212       11.029  -10.204  32.239  1.00 73.68          c
ATOM   14071  0    LEU D 212       11.542   -9.190  32.714  I.00 71.62          0
ATOM   14072  CB   LEU D 212        9.487  -11.122  33.979  1.00 72.17          c
ATOM   14073  CG   LEU D 212        8.145  -10.887  34.685  1.00 72.53          c
ATOM   14074  CD1  LEU D 212        8.196  -11.457  36.090  I.00 74.02          c
ATOM   14075  CD2  LEU D 212        7.798   -9.407  34.715  1.00 61.04          c
ATOM   14076  N    SER D 213       11.688  -11.029  31.431  1.00 72.81          N
ATOM   14077  CA   SER D 213       13.084  -10.788  31.096  1.00 64.86          c
ATOM   14078  C    SER D 213       13.278  -10.199  29.710  1.00 73.82          c
ATOM   14079  O    SER D 213       14.417  -10.031  29.274  1.00 77.15          0
ATOM   14080  CB   SER D 213       13.884  -12.080  31.187  1.00 77.35          c
ATOM   14081  OG   SER D 213       13.604  -12.922  30.078  I.00 78.56          0
ATOM   14082  N    ALA D 214       12.184   -9.898  29.012  1.00 76.81          N
ATOM   14083  CA   ALA D 214       12.288   -9.381  27.651  1.00 78.24          c
ATOM   14084  C    ALA D 214       13.198   -8.156  27.626  I.00 80.88          c
ATOM   14085  O    ALA D 214       13.306   -7.432  28.621  1.00 77.50          0
ATOM   14086  CB   ALA D 214       10.924   -9.041  27.098  1.00 71.79          c
ATOM   14087  O    ARG D 215       14.169   -4.715  25.194  I.00 82.07          0
ATOM   14088  N    ARG D 215       13.877   -7.944  26.499  1.00 83.87          N
ATOM   14089  CA   ARG D 215       14.714   -6.761  26.324  1.00 81.98          c
ATOM   14090  c    ARG D 215       13.835   -5.538  26.040  1.00 82.49          c
ATOM   14091  CB   ARG D 215       15.725   -6.975  25.194  1.00 74.26          c
ATOM   14092  O    LEU D 216       12.329   -3.851  28.849  1.00 79.45          0
ATOM   14093  N    LEU D 216       12.716   -5.443  26.759  1.00 76.39          N
ATOM   14094  CA.  LEU D 216       11.732   -4.381  26.593  I.00 76.45          c
ATOM   14095  C    LEU D 216       11.626   -3.561  27.878  1.00 78.58          c
ATOM   14096  CB   LEU D 216       10.370   -4.973  26.219  1.00 77.42          c
ATOM   14097  CG   LEU D 216        9.988   -5.015  24.736  I.00 79.63          c
ATOM   14098  CD1  LEU D 216        9.616   -3.613  24.226  1.00 86.03          c
ATOM   14099  CD2  LEU D 216       11.107   -5.624  23.895  1.00 82.84          c
ATOM   14100  N    SER D 217       10.746   -2.556  27.894  I.00 71.36          N
ATOM   14101  CA   SER D 217       10.625   -1.649  29.049  1.00 73.99          c
ATOM   14102  C    SER D 217        9.937   -2.299  30.249  1.00 73.27          c
ATOM   14103  O    SER D 217        9.367   -3.382  30.146  I.00 73.02          0
ATOM   14104  CB   SER D 217        9.864   -0.368  28.670  1.00 70.42          c
ATOM   14105  OG   SER D 217        8.455   -0.539  28.755  1.00 64.68          0
ATOM   14106  N    LYS D 218        9.983   -1.618  31.389  1.00 72.44          N
ATOM   14107  CA   LYS D 218        9.373   -2.140  32.601  1.00 71.39          c
ATOM   14108  C    LYS D 218        7.850   -2.211  32.468  1.00 69.44          c
ATOM   14109  O    LYS D 218        7.233   -3.257  32.691  1.00 67.07          0
ATOM   14110  CB   LYS D 218        9.779   -1.283  33.798  I.00 71.16          c
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ATOM   14111  CG   LYS  D  218      11.279   -1.105   33.899   1.00  70.93           C
ATOM   14112  CD   LYS  D  218      11.719   -0.533   35.226   1.00  64.16           C
ATOM   14113  CE   LYS  D  218      13.231   -0.586   35.353   1.00  66.48           C
ATOM   14114  NZ   LYS  D  218      13.707   -2.007   35.420   1.00  69.69           N
ATOM   14115  N    SER  D  219       7.247   -1.103   32.072   1.00  68.98           N
ATOM   14116  CA   SER  D  219       5.802   -1.045   31.966   1.00  68.96           C
ATOM   14117  C    SER  D  219       5.251   -2.006   30.914   1.00  69.54           C
ATOM   14118  0    SER  D  219       4.235   -2.668   31.133   1.00  67.10           0
ATOM   14119  CB   SER  D  219       5.391    0.379   31.663   1.00  62.14           C
ATOM   14120  OG   SER  D  219       6.151    1.249   32.481   1.00  69.44           0
ATOM   14121  N    ARG  D  220       5.927   -2.085   29.774   1.00  69.37           N
ATOM   14122  CA   ARG  D  220       5.512   -2.999   28.716   1.00  71.76           C
ATOM   14123  C    ARG  D  220       5.616   -4.446   29.191   1.00  71.81           C
ATOM   14124  O    ARG  D  220       4.716   -5.251   28.935   1.00  71.49           0
ATOM   14125  CB   ARG  D  220       6.356   -2.788   27.454   1.00  76.81           C
ATOM   14126  N    ARG  D  221       6.707   -4.767   29.890   1.00  70.35           N
ATOM   14127  CA   ARG  D  221       6.872   -6.093   30.493   1.00  74.56           C
ATOM   14128  C    ARG  D  221       5.765   -6.334   31.515   1.00  71.67           C
ATOM   14129  O    ARG  D  221       5.283   -7.460   31.671   1.00  68.98           O
ATOM   14130  CB   ARG  D  221       8.248   -6.238   31.152   1.00  69.28           C
ATOM   14131  CG   ARG  D  221       9.299   -6.892   30.275   1.00  72.49           C
ATOM   14132  CD   ARG  D  221      10.616   -6.120   30.304   1.00  70.32           C
ATOM   14133  NE   ARG  D  221      11.349   -6.271   31.556   1.00  71.51           N
ATOM   14134  CZ   ARG  D  221      12.343   -5.473   31.937   1.00  75.38           C
ATOM   14135  NH1  ARG  D  221      12.705   -4.452   31.178   1.00  78.91           N
ATOM   14136  NH2  ARG  D  221      12.967   -5.682   33.085   1.00  74.52           N
ATOM   14137  N    LEU  D  222       5.365   -5.265   32.199   1.00  66.42           N
ATOM   14138  CA   LEU  D  222       4.324   -5.353   33.214   1.00  69.15           C
ATOM   14139  C    LEU  D  222       3.000   -5.795   32.616   1.00  72.61           C
ATOM   14140  O    LEU  D  222       2.491   -6.871   32.959   1.00  71.70           O
ATOM   14141  CB   LEU  D  222       4.146   -4.014   33.932   1.00  69.44           C
ATOM   14142  CG   LEU  D  222       3.121   -4.001   35.068   1.00  65.38           C
ATOM   14143  CD2  LEU  D  222       3.273   -2.733   35.881   1.00  60.06           C
ATOM   14144  CD1  LEU  D  222       3.272   -5.226   35.972   1.00  64.77           C
ATOM   14145  N    GLU  D  223       2.449   -4.969   31.723   1.00  76.19           N
ATOM   14146  CA   GLU  D  223       1.169   -5.276   31.089   1.00  71.32           C
ATOM   14147  C    GLU  D  223       1.247   -6.608   30.357   1.00  70.60           C
ATOM   14148  O    GLU  D  223       0.279   -7.369   30.347   1.00  70.81           O
ATOM   1414 9  CB   GLU  D  223       0.737   -4.159   30.139   1.00  74.66           C
ATOM   14150  CG   GLU  D  223      -0.785   -4.120   29.925   1.00  86.29           C
ATOM   14151  CD   GLU  D  223      -1.374   -2.705   29.946   1.00  89.64           C
ATOM   14152  OE1  GLU  D  223      -0.719   -1.770   29.431   1.00  86.82           0
ATOM   14153  OE2  GLU  D  223      -2.494   -2.537   30.484   1.00  91.25           0
ATOM   14154  N    ASM  D  224       2.408   -6.910   29.779   1.00  69.00           N
ATOM   14155  CA   ASN  D  224       2.626   -8.233   29.181   1.00  73.79           C
ATOM   14156  C    ASN  D  224       2.409   -9.370   30.173   1.00  70.40           C
ATOM   14157  O    ASM  D  224       2.009  -10.468   29.788   1.00  70.92           0
ATOM   14158  CB   ASN  D  224       4.029   -8.349   28.589   1.00  73.21           C
ATOM   14159  CG   ASN  D  224       4.119   -7.808   27.174   1.00  75.72           C
ATOM   14160  OD1  ASN  D  224       3.101   -7.570   26.506   1.00  70.44           0
ATOM   14161  ND2  ASN  D  224       5.350   -7.624   26.701   1.00  70.19           N
ATOM   14162  N    LEU  D  225       2.660   -9.113   31.452   1.00  71.46           N
ATOM   14163  CA   LEU  D  225       2.404  -10.141   32.446   1.00  70.29           C
ATOM   14164  C    LEU  D  225       0.953  -10.141   32.932   1.00  70.44           C
ATOM   14165  O    LEU  D  225       0.388  -11.214   33.110   1.00  68.37           O
ATOM   14166  CB   LEU  D  225       3.350  -10.006   33.636   1.00  69.29           C
ATOM   14167  CG   LEU  D  225       3.278  -11.281   34.475   1.00  72.65           C
ATOM   14168  GDI  LEU  D  225       4.658  -11.856   34.760   1.00  71.10           C
ATOM   14169  CD2  LEU  D  225       2.503  -11.031   35.761   1.00  68.49           C
ATOM   14170  N    ILE  D  226       0.345   -8.968   33.143   1.00  69.69           N
ATOM   14171  CA   ILE  D  226      -1.053   -8.940   33.582   1.00  71.60           C
ATOM   14172  C    ILE  D  226      -1.956   -9.542   32.517   1.00  72.33           C
ATOM   1417 3  0    ILE  D  226      -2.946  -10.195   32.834   1.00  77.34           0
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ATOM	14174	CB	ILE	D	226	-1 .553	-7 .496	33..940	1 ,00	76..77	C
ATOM	14175	CGI	ILE	D	226	-1 ,764	--6..601	32.,700	1 ,00	79..03	C
ATOM	14176	CG2	ILE	D	226	-0 ..586	-6,,854	34..911	1 ,00	77 ,39	C
ATOM	14177	GDI	ILE	D	226	-3 ..161	-6 .671	32.,003	1 ,00	76..13	C
ATOM	14178	N	ALA	D	227	-1 „611	-9. .303	.3.1. ,254	1 ,00	70..84	N
ATOM	14179	CA	ALA	D	227	-2 .361	-9,,822	30..120	1 ,00	70,.69	C
ATOM	14180	C	ALA	D	227	-2 .542	-11 ,328	30..239	1 ,00	71 ,37	C
ATOM	14181	0	ALA	D	227	-3 „566	-11 .881	29.,824	1 ,00	68..70	0
ATOM	14182	CB	ALA	D	227	-1 .656	--9.,481	28..830	1 ,00	70..87	C
ATOM	14183	N	GLN	D	228	-1 .546	-11 ,994	30..812	1 ,00	69,.11	N
ATOM	14184	CA	GLN	D	228	-1 „641	-13..432	31.,008	I ,00	72 .0.3	C
ATOM	14185	C	GLN	D	228	-2 ..336	-13..731	32.,315	1 ,00	74 .63	C
ATOM	14186	O	GLN	D	228	-2 .393	-14 ,882	32. 738	1 ,00	78 ,34	O
ATOM	14187	CB	GLN	D	228	-0 ..266	-14 .087	30.,986	1 ,00	72 .94	C
ATOM	14188	CG	GLN	D	228	-0 „123	-15..157	29.,925	1 ,00	75..97	C
ATOM	14189	CD	GLN	D	228	0 ..769	-14 ,721	28.. 787	1 ,00	7.3,.29	C
ATOM	14190	OE1	GLN	D	228	1 .568	-15..497	28.,270	1 ,00	74 .69	0
ATOM	14191	NE2	GLN	D	228	0 „648	-13. 466	28.,400	1 ,00	75..75	N
ATOM	14192	N	LEU	D	229	-2 .859	-12.,688	32.. 954	1 ,00	76,.21	N
ATOM	14193	CA	LEU	D	229	-3 ..548	-12.,846	34.. 231	1 ,00	81 ,55	C
ATOM	14194	C	LEU	D	229	-5 „023	-12 .437	.34.,135	1 ,00	84 .10	C
ATOM	14195	O	LEU	D	229	-5 ..373	-11 ,240	34.,112	1 ,00	79..67	O
ATOM	14196	CB	LEU	D	229	-2 .832	-12.,050	35.. 324	1 ,00	81 ,03	C
ATOM	14197	CG	LEU	D	229	-1 „440	-12 .597	.35.,647	I ,00	76..35	C
ATOM	14198	CD1	LEU	D	229	-0 ..823	-11 ,857	36 ,815	1 ,00	65..95	C
ATOM	14199	CD2	LEU	D	229	-1 .516	-14 ,099	35. 909	1 ,00	79 ,77	C
ATOM	14200	O	PRO	D	230	-7 „762	-12 .722	3 6 ,213	I ,00	86..67	0
ATOM	14201	N	FRO	D	230	-5 „893	-13..458	34.,095	1 ,00	85..86	N
ATOM	142 02	CA	PRO	D	230	-7 ..338	-13.,312	33. 935	1 ,00	89 ,39	C
ATOM	14203	C	PRO	D	230	-7 .934	-12..431	35.,031	1 ,00	87 .36	C
ATOM	142 04	CB	FRO	D	230	-7 ,856	-14 .758	34.,046	1 ,00	84 .84	C
ATOM	14205	CG	PRO	D	230	-6 ..663	-15.,634	33.. 924	1 ,00	77 ,37	C
ATOM	14206	CD	PRO	D	230	-5 ..512	-14 .845	34.,420	1 ,00	80..92	C
ATOM	142 07	O	GLY	D	231	-8 „898	-8. 540	3 6 ,875	1 ,00	96..81	0
ATOM	14208	N	GLY	D	231	-8 ..609	-11 ,357	34.. 643	1 ,00	90,.64	N
ATOM	14209	CA	GLY	D	231	-9 ..318	-10,,527	35.. 601	1 ,00	89,.77	C
ATOM	14210	C	GLY	D	231	-8 „452	-9. 618	3 6 ,459	1 ,00	92 .77	C
ATOM	14211	O	GLU	D	232	-5 ..448	-7 ,787	35.,927	1 ,00	84 .19	0
ATOM	14212	N	GLU	D	232	-7 .219	-10.,039	36. 731	1 ,00	89 ,13	N
ATOM	14213	CA	GLU	D	232	-6 „339	-9 .248	.37.,581	I ,00	88..34	C
ATOM	14214	C	GLU	D	232	-6 ,079	-7 .886	36.,975	1 ,00	83..64	C
ATOM	14215	CB	GLU	D	232	-5 .007	-9.,954	37. 813	1 ,00	8.3 ,72	C
ATOM	14216	CG	GLU	D	232	-4 .166	-9 ,272	38.,873	1 ,00	81 .64	C
ATOM	14217	CD	GLU	D	232	-4 ,524	-9.. 731	40,,269	1 ,00	84 .88	C
ATOM	14218	OE1	GLU	D	232	-5 ..044	-10.,863	40.. .397	1 ,00	81 ,91	0
ATOM	14219	OE2	GLU	D	232	-4 .287	-8.,966	41 .233	1 ,00	84 .16	0
ATOM	14220	O	LYS	D	233	-3 „998	-6. 142	.37.,847	1 ,00	81 .91	0
ATOM	14221	N	LYS	D	233	-6 ..570	-6.,840	37..631	1 ,00	81 ,55	N
ATOM	14222	CA	LYS	D	233	-6 ..227	-5.,490	37 .228	1 ,00	85,.96	C
ATOM	14223	C	LYS	D	233	-4 „704	-5. 365	.37.,202	1 ,00	86..2.3	C
ATOM	14224	CB	LYS	D	233	-6 ..845	-4 ,454	38.,174	1 ,00	83..17	C
ATOM	14225	O	LYS	D	234	-1 .273	-3.,359	38.. 152	1 ,00	83,.69	0
ATOM	14226	N	LYS	D	234	-4 „195	-4 .406	3 6 ,435	I ,00	89..86	N
ATOM	14227	CA	LYS	D	234	-2 ..762	-4 ,139	36 ,426	1 ,00	88..13	C
ATOM	14228	C	LYS	D	234	-2 ..394	-.3.,273	37. 635	1 ,00	86 ,09	C
ATOM	14229	CB	LYS	D	234	-2 „338	-3.. 465	.35.,117	I ,00	85..26	C
ATOM	14230	O	ASM	D	235	-3 „348	-1 .937	41 „691	1 ,00	75..16	0
ATOM	142 31	N	ASN	D	235	-3 .352	-2.,453	38. 076	1 ,00	8.1 ,09	N
ATOM	14232	CA	ASN	D	235	-3 ,223	-1 ,652	39.,296	1 ,00	81 .00	C
ATOM	14233	C	ASM	D	235	-3 „465	-2 .461	40,,577	1 ,00	79..04	C
ATOM	14234	CB	ASN	D	235	-4 .197	-0.,473	39 .257	1 ,00	76,.18	C
ATOM	14235	CG	ASN	D	235	-3 ..593	0 ,762	38.,633	1 ,00	82 .29	C
ATOM	14236	OD1	ASN	D	235	-3 „180	1 .687	3 9 ,335	1 ,00	88..13	0

ATOM	14237	ND2	ASN	D	235	-3.538	0.791	37.306	1.00	90.62	N
ATOM	14238	O	GLY	D	236	-1.822	-4.254	42.213	1.00	69.55	O
ATOM	14239	N	GLY	D	236	-3.818	-3.733	40.409	1.00	76.74	N
ATOM	14240	CA	GLY	D	236	-4.088	-4.620	41.526	1.00	74.90	C
ATOM	14241	C	GLY	D	236	-2.905	-4.779	42.461	I.00	71.91	C
ATOM	14242	N	LEU	D	237	-3.113	-5.495	43.554	1.00	70.48	N
ATOM	14243	CA	LEU	D	237	-2.030	-5.719	44.493	1.00	69.09	C
ATOM	14244	C	LEU	D	237	-0.913	-6.484	43.789	I.00	70.04	C
ATOM	14245	O	LEU	D	237	0.262	-6.100	43.838	1.00	67.32	0
ATOM	14246	CB	LEU	D	237	-2.522	-6.485	45.717	1.00	63.80	C
ATOM	14247	CG	LEU	D	237	-1.499	-6.559	46.842	I.00	63.79	C
ATOM	14248	GDI	LEU	D	237	-1.050	-5.165	47.255	1.00	65.67	C
ATOM	14249	CD2	LEU	D	237	-2.067	-7.323	48.011	1.00	72.04	C
ATOM	14250	N	PHE	D	238	-1.303	-7.551	43.106	1.00	66.36	N
ATOM	14251	CA	FHE	D	238	-0.355	-8.394	42.425	1.00	64.20	C
ATOM	14252	C	PHE	D	238	0.401	-7.622	41.346	1.00	68.25	C
ATOM	14253	O	PHE	D	238	1.576	-7.881	41.110	1.00	71.31	0
ATOM	14254	CB	PHE	D	238	-1.055	-9.597	41.825	I.00	62.56	C
ATOM	14255	CG	PHE	D	238	-0.137	-10.736	41.541	1.00	69.38	C
ATOM	14256	CD1	PHE	D	238	0.152	-11.675	42.525	1.00	70.98	C
ATOM	14257	CD2	PHE	D	238	0.450	-10.873	40.303	I.00	65.82	C
ATOM	14258	CE1	PHE	D	238	1.003	-12.741	42.273	1.00	71.54	C
ATOM	14259	CE2	PHE	D	238	1.306	-11.942	40.044	1.00	72.06	C
ATOM	14260	CZ	PHE	D	238	1.579	-12.876	41.033	I.00	70.18	C
ATOM	14261	N	GLY	D	239	-0.261	-6.670	40.701	1.00	65.79	N
ATOM	14262	CA	GLY	D	239	0.388	-5.881	39.675	1.00	62.33	C
ATOM	14263	C	GLY	D	239	1.451	-4.977	40.262	I.00	68.28	C
ATOM	14264	O	GLY	D	239	2.564	-4.890	39.740	1.00	68.71	0
ATOM	14265	N	ASN	D	240	1.105	-4.306	41.357	1.00	70.41	N
ATOM	14266	CA	ASN	D	240	2.034	-3.416	42.051	1.00	70.18	C
ATOM	14267	C	ASN	D	240	3.246	-4.164	42.581	1.00	64.39	C
ATOM	14268	O	ASN	D	240	4.356	-3.634	42.611	1.00	65.49	0
ATOM	14269	CB	ASN	D	240	1.338	-2.696	43.205	1.00	71.42	C
ATOM	14270	CG	ASN	D	240	0.324	-1.676	42.732	I.00	73.16	C
ATOM	14271	OD1	ASN	D	240	0.452	-0.481	43.002	1.00	74.39	0
ATOM	14272	ND2	ASN	D	240	-0.698	-2.143	42.029	1.00	74.73	N
ATOM	14273	N	LEU	D	241	3.031	-5.397	43.011	I.00	65.10	N
ATOM	14274	CA	LEU	D	241	4.145	-6.226	43.435	1.00	65.34	C
ATOM	14275	C	LEU	D	241	5.041	-6.547	42.241	1.00	65.48	C
ATOM	14276	O	LEU	D	241	6.259	-6.475	42.344	I.00	65.34	O
ATOM	14277	CB	LEU	D	241	3.652	-7.511	44.096	1.00	64.96	C
ATOM	14278	CG	LEU	D	241	3.037	-7.396	45.494	1.00	66.01	C
ATOM	14279	CD1	LEU	D	241	2.375	-8.719	45.834	1.00	64.23	C
ATOM	14280	CD2	LEU	D	241	4.065	-7.014	46.554	1.00	59.79	C
ATOM	14281	N	ILE	D	242	4.439	-6.882	41.104	1.00	64.20	N
ATOM	14282	CA	ILE	D	242	5.220	-7.183	39.910	1.00	64.82	C
ATOM	14283	C	ILE	D	242	5.952	-5.922	39.450	I.00	65.58	C
ATOM	14284	O	ILE	D	242	7.121	-5.983	39.048	1.00	63.51	O
ATOM	14285	CB	ILE	D	242	4.343	-7.740	38.768	1.00	63.77	C
ATOM	14286	CGI	ILE	D	242	3.671	-9.038	39.191	I.00	57.39	C
ATOM	14287	CG2	ILE	D	242	5.181	-8.020	37.536	1.00	60.48	C
ATOM	14288	CD1	ILE	D	242	4.608	-10.239	39.180	1.00	68.57	C
ATOM	14289	N	ALA	D	243	5.264	-4.785	39.521	I.00	59.80	N
ATOM	14290	CA	ALA	D	243	5.884	-3.493	39.257	1.00	62.29	C
ATOM	14291	C	ALA	D	243	7.118	-3.305	40.139	1.00	67.11	C
ATOM	14292	O	ALA	D	243	8.194	-2.918	39.664	I.00	64.54	0
ATOM	14293	CB	ALA	D	243	4.885	-2.358	39.489	1.00	52.97	C
ATOM	14294	N	LEU	D	244	6.953	-3.586	41.429	1.00	68.82	N
ATOM	14295	CA	LEU	D	244	8.040	-3.438	42.388	1.00	66.23	C
ATOM	14296	C	LEU	D	244	9.216	-4.318	41.996	1.00	58.76	C
ATOM	14297	O	LEU	D	244	10.346	-3.859	41.973	1.00	59.22	O
ATOM	14298	CB	LEU	D	244	7.564	-3.778	43.801	1.00	63.16	C
ATOM	14299	CG	LEU	D	244	8.508	-3.329	44.916	I.00	61.26	C

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ATOM   14300   GDI  LEU  D  244        8.617   -1.810   44.964   1.00  63.46          C
ATOM   14301   CD2  LEU  D  244        8.049   --3.877  46.248   1.00  65.60          C
ATOM   14302   N    SER. D  245        8.921   -5.573   41.663   1.00  61.02          N
ATOM   14303   CA   SER  D  245        9.914   -6.548   41.228   1.00  64.12          C
ATOM   14304   C    SER  D  245       10.684   -6.095   39.992   1.00  67.28          C
ATOM   14305   O    SER  D  245       11.870   -6.393   39.863   1.00  64.27          0
ATOM   14306   CB   SER  D  245        9.254   -7.900   40.929   1.00  64.67          C
ATOM   14307   OG   SER  D  245        8.472   -8.363   42.014   1.00  66.69          0
ATOM   14308   N    LEU  D  246       10.006   --5.395  39.081   1.00  65.87          N
ATOM   14309   CA   LEU  D  246       10.628   -4.956   37.828   1.00  66.05          C
ATOM   14310   C    LEU  D  246       11.555   -3.772   .38.072  1.00  69.00          C
ATOM   14311   O    LEU  D  246       12.494   --3.529  37.301   1.00  71.49          0
ATOM   14312   CB   LEU  D  246        9.564   -4.598   36.777   1.00  64.55          C
ATOM   14313   CG   LEU  D  246        8.910   -5.817   36.124   1.00  61.02          C
ATOM   14314   CD2  LEU  D  246        9.922   --6.536  35.271   1.00  69.08          C
ATOM   14315   CD1  LEU  D  246        7.724   -5.451   35..301   1.00  59.09          C
ATOM   14316   O    GLY  D  247       12.113    0.429   39.655   1.00  59.43          0
ATOM   14317   N    GLY  D  247       11.301   -3.046   39.154   1.00  62.50          N
ATOM   14318   CA   GLY  D  247       12.174   -.1.956   39.542   1.00  61.08          C
ATOM   14319   C    GLY  D  247       11.478   -0.614   39.518   1.00  63.14          C
ATOM   14320   0    LEU  D  248        9.765    0.610   41.673   1.00  71.08          0
ATOM   14321   N    LEU  D  248       10.162   --0.650  39.356   1.00  66.17          N
ATOM   14322   CA   LEU  D  248        9.366    0.562   39.309   1.00  65.32          C
ATOM   14323   C    LEU  D  248        9.139    1.080   40.719   1.00  68..30          C
ATOM   14324   CB   LEU  D  248        8.041    0.297   38.596   1.00  69.22          C
ATOM   14325   CG   LEU  D  248        8.214   -0.159   37.141   1.00  63.33          C
ATOM   14326   CD1  LEU  D  248        6.941   -0.742   3 6.583  1.00  60.3 6          C
ATOM   14327   CD2  LEU  D  248        8.661    1.015   36.310   1.00  65.26          C
ATOM   14328   O    THR  D  249        5.960    3.835   42.644   1.00  70.92          0
ATOM   14329   N    THR  D  249        8.238    2.045   40.848   1.00  69.74          N
ATOM   14330   CA   THR  D  249        8.007    2.714   42.120   1.00  68.71          C
ATOM   14331   C    THR  D  249        6.526    2.754   42.454   1.00  68.88          C
ATOM   14332   CB   THR  D  249        8.560    4.156   42.097   1.00  71.93          C
ATOM   14333   OG1  THR  D  249        9.780    4.189   41.354   1.00  79.23          0
ATOM   14334   CG2  THR  D  249        8.837    4.666   43.506   1.00  70.94          C
ATOM   14335   O    PRO  D  250        4.766    2.439   44.937   1.00  71.13          0
ATOM   14336   N    PRO  D  250        5.894    1.576   42.551   1.00  65.42          N
ATOM   14337   CA   PRO  D  250        4.439    1.549   42.734   1.00  67.18          C
ATOM   14338   C    PRO  D  250        3.982    2.271   44.004   1.00  72.53          C
ATOM   14339   CB   PRO  D  250        4.118    0.052   42.810   1.00  68.58          C
ATOM   14340   CG   FRO  D  250        5.395   --0.596  43.262   1.00  68.10          C
ATOM   14341   CD   PRO  D  250        6.497    0.235   42.667   1.00  69.68          C
ATOM   14342   O    ASN  D  251        0.213    1.817   44.946   1.00  70.76          0
ATOM   14343   N    ASM  D  251        2.730    2.720   44.006   1.00  76.73          N
ATOM   14344   CA   ASN  D  251        2.091    3.310   45.176   1.00  7.1.80          C
ATOM   14345   C    ASN  D  251        1.039    2.337   45.706   1.00  71.77          C
ATOM   14346   CB   ASN  D  251        1.464    4.663   44.821   1.00  73.67          C
ATOM   14347   CG   ASN  D  251        0.905    5.402   46.034   1.00  76.66          C
ATOM   14348   OD1  ASN  D  251        0.280    4.810   46.906   1.00  78.26          0
ATOM   14349   ND2  ASN  D  251        1.131    6.708   46.084   1.00  74.12          N
ATOM   14350   O    PHE  D  252       -1.669    1.115   49.196   1.00  83.29          0
ATOM   14351   N    PHE  D  252        1.071    2.090   47.011   1.00  73.37          N
ATOM   14352   CA   PHE  D  252        0.159    1.129   47.617   1.00  74.77          C
ATOM   14353   C    PHE  D  252       -1.004    1.784   48.408   1.00  81.52          C
ATOM   14354   CB   PHE  D  252        0.953    0.174   48.522   1.00  76.95          C
ATOM   14355   CG   PHE  D  252        1.794   -0.845   47.765   1.00  73.92          C
ATOM   14356   CD1  PHE  D  252        1.240   --2.039  47.336   1.00  71.73          C
ATOM   14357   CD2  PHE  D  252        3.140   -0.609   47.502   1.00  71.45          C
ATOM   14358   CE1  PHE  D  252        2.009   -2.980   46.641   1.00  73.28          C
ATOM   14359   CE2  PHE  D  252        3.911   --1.543  46.817   1.00  69.66          C
ATOM   14360   CZ   PHE  D  252        3.342   -2.730   46..37 9  1.00  68.49          C
ATOM   14361   O    LYS  D  253       -4.616    3.285   49.432   1.00  88.66          0
ATOM   143 62   N    LYS  D  253       -.1.276    3.070   48.176   1.00  78.58          N
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ATOM   14363  CA   LYS  D  253      -2.335    3.774   48.917   1.00  82.61          C
ATOM   14364  C    LYS  D  253      -3.745    3.294   48.572   1.00  85.71          C
ATOM   14365  CB   LYS  D  253      -2.259    5.289   48.691   1.00  78.80          C
ATOM   14366  O    SER  D  254      -6.547    0.537   47.687   1.00  92.28          0
ATOM   14367  N    SER  D  254      -3.979    2.911   47.322   1.00  84.97          N
ATOM   14368  CA   SER  D  254      -5.300    2.430   46.934   1.00  84.48          C
ATOM   14369  C    SER  D  254      -5.470    0.962   47.275   1.00  88.64          C
ATOM   14370  CB   SER  D  254      -5.547    2.643   45.441   1.00  80.30          C
ATOM   14371  OG   SER  D  254      -5.787    4.008   45.172   1.00  96.06          0
ATOM   14372  O    ASN  D  255      -5.582   -2.679   48.854   1.00  84.68          0
ATOM   14373  N    ASM  D  255      -4.400    0.194   47.095   1.00  83.28          N
ATOM   14374  CA   ASN  D  255      -4.426   -1.249   47.296   1.00  80.66          C
ATOM   14375  C    ASN  D  255      -4.917   -1.651   48.687   1.00  84.72          C
ATOM   14376  CB   ASN  D  255      -3.031   -1.828   47.051   1.00  81.19          C
ATOM   14377  CG   ASN  D  255      -2.576   -1.671   45.611   1.00  82.04          C
ATOM   14378  OD1  ASN  D  255      -2.388   -2.659   44.904   1.00  81.86          0
ATOM   14379  ND2  ASN  D  255      -2.407   -0.423   45.164   1.00  83.79          N
ATOM   14380  O    PHE  D  256      -5.799    0.292   52.828   1.00  86.73          O
ATOM   14381  N    PHE  D  256      -4.581   -0.835   49.682   1.00  84.81          N
ATOM   14382  CA   PHE  D  256      -4.999   -1.087   51.053   1.00  84.61          C
ATOM   14383  C    PHE  D  256      -5.738    0.118   51.615   1.00  86.48          C
ATOM   14384  CB   PHE  D  256      -3.807   -1.401   51.958   1.00  81.89          C
ATOM   14385  CG   PHE  D  256      -2.998   -2.593   51.541   1.00  77.61          C
ATOM   14386  CD1  PHE  D  256      -3.400   -3.874   51.881   1.00  73.13          C
ATOM   14387  CD2  PHE  D  256      -1.809   -2.427   50.852   1.00  75.52          C
ATOM   14388  CE1  PHE  D  256      -2.648   -4.971   51.512   1.00  76.29          C
ATOM   14389  CE2  PHE  D  256      -1.048   -3.519   50.480   1.00  75.78          C
ATOM   14390  CZ   PHE  D  256      -1.465   -4.793   50.811   1.00  75.76          C
ATOM   14391  O    ASP  D  257      -7.242    2.908   53.342   1.00  85.28          0
ATOM   14392  N    ASP  D  257      -6.265    0.954   50.727   1.00  87.59          N
ATOM   14393  CA   ASP  D  257      -7.126    2.079   51.101   1.00  90.57          C
ATOM   14394  C    ASP  D  257      -6.609    2.879   52.295   1.00  85.37          C
ATOM   14395  CB   ASP  D  257      -8.548    1.579   51.397   1.00  97.97          C
ATOM   14396  CG   ASP  D  257      -9.428    1.510   50.141   1.00104.49          C
ATOM   14397  OD2  ASP  D  257      -9.535    0.413   49.536   1.00104.37          0
ATOM   14398  OD1  ASP  D  257     -10.022    2.556   49.769   1.00102.03          0
ATOM   14399  O    LEU  D  258      -5.983    6.219   52.395   1.00  77.47          0
ATOM   14400  N    LEU  D  258      -5.464    3.529   52.125   1.00  84.82          N
ATOM   14401  CA   LEU  D  258      -4.825    4.274   53.208   1.00  80.89          C
ATOM   14402  C    LEU  D  258      -5.151    5.766   53.172   1.00  79.52          C
ATOM   14403  CB   LEU  D  258      -3.306    4.079   53.161   1.00  81.32          C
ATOM   14404  CG   LEU  D  258      -2.772    2.662   53.420   1.00  83.86          C
ATOM   14405  CD1  LEU  D  258      -2.775    1.839   52.155   1.00  86.52          C
ATOM   14406  CD2  LEU  D  258      -1.374    2.688   54.016   1.00  84.31          C
ATOM   14407  O    ALA  D  259      -4.025    9.555   52.518   1.00  81.52          0
ATOM   14408  N    ALA  D  259      -4.487    6.527   54.030   1.00  79.97          N
ATOM   14409  CA.  ALA  D  259      -4.751    7.952   54.141   1.00  78.30          C
ATOM   14410  C    ALA  D  259      -3.702    8.739   53.383   1.00  82.62          C
ATOM   14411  CB   ALA  D  259      -4.779    8.375   55.597   1.00  79.36          C
ATOM   14412  O    GLU  D  260      -1.227    7.041   51.886   1.00  79.12          0
ATOM   14413  N    GLU  D  260      -2.440    8.489   53.726   1.00  82.10          N
ATOM   14414  CA   GLU  D  260      -1.317    9.125   53.057   1.00  76.64          C
ATOM   14415  C    GLU  D  260      -0.752    8.165   52.016   1.00  74.95          C
ATOM   14416  CB   GLU  D  260      -0.252    9.540   54.073   1.00  70.84          C
ATOM   14417  O    ASP  D  261       2.127    6.700   51.956   1.00  76.19          O
ATOM   14418  N    ASP  D  261       0.247    8.606   51.259   1.00  77.10          N
ATOM   14419  CA   ASP  D  261       0.827    7.758   50.221   1.00  76.24          C
ATOM   14420  C    ASP  D  261       1.661    6.623   50.821   1.00  78.20          C
ATOM   14421  CB   ASP  D  261       1.684    8.590   49.261   1.00  74.38          C
ATOM   14422  CG   ASP  D  261       0.867    9.240   48.149   1.00  82.31          C
ATOM   14423  OD1  ASP  D  261       0.132    8.516   47.439   1.00  79.61          0
ATOM   14424  OD2  ASP  D  261       0.956   10.480   47.986   1.00  88.03          0
ATOM   14425  O    ALA  D  262       3.320    2.907   48.719   1.00  72.55          0
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ATOM   14426  N    ALA D 262       1.837   5.562  50.047  1.00 78.02          N
ATOM   14427  CA   ALA D 262       2.710   4.469  50.441  1.00 72.53          C
ATOM   14428  C    ALA D 262       3.520   4.009  49.240  1.00 75.55          C
ATOM   14429  CB   ALA D 262       1.912   3.331  51.016  1.00 75.98          C
ATOM   14430  O    LYS D 263       7.270   4.246  48.864  1.00 71.52          0
ATOM   14431  N    LYS D 263       4.433   4.870  48.801  1.00 79.54          N
ATOM   14432  CA   LYS D 263       5.245   4.597  47.620  1.00 75.16          C
ATOM   14433  C    LYS D 263       6.524   3.849  47.972  1.00 72.76          C
ATOM   14434  CB   LYS D 263       5.576   5.901  46.889  1.00 75.26          C
ATOM   14435  CG   LYS D 263       4.444   6.412  46.000  1.00 75.73          C
ATOM   14436  CD   LYS D 263       4.883   7.582  45.141  1.00 66.96          C
ATOM   14437  CE   LYS D 263       4.731   8.888  45.890  1.00 82.37          C
ATOM   14438  NZ   LYS D 263       5.082  10.062  45.033  1.00 82.83          N
ATOM   14439  O    LEU D 264       8.399   1.741  45.158  1.00 69.32          O
ATOM   14440  N    LEU D 264       6.769   2.764  47.249  1.00 72.24          N
ATOM   14441  CA   LEU D 264       7.901   1.886  47.529  1.00 75.77          C
ATOM   14442  C    LEU D 264       8.835   1.706  46.313  1.00 73.61          C
ATOM   14443  CB   LEU D 264       7.394   0.523  48.015  1.00 72.28          C
ATOM   14444  CG   LEU D 264       6.574   0.526  49.307  1.00 75.10          C
ATOM   14445  CD1  LEU D 264       6.493  -0.862  49.906  1.00 70.61          C
ATOM   14446  CD2  LEU D 264       7.169   1.488  50.315  1.00 79.09          C
ATOM   14447  O    GLR D 265      13.157   1.297  46.680  1.00 67.05          0
ATOM   14448  N    GLN D 265      10.125   1.533  46.580  1.00 66.42          N
ATOM   14449  CA   GLN D 265      11.079   1.347  45.500  1.00 71.93          C
ATOM   14450  C    GLR D 265      12.332   0.672  46.013  1.00 67.06          C
ATOM   14451  CB   GLN D 265      11.435   2.681  44.846  1.00 70.54          C
ATOM   14452  CG   GLN D 265      12.077   2.524  43.476  1.00 72.87          C
ATOM   14453  CD   GLN D 265      12.913   3.723  43.069  1.00 78.15          C
ATOM   14454  OE1  GLN D 265      13.073   4.682  43.832  1.00 78.98          0
ATOM   14455  NE2  GLN D 265      13.461   3.669  41.860  1.00 77.75          N
ATOM   14456  O    LEU D 266      15.719  --0.987  47.050  1.00 71.48          0
ATOM   14457  N    LEU D 266      12.467  -0.602  45.674  1.00 63.68          N
ATOM   14458  CA   LEU D 266      13.556  -1.444  46.159  1.00 63.24          C
ATOM   14459  C    LEU D 266      14.945  -0.806  46.127  1.00 64.40          C
ATOM   14460  CB   LEU D 266      13.565  -2.739  45.365  1.00 59.52          C
ATOM   14461  CG   LEU D 266      12.291  -3.544  45.636  1.00 64.98          C
ATOM   14462  CD1  LEU D 266      12.125  -4.707  44.664  1.00 67.20          C
ATOM   14463  CD2  LEU D 266      12.311  -4.043  47.070  1.00 62.52          C
ATOM   14464  O    SER D 267      18.049   1.939  46.261  1.00 68.63          0
ATOM   14465  N    SER D 267      15.249  -0.042  45.087  1.00 70.11          N
ATOM   14466  CA   SER D 267      16.572   0.578  44.946  1.00 66.60          C
ATOM   14467  C    SER D 267      16.879   1.708  45.941  1.00 68.75          C
ATOM   14468  CB   SER D 267      16.736   1.119  43.522  1.00 65.97          C
ATOM   14469  OG   SER D 267      15.597   1.873  43.130  1.00 70.12          0
ATOM   14470  O    LYS D 268      16.142   2.103  49.139  1.00 68.60          0
ATOM   14471  N    LYS D 268      15.847   2.422  46.404  1.00 69.52          N
ATOM   14472  CA.  LYS D 268      16.046   3.588  47.272  1.00 68.52          C
ATOM   14473  C    LYS D 268      16.531   3.152  48.646  1.00 72.05          C
ATOM   14474  CB   LYS D 268      14.765   4.416  47.399  1.00 73.09          C
ATOM   14475  O    ASP D 269      17.571   3.169  52.792  1.00 82.60          0
ATOM   14476  N    ASP D 269      17.389   3.970  49.253  1.00 80.61          N
ATOM   14477  CA   ASP D 269      18.095   3.607  50.485  1.00 82.64          C
ATOM   14478  C    ASP D 269      17.188   3.612  51.707  1.00 81.83          C
ATOM   14479  CB   ASP D 269      19.281   4.556  50.719  1.00 81.64          C
ATOM   14480  CG   ASP D 269      18.946   6.008  50.414  1.00 85.40          C
ATOM   14481  OD2  ASP D 269      19.455   6.897  51.131  1.00 90.19          O
ATOM   14482  OD1  ASP D 269      18.182   6.262  49.457  1.00 82.42          O
ATOM   14483  O    THR D 270      13.044   3.197  53.369  1.00 84.14          0
ATOM   14484  N    THR D 270      15.979   4.113  51.518  1.00 83.44          N
ATOM   14485  CA   THR D 270      15.047   4.284  52.615  1.00 82.58          C
ATOM   14486  C    THR D 270      13.997   3.176  52.594  1.00 81.48          C
ATOM   14487  CB   THR D 270      14.380   5.669  52.538  1.00 79.45          C
ATOM   14488  OG1  THR D 270      13.551   5.741  51.375  1.00 80.35          0
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ATOM   14489   CG2  THR  D  270       15.440    6.750   52.429   1.00  81.81          C
ATOM   14490   N    TYR  D  271       14.196    2.196   51.717   1.00  75.47          M
ATOM   14491   CA   TYR  D  271       13.168    1.199   51.436   1.00  74.07          C
ATOM   144 92  C    TYR  D  271       12.816    0.325   52.632   1.00  75.52          C
ATOM   144 93  0    TYR  D  271       11.645    0.054   52.886   1.00  76.96          0
ATOM   14494   CB   TYR  D  271       13.591    0.291   50.280   1.00  71.04          C
ATOM   14495   CG   TYR  D  271       12.667   -0.890   50.120   1.00  67.24          C
ATOM   144 96  GDI  TYR  D  271       11.448   -0.754   49.475   1.00  67.36          C
ATOM   144 97  CD2  TYR  D  271       12.998   -2.133   50.634   1.00  64.50          C
ATOM   14498   CE1  TYR  D  271       10.599   -1.819   49.339   1.00  65.71          C
ATOM   144 99  CE2  TYR  D  271       12.146   -3.203   50.504   1.00  60.92          C
ATOM   14500   CZ   TYR  D  271       10.951   --3.039   49.858   1.00  60.98          C
ATOM   14501   OH   TYR  D  271       10.105   -4.108   49.716   1.00  64.09          0
ATOM   14502   N    ASP  D  272       13.825   -0.157   53.341   1.00  77.17          M
ATOM   14503   CA   ASP  D  272       13.567   --1.022   54.477   1.00  77.89          C
ATOM   14504   C    ASP  D  272       12.740   -0.290   55.526   1.00  79.59          C
ATOM   14505   O    ASP  D  272       11.889   -0.887   56.167   1.00  81.87          0
ATOM   14506   CB   ASP  D  272       14.874   -1.531   55.066   1.00  74..34          C
ATOM   14507   CG   ASP  D  272       15.480   -2.635   54.234   1.00  83.44          C
ATOM   14508   OD2  ASP  D  272       16.726   -2.773   54.210   1.00  84.97          0
ATOM   14509   OD1  ASP  D  272       14.693   -3..365   53.594   1.00  81..34          0
ATOM   14510   K    ASP  D  273       12.985    1.005   55.684   1.00  73.26          K
ATOM   14511   CA   ASP  D  273       12.171    1.827   56.574   1.00  85.18          C
ATOM   14512   C    ASP  D  273       10.791    2.055   55.973   1.00  83.62          C
ATOM   14513   O    ASP  D  273        9.782    1.935   56.658   1.00  84.24          0
ATOM   14514   CB   ASP  D  273       12.851    3.176   56.853   1.00  88.46          C
ATOM   14515   CG   ASP  D  273       14.034    3.050   57.801   1.00  95.69          C
ATOM   14516   OD1  ASP  D  273       13.863    2.424   58.871   1.00  97.40          0
ATOM   14517   OD2  ASP  D  273       15.133    3.563   57.476   1.00  98.92          0
ATOM   14518   N    ASP  D  274       10.765    2.381   54.684   1.00  81.22          M
ATOM   14519   CA   ASP  D  274        9.534    2.691   53.972   1.00  79.01          C
ATOM   14520   C    ASP  D  274        8.547    1.535   53.988   1.00  79.14          C
ATOM   14521   O    ASP  D  274        7.332    1.733   54.047   1.00  83.57          0
ATOM   14522   CB   ASP  D  274        9.856    3.076   52.533   1.00  77.83          C
ATOM   14523   CG   ASP  D  274       10.558    4.412   52.437   1.00  82.53          C
ATOM   14524   OD2  ASP  D  274       11.406    4.575   51.539   1.00  85.13          0
ATOM   14525   OD1  ASP  D  274       10.267    5.295   53.269   1.00  83.41          0
ATOM   14526   K    LEU  D  275        9.082    0.326   53.920   1.00  77.59          K
ATOM   14527   CA   LEU  D  275        8.278   -0.874   53.966   1.00  73.36          C
ATOM   14528   C    LEU  D  275        7.703   -1.053   55.360   1.00  77.73          C
ATOM   14529   O    LEU  D  275        6.560   --1.469   55.516   1.00  78.00          0
ATOM   14530   CB   LEU  D  275        9.114   -2.088   53.577   1.00  71.05          C
ATOM   14531   CG   LEU  D  275        8.353   -3.409   53.651   1.00  73.18          C
ATOM   14532   CD1  LEU  D  275        7.118   --3.365   52.753   1.00  73.23          C
ATOM   14533   CD2  LEU  D  275        9.235   -4.575   53.288   1.00  60.00          C
ATOM   14534   N    ASP  D  276        8.503   -0.723   56.372   1.00  80.11          M
ATOM   14535   CA.  ASP  D  276        8.104   -0.904   57.767   1.00  78.52          C
ATOM   14536   C    ASP  D  276        7.010    0.064   58.163   1.00  80.58          C
ATOM   14537   O    ASP  D  276        6.079   -0.311   58.869   1.00  79.52          0
ATOM   14538   CB   ASP  D  276        9.300   -0.749   58.698   1.00  79.77          C
ATOM   14539   CG   ASP  D  276       10.182   --1.985   58.710   1.00  89.26          C
ATOM   14540   OD1  ASP  D  276        9.871   -2.944   57.964   1.00  86.40          0
ATOM   14541   OD2  ASP  D  276       11.190   -1.994   59.453   1.00  95.11          0
ATOM   14542   K    ASN  D  277        7.118    1.308   57.706   1.00  81.81          K
ATOM   14543   CA   ASN  D  277        6.049    2.262   57.915   1.00  81.97          C
ATOM   14544   C    ASM  D  277        4.769    1.765   57.279   1.00  81.45          C
ATOM   14545   O    ASM  D  277        3.680    2.049   57.764   1.00  85.08          0
ATOM   14546   CB   A.SM D  277        6..396    3.630   57..348   1.00  87.28          C
ATOM   14547   CG   ASM  D  277        5.221    4.591   57.417   1.00  91.76          C
ATOM   14548   OD1  ASM  D  277        4.628    4.947   56.396   1.00101 .10          0
ATOM   14549   KD2  ASN  D  277        4.860    4.996   58.633   1.00  94.09          K
ATOM   14550   N    LEU  D  278        4.905    1.022   56.189   1.00  79.24          M
ATOM   14551   CA.  LEU  D  278        3.745    0.454   55.532   1.00  77.80          C
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ATOM	14552	c	LEU	D	278	3.233	-0.756	56.292	1.00	73.48	c
ATOM	14553	O	LEU	D	278	2,055	-0.840	56,607	1,00	72.71	O
ATOM	14554	CB	LEU	D	278	4.059	0,058	54:089	1,00	79,21	C
ATOM	14555	CG	LEU	D	278	2.816	-0:508	53:388	1.00	76.49	c
ATOM	14556	GDI	LEU	D	278	1,719	0.537	53,358	1,00	71,77	c
ATOM	14557	CD2	LEU	D	278	3.101	-1,021	51:988	1,00	74,53	c
ATOM	14558	N	LEU	D	279	4.119	-1,699	56:573	1,00	76,22	N
ATOM	14559	CA.	LEU	D	279	3,730	-2.930	57,257	1,00	76,86	C
ATOM	14560	C	LEU	D	279	3.146	-2,670	58:651	1,00	73.46	C
ATOM	14561	O	LEU	D	279	2.397	-3,484	59:177	1,00	74,61	O
ATOM	14562	CB	LEU	D	279	4,929	-3.873	57,360	I,00	75.67	C
ATOM	14563	CG	LEU	D	279	5.441	-4.409	56:021	1,00	77.39	c
ATOM	14564	GDI	LEU	D	279	6.727	-5,221	56.204	1,00	73,88	c
ATOM	14565	CD2	LEU	D	279	4.356	-5:236	55:332	1.00	74.76	c
ATOM	14566	N	ALA	D	280	3,491	-1.530	59,238	1,00	71.69	N
ATOM	14567	CA	ALA	D	280	2.946	-1,133	60:529	1,00	71,56	C
ATOM	14568	c	ALA	D	280	1.471	-0:829	60:376	1.00	74.16	c
ATOM	14569	0	ALA	D	280	0,625	-1.461	60,997	1,00	73,33	0
ATOM	14570	CB	ALA	D	280	3.685	0,076	61:075	1,00	71,65	c
ATOM	14571	N	GLN	D	281	1.192	0,148	59.519	1,00	73,86	N
ATOM	14572	CA.	GLN	D	281	-0,150	0.534	59,129	1,00	65,41	C
ATOM	14573	C	GLN	D	281	-0.979	-0:591	58:517	1,00	68.34	C
ATOM	14574	O	GLN	D	281	-2.193	-0,542	58.558	1,00	71,02	O
ATOM	14575	CB	GLN	D	281	-0,069	1:692	58,136	I,00	65.94	C
ATOM	14576	N	ILE	D	282	-0.340	-1:609	57:954	1,00	76.65	N
ATOM	14577	CA	ILE	D	282	-1.067	-2,532	57.075	1,00	77,39	C
ATOM	14578	C	ILE	D	282	-1,112	-3:983	57,539	I,00	74.80	C
ATOM	14579	O	ILE	D	282	-2,059	-4.699	57,225	1,00	73.89	0
ATOM	14580	CB	ILE	D	282	-0.485	-2,479	55.629	1,00	74,97	c
ATOM	14581	CGI	ILE	D	282	-1.601	-2:160	54,646	1.00	69.43	c
ATOM	14582	CG2	ILE	D	282	0,304	-3.730	55,249	1,00	73.03	c
ATOM	14583	GD1	ILE	D	282	-2.011	-0,741	54.767	1,00	79,72	c
ATOM	14584	N	GLY	D	283	-0.099	-4:422	58.280	1.00	72.86	N
ATOM	14585	C	GLY	D	283	1,165	-6.550	58,566	1,00	77,54	C
ATOM	14586	CA	GLY	D	283	-0.108	-5,767	58.809	1,00	69,98	C
ATOM	14587	O	GLY	D	283	1.693	-8,587	57.460	1,00	81,51	O
ATOM	14588	N	ASP	D	284	1,648	-7.183	59,625	1,00	73,93	N
ATOM	14589	CA	ASP	D	284	2.725	-8.162	59:564	1,00	77.02	C
ATOM	14590	C	ASP	D	284	2.404	-9,299	58.596	1,00	77,00	c
ATOM	14591	O	ASP	D	284	3,302	-9:955	58,072	I,00	82.96	0
ATOM	14592	CB	ASP	D	284	2,980	-8.703	60,977	1,00	79.98	c
ATOM	14593	CG	ASP	D	284	3.884	-9,894	61.003	1,00	87,89	c
ATOM	14594	OD2	ASP	D	284	3.366	-11:033	61:118	1.00	89.81	0
ATOM	14595	OD1	ASP	D	284	5,114	-9.684	60,935	1,00	96.99	0
ATOM	14596	N	GLN	D	285	1.118	-9,529	58..359	1,00	76,26	N
ATOM	14597	CA	GLN	D	285	0.667	-10:603	57.479	1.00	74.78	c
ATOM	14598	C	GLN	D	285	1,228	-10.465	56,064	1,00	79,19	C
ATOM	14599	O	GLN	D	285	1.472	-11,458	55..376	1,00	78,01	0
ATOM	14600	CB	GLN	D	285	-0.853	-10,615	57.437	1,00	71,67	c
ATOM	14601	CG	GLN	D	285	-1,448	-9.221	57,315	1,00	70,30	c
ATOM	14602	CD	GLN	D	285	-2:949	-9,242	57:431	1,00	73.30	c
ATOM	14603	OE1	GLN	D	285	-3.552	-10,314	57.510	1,00	72,49	0
ATOM	14604	NE2	GLN	D	285	-3,569	-8:063	57,446	I,00	72.51	N
ATOM	14605	N	TYR	D	286	1:429	-9:216	55:652	1,00	80.56	N
ATOM	14606	CA	TYR	D	286	1.901	-8,880	54.314	1,00	80,17	C
ATOM	14607	C	TYR	D	286	3,421	-8:737	54,219	I,00	79.21	C
ATOM	14608	O	TYR	D	286	3,913	-7.935	53,427	1,00	77.96	O
ATOM	14609	CB	TYR	D	286	1.256	-7,567	53.845	1,00	71,59	c
ATOM	14610	CG	TYR	D	286	-0,241	-7:619	53:754	1.00	75.29	c
ATOM	14611	CD1	TYR	D	286	-0,868	-8.544	52,936	1,00	76.74	c
ATOM	14612	CD2	TYR	D	286	-1.030	-6,738	54.477	1,00	72,15	c
ATOM	14613	CE1	TYR	D	286	-2.237	-8:597	52.847	1.00	77.52	c
ATOM	14614	CE2	TYR	D	286	-2,396	-6.777	54,393	1,00	71,71	c

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ATOM  14615  CZ   TYR D 286     -2.999  -7.709  53.574  1.00 76.39           C
ATOM  14616  OH   TYR D 286     -4.368  -7.758  53.479  1.00 78.49           O
ATOM  14617  N    ALA D 287      4.170  -9.492  55.016  1.00 77.81           N
ATOM  14618  CA   ALA D 287      5.625  -y.321  55.024  1.00 78.97           C
ATOM  14619  C    ALA D 287      6.329 -10.393  54.201  1.00 79.43           C
ATOM  14620  O    ALA D 287      7.400 -10.148  53.658  1.00 79.30           0
ATOM  14621  CB   ALA D 287      6.155  -9.319  56.443  1.00 78.67           C
ATOM  14622  N    ASP D 288      5.739 -11.583  54.125  1.00 78.96           N
ATOM  14623  CA   ASP D 288      6.277 -12.628  53.267  1.00 77.20           C
ATOM  14624  c    ASP D 288      6.039 -12.257  51.803  1.00 79.13           C
ATOM  14625  0    ASP D 288      6.827 -12.606  50.912  1.00 79.15           0
ATOM  14626  CB   ASP D 288      5.644 -13.978  53.589  1.00 73.82           C
ATOM  14627  CG   ASP D 288      6.280 -14.647  54.784  1.00 81.24           C
ATOM  14628  OD1  ASP D 288      7.420 -14.273  55.135  1.00 77.71           0
ATOM  14629  OD2  ASP D 288      5.646 -15.554  55.366  1.00 83.66           0
ATOM  14630  N    LEU D 289      4.943 -11.538  51.580  1.00 77.42           N
ATOM  14631  CA   LEU D 289      4.558 -11.070  50.265  1.00 72.75           C
ATOM  14632  C    LEU D 289      5.651 -10.183  49.710  1.00 70.40           C
ATOM  14633  O    LEU D 289      6.317 -10.540  48.741  1.00 71.94           O
ATOM  14634  CB   LEU D 289      3.230 -10.316  50.335  1.00 72.99           C
ATOM  14635  CG   LEU D 289      2.472 -10.172  49.019  1.00 70.44           C
ATOM  14636  CD2  LEU D 289      1.174  -9.428  49.227  1.00 64.12           C
ATOM  14637  CD1  LEU D 289      2.228 -11.532  48.363  1.00 71.10           C
ATOM  14638  N    PHE D 290      5.860  -9.040  50.347  1.00 69.82           N
ATOM  14639  CA   PHE D 290      6.897  -8.119  49.904  1.00 71.68           C
ATOM  14640  C    PHE D 290      8.288  -8.751  49.911  1.00 68.60           C
ATOM  14641  O    PHE D 290      9.184  -8.287  49.216  1.00 70.70           0
ATOM  14642  CB   PHE D 290      6.890  -6.854  50.760  1.00 70.13           C
ATOM  14643  CG   PHE D 290      5.735  -5.934  50.471  1.00 69.53           C
ATOM  14644  CD2  PHE D 290      5.893  -4.842  49.633  1.00 69.59           C
ATOM  14645  CD1  PHE D 290      4.490  -6.164  51.033  1.00 68.32           C
ATOM  14646  CE2  PHE D 290      4.829  -3.988  49.367  1.00 72.48           C
ATOM  14647  CE1  PHE D 290      3.425  -5.320  50.773  1.00 68.21           C
ATOM  14648  CZ   PHE D 290      3.592  -4.227  49.941  1.00 70.13           C
ATOM  14649  N    LEU D 291      8.469  -9.816  50.680  1.00 71.46           N
ATOM  14650  CA   LEU D 291      9.749 -10.502  50.696  1.00 70.03           C
ATOM  14651  C    LEU D 291      9.904 -11.277  49.393  1.00 71.48           C
ATOM  14652  O    LEU D 291     10.953 -11.226  48.742  1.00 69.53           0
ATOM  14653  CB   LEU D 291      9.859 -11.432  51.902  1.00 67.33           C
ATOM  14654  CG   LEU D 291     11.040 -12.404  51.872  1.00 67.81           C
ATOM  14655  CD2  LEU D 291     10.896 -13.455  52.958  1.00 73.85           C
ATOM  14656  GDI  LEU D 291     12.373 -11.684  51.988  1.00 64.71           C
ATOM  14657  N    ALA D 292      8.839 -11.978  49.018  1.00 68.45           N
ATOM  14658  CA   ALA D 292      8.792 -12.708  47.766  1.00 66.70           C
ATOM  14659  C    ALA D 292      9.144 -11.810  46.580  1.00 69.51           C
ATOM  14660  O    ALA D 292      9.936 -12.190  45.714  1.00 73.31           0
ATOM  14661  CB   ALA D 292      7.425 -13.318  47.576  1.00 69.96           C
ATOM  14662  N    ALA D 293      8.568 -10.614  46.558  1.00 68.57           N
ATOM  14663  CA   ALA D 293      8.776  -9.664  45.465  1.00 69.72           C
ATOM  14664  C    ALA D 293     10.233  -9.232  45.344  1.00 70.26           C
ATOM  14665  O    ALA D 293     10.799  -9.230  44.250  1.00 71.10           0
ATOM  14666  CB   ALA D 293      7.881  -8.446  45.648  1.00 62.29           C
ATOM  14667  N    LYS D 294     10.836  -8.861  46.468  1.00 71.57           N
ATOM  14668  CA   LYS D 294     12.215  -8.389  46.467  1.00 71.41           C
ATOM  14669  C    LYS D 294     13.123  -9.458  45.881  1.00 70.44           C
ATOM  14670  O    LYS D 294     14.044  -9.170  45.112  1.00 67.12           0
ATOM  14671  CB   LYS D 294     12.650  -8.009  47.883  1.00 72.88           C
ATOM  14672  CG   LYS D 294     14.144  -8.024  48.116  1.00 73.79           C
ATOM  14673  CD   LYS D 294     14.449  -7.769  49.575  1.00 75.50           C
ATOM  14674  CE   LYS D 294     15.824  -8.293  49.958  1.00 86.32           C
ATOM  14675  NZ   LYS D 294     16.161  -7.937  51.368  1.00 84.92           N
ATOM  14676  N    ASN D 295     12.829 -10.704  46.220  1.00 71.30           N
ATOM  14677  CA.  ASM D 295     13.566 -11.816  45.665  1.00 66.96           C
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ATOM   14678   c    ASN  D  295      13.374  --11.939   44.162   1.00  68.38          c
ATOM   14679   O    ASM  D  295      14.335  --12.164   43.430   1.00  69.88          O
ATOM   14680   CB   ASN  D  295      13.162  -13.097    46..376   1.00  75.43          c
ATOM   14681   CG   ASN  D  295      13.820  --13.224   47.740   1.00  80.01          c
ATOM   14682   OD1  ASN  D  295      15.048  -13.120    47.865   I.00  81.3.3          0
ATOM   14683   ND2  ASN  D  295      13.010  -13.423    48.771   1.00  7.1.90          N
ATOM   14684   N    LEU  D  296      12.136  -11.783    43.705   1.00  70.18          N
ATOM   14685   CA.  LEU  D  296      11.851  -11.727    42.276   I.00  68.63          C
ATOM   14686   C    LEU  D  296      12.727  -10.680    41.623   1.00  67.37          C
ATOM   14687   O    LEU  D  296      13.452  -10.960    40.672   1.00  65.67          O
ATOM   14688   CB   LEU  D  296      10.384  -11.400    42.032   I.00  66.99          c
ATOM   14689   CG   LEU  D  296       9.878  -11.506    40.596   1.00  70.13          c
ATOM   14690   GDI  LEU  D  296      10.279  -12.832    39.984   1.00  70.45          c
ATOM   14691   CD2  LEU  D  296       8.366  -11.343    40.573   1.00  69.37          c
ATOM   14692   N    SEP. D  297      12.686   -9.479    42.182   1.00  66.91          N
ATOM   14693   CA   SEP. D  297      13.475   -8.371    41.676   1.00  65.16          C
ATOM   14694   c    SER  D  297      14.951   -8.707    41.471   1.00  65.92          c
ATOM   14695   0    SER  D  297      15.596   -8.1.18    40.615   I.00  68.89          0
ATOM   14696   CB   SER  D  297      13.360   -7.185    42.611   1.00  67.80          c
ATOM   14697   OG   SER  D  297      14.227   -7.355    43.716   1.00  74.48          0
ATOM   14698   N    ASP  D  298      15.485   -9.640    42.253   I.00  67.92          N
ATOM   14699   CA   ASP  D  298      16.884  -10.049    42.105   1.00  71.45          c
ATOM   14700   c    ASP  D  298      17.126  -10.904    40.853   1.00  70.36          c
ATOM   147 01  0    ASP  D  298      18.091  -10.690    40.118   I.00  67.50          0
ATOM   14702   CB   ASP  D  298      17.357  -10.822    43.339   1.00  70.16          c
ATOM   147 03  CG   ASP  D  298      17.625   -9.923    44.5.19   1.00  7.1.13          c
ATOM   147 04  OD1  ASP  D  298      17.923   -8.731    44.297   I.00  70.80          0
ATOM   14705   OD2  ASP  D  298      17.539  -10.409    45.668   1.00  74.97          0
ATOM   147 06  N    ALA  D  299      16.264  -11.887    40.626   1.00  70.99          N
ATOM   147 07  CA   ALA  D  299      16.370  -12.712    39.433   1.00  67.08          c
ATOM   147 08  C    ALA  D  299      16.050  -11.890    38.189   1.00  62.78          c
ATOM   14709   O    ALA  D  299      16.614  -12.112    37.135   1.00  6.3.48          0
ATOM   14710   CB   ALA  D  299      15.449  -13.907    39.536   1.00  69.23          c
ATOM   14711   N    ILE  D  300      15.146  -10.931    38.327   I.00  62.67          N
ATOM   14712   CA   ILE  D  300      14.772  -10.067    37.2.15   1.00  64.22          c
ATOM   14713   c    ILE  D  300      15.953   -9.209    36.766   1.00  68.61          c
ATOM   14714   0    ILE  D  300      16.260   -9.134    35.573   I.00  68.44          0
ATOM   14715   CB   ILE  D  300      13.572   -9.168    37.588   1.00  65.07          c
ATOM   14716   CGI  ILE  D  300      12.267   -9.955    37.445   1.00  66.01          c
ATOM   14717   CG2  ILE  D  300      13.533   -7.9.19   3 6.726   I.00  63.98          c
ATOM   14718   CD1  ILE  D  300      11.034   -9.162    37.777   1.00  65.40          c
ATOM   14719   N    LEU  D  301      16.625   -8.578    37.722   1.00  64.64          N
ATOM   14720   CA   LEU  D  301      17.817   -7.799    37.425   1.00  59.79          c
ATOM   14721   C    LEU  D  301      18.898   -8.660    36.733   1.00  68.13          c
ATOM   14722   O    LEU  D  301      19.469   -8.241    35.728   1.00  67.98          0
ATOM   14723   CB   LEU  D  301      18.357   -7.177    38.707   1.00  62.48          c
ATOM   147 24  CG   LEU  D  301      19.323   -5.993    38.633   I.00  70.56          c
ATOM   14725   GD1  LEU  D  301      18.713   -4.809    37.871   1.00  69.09          c
ATOM   14726   CD2  LEU  D  301      19.707   -5.567    40.041   1.00  60.73          c
ATOM   14727   N    LEU  D  302      19.162   -9.857    37.265   I.00  62.80          N
ATOM   14728   CA   LEU  D  302      20.152  -10.779    36.703   1.00  64.27          c
ATOM   14729   c    LEU  D  302      19.860  -11.163    35.233   1.00  64.97          c
ATOM   14730   0    LEU  D  302      20.770  -11.267    .34.413   I.00  64.0.3          0
ATOM   14731   CB   LEU  D  302      20.222  -12.045    37.568   1.00  66.55          c
ATOM   14732   CG   LEU  D  302      21.474  -12.531    38.324   1.00  68.26          c
ATOM   147 33  GDI  LEU  D  302      22.471  -11.441    .38.722   I.00  64.64          c
ATOM   147 34  CD2  LEU  D  302      21.041  -13.302    39.571   1.00  70.37          c
ATOM   147 35  N    SER  D  303      18.590  -11.370    34.904   1.00  62.66          N
ATOM   14736   CA   SER  D  303      18.207  -11.780    33.563   1.00  59.85          c
ATOM   147 37  C    SER  D  303      18.069  -10.590    32.615   1.00  67.67          c
ATOM   14738   O    SER  D  303      17.870  -10.777    31.4.15   1.00  69.56          0
ATOM   147 39  CB   SER  D  303      16.898  -12.559    33.593   1.00  67.63          c
ATOM   147 40  OG   SER  D  303      15.794  -11.671    3.3.588   I.00  72.34          0
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ATOM   14741  N    ASP D 304      18.139  -9.378  33.164  1.00 63.20           N
ATOM   14742  C    ASP D 304      19.773  -8.115  31.870  1.00 69.47           C
ATOM   14743  CA   ASP D 304      18.336  -8.172  32.368  1.00 60.40           C
ATOM   14744  O    ASP D 304      20.054  -7.602  30.784  1.00 69.03           0
ATOM   14745  CB   ASP D 304      18.031  -6.921  33.183  I.00 65.01           C
ATOM   14746  CG   ASP D 304      16.541  -6.621  33.259  1.00 73.15           C
ATOM   14747  OD1  ASP D 304      15.743  -7.412  32.695  1.00 72.65           0
ATOM   14748  OD2  ASP D 304      16.177  -5.594  33.882  I.00 74.76           0
ATOM   14749  N    1LE D 305      20.688  -8.632  32.685  1.00 64.68           N
ATOM   14750  C    ILE D 305      22.229  -9.830  31.295  1.00 62.28           C
ATOM   14751  CA   ILE D 305      22.083  -8.698  32.301  I.00 61.61           C
ATOM   14752  O    ILE D 305      22.685  -9.612  30.177  1.00 63.27           0
ATOM   14753  CB   ILE D 305      23.020  -8.921  33.518  1.00 60.00           C
ATOM   14754  CGI  ILE D 305      23.434  -7.584  34.149  1.00 65.63           C
ATOM   14755  CG2  ILE D 305      24.273  -9.609  33.078  1.00 54.96           C
ATOM   14756  CD1  ILE D 305      22.534  -7.081  35.255  1.00 56.78           C
ATOM   14757  O    LEU D 306      20.190 -13.595  31.816  1.00 64.11           0
ATOM   14758  N    LEU D 306      21.801 -11.026  31.694  I.00 61.92           N
ATOM   14759  CA   LEU D 306      21.897 -12.219  30.851  1.00 65.62           C
ATOM   14760  C    LEU D 306      20.576 -12.973  30.826  1.00 65.67           C
ATOM   14761  CB   LEU D 306      23.011 -13.156  31.336  I.00 61.71           C
ATOM   14762  CG   LEU D 306      23.148 -14.479  30.576  1.00 59.78           C
ATOM   14763  CD2  LEU D 306      24.026 -15.462  31.332  1.00 55.37           C
ATOM   14764  CD1  LEU D 306      23.702 -14.222  29.180  I.00 59.42           C
ATOM   14765  O    ARG D 307      17.451 -15.424  30.205  1.00 73.15           0
ATOM   14766  N    ARG D 307      19.915 -12.934  29.672  1.00 65.45           N
ATOM   14767  CA   ARG D 307      18.544 -13.403  29.516  I.00 64.95           C
ATOM   14768  C    ARG D 307      18.369 -14.921  29.551  1.00 71.37           C
ATOM   14769  CB   ARG D 307      17.974 -12.863  28.207  1.00 68.65           C
ATOM   14770  CG   ARG D 307      16.536 -13.220  28.001  1.00 72.04           C
ATOM   14771  CD   ARG D 307      15.909 -12.419  26.888  1.00 79.83           C
ATOM   14772  NE   ARG D 307      14.497 -12.760  26.757  1.00 84.20           N
ATOM   14773  CZ   ARG D 307      14.017 -13.614  25.860  1.00 86.66           C
ATOM   14774  NH1  ARG D 307      12.715 -13.872  25.824  I.00 88.44           N
ATOM   14775  NH2  ARG D 307      14.836 -14.202  24.995  1.00 84.70           N
ATOM   14776  O    VAL D 308      21.412 -17.477  29.306  1.00 58.31           0
ATOM   14777  N    VAL D 308      19.229 -15.649  28.841  I.00 66.02           N
ATOM   14778  CA   VAL D 308      19.116 -17.103  28.772  1.00 68.25           C
ATOM   14779  C    VAL D 308      20.252 -17.815  29.504  1.00 63.66           C
ATOM   14780  CB   VAL D 308      19.098 -17.596  27.317  I.00 68.71           C
ATOM   14781  CG2  VAL D 308      18.193 -16.713  26.462  1.00 67.59           C
ATOM   14782  CGI  VAL D 308      18.638 -19.045  27.268  1.00 66.89           C
ATOM   14783  O    ASN D 309      22.415 -19.142  32.815  1.00 66.76           0
ATOM   14784  N    ASM D 309      19.880 -18.802  30.329  1.00 68.40           N
ATOM   14785  CA   ASN D 309      20.779 -19.629  31.153  1.00 66.00           C
ATOM   14786  C    ASN D 309      21.302 -18.888  32.351  1.00 67.54           C
ATOM   14787  CB   ASN D 309      21.960 -20.165  30.349  I.00 65.06           C
ATOM   14788  CG   ASN D 309      21.547 -21.214  29.357  1.00 69.97           C
ATOM   14789  OD1  ASN D 309      20.453 -21.778  29.449  1.00 72.52           0
ATOM   14790  ND2  ASN D 309      22.419 -21.491  28.399  I.00 75.31           N
ATOM   14791  O    THR D 310      21.445 -17.283  36.212  1.00 70.32           0
ATOM   14792  N    THR D 310      20.468 -17.981  32.847  1.00 69.70           N
ATOM   14793  CA   THR D 310      20.818 -17.067  33.916  I.00 60.60           C
ATOM   14794  C    THR D 310      20.789 -17.739  35.277  1.00 69.58           C
ATOM   14795  CB   THR D 310      19.868 -15.860  33.906  1.00 67.54           C
ATOM   14796  OG1  THR D 310      19.464 -15.540  35.238  I.00 68.31           O
ATOM   14797  CG2  THR D 310      18.648 -16.171  33.078  1.00 63.02           C
ATOM   14798  O    GLU D 311      21.246 -21.100  37.911  1.00 74.34           O
ATOM   14799  N    GLU D 311      20.049 -18.838  35.382  1.00 72.70           N
ATOM   14800  CA   GLU D 311      19.922 -19.548  36.648  1.00 71.45           C
ATOM   14801  C    GLU D 311      21.065 -20.539  36.828  1.00 73.84           C
ATOM   14802  CB   GLU D 311      18.571 -20.266  36.735  1.00 71.99           C
ATOM   14803  CG   GLU D 311      18.416 -21.452  35.786  I.00 78.76           C
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ATOM   14804  CD   GLU  D  311      18.043  --21.050  34.365  1.00  83.56           C
ATOM   14805  OE1  GLU  D  311      17.483  --19.928  34.177  1.00  75.95           O
ATOM   14806  OE2  GLU  D  311      18.315  -21.872   33.446  1.00  78.09           0
ATOM   14807  O    ILE  D  312      25.339  --21.783  35.497  1.00  63.01           0
ATOM   14808  N    ILE  D  312      21.849  -20.738   35.772  I.00  70.97           N
ATOM   14809  CA   ILE  D  312      22.956  -21.695   35.824  1.00  68.09           C
ATOM   14810  C    ILE  D  312      24.325  -21.088   35.493  1.00  67.70           C
ATOM   14811  CB   ILE  D  312      22.715  -22.888   34.859  I.00  71.91           C
ATOM   14812  CGI  ILE  D  312      22.771  -22.434   33.398  1.00  68.88           C
ATOM   14813  CG2  ILE  D  312      21.400  -23.588   35.178  1.00  72.69           C
ATOM   14814  CD1  ILE  D  312      22.117  -23.408   32.447  I.00  70.20           C
ATOM   14815  O    THR  D  313      25.451  -17.298   36.299  1.00  66.49           0
ATOM   14816  N    THR  D  313      24.376  -19.792   35.221  1.00  67.65           N
ATOM   14817  CA   THR  D  313      25.656  -19.209   34.861  1.00  62.14           C
ATOM   14818  C    THR  D  313      26.165  -18.210   35.898  1.00  61.51           C
ATOM   14819  CB   THR  D  313      25.572  -18.525   33.505  1.00  64.51           C
ATOM   14820  OG1  THR  D  313      24.904  -19.390   32.575  1.00  60.99           0
ATOM   14821  CG2  THR  D  313      26.961  -18.172   33.003  I.00  53.93           C
ATOM   14822  O    LYS  D  314      29.290  -16.763   35.291  1.00  64.34           0
ATOM   14823  N    LYS  D  314      27.403  -18.415   36.333  1.00  64.74           N
ATOM   14824  CA.  LYS  D  314      28.101  -17.507   37.236  I.00  60.56           C
ATOM   14825  C    LYS  D  314      28.833  -16.467   36.405  1.00  65.06           C
ATOM   14826  CB   LYS  D  314      29.086  -18.269   38.115  1.00  64.44           C
ATOM   14827  CG   LYS  D  314      28.486  -19.471   38.814  I.00  66.93           C
ATOM   14828  CD   LYS  D  314      29.556  -20.286   39.525  1.00  70.38           C
ATOM   14829  CE   LYS  D  314      28.933  -21.390   40.370  1.00  74.82           C
ATOM   14830  NZ   LYS  D  314      29.964  -22.372   40.818  I.00  79.00           N
ATOM   14831  O    ALA  D  315      28.953  -13.875   33.803  1.00  48.02           0
ATOM   14832  N    ALA  D  315      28.964  -15.264   36.953  1.00  57.50           N
ATOM   14833  CA   ALA  D  315      29.391  -14.118   36.171  1.00  48.15           C
ATOM   14834  C    ALA  D  315      28.483  -13.906   34.946  1.00  48.67           C
ATOM   14835  CB   ALA  D  315      30.852  -14.283   35.754  1.00  44.20           C
ATOM   14836  N    PRO  D  316      27.169  -13.751   35.182  1.00  49.36           N
ATOM   14837  CA.  PRO  D  316      26.236  -13.467   34.080  I.00  49.86           C
ATOM   14838  C    PRO  D  316      26.656  -12.266   33.210  1.00  53.07           C
ATOM   14839  O    PRO  D  316      26.412  -12.274   31.994  1.00  50.13           O
ATOM   14840  CB   PRO  D  316      24.923  -13.148   34.808  I.00  50.43           C
ATOM   14841  CG   PRO  D  316      25.348  -12.635   36.134  1.00  53.36           C
ATOM   14842  CD   PRO  D  316      26.522  -13.542   36.488  1.00  53.17           C
ATOM   14843  N    LEU  D  317      27.285  -11.256   33.813  I.00  47.89           N
ATOM   14844  CA   LEU  D  317      27.704  -10.108   33.034  1.00  44.09           C
ATOM   14845  C    LEU  D  317      28.759  -10.481   32.026  1.00  43.81           C
ATOM   14846  O    LEU  D  317      28.591  -10.231   30.824  1.00  52.12           0
ATOM   14847  CB   LEU  D  317      28.236   -8.967   33.914  1.00  43.93           C
ATOM   14848  CG   LEU  D  317      28.724   -7.887   32.935  1.00  44.19           C
ATOM   14849  CD1  LEU  D  317      27.537   -7.109   32.342  1.00  41.05           C
ATOM   14850  CD.2 LEU  D  317      29.797   -6.987   33.494  I.00  45.47           C
ATOM   14851  N    SEP. D  318      29.858  -11.057   32.499  1.00  46.33           N
ATOM   14852  CA   SER  D  318      30.917  -11.467   31.577  1.00  41.65           C
ATOM   14853  C    SER  D  318      30.363  -12.446   30.557  I.00  44.39           C
ATOM   14854  O    SER  D  318      30.662  -12.321   29.366  1.00  46.07           0
ATOM   14855  CB   SER  D  318      32.096  -12.059   32.324  1.00  47.99           C
ATOM   14856  OG   SER  D  318      32.942  -11.036   32.842  I.00  49.08           0
ATOM   14857  N    ALA  D  319      29.505  -13.367   30.992  1.00  41.16           N
ATOM   14858  CA   ALA  D  319      28.907  -14.301   30.033  1.00  46.05           C
ATOM   14859  C    ALA  D  319      28.144  -13.574   28.909  I.00  50.56           C
ATOM   14860  O    ALA  D  319      28.289  -13.933   27.729  1.00  50.40           0
ATOM   14861  CB   ALA  D  319      27.999  -15.289   30.735  1.00  43.78           C
ATOM   14862  N    SER  D  320      27.353  -12.552   29.250  1.00  44.55           N
ATOM   14863  CA   SER  D  320      26.605  -11.839   28.211  1.00  47.77           C
ATOM   14864  C    SER  D  320      27.565  -11.029   27.332  1.00  44.55           C
ATOM   14865  O    SER  D  320      27.326  -10.871   26.142  1.00  49.53           0
ATOM   14866  CB   SER  D  320      25.512  -10.933   28.816  I.00  47.26           C
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ATOM  14867  OG   SER  D 320     26.081  -9.883  29.571  1.00 47.56      O
ATOM  14868  N    MET  D 321     28.664 --10.533  27.886  1.00 45.53      N
ATOM  14869  CA   MET  D 321     29.679  -9.931  27.025  1.00 43.51      C
ATOM  14870  C    MET  D 321     30.254 --10.991  26.115  1.00 45.34      C
ATOM  14871  O    MET  D 321     30.409 -10.765  24.915  I.00 49.75      0
ATOM  14872  CB   MET  D 321     30.790  -9.268  27.837  1.00 39.36      C
ATOM  14873  CG   MET  D 321     30.313  -8.099  28.697  1.00 46.23      C
ATOM  14874  SD   MET  D 321     29.471  -6.818  27.704  I.00 45.75      S
ATOM  14875  CE   MET  D 321     27.736  -7.290  27.952  1.00 53.22      C
ATOM  14876  N    ILE  D 322     30.530 --12.168  26.677  1.00 50.77      N
ATOM  14877  CA   ILE  D 322     31.084 -13.278  25.894  I.00 46.88      C
ATOM  14878  C    ILE  D 322     30.105 -13.660  24.799  1.00 46.24      C
ATOM  14879  O    ILE  D 322     30.491 -13.852  23.651  1.00 49.16      O
ATOM  14880  CB   ILE  D 322     31.403 -14.491  26.770  1.00 46.28      C
ATOM  14881  CGI  ILE  D 322     32.642 -14.203  27.602  1.00 43.50      C
ATOM  14882  CG2  ILE  D 322     31.626 -15.741  25.911  1.00 44.13      C
ATOM  14883  CD1  ILE  D 322     32.904 -15.239  28.648  1.00 42.34      C
ATOM  14884  N    LYS  D 323     28.828 -13.718  25.147  I.00 45.09      N
ATOM  14885  CA   LYS  D 323     27.793 -14.001  24.156  1.00 43.96      C
ATOM  14886  C    LYS  D 323     27.719 -12.941  23.045  1.00 50.51      C
ATOM  14887  0    LYS  D 323     27.453 -13.297  21.901  I.00 53.85      0
ATOM  14888  CB   LYS  D 323     26.435 -14.135  24.847  1.00 49.19      C
ATOM  14889  CG   LYS  D 323     25.292 -14.550  23.929  1.00 54.79      C
ATOM  14890  CD   LYS  D 323     24.059 -14.945  24.733  I.00 55.46      C
ATOM  14891  CE   LYS  D 323     22.873 -15.330  23.842  1.00 61.32      C
ATOM  14892  NZ   LYS  D 323     22.193 -14.142  23.238  1.00 67.05      N
ATOM  14893  N    ARG  D 324     27.957 -11.659  23.369  I.00 42.93      N
ATOM  14894  CA   ARG  D 324     27.978 -10.610  22.344  1.00 44.13      C
ATOM  14895  C    ARG  D 324     29.122 -10.900  21.417  1.00 48.73      C
ATOM  14896  O    ARG  D 324     28.973 -10.886  20.194  1.00 51.39      0
ATOM  14897  CB   ARG  D 324     28.162  -9.181  22.918  1.00 46.42      C
ATOM  14898  CG   ARG  D 324     26.966  -8.541  23.640  1.00 42.27      C
ATOM  14899  CD   ARG  D 324     27.007  -6.964  23.578  1.00 43.55      C
ATOM  14900  NE   ARG  D 324     26.517  -6.356  24.821  I.00 50.95      N
ATOM  14901  CZ   ARG  D 324     26.805  -5.125  25.254  1.00 47.84      C
ATOM  14902  NH1  ARG  D 324     27.589  -4.315  24.555  1.00 41.00      N
ATOM  14903  NH2  ARG  D 324     26.305  -4.709  26.413  I.00 48.53      N
ATOM  14904  N    TYR  D 325     30.281 -11.138  22.023  1.00 47.44      N
ATOM  14905  CA   TYR  D 325     31.480 -11.454  21.283  1.00 44.36      C
ATOM  14906  C    TYR  D 325     31.250 -12.611  20.286  I.00 50.57      C
ATOM  14907  O    TYR  D 325     31.553 -12.475  19.091  1.00 46.51      O
ATOM  14908  CB   TYR  D 325     32.618 -11.810  22.244  1.00 48.33      C
ATOM  14909  CG   TYR  D 325     33.843 -12.200  21.475  1.00 50.53      C
ATOM  14910  CD1  TYR  D 325     34.717 -11.220  21.016  1.00 44.04      C
ATOM  14911  CD2  TYR  D 325     34.097 -13.544  21.136  1.00 45.97      C
ATOM  14912  CE1  TYR  D 325     35.829 -11.546  20.272  1.00 42.84      C
ATOM  14913  CE2  TYR  D 325     35.215 -13.883  20.382  I.00 45.21      C
ATOM  14914  CZ   TYR  D 325     36.084 -12.881  19.956  1.00 50.63      C
ATOM  14915  OH   TYR  D 325     37.210 -13.169  19.204  1.00 53.14      0
ATOM  14916  N    ASP  D 326     30.732 -13.739  20.786  I.00 49.05      N
ATOM  14917  CA   ASP  D 326     30.440 -14.911  19.947  1.00 48.30      C
ATOM  14918  C    ASP  D 326     29.434 -14.617  18.823  1.00 52.62      C
ATOM  14919  0    ASP  D 326     29.617 -15.043  17.676  I.00 52.67      0
ATOM  14920  CB   ASP  D 326     29.917 -16.071  20.799  1.00 42.57      C
ATOM  14921  CG   ASP  D 326     30.997 -16.694  21.670  1.00 49.23      C
ATOM  14922  OD1  ASP  D 326     32.180 -16.546  21.328  I.00 51.47      0
ATOM  14923  OD2  ASP  D 326     30.662 -17.324  22.698  1.00 49.09      0
ATOM  14924  N    GUI  D 327     28.370 -13.887  19.142  1.00 53.03      N
ATOM  14925  CA   GLU  D 327     27.353 -13.607  18.133  1.00 51.44      C
ATOM  14926  C    GLU  D 327     27.865 -12.609  17.110  1.00 49.50      C
ATOM  14927  O    GLU  D 327     27.502 -12.683  15.953  1.00 51.01      0
ATOM  14928  CB   GLU  D 327     26.075 -13.110  18.790  1.00 54.63      C
ATOM  14929  CG   GLU  D 327     25.287 -14.217  19.445  I.00 55.14      C
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ATOM   14930  CD  GLU D 327     23.918 --13.760  19.859  1.00 64.72           C
ATOM   14931  OE1 GLU D 327     23.665 --12.542  19.768  1.00 71.21           O
ATOM   14932  OE2 GLU D 327     23.100 -14.607  20.273  1.00 68.87           0
ATOM   14933  N   HIS D 328     28.737 --11.703  17.542  1.00 49.08           N
ATOM   14934  CA. HIS D 328     29.352 -10.730  16.648  I.00 46.69           C
ATOM   14935  C   HIS D 328     30.148 -11.514  15.601  1.00 47.61           C
ATOM   14936  O   HIS D 328     30.069 -11.233  14.408  1.00 49.27           O
ATOM   14937  CB  HIS D 328     30.211  -9.731  17.473  I.00 45.05           C
ATOM   14938  CG  HIS D 328     30.894  -8.644  16.677  1.00 45.62           C
ATOM   14939  ND1 HIS D 328     31.091  -7.375  17.183  1.00 43.52           N
ATOM   14940  CD2 HIS D 328     31.488  -8.651  15.456  I.00 44.68           C
ATOM   14941  CE1 HIS D 328     31.742  -6.640  16.297  1.00 43.95           C
ATOM   14942  NE2 HIS D 328     31.991  -7.388  15.237  1.00 44.34           N
ATOM   14943  N   HIS D 329     30.869 -12.538  16.048  1.00 51.63           N
ATOM   14944  CA  HIS D 329     31.681 -13.353  15.142  1.00 49.92           C
ATOM   14945  C   HIS D 329     30.845 -14.116  14.127  1.00 53.30           C
ATOM   14946  O   HIS D 329     31.131 -14.069  12.925  1.00 52.30           0
ATOM   14947  CB  HIS D 329     32.543 -14.354  15.907  I.00 45.82           C
ATOM   14948  CG  HIS D 329     33.293 -15.289  15.007  1.00 53.75           C
ATOM   14949  ND1 HIS D 329     32.919 -16.603  14.815  1.00 47.46           N
ATOM   14950  CD2 HIS D 329     34.376 -15.088  14.221  I.00 54.66           C
ATOM   14951  CE1 HIS D 329     33.754 -17.175  13.966  1.00 51.92           C
ATOM   14952  NE2 HIS D 329     34.646 -16.277  13.589  1.00 54.30           N
ATOM   14953  N   GLN D 330     29.819 -14.815  14.610  I.00 51.71           N
ATOM   14954  CA  GLN D 330     28.895 -15.508  13.718  1.00 48.44           C
ATOM   14955  C   GLN D 330     28.241 -14.543  12.730  1.00 55.31           C
ATOM   14956  O   GLN D 330     28.246 -14.823  11.529  I.00 55.90           0
ATOM   14957  CB  GLN D 330     27.845 -16.266  14.525  1.00 50.63           C
ATOM   14958  CG  GLN D 330     28.384 -17.558  15.143  1.00 55.11           C
ATOM   14959  CD  GLN D 330     27.947 -17.767  16.591  1.00 63.43           C
ATOM   14960  OE1 GLN D 330     26.888 -17.288  17.010  1.00 63.63           0
ATOM   14961  KE2 GLN D 3.30     28.772 -18.483  17..369  1.00 62.16           N
ATOM   14962  N   ASP D 331     27.716 -13.400  13.206  1.00 54.32           N
ATOM   14963  CA. ASP D 331     27.075 -12.450  12.296  I.00 47.73           C
ATOM   14964  C   ASP D 331     28.108 -11.939  11.311  1.00 52.66           C
ATOM   14965  O   ASP D 331     27.796 -11.671  10.158  1.00 55.56           O
ATOM   14966  CB  ASP D 331     26.454 -11.233  13.014  I.00 54.67           C
ATOM   14967  CG  ASP D 331     25.588 -11.601  14.228  1.00 61.53           C
ATOM   14968  OD1 ASP D 331     25.062 -12.745  14.287  1.00 55.47           O
ATOM   14969  OD2 ASP D 331     25.450 -10.717  15.133  I.00 61.90           O
ATOM   14970  N   LEU D 332     29.343 -11.781  11.768  1.00 48.29           N
ATOM   14971  CA  LEU D 332     30.369 -11.241  10.887  1.00 47.51           C
ATOM   14972  C   LEU D 332     30.766 -12.257   9.836  1.00 56.13           C
ATOM   14973  O   LEU D 332     30.948 -11.895   8.676  1.00 57.51           0
ATOM   14974  CB  LEU D 3.32     31.594 -10.801  11.669  1.00 47.75           C
ATOM   14975  CG  LEU D 332     32.686 -10.141  10.830  1.00 47.52           C
ATOM   14976  CD1 LEU D 332     32.193  -8.840  10.196  I.00 50.76           C
ATOM   14977  CD2 LEU D 3.32     33.886  -9.886  11.701  1.00 45.13           C
ATOM   14978  N   THR D 333     30.889 -13.523  10.243  1.00 51.19           N
ATOM   14979  CA. TH.R D 333     31.202 -14.602   9.313  I.00 50.72           C
ATOM   14980  C   THR D 333     30.131 -14.648   8.213  1.00 57.94           C
ATOM   14981  O   THR D 333     30.438 -14.578   7.017  1.00 59.98           0
ATOM   14982  CB  THR D 333     31.307 -15.975  10.047  I.00 50.23           C
ATOM   14983  OG1 THR D 333     32.437 -15.964  10.934  1.00 49.14           0
ATOM   14984  CG2 THR D 333     31.480 -17.122   9.048  1.00 49.44           C
ATOM   14985  N   LEU D 334     28.871 -14.732   8.625  I.00 55.01           N
ATOM   14986  CA  LEU D 334     27.766 -14.765   7.676  1.00 57.12           C
ATOM   14987  C   LEU D 334     27.747 -13.538   6.782  1.00 57.56           C
ATOM   14988  O   LEU D 334     27.688 -13.658   5.567  1.00 62.29           O
ATOM   14989  CB  LEU D 334     26.423 -14.887   8.403  1.00 58.32           C
ATOM   14990  CG  LEU D 3.34     25.192 -14.746   7.500  1.00 60.79           C
ATOM   14991  CD1 LEU D 334     25.217 -15.805   6.398  1.00 62.07           C
ATOM   14992  CD2 LEU D 334     23.895 -14.827   8.297  I.00 60.76           C
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ATOM  14993   N    LEU D 335    27.790 --12.359    7.383  1.00 58.90    N
ATOM  14994   CA   LEU D 335    27,706 --11.118    6,615  1,00 59.42    C
ATOM  14995   C    LEU D 335    28.792  -11,057    5.535  1.00 60,26    C
ATOM  14996   O    LEU D 335    28.512 --10.699    4.396  1.00 63.64    0
ATOM  14997   CB   LEU D 335    27,806   -9.897    7,538  1,00 52.41    C
ATOM  14998   CG   LEU D 335    27.980   -8,581    6.788  1.00 58,44    C
ATOM  14999   CD1  LEU D 335    26.714   -8,254    6.003  1.00 60,64    C
ATOM  15000   CD2  LEU D 335    28,333   ~7.452    7,731  1,00 61,39    C
ATOM  15001   O    LYS D 336    30.959  -12,134    2.602  1,00 67.85    0
ATOM  15002   N    LYS D 336    30.022  -11,421    5.892  1.00 59,05    N
ATOM  15003   CA   LYS D 336    31,116  -11.489    4,911  1,00 64.23    C
ATOM  15004   C    LYS D 336    30.796  -12.465    3.774  1,00 66.21    C
ATOM  15005   CB   LYS D 336    32.429  -11,893    5.585  1,00 57,92    C
ATOM  15006   CG   LYS D 336    33.289  -10.716    6,025  1.00 60.09    C
ATOM  15007   CD   LYS D 336    34,326  -11.123    7,073  1,00 52.91    C
ATOM  15008   CE   LYS D 336    35..358 -10,019    7.280  1.00 54,00    C
ATOM  15009   NZ   LYS D 336    36.379  -10.386    8.299  1.00 54.40    N
ATOM  15010   O    ALA D 337    29,147  -14.003    0,938  1,00 67.01    O
ATOM  15011   N    ALA D 337    30..339 -13,663    4.119  1.00 62,98    N
ATOM  15012   CA   ALA D 337    29.965  -14,642    3.102  1,00 61,94    C
ATOM  15013   C    ALA D 337    28,921  -14.060    2,147  1,00 65.00    C
ATOM  15014   CB   ALA D 337    29.445  -15,923    3.759  1,00 56.24    C
ATOM  15015   O    LEU D 338    26.942  -11,991   -0.253  1,00 72,11    0
ATOM  15016   N    LEU D 338    27,797  -13.605    2,699  1,00 66.10    N
ATOM  15017   CA   LEU D 338    26.727  -13.007    1.900  1,00 63.60    C
ATOM  15018   C    LEU D 338    27.230  -11,935    0.940  1,00 66,86    C
ATOM  15019   CB   LEU D 338    25,655  -12.382    2,791  1,00 66.65    C
ATOM  1502 0  CG   LEU D 338    24,879  -13.168    3,842  1,00 62.83    C
ATOM  1502 1  GDI  LEU D 338    23.879  -12,213    4.452  1,00 62,29    C
ATOM  1 5022  CD2  LEU D 338    24.193  -14,400    3,280  1.00 55,77    C
ATOM  1502 3  O    VAL D 339    29,379   -9.655   -1,554  1,00 71.27    0
ATOM  1502 4  N    VAL D 339    27.970  -10,957    1.458  1.00 65,11    N
ATOM  1502 5  CA   VAL D 339    28.413   -9.821    0.642  1,00 66.90    C
ATOM  15026   C    VAL D 339    29,361  -10.259   -0,475  1,00 69.01    C
ATOM  1502 7  CB   VAL D 339    29.103   -8,736    1.511  1,00 62,70    C
ATOM  1502 8  CGI  VAL D 339    29.636   -7,601    0.663  1,00 55,14    C
ATOM  15029   CG2  VAL D 339    28,146   -8.216    2,562  1,00 61.66    C
ATOM  15030   O    ARG D 340    30.643  -12,412   -3.519  1,00 73.64    0
ATOM  15031   N    A.P.G D 340   30.136  -11,312   -0.217  1,00 64,62    N
ATOM  15032   CA   ARG D 340    31,044  -11.869   -1,229  1,00 70.76    C
ATOM  15033   C    ARG D 340    30,259  -12.511   -2,357  1,00 71.63    C
ATOM  15034   CB   ARG D 340    31.999  -12,919   -0.630  1,00 66,01    C
ATOM  15035   CG   ARG D 340    33,090  -12.380    0,277  1.00 68.08    C
ATOM  15036   CD   ARG D 340    34,263  -11.763   -0,493  1,00 71.85    C
ATOM  15037   NE   ARG D 340    35.440  -11,640    0..371 1.00 78,47    N
ATOM  15038   CZ   ARG D 340    36.575  -11.028    0.042  1.00 76.77    C
ATOM  15039   NH1  ARG D 340    36,723  -10.451   -1,144  1,00 74.29    N
ATOM  15040   NH2  ARG D 340    37.567  -10,984    0.918  1.00 74,66    N
ATOM  15041   O    GLN D 341    26.818  -13,516   -4.734  1,00 68,27    O
ATOM  15042   N    GLN D 341    29,163  -13.178   -2,001  1,00 72.05    N
ATOM  15043   CA   GLN D 341    28,361  -13.935   -2.962  1,00 71.11    C
ATOM  15044   C    GLN D 341    27.288  -13,110   -3.681  1,00 68,99    C
ATOM  15045   CB   GLN D 341    27,693  -15.125   -2,263  1,00 73.57    C
ATOM  15046   O    GLN D 342    25.608   -9.297   -5,137  1,00 82.15    0
ATOM  15047   N    GLN D 342    26.895  -11,961   -3.136  1,00 69,07    N
ATOM  15048   CA   GLN D 342    25,779  -11.214   -3,730  1,00 68.87    C
ATOM  15049   C    GLN D 342    26,124   -9.799   -4,143  1,00 73.90    C
ATOM  15050   CB   GLN D 342    24.595  -11,144   -2.770  1,00 70,24    C
ATOM  15051   CG   GLN D 342    24,036  -12.477   -2,337  1.00 70.99    C
ATOM  15052   CD   GLN D 342    22,770  -12.315   -1,517  1,00 77.92    C
ATOM  15053   OE1  GLN D 342    22.512  -13,091   -0.591  1.00 75,30    0
ATOM  15054   NE2  GLN D 342    21.964  -11.305   -1.861  1.00 75.54    N
ATOM  15055   O    LEU D 343    29,291   -6.654   -2,856  1,00 73.27    O
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ATOM	15056	N	LEU	D	343	26..955	-9.129	--3.,357	1.00	73..48	N
ATOM	15057	CA	LEU	D	343	27.,355	-7.768	-3.,688	1,00	72.85	C
ATOM	15058	C	LEU	D	343	28..857	-7,549	-3..583	1,00	73,.62	C
ATOM	15059	CB	LEU	D	343	26..633	-6,769	-2.782	1.00	75..41	C
ATOM	15060	CG	LEU	D	343	25,224	-6..354	-3.,215	1,00	76.,45	C
ATOM	15061	CD2	LEU	D	343	24..850	-4,999	-2.626	1,00	77,.12	C
ATOM	15062	CD1	LEU	D	343	24.173	-7,416	-2.884	1,00	78..07	C
ATOM	15063	O	PRO	D	344	32.,920	-6.855	-4,207	1,00	77,89	0
ATOM	15064	N	FRO	D	344	29..649	--8.,336	-4,339	1,00	75..35	N
ATOM	15065	CA	PRO	D	344	31..112	-8.,390	-4.205	1,00	74,31	C
ATOM	15066	C	PRO	D	344	31.,773	-7.082	-4,572	I,00	72.85	C
ATOM	15067	CB	PRO	D	344	31..527	--9..487	-5.,200	1,00	73..54	C
ATOM	15068	CG	PRO	D	344	30.259	-10.,159	-5.610	1,00	73,81	C
ATOM	15069	CD	PRO	D	344	29..192	-9,131	--5.,490	1.00	72.92	C
ATOM	15070	N	GLU	D	345	31.,051	--6..234	-5.,292	1,00	73..02	N
ATOM	15071	CA	GLU	D	345	31..583	-4,950	-5..715	1,00	74,67	C
ATOM	15072	C	GLU	D	345	31..456	-3.,924	-4.581	1.00	77.81	C
ATOM	15073	O	GLU	D	345	31.,897	-2.776	-4,696	1,00	72,97	0
ATOM	15074	CB	GLU	D	345	30..862	-4,469	-6..982	1,00	71,64	C
ATOM	15075	N	LYS	D	346	30..852	-4,353	--3..479	1,00	78..02	N
ATOM	15076	CA.	LYS	D	346	30.,656	-3.478	-2.,333	1,00	74,58	C
ATOM	15077	C	LYS	D	346	31..537	--3.,902	-1,157	1,00	72.93	C
ATOM	15078	O	LYS	D	346	31..543	-3.,250	--0..115	1,00	75,.11	O
ATOM	15079	CB	LYS	D	346	29.,181	-3..466	-1,919	I,00	70..71	C
ATOM	15080	N	TYR	D	347	32..291	--4.983	-1,333	1,00	70..00	N
ATOM	15081	CA	TYR	D	347	33. 063	-5,556	-0. 240	1,00	66,08	C
ATOM	15082	C	TYR	D	347	34.,181	-4.632	0,257	I,00	65..82	C
ATOM	15083	O	TYR	D	347	34.,428	--4.551	1,458	1,00	66..52	O
ATOM	15084	CB	TYR	D	347	33. 661	-6.,906	-0. 657	1,00	60,52	C
ATOM	15085	CG	TYR	D	347	34..211	-7,698	0,508	1.00	62.22	C
ATOM	15086	CD1	TYR	D	347	35.,470	-7.426	1,031	1,00	64.85	C
ATOM	15087	CD2	TYR	D	347	33..464	-8.,702	1.099	1,00	62,99	C
ATOM	15088	CE1	TYR	D	347	35..966	-8.,133	2.104	1.00	63..95	C
ATOM	15089	CE2	TYR	D	347	33.,952	-9. 412	2,169	1,00	64.54	C
ATOM	15090	CZ	TYR	D	347	35..201	-9.,127	2.666	1,00	65,.70	C
ATOM	15091	OH	TYR	D	347	35..688	-9.,840	3..736	1,00	68,.79	0
ATOM	15092	N	LYS	D	348	34.,866	-3.955	-0.,656	1,00	66..14	N
ATOM	15093	CA	LYS	D	348	35..990	--3.,104	-0.,272	1,00	70..02	C
ATOM	15094	C	LYS	D	348	35. 514	-.1,906	0.553	1,00	70,60	C
ATOM	15095	O	LYS	D	348	36.,133	-1.534	1,553	I,00	67.37	0
ATOM	15096	CB	LYS	D	348	36.,756	-2.622	-1,510	1,00	70..01	C
ATOM	15097	N	GLU	D	349	34. 410	-.1,306	0.124	1,00	71,53	N
ATOM	15098	CA	GLU	D	349	33..814	-0.,212	0..868	1.00	69..81	C
ATOM	15099	C	GLU	D	349	33.,427	--0..650	2,272	1,00	66..53	C
ATOM	15100	O	GLU	D	349	33..702	0,052	3..248	1,00	67,96	0
ATOM	15101	CB	GLU	D	349	32..589	0,326	0..133	1.00	76..23	C
ATOM	15102	CG	GLU	D	349	31.,934	1.511	0,811	1,00	78...30	C
ATOM	15103	CD	GLU	D	349	30..873	2,137	-0..050	1,00	87,46	C
ATOM	15104	OE1	GLU	D	349	29..971	1,403	--0..515	1,00	90,.94	0
ATOM	15105	OE2	GLU	D	349	30.,947	3..363	-0.,276	1,00	92.56	0
ATOM	15106	N	1LE	D	350	32..807	--1.823	2,372	1,00	64.10	N
ATOM	15107	CA	ILE	D	350	32..256	-2.,290	3..639	1,00	63,.67	C
ATOM	15108	C	ILE	D	350	33.,317	-2.672	4,665	I,00	61.61	C
ATOM	15109	O	ILE	D	350	33..192	-2.327	5,844	1,00	63..76	0
ATOM	15110	CB	ILE	D	350	31..321	-3.,491	3.436	1,00	57,65	C
ATOM	15111	CGI	ILE	D	350	30.,058	-3..055	2,694	I,00	57,13	C
ATOM	15112	CG2	ILE	D	350	30.,923	-4.085	4,773	1,00	55..00	C
ATOM	15113	CD1	ILE	D	350	29. 152	-4,208	2.289	1,00	56,65	C
ATOM	15114	N	PHE	D	351	34..374	-3.,345	4,225	1.00	64.31	N
ATOM	15115	CA	PHE	D	351	35.,324	--3..934	5,172	1,00	59..16	C
ATOM	15116	C	PHE	D	351	36.,722	-3.,328	5..192	1,00	60,.07	C
ATOM	15117	O	PHE	D	351	37..442	-3.,502	6..175	1.00	63..15	0
ATOM	15118	CB	PHE	D	351	35,432	-5. 433	4,910	1,00	57.87	C

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ATOM   15119   CG   PHE  D  351    34..148   -6.153    5..106   1.00  55..10   C
ATOM   15120   GDI  FHE  D  351    33,,646   --6..349  6,373    1,00  57.17    C
ATOM   15121   CD2  PHE  D  351    33..427   -6.,603   4.031    1,00  53..35   C
ATOM   15122   CE1  PHE  D  351    32..444   -6,993    6..559   1.00  59..74   C
ATOM   1512 3  CE2  PHE  D  351    .32.,236  -7.245    4,214    1,00  54.89    C
ATOM   15124   CZ   PHE  D  351    31..739   -7,,438   5..480   1,00  52,40    C
ATOM   15125   N    PHE  D  352    37.123    -2.,624   4.139    1,00  62,09    N
ATOM   1512 6  CA.  PHE  D  352    .38.,471  -2.052    4,123    1,00  64.67    C
ATOM   15127   C    PHE  D  352    38..487   --0.,539  4,301    1,00  69..74   C
ATOM   15128   O    PHE  D  352    39..485   0,022     4.771    1,00  71,38    O
ATOM   15129   CB   PHE  D  352    .39.,196  -2..397   2,826    1,00  64.31    C
ATOM   15130   CG   PHE  D  352    39..706   --3..801  2,768    1,00  63..73   C
ATOM   15131   GDI  PHE  D  352    40. 953   -4,120    3.277    1,00  71,40    C
ATOM   15132   CD2  PHE  D  352    38.,952   -4,800    2,194    1.00  66..62   C
ATOM   15133   CEl  FHE  D  352    41,435    --5..418  3,221    1,00  70..77   C
ATOM   15134   CE2  PHE  D  352    39.425    -6.,098   2.136    1,00  70,.42   C
ATOM   15135   CZ   PHE  D  352    40..669   -6,407    2.649    1.00  71.02    C
ATOM   15136   N    ASP  D  353    .37.,386  0.112     3,928    1,00  65..20   N
ATOM   15137   CA   ASP  D  353    37...325  1,575     3..840   1,00  68,.40   C
ATOM   15138   C    ASP  D  353    36..841   2,253     5..140   1,00  70..39   C
ATOM   15139   0    ASP  D  353    .35.,638  2..331    5,422    1,00  70..85   0
ATOM   15140   CB   ASP  D  353    36,425    1.974     2,665    1,00  67.75    C
ATOM   15141   CG   ASP  D  353    36..480   3,458     2.358    1,00  73..25   C
ATOM   15142   OD1  ASP  D  353    .37.,410  4.138     2,848    1,00  74.31    0
ATOM   15143   OD2  ASP  D  353    35.,590   3..941    1,618    1,00  76..55   0
ATOM   15144   O    GLN  D  354    36. 023   5,074     7.963    1,00  68,93    0
ATOM   15145   N    GLN  D  354    .37 ,798  2.751     5,915    1,00  68..99   N
ATOM   15146   CA   GLN  D  354    37.,516   3..387    7,196    1,00  68..77   C
ATOM   15147   C    GLN  D  354    36. 765   4,703     7.067    1,00  67,47    C
ATOM   15148   CB   GLN  D  354    38.,810   3,642     7,959    1.00  64.21    C
ATOM   15149   CG   GLN  D  354    39.,660   2.423     8,193    1,00  71.45    C
ATOM   15150   CD   GLN  D  354    40..734   2,706     9.218    1,00  77,32    C
ATOM   15151   OE1  GLN  D  354    40..677   3,723     9..919   1.00  73..83   0
ATOM   15152   NE2  GLN  D  354    41,727    1.823     9,309    1,00  71.81    N
ATOM   15153   O    SEP. D  355    34..037   7,,128    6...363  1.00  72,82    0
ATOM   15154   N    SER  D  355    36..985   5,419     5..969   1,00  71,00    N
ATOM   15155   CA.  SER  D  355    36,286    6.680     5,722    1,00  66..31   C
ATOM   15156   C    SER  D  355    34.,781   6,458     5,663    1,00  65..91   C
ATOM   15157   CB   SER  D  355    36. 768   7,320     4.427    1,00  67,63    C
ATOM   15158   OG   SER  D  355    36,566    6..434    3,339    1,00  71.78    0
ATOM   15159   O    LYS  D  356    33.,307   4.244     6,950    1,00  65..44   0
ATOM   15160   N    LYS  D  356    34. .342   5,512     4.838    1,00  64,23    N
ATOM   15161   CA   LYS  D  356    32..929   5,154     4,762    1.00  61.25    C
ATOM   15162   C    LYS  D  356    32.,478   4.541     6,083    1,00  62.42    C
ATOM   15163   CB   LYS  D  356    32..669   4,189     3..603   1.00  67,41    C
ATOM   15164   O    ASN  D  357    29..234   2,135     8..174   1.00  60..91   O
ATOM   15165   N    ASM  D  357    .31.,171  4.362     6,241    1,00  57.84    N
ATOM   15166   CA   ASN  D  357    30..601   3,988     7..532   1.00  57,12    C
ATOM   15167   C    ASN  D  357    30..229   2,516     7.562    1,00  59,.11   C
ATOM   15168   CB   ASN  D  357    29.,349   4.838     7,877    1,00  60..28   C
ATOM   15169   CG   ASN  D  357    29.,685   6,266     8,377    1,00  63..24   C
ATOM   15170   OD1  ASN  D  357    30..828   6,594     8.714    1,00  64,61    0
ATOM   15171   ND2  ASN  D  357    28.,662   7.112     8,434    1,00  63..39   N
ATOM   15172   O    GLY  D  358    31.,248   0..103    9,147    1,00  53..18   0
ATOM   15173   N    GLY  D  358    31. 038   1,687     6.909    1,00  62,97    N
ATOM   15174   CA   GLY  D  358    .30.,792  0..259    6,838    1,00  56..89   C
ATOM   1517 5  C    GLY  D  358    31.,275   --0..461  8,071    1,00  54.30    C
ATOM   1517 6  O    TYR  D  359    33. 870   -.1,763   10. 716  1,00  56,59    O
ATOM   15177   N    TYR  D  359    31.,726   -1,705    7,927    1.00  56..47   N
ATOM   15178   CA   TYR  D  359    32.,255   -2.409    9,084    1,00  53..34   C
ATOM   1517 9  C    TYR  D  359    33..587   -1,825    9.515    1.00  54,14    C
ATOM   15180   CB   TYR  D  359    32..418   -3.,894   8..812   1.00  56..64   C
ATOM   15181   CG   TYR  D  359    .32.,868  -4.652    10.,029  1,00  52..35   C
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ATOM	15182	GDI	TYR	D	359	31.978	-4.928	11.057	1.00	51.88	C
ATOM	15183	CD2	TYR	D	359	34.182	-5.082	10.159	1.00	49.68	C
ATOM	15184	CE1	TYR	D	359	32.385	-5.620	12.174	1.00	54.84	C
ATOM	15185	CE2	TYR	D	359	34.599	-5.780	11.266	1.00	46.91	C
ATOM	15186	CZ	TYR	D	359	33.705	-6.049	12.273	I.00	52.18	C
ATOM	15187	OH	TYR	D	359	34.109	-6.749	13.391	1.00	48.07	0
ATOM	15188	O	ALA	D	360	36.393	0.976	10.331	1.00	61.93	0
ATOM	15189	N	ALA	D	360	34.392	-1.385	8.549	I.00	54.82	N
ATOM	15190	CA	ALA	D	360	35.707	-0.801	8.848	1.00	60.06	C
ATOM	15191	C	ALA	D	360	35.571	0.583	9.497	1.00	61.13	C
ATOM	15192	CB	ALA	D	360	36.567	-0.716	7.582	I.00	56.88	C
ATOM	15193	O	GLY	D	361	34.257	3.230	12.039	1.00	58.28	0
ATOM	15194	N	GLY	D	361	34.533	1.319	9.125	1.00	58.62	N
ATOM	15195	CA	GLY	D	361	34.301	2.621	9.727	1.00	60.97	C
ATOM	15196	C	GLY	D	361	33.885	2.454	11.172	1.00	56.97	C
ATOM	15197	O	TYR	D	362	33.765	0.941	14.850	1.00	50.06	0
ATOM	15198	N	TYR	D	362	33.107	1.411	11.408	1.00	54.56	N
ATOM	15199	CA.	TYR	D	362	32.612	1.030	12.720	I.00	51.86	C
ATOM	15200	C	TYR	D	362	33.738	0.595	13.666	1.00	54.17	C
ATOM	15201	CB	TYR	D	362	31.613	-0.098	12.521	1.00	45.90	C
ATOM	15202	CG	TYR	D	362	30.933	-0.647	13.737	I.00	50.05	C
ATOM	15203	CD1	TYR	D	362	30.349	0.196	14.693	1.00	48.53	C
ATOM	15204	CD2	TYR	D	362	30.800	-2.022	13.900	1.00	48.90	C
ATOM	15205	CE1	TYR	D	362	29.675	-0.343	15.794	I.00	49.81	C
ATOM	15206	CE2	TYR	D	362	30.148	-2.558	14.988	1.00	48.66	C
ATOM	15207	CZ	TYR	D	362	29.584	-1.730	15.927	1.00	43.50	C
ATOM	15208	OH	TYR	D	362	28.933	-2.296	16.997	I.00	44.48	0
ATOM	15209	O	ILE	D	363	37.477	0.585	14.994	1.00	54.11	0
ATOM	15210	N	ILE	D	363	34.673	-0.178	13.136	1.00	53.63	N
ATOM	15211	CA	ILE	D	363	35.733	-0.692	13.970	1.00	54.77	C
ATOM	15212	C	ILE	D	363	36.937	0.228	13.949	1.00	51.83	C
ATOM	15213	CB	ILE	D	363	36.154	-2.101	13.544	1.00	53.22	C
ATOM	15214	CGI	ILE	D	363	34.965	-3.065	13.635	1.00	51.77	C
ATOM	15215	CG2	ILE	D	363	37.273	-2.575	14.423	I.00	51.18	C
ATOM	15216	CD1	ILE	D	363	34.429	-3.254	15.036	1.00	43.05	C
ATOM	15217	O	ASP	D	364	39.426	3.559	12.503	1.00	69.04	0
ATOM	15218	N	ASP	D	364	37.350	0.636	12.766	I.00	53.41	N
ATOM	15219	CA	ASP	D	364	38.628	1.320	12.676	1.00	60.41	C
ATOM	15220	C	ASP	D	364	38.489	2.791	12.326	1.00	61.52	C
ATOM	15221	CB	ASP	D	364	39.526	0.587	11.676	I.00	56.54	C
ATOM	15222	CG	ASP	D	364	39.998	-0.763	12.219	1.00	59.30	C
ATOM	15223	OD1	ASP	D	364	40.415	-0.797	13.403	1.00	54.09	0
ATOM	15224	OD2	ASP	D	364	39.932	-1.778	11.486	1.00	60.53	0
ATOM	15225	O	GLY	D	365	36.858	4.791	13.973	1.00	69.21	0
ATOM	15226	N	GLY	D	365	37.316	3.191	11.856	1.00	60.49	N
ATOM	15227	CA	GLY	D	365	37.058	4.595	11.606	1.00	65.01	C
ATOM	15228	C	GLY	D	365	36.480	5.186	12.870	I.00	66.79	C
ATOM	15229	O	GLY	D	366	32.778	6.996	14.890	1.00	70.78	0
ATOM	15230	N	GLY	D	366	35.550	6.120	12.723	1.00	64.13	N
ATOM	15231	CA.	GLY	D	366	34.929	6.720	13.887	I.00	64.73	C
ATOM	15232	C	GLY	D	366	33.434	6.468	13.989	1.00	68.80	C
ATOM	15233	O	ALA	D	367	31.486	3.745	14.767	1.00	59.40	0
ATOM	15234	N	ALA	D	367	32.897	5.663	13.075	I.00	59.61	N
ATOM	15235	CA	ALA	D	367	31.466	5.408	13.028	1.00	55.04	C
ATOM	15236	C	ALA	D	367	30.932	4.725	14.282	1.00	55.24	C
ATOM	15237	CB	ALA	D	367	31.123	4.579	11.810	I.00	52.95	C
ATOM	15238	N	SEP.	D	368	29.835	5.259	14.792	1.00	56.25	N
ATOM	15239	CA	SER	D	368	29.127	4.685	15.921	1.00	52.61	C
ATOM	15240	C	SER	D	368	28.246	3.532	15.495	1.00	49.16	C
ATOM	15241	O	SER	D	368	28.030	3.311	14.307	1.00	51.44	0
ATOM	15242	CB	SER	D	368	28.244	5.738	16.577	1.00	49.82	C
ATOM	15243	OG	SER	D	368	27.192	6.046	15.687	1.00	51.76	0
ATOM	15244	N	GLN	D	369	27.695	2.838	16.479	I.00	47.30	N

ATOM	15245	CA	GLN	D	369	26.760	1.765	16.217	1.00	49.94	C
ATOM	15246	C	GLN	D	369	25.663	2.265	15.308	1.00	53.35	C
ATOM	15247	O	GLN	D	369	25.421	1.681	14.253	1.00	55.41	0
ATOM	15248	CB	GLN	D	369	26.168	1.244	17.514	1.00	48.60	C
ATOM	15249	CG	GLN	D	369	25.157	0.143	17.343	1.00	48.02	C
ATOM	15250	CD	GLN	D	369	24.863	-0.520	18.661	1.00	53.29	C
ATOM	15251	OE1	GLN	D	369	25.765	-1.074	19.299	1.00	58.14	0
ATOM	15252	NE2	GLN	D	369	23.619	-0.446	19.103	1.00	51.76	N
ATOM	15253	N	GLU	D	370	25.041	3.374	15.715	1.00	54.95	N
ATOM	15254	CA	GLU	D	370	23.916	3.989	15.007	1.00	52.31	C
ATOM	15255	C	GLU	D	370	24.245	4.335	13.554	1.00	55.12	C
ATOM	15256	O	GLU	D	370	23.516	3.942	12.636	1.00	60.43	0
ATOM	15257	CB	GLU	D	370	23.473	5.246	15.764	1.00	59.04	C
ATOM	15258	CG	GLU	D	370	22.158	5.837	15.323	1.00	69.18	C
ATOM	15259	CD	GLU	D	370	21.631	6.896	16.294	1.00	75.48	C
ATOM	15260	OE1	GLU	D	370	21.020	7.875	15.822	1.00	79.80	0
ATOM	15261	OE2	GLU	D	370	21.818	6.743	17.523	1.00	80.03	0
ATOM	15262	N	GLU	D	371	25.341	5.063	13.347	1.00	52.36	N
ATOM	15263	CA	GLU	D	371	25.808	5.368	11.999	1.00	50.34	C
ATOM	15264	C	GLU	D	371	26.072	4.090	11.204	1.00	54.72	C
ATOM	15265	0	GLU	D	371	25.795	4.045	10.011	1.00	60.62	0
ATOM	15266	CB	GLU	D	371	27.067	6.253	12.046	1.00	55.30	C
ATOM	15267	CG	GLU	D	371	26.792	7.730	12.419	1.00	59.52	C
ATOM	15268	CD	GLU	D	371	28.025	8.519	12.934	1.00	70.18	C
ATOM	15269	OE1	GLU	D	371	27.861	9.713	13.277	1.00	75.16	0
ATOM	15270	OF.2	GLU	D	371	29.144	7.966	13.019	1.00	67.86	0
ATOM	15271	N	PHE	D	372	26.577	3.044	11.867	1.00	56.97	N
ATOM	15272	CA	PHE	D	372	26.896	1.773	11.189	1.00	57.65	C
ATOM	15273	C	PHE	D	372	25.638	1.089	10.688	1.00	56.85	C
ATOM	15274	O	PHE	D	372	25.607	0.532	9.593	1.00	60.97	0
ATOM	15275	CB	PHE	D	372	27.668	0.815	12.114	1.00	53.07	C
ATOM	15276	CG	PHE	D	372	27.761	-0.602	11.588	1.00	53.59	C
ATOM	15277	CD1	PHE	D	372	28.313	-0.865	10.346	1.00	51.54	C
ATOM	15278	CD2	PHE	D	372	27.308	-1.665	12.343	1.00	54.99	C
ATOM	15279	CE1	PHE	D	372	28.407	-2.154	9.868	1.00	55.50	C
ATOM	15280	CE2	PHE	D	372	27.409	-2.966	11.876	1.00	51.52	C
ATOM	15281	CZ	PHE	D	372	27.955	-3.210	10.632	1.00	54.81	C
ATOM	15282	N	TYR	D	373	24.610	1.123	11.519	1.00	55.75	N
ATOM	15283	CA	TYR	D	373	23.324	0.568	11.166	1.00	57.26	C
ATOM	15284	C	TYR	D	373	22.666	1.337	10.005	1.00	65.03	C
ATOM	15285	O	TYR	D	373	22.122	0.714	9.090	1.00	68.09	0
ATOM	15286	CB	TYR	D	373	22.422	0.562	12.392	1.00	50.53	C
ATOM	15287	CG	TYR	D	373	22.769	-0.491	13.406	1.00	52.82	C
ATOM	15288	CD1	TYR	D	373	23.671	-1.520	13.106	1.00	54.67	C
ATOM	15289	CD2	TYR	D	373	22.185	-0.479	14.664	1.00	49.26	C
ATOM	15290	CE1	TYR	D	373	23.973	-2.496	14.042	1.00	45.22	C
ATOM	15291	CE2	TYR	D	373	22.472	-1.446	15.598	1.00	49.32	C
ATOM	15292	CZ	TYR	D	373	23.368	-2.454	15.283	1.00	52.42	C
ATOM	15293	OH	TYR	D	373	23.647	-3.405	16.235	1.00	59.26	0
ATOM	15294	N	LYS	D	374	22.713	2.673	10.036	1.00	62.39	N
ATOM	15295	CA	LYS	D	374	22.145	3.475	8.950	1.00	62.94	C
ATOM	15296	C	LYS	D	374	22.754	3.046	7.630	1.00	67.54	C
ATOM	15297	0	LYS	D	374	22.047	2.892	6.637	1.00	71.30	0
ATOM	15298	CB	LYS	D	374	22.374	4.978	9.166	1.00	57.51	C
ATOM	15299	N	PHE	D	375	24.065	2.827	7.638	1.00	63.85	N
ATOM	15300	CA	PHE	D	375	24.805	2.454	6.432	1.00	66.29	C
ATOM	15301	C	PHE	D	375	24.464	1.050	5.945	1.00	66.76	C
ATOM	15302	O	PHE	D	375	24.402	0.814	4.745	1.00	69.50	0
ATOM	15303	CB	PHE	D	375	26.320	2.559	6.699	1.00	67.06	C
ATOM	15304	CG	PHE	D	375	27.205	2.021	5.583	1.00	68.03	C
ATOM	15305	CD1	PHE	D	375	27.816	2.888	4.686	1.00	64.60	C
ATOM	15306	CD2	PHE	D	375	27.471	0.658	5.466	1.00	69.87	C
ATOM	15307	CE1	PHE	D	375	28.639	2.408	3.683	1.00	67.35	C

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ATOM   15308  CE2  PHE  D  375     28..290    0.171     4.453   1.00  64.06          C
ATOM   15309  CZ   FHE  D  375     28,,876    1.043     3,566   1,00  64.21          C
ATOM   15310  N    ILE  D  376     24..266    0,118     6..874  1,00  66,,36         N
ATOM   15311  CA   ILE  D  376     24..262   -1.302     6..528  1.00  64.24          C
ATOM   15312  C    ILE  D  376     22.,865   -1.892    6,423   1,00  64.56          C
ATOM   15313  O    ILE  D  376     22..699   -2.,986    5..900  1,00  69,,35         0
ATOM   15314  CB   ILE  D  376     25..083   -2.,149    7.558   1,00  62,34          C
ATOM   15315  CGI  ILE  D  376     25,643    -3.420    6,905   1,00  60..94         C
ATOM   15316  CG2  ILE  D  376     24..240   -2.522    8.757   1,00  59..38         C
ATOM   15317  CD1  ILE  D  376     26..684   -3.,153    5..842  1,00  62,37          C
ATOM   15318  N    LYS  D  377     21.,858   -1.179    6,915   I,00  70..43         N
ATOM   15319  CA   LYS  D  377     20..474   --1.654   6.792   1,00  72.81          C
ATOM   15320  C    LYS  D  377     20.040    -.1,861   5.330   1,00  71,66          C
ATOM   15321  O    LYS  D  377     19..515   -2..925   5.012   1.00  73..08         0
ATOM   15322  CB   LYS  D  377     19.,491   --0..703  7,496   1,00  66..25         C
ATOM   15323  CG   LYS  D  377     18,110    -1,306    7.664   1,00  70,,89         C
ATOM   15324  CD   LYS  D  377     17.161    -0..362   8..383  1.00  75..39         C
ATOM   15325  CE   LYS  D  377     15.,747   -0.907    8,381   1,00  71.43          C
ATOM   15326  NZ   LYS  D  377     14.775    0,088     8..905  1,00  88,,17         N
ATOM   15327  N    PRO  D  378     20..260   -0.,867    4.441   1,00  65,.96         N
ATOM   15328  CA.  PRO  D  378     19.,879   -1.092    3,041   1,00  66..54         C
ATOM   15329  C    PRO  D  378     20..520   -2.320    2.392   1,00  69..06         C
ATOM   15330  O    PRO  D  378     19..813   -3.,112    1.758   1,00  68,.23         0
ATOM   15331  CB   PRO  D  378     20.,350   0..187    2,338   I,00  70..29         C
ATOM   15332  CG   PRO  D  378     21..241   0..881    3.298   1,00  72.31          C
ATOM   15333  CD   PRO  D  378     20.728    0,515     4.643   1,00  68,24          C
ATOM   15334  N    ILE  D  379     21.,829   -2.484    2,557   I,00  75..36         N
ATOM   15335  CA   ILE  D  379     22.,554   --3..621  1,969   1,00  67.66          C
ATOM   15336  C    ILE  D  379     21.965    -4,957    2.443   1,00  69,12          C
ATOM   15337  O    ILE  D  379     21..815   -5..900   1.664   1.00  70..89         O
ATOM   15338  CB   ILE  D  379     24.,051   --3..536  2,309   1,00  65..02         C
ATOM   15339  CGI  ILE  D  379     24..702   -2.,424    1.497   1,00  68,.28         C
ATOM   15340  CG2  ILE  D  379     24..747   -4.822    1.995   1.00  72.17          C
ATOM   15341  CD1  ILE  D  379     26.,071   -2.053    1,979   1,00  68..00         C
ATOM   15342  N    LEU  D  380     21..602   -5.,018    3..721  1,00  70,.15         N
ATOM   15343  CA   LEU  D  380     20..948   -8,194    4.283   1,00  68,.74         C
ATOM   15344  C    LEU  D  380     19.,632   -6.505    3,589   1,00  71.40          C
ATOM   15345  O    LEU  D  380     19..178   --7.644   3.574   1,00  66..86         0
ATOM   15346  CB   LEU  D  380     20.686    -6.,001    5.769   1,00  63,36          C
ATOM   15347  CG   LEU  D  380     21.,896   -5..974   6,676   I,00  62.45          C
ATOM   15348  CD1  LEU  D  380     21.,402   --5..939  8,101   1,00  55..78         C
ATOM   15349  CD2  LEU  D  380     22.767    -7,211    6.429   1,00  61,85          C
ATOM   15350  O    GLU  D  381     17.092    -6.880    0.464   1.00  72.22          0
ATOM   15351  N    GLU  D  381     19.,011   --5..475  3,026   1,00  72.48          N
ATOM   15352  CA   GLU  D  381     17.706    -5.,631    2.400   1,00  69,.58         C
ATOM   15353  C    GLU  D  381     17.838    -6.031    0..940  1.00  69..94         C
ATOM   15354  CB   GLU  D  381     16.,904   -4.345    2,568   1,00  74.81          C
ATOM   15355  CG   GLU  D  381     16..600   -4,088    4.040   1,00  73,.95         C
ATOM   15356  CD   GLU  D  381     15.813    -2.,833    4.295   1,00  72,76          C
ATOM   15357  OE1  GLU  D  381     16.,150   -1.784    3,697   1,00  76..67         0
ATOM   15358  OE2  GLU  D  381     14.860    -2.903    5.110   1,00  72.17          0
ATOM   15359  O    LYS  D  382     19..492   -7,931    -2.305  1,00  84,01          0
ATOM   15360  N    LYS  D  382     18.,823   -5..468   0,249   I,00  70..05         N
ATOM   15361  CA   LYS  D  382     19..130   --5..883  -1.115  1,00  69..39         C
ATOM   15362  C    LYS  D  382     19.491    -7,370    -1.209  1,00  76,73          C
ATOM   15363  CB   LYS  D  382     20.,277   -5..042   -1,683  I,00  66..59         C
ATOM   15364  O    MET  D  383     18.,266   -10..121  1,001   1,00  76..94         0
ATOM   15365  N    MET  D  383     19.783    -8.,002    -0.068  1,00  71,70          N
ATOM   15366  CA   MET  D  383     20..302   -9.375    --0..044 1.00  72.73          C
ATOM   15367  C    MET  D  383     19.,362   -10..431  0,537   1,00  75..38         C
ATOM   15368  CB   MET  D  383     21..602   -9.,433    0..748  1,00  74,15          C
ATOM   15369  CG   MET  D  383     22..747   -8..638   0..175  1.00  77.37          C
ATOM   15370  SD   MET  D  383     24.,270   -9.077    1,036   1,00  77.93          S
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ATOM	15371	CE	MET	D	383	25.398	-7.911	0.311	1.00	75.24	C
ATOM	15372	O	ASP	D	384	17.821	-13.310	2.884	1.00	78.22	0
ATOM	15373	N	ASP	D	384	19.830	-11.679	0.561	1.00	74.30	N
ATOM	15374	CA	ASP	D	384	18.944	-12.812	0.813	1.00	71.90	C
ATOM	15375	C	ASP	D	384	18.880	-13.372	2.238	1.00	75.67	C
ATOM	15376	CB	ASP	D	384	19.297	-13.944	-0.139	1.00	74.19	C
ATOM	15377	CG	ASP	D	384	18.478	-13.900	-1.408	1.00	82.20	C
ATOM	15378	OD1	ASP	D	384	18.081	-12.784	-1.804	1.00	88.93	0
ATOM	15379	OD2	ASP	D	384	18.214	-14.968	-2.002	1.00	86.65	0
ATOM	15380	N	GLY	D	385	19.972	-13.944	2.733	1.00	72.86	N
ATOM	15381	CA	GLY	D	385	19.918	-14.620	4.025	1.00	67.03	C
ATOM	15382	C	GLY	D	385	19.899	-13.686	5.220	1.00	63.64	C
ATOM	15383	O	GLY	D	385	20.213	-14.071	6.343	1.00	63.17	0
ATOM	15384	N	THR	D	386	19.500	-12.447	4.984	1.00	67.93	N
ATOM	15385	CA	THR	D	386	19.666	-11.399	5.973	1.00	65.15	C
ATOM	15386	C	THR	D	386	18.543	-11.285	7.006	1.00	65.05	C
ATOM	15387	O	THR	D	386	18.615	-10.441	7.895	1.00	67.71	O
ATOM	15388	CB	THR	D	386	19.811	-10.081	5.272	1.00	64.06	C
ATOM	15389	OG1	THR	D	386	18.883	-10.050	4.184	1.00	72.99	O
ATOM	15390	CG2	THR	D	386	21.204	-9.953	4.704	1.00	67.81	C
ATOM	15391	N	GLU	D	387	17.525	-12.134	6.904	1.00	61.15	N
ATOM	15392	CA	GLU	D	387	16.378	-12.064	7.806	1.00	61.45	C
ATOM	15393	C	GLU	D	387	16.767	-12.007	9.273	1.00	64.71	C
ATOM	15394	0	GLU	D	387	16.345	-11.097	9.999	1.00	70.45	0
ATOM	15395	CB	GLU	D	387	15.439	-13.252	7.582	1.00	61.80	C
ATOM	15396	N	GLU	D	388	17.570	-12.967	9.719	1.00	63.87	N
ATOM	15397	CA	GLU	D	388	17.925	-13.032	11.129	1.00	62.63	C
ATOM	15398	C	GLU	D	388	18.802	-11.845	11.516	1.00	65.11	C
ATOM	15399	O	GLU	D	388	18.840	-11.447	12.681	1.00	70.81	0
ATOM	15400	CB	GLU	D	388	18.621	-14.353	11.452	1.00	64.95	C
ATOM	15401	N	LEU	D	389	19.491	-11.268	10.538	1.00	60.50	N
ATOM	15402	CA	LEU	D	389	20.350	-10.131	10.801	1.00	56.19	C
ATOM	15403	C	LEU	D	389	19.506	-8.885	11.077	1.00	63.42	C
ATOM	15404	O	LEU	D	389	19.854	-8.045	11.914	1.00	62.59	0
ATOM	15405	CB	LEU	D	389	21.300	-9.884	9.620	1.00	62.65	C
ATOM	15406	CG	LEU	D	389	22.307	-10.953	9.162	1.00	61.12	C
ATOM	15407	CD1	LEU	D	389	23.248	-10.431	8.064	1.00	55.77	C
ATOM	15408	CD2	LEU	D	389	23.111	-11.544	10.323	1.00	53.24	C
ATOM	15409	N	LEU	D	390	18.394	-8.770	10.358	1.00	67.09	N
ATOM	15410	CA	LEU	D	390	17.538	-7.593	10.436	1.00	56.93	C
ATOM	15411	C	LEU	D	390	16.712	-7.589	11.722	1.00	57.51	C
ATOM	15412	O	LEU	D	390	16.489	-6.537	12.327	1.00	61.46	0
ATOM	15413	CB	LEU	D	390	16.645	-7.514	9.199	1.00	60.46	C
ATOM	15414	CG	LEU	D	390	17.399	-6.992	7.969	1.00	61.51	C
ATOM	15415	CD1	LEU	D	390	16.589	-7.117	6.715	1.00	61.68	C
ATOM	15416	CD2	LEU	D	390	17.772	-5.557	8.188	1.00	62.58	C
ATOM	15417	N	VAL	D	391	16.280	-8.757	12.172	1.00	57.12	N
ATOM	15418	CA	VAL	D	391	15.687	-8.835	13.506	1.00	60.82	C
ATOM	15419	C	VAL	D	391	16.651	-8.285	14.581	1.00	60.81	C
ATOM	15420	0	VAL	D	391	16.234	-7.577	15.505	1.00	63.01	0
ATOM	15421	CB	VAL	D	391	15.274	-10.269	13.848	1.00	59.34	C
ATOM	15422	CGI	VAL	D	391	15.180	-10.468	15.359	1.00	52.15	C
ATOM	15423	CG2	VAL	D	391	13.956	-10.600	13.179	1.00	53.51	C
ATOM	15424	N	LYS	D	392	17.942	-8.574	14.428	1.00	62.54	N
ATOM	15425	CA	LYS	D	392	18.961	-8.103	15.368	1.00	55.77	C
ATOM	15426	C	LYS	D	392	19.207	-6.610	15.213	1.00	58.69	C
ATOM	15427	O	LYS	D	392	19.283	-5.890	16.203	1.00	56.94	0
ATOM	15428	CB	LYS	D	392	20.265	-8.870	15.182	1.00	57.74	C
ATOM	15429	CG	LYS	D	392	20.151	-10.335	15.522	1.00	56.18	C
ATOM	15430	CD	LYS	D	392	21.491	-10.994	15.543	1.00	53.51	C
ATOM	15431	CE	LYS	D	392	21.366	-12.399	16.075	1.00	58.26	C
ATOM	15432	NZ	LYS	D	392	22.715	-13.005	16.286	1.00	69.61	N
ATOM	15433	N	LEU	D	393	19.312	-6.147	13.973	1.00	53.61	N

ATOM	15434	CA	LEU	D	393	19.445	-4.720	13.706	1.00	54.75	C
ATOM	15435	C	LEU	D	393	18.257	-3.914	14.311	1.00	58.09	C
ATOM	15436	O	LEU	D	393	18.435	-2.834	14.859	1.00	57.82	0
ATOM	15437	CB	LEU	D	393	19.571	-4.487	12.189	1.00	52.38	C
ATOM	15438	CG	LEU	D	393	20.233	-3.195	11.706	1.00	56.05	C
ATOM	15439	GD1	LEU	D	393	20.841	-3.370	10.339	1.00	54.76	C
ATOM	15440	CD2	LEU	D	393	19.242	-2.055	11.664	1.00	54.39	C
ATOM	15441	N	ASM	D	394	17.054	-4.463	14.245	1.00	60.02	N
ATOM	15442	CA	ASN	D	394	15.906	-3.792	14.829	1.00	59.87	C
ATOM	15443	C	ASN	D	394	15.903	-3.850	16.340	1.00	64.01	C
ATOM	15444	0	ASK	D	394	15.481	-2.898	17.002	1.00	70.23	0
ATOM	15445	CB	ASN	D	394	14.605	-4.386	14.291	1.00	63.74	C
ATOM	15446	CG	ASN	D	394	14.207	-3.772	12.991	1.00	65.01	C
ATOM	15447	OD1	ASK	D	394	13.547	-2.736	12.966	1.00	73.34	0
ATOM	15448	ND2	ASN	D	394	14.641	-4.375	11.892	1.00	65.57	K
ATOM	15449	N	AP.G	D	395	16.371	-4.959	16.896	1.00	61.39	K
ATOM	15450	CA	ARG	D	395	16.478	-5.050	18.339	1.00	60.20	C
ATOM	15451	C	ARG	D	395	17.741	-4.331	18.850	1.00	59.95	C
ATOM	15452	O	ARG	D	395	18.052	-4.412	20.030	1.00	59.12	0
ATOM	15453	CB	ARG	D	395	16.475	-6.515	18.769	1.00	60.87	C
ATOM	15454	N	GLU	D	396	18.449	-3.627	17.960	1.00	60.29	N
ATOM	15455	CA	GLU	D	396	19.742	-2.989	18.270	1.00	62.05	C
ATOM	15456	C	GLU	D	396	20.739	-3.974	18.896	1.00	60.27	C
ATOM	15457	0	GLU	D	396	21.359	-3.699	19.921	1.00	61.64	0
ATOM	15458	CB	GLU	D	396	19.552	-1.778	19.199	1.00	61.91	C
ATOM	15459	CG	GLU	D	396	19.148	-0.488	18.466	1.00	65.69	C
ATOM	15460	CD	GLU	D	396	18.648	0.626	19.386	1.00	74.01	C
ATOM	15461	OE1	GLU	D	396	19.177	0.787	20.514	1.00	68.41	0
ATOM	15462	OE2	GLU	D	396	17.721	1.358	18.964	1.00	80.46	0
ATOM	15463	O	ASP	D	397	22.323	-8.188	17.699	1.00	59.16	0
ATOM	15464	N	ASP	D	397	20.899	-5.119	18.257	1.00	56.63	K
ATOM	15465	CA	ASP	D	397	21.646	-6.216	18.838	1.00	56.68	C
ATOM	15466	C	ASP	D	397	22.406	-6.983	17.765	1.00	53.02	C
ATOM	15467	CB	ASP	D	397	20.694	-7.142	19.573	1.00	58.65	C
ATOM	15468	CG	ASP	D	397	21.408	-8.ill	20.452	1.00	65.99	C
ATOM	15469	OD2	ASP	D	397	21.390	-9.316	20.128	1.00	74.83	0
ATOM	15470	OD1	ASP	D	397	21.993	-7.664	21.463	1.00	69.81	0
ATOM	15471	O	LEU	D	398	25.537	-5.213	16.030	1.00	50.46	0
ATOM	15472	N	LEU	D	398	23.138	-6.259	16.930	1.00	54.51	N
ATOM	15473	CA	LEU	D	398	23.798	-6.795	15.747	1.00	50.91	C
ATOM	15474	C	LEU	D	398	25.257	-6.388	15.803	1.00	53.97	C
ATOM	15475	CB	LEU	D	398	23.148	-6.239	14.477	1.00	51.47	C
ATOM	15476	CG	LEU	D	398	23.400	-6.735	13.049	1.00	50.98	C
ATOM	15477	CD2	LEU	D	398	23.859	-5.619	12.114	1.00	52.36	C
ATOM	15478	CD1	LEU	D	398	24.354	-7.900	12.997	1.00	52.56	C
ATOM	15479	O	LEU	D	399	28.760	-5.131	16.500	1.00	46.89	0
ATOM	15480	N	LEU	D	399	26.178	-7.336	15.591	1.00	52.61	N
ATOM	15481	CA	LEU	D	399	27.616	-7.041	15.616	1.00	47.88	C
ATOM	15482	C	LEU	D	399	27.996	-6.061	16.734	1.00	47.75	C
ATOM	15483	CB	LEU	D	399	28.071	-6.458	14.275	1.00	46.33	C
ATOM	15484	CG	LEU	D	399	27.997	-7.290	12.998	1.00	51.16	C
ATOM	15485	CD1	LEU	D	399	27.652	-6.412	11.816	1.00	50.61	C
ATOM	15486	CD2	LEU	D	399	29.309	-8.007	12.738	1.00	49.62	C
ATOM	15487	O	ARG	D	400	29.805	-6.570	19.582	1.00	39.45	0
ATOM	15488	N	ARG	D	400	27.435	-6.244	17.928	1.00	45.63	N
ATOM	15489	CA	ARG	D	400	27.736	-5.352	19.055	1.00	44.55	C
ATOM	15490	C	ARG	D	400	29.191	-5.477	19.590	1.00	45.18	C
ATOM	15491	CB	ARG	D	400	26.741	-5.604	20.201	1.00	41.89	C
ATOM	15492	CG	ARG	D	400	25.272	-5.258	19.865	1.00	50.55	C
ATOM	15493	CD	ARG	D	400	24.866	-3.834	20.348	1.00	51.74	C
ATOM	15494	KE	ARG	D	400	24.635	-3.812	21.789	1.00	44.33	N
ATOM	15495	CZ	ARG	D	400	24.890	-2.789	22.591	1.00	46.27	C
ATOM	15496	NH1	ARG	D	400	25.355	-1.642	22.115	1.00	49.02	N

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ATOM  15497  NH2  ARG  D 400   24.659  -2,918  23.884  1.00 49.80   N
ATOM  15498  O    LYS  D 401   29,424  -4.900  22,487  1,00 40.49   O
ATOM  15499  R    LYS  D 401   29.721  -4,339  20.045  1.00 39,22   R
ATOM  15500  CA   LYS  D 401   30.954  -4,282  20.814  1.00 37.54   c
ATOM  15501  C    LYS  D 401   30,576  -4.598  22,239  1,00 38.12   C
ATOM  15502  CB   LYS  D 401   31.637  -2,934  20.682  1.00 37,23   C
ATOM  15503  CG   LYS  D 401   32.112  -2,636  19.262  1,00 41,95   c
ATOM  15504  CD   LYS  D 401   32,141  -1.127  18,981  1,00 39.97   c
ATOM  15505  CE   LYS  D 401   32.496  -0.823  17,522  1,00 44.74   c
ATOM  15506  NZ   LYS  D 401   33.186   0,489  17.324  1,00 46,53   N
ATOM  15507  O    GLN  D 402   30,774  -3.531  26,529  1,00 41.11   O
ATOM  15508  R    GLR  D 402   31.528  -4,611  23,169  1,00 38.15   N
ATOM  15509  CA   GLR  D 402   31.157  -4,882  24.560  1,00 37,88   C
ATOM  15510  c    GLN  D 402   31.356  -3,635  25,443  1.00 39.35   c
ATOM  15511  CB   GLN  D 402   31,941  -6.077  25,134  1,00 37.81   c
ATOM  15512  CG   GLR  D 402   31.708  -7,445  24.414  1.00 40,89   c
ATOM  15513  CD   GLN  D 402   32.441  -7,552  23.089  1,00 38.56   c
ATOM  15514  OE1  GLN  D 402   33,635  -7.303  23,017  1,00 40.93   0
ATOM  15515  RE2  GLR  D 402   31.722  -7,873  22.032  1,00 40,94   R
ATOM  15516  O    ARG  D 403   31.724   0,033  23.663  1,00 43,34   O
ATOM  15517  N    ARG  D 403   32,205  -2.724  24,988  1,00 33.38   N
ATOM  15518  CA   ARG  D 403   32.255  -1,385  25,539  1,00 41.60   C
ATOM  15519  c    ARG  D 403   31.370  -0,427  24.737  1,00 42,15   c
ATOM  1552 0 CB   ARG  D 403   33,673  -0.891  25,571  1,00 41.36   c
ATOM  1552 1 CG   ARG  D 403   34.514  -1,718  26,513  1,00 41.73   c
ATOM  15522  CD   ARG  D 403   34.093  -1,481  27.950  1,00 42,00   c
ATOM  1552 3 NE   ARG  D 403   35,307  -1.441  28,730  1,00 44.72   N
ATOM  1552 4 CZ   ARG  D 403   35,832  -0.356  29,260  1,00 43.64   c
ATOM  1552 5 NH1  ARG  D 403   36.967  -0,470  29.909  1,00 48,97   N
ATOM  1552 6 NH2  ARG  D 403   35.238   0,826  29,149  1.00 42.69   N
ATOM  1552 7 N    THR  D 404   30,190  -0.166  25,263  1,00 36.86   N
ATOM  1552 8 CA   THR  D 404   29.175   0,509  24.486  1.00 41,07   C
ATOM  1552 9 c    THR  D 404   28,483   1,537  25.351  1.00 42.11   c
ATOM  15530  O    THR  D 404   28,544   1.447  26,586  1,00 41.30   0
ATOM  15531  CB   THR  D 404   28.126  -0,476  23.925  1.00 43,44   c
ATOM  15532  OG1  THR  D 404   27.544  -1,214  25.015  1,00 49,32   0
ATOM  15533  CG2  THR  D 404   28,752  -1.442  22,933  1,00 38.78   c
ATOM  15534  R    PHE  D 405   27,824   2,492  24,687  1,00 45.50   R
ATOM  15535  CA   PHE  D 405   27.129   3,609  25..340 1,00 42,20   C
ATOM  15536  C    PHE  D 405   26,132   3.145  26,411  1,00 47.56   C
ATOM  15537  O    PHE  D 405   25,910   3.860  27,382  1,00 53.85   O
ATOM  15538  CB   PHE  D 405   26.406   4,477  24.285  1,00 45,91   c
ATOM  15539  CG   PHE  D 405   25,360   3,722  23,483  1.00 52,91   c
ATOM  15540  CD2  PHE  D 405   24,054   3.612  23,944  1,00 48.07   c
ATOM  15541  CD1  PHE  D 405   25.694   3,103  22.286  1,00 46,94   c
ATOM  15542  CE2  PHE  D 405   23.Ill    2,904  23.240  1.00 44.52   c
ATOM  15543  CE1  PHE  D 405   24,746   2.394  21,564  1,00 48.61   c
ATOM  15544  CZ   PHE  D 405   23.456   2,296  22.043  1,00 51,42   c
ATOM  15545  N    ASP  D 406   25.550   1,951  26.257  1,00 47,55   N
ATOM  15546  CA.  ASP  D 406   24,505   1.500  27,184  1,00 47.17   C
ATOM  15547  C    ASP  D 406   24,962   0,661  28,375  1,00 46.50   C
ATOM  15548  O    ASP  D 406   24.125   0,141  29.108  1,00 48,70   0
ATOM  15549  CB   ASP  D 406   23,425   0.709  26,444  1,00 41.21   c
ATOM  15550  CG   ASP  D 406   23,993  -0.403  25,602  1,00 49.42   c
ATOM  15551  OD1  ASP  D 406   25.047  -0,184  24.983  1,00 56,50   0
ATOM  15552  OD2  ASP  D 406   23,385  -1.490  25,534  1,00 51.64   0
ATOM  15553  N    ASM  D 407   26,258   0.555  28,620  1,00 41.18   N
ATOM  15554  CA   A.SN D 407   26.690  -0,169  29.807  1,00 40,92   C
ATOM  15555  c    ASN  D 407   26,447   0,602  31,077  1.00 42.42   c
ATOM  15556  O    ASM  D 407   26,713   0.106  32,165  1,00 44.77   0
ATOM  15557  CB   ASR  D 407   28.168  -0,521  29.712  1.00 43,16   c
ATOM  15558  CG   ASN  D 407   28.427  -1,601  28.710  1.00 38.14   c
ATOM  15559  OD1  ASN  D 407   27,525  -2.348  28,369  1,00 35.70   0
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ATOM	15560	ND2	ASN	D	407	29.654	-1,665	28,202	1.00	40.11	N
ATOM	15561	N	GLY	D	408	25,929	1.820	30,929	1,00	47.23	N
ATOM	15562	CA	GLY	D	408	25.646	2,698	32.052	1,00	42,00	C
ATOM	15563	C	GLY	D	408	24.650	2,114	33,004	1.00	39.86	C
ATOM	15564	O	GLY	D	408	24,626	2.484	34,170	1,00	44.46	0
ATOM	15565	N	SER	D	409	23.840	1,180	32.527	1,00	40,52	N
ATOM	15566	CA	SER	D	409	22.781	0,634	33.378	1,00	45,51	C
ATOM	15567	C	SER	D	409	23,276	-0.405	34,362	1,00	47.89	C
ATOM	15568	O	SER	D	409	22.520	-0,847	35,217	1,00	55.79	O
ATOM	15569	CB	SER	D	409	21.676	0,035	32.532	1,00	38,15	C
ATOM	15570	OG	SER	D	409	22,248	-0.679	31,461	I,00	57.68	0
ATOM	15571	O	1LE	D	410	26,366	-0,328	36,519	1,00	52.54	0
ATOM	15572	N	ILE	D	410	24.541	-0,802	34.254	1,00	49,94	N
ATOM	15573	CA	ILE	D	410	25,077	-1,820	35,152	1.00	46.22	C
ATOM	15574	C	ILE	D	410	25,516	-1.231	36,482	1,00	48.60	C
ATOM	15575	CB	ILE	D	410	26.286	-2,556	34.543	1,00	48,83	C
ATOM	15576	CGI	ILE	D	410	25,886	-3,343	33,297	1.00	47,99	C
ATOM	15577	CG2	ILE	D	410	26,909	-3.448	35,568	1,00	41.59	C
ATOM	15578	CD1	ILE	D	410	27.031	-3,532	32,342	1,00	51,19	C
ATOM	15579	N	PRO	D	411	24.940	-1,750	37.578	1,00	52,72	N
ATOM	15580	CA.	PRO	D	411	25,261	-1..386	38,962	1,00	47,68	C
ATOM	15581	C	PRO	D	411	26,529	-2,075	39,457	1,00	49.60	C
ATOM	15582	O	PRO	D	411	26.846	-3,193	39.028	1,00	46,33	O
ATOM	15583	CB	PRO	D	411	24,044	-1.886	39,763	I,00	49.80	C
ATOM	15584	CG	PRO	D	411	23,069	-2,436	38,759	1,00	52.23	C
ATOM	15585	CD	PRO	D	411	23.884	-2,771	37.525	1,00	53,95	C
ATOM	15586	N	HIS	D	412	27,214	-1.412	40,380	I,00	51.79	N
ATOM	15587	CA	HI S	D	412	28,470	-1.897	40,915	1,00	49.02	C
ATOM	15588	C	HIS	D	412	28..340	-3,304	41.500	1,00	51,96	C
ATOM	15589	O	HIS	D	412	29,282	-4,087	41,386	1.00	54.70	O
ATOM	15590	CB	HI S	D	412	29,039	-0.906	41,962	1,00	44.82	C
ATOM	15591	CG	HIS	D	412	28..348	-0,933	43.294	1,00	50,54	C
ATOM	15592	ND1	HIS	D	412	27,100	-0,381	43,502	1.00	58.79	N
ATOM	15593	CD2	HI S	D	412	28,751	-1.410	44,499	1,00	54.41	C
ATOM	15594	CE1	HIS	D	412	26.750	-0,546	44.767	1,00	53,18	C
ATOM	15595	NE2	HIS	D	412	27.734	-1,164	45.395	1,00	53,79	N
ATOM	15596	N	GLN	D	413	27,181	-3.623	42,089	1,00	53.50	N
ATOM	15597	CA	GLN	D	413	26,938	-4,927	42,720	1,00	50.92	C
ATOM	15598	C	GLN	D	413	27.162	-6,104	41.766	1,00	51,44	C
ATOM	15599	O	GLN	D	413	27,491	-7.205	42,199	I,00	58.93	0
ATOM	15600	CB	GLN	D	413	25,519	-5.012	43,288	1,00	49.10	C
ATOM	15601	CG	GLN	D	413	25.259	-4,125	44.493	1,00	57,25	C
ATOM	15602	CD	GLN	D	413	24,552	-2,812	44,117	1.00	59.15	C
ATOM	15603	OE1	GLN	D	413	24,387	-2.498	42,936	1,00	54.62	0
ATOM	15604	NE2	GLN	D	413	24.127	-2,056	45.124	1,00	55,07	N
ATOM	15605	N	ILE	D	414	26,999	-5,877	40,470	1.00	51.70	N
ATOM	15606	CA.	ILE	D	414	27,309	-6.915	39,487	1,00	47.05	C
ATOM	15607	C	ILE	D	414	28.835	-7,125	39.352	1,00	48,98	C
ATOM	15608	O	ILE	D	414	29.304	-8,246	39.490	1,00	54,19	O
ATOM	15609	CB	ILE	D	414	26,670	-6.576	38,137	1,00	45.15	C
ATOM	15610	CGI	ILE	D	414	25,153	-6,751	38,236	1,00	48.01	C
ATOM	15611	CG2	ILE	D	414	27.192	-7,446	37.035	1,00	43,64	C
ATOM	15612	CDI	ILE	D	414	24,694	-8.173	38,147	I,00	45.27	C
ATOM	15613	N	HI S	D	415	29,617	-6,069	39,117	1,00	49.95	N
ATOM	15614	CA	HIS	D	415	31.078	-6,218	39.071	1,00	52,52	C
ATOM	15615	C	HIS	D	415	31,637	-6.728	40,396	I,00	54.55	C
ATOM	15616	O	HI S	D	415	32,661	-7.419	40,432	1,00	50.57	0
ATOM	15617	CB	HIS	D	415	31.772	-4,906	38.725	1,00	44,27	C
ATOM	15618	CG	HIS	D	415	31,401	-4,353	37,387	1.00	47.91	C
ATOM	15619	ND1	HI S	D	415	31,678	-5.002	36,205	1,00	47.43	N
ATOM	15620	CD2	HIS	D	415	30.803	-3,187	37.044	1,00	45,32	C
ATOM	15621	CE1	HIS	D	415	31.252	-4,269	35,191	1.00	49.50	C
ATOM	15622	NE2	HI S	D	415	30,728	-3.157	35,675	1,00	46.48	N

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ATOM  15623  N    LEU  D 416     30.967   -6.350   41.483  1.00 56.81    N
ATOM  15624  CA   LEU  D 416     31.423   -6.695   42.821  1.00 57.46    C
ATOM  15625  C    LEU  D 416     31.267   -8.192   43.023  1.00 53.69    C
ATOM  15626  O    LEU  D 416     32.127   -8.837   43.617  1.00 51.77    0
ATOM  15627  CB   LEU  D 416     30.636   -5.922   43.894  I.00 50.14    C
ATOM  15628  CG   LEU  D 416     30.834   -6.336   45.361  1.00 51.08    C
ATOM  15629  CD1  LEU  D 416     32.242   -6.043   45.801  1.00 50.27    C
ATOM  15630  CD2  LEU  D 416     29.837   -5.661   46.303  I.00 46.00    C
ATOM  15631  N    GLY  D 417     30.136   -8.707   42.542  1.00 55.39    N
ATOM  15632  CA   GLY  D 417     29.780  -10.107   42.669  1.00 55.58    C
ATOM  15633  C    GLY  D 417     30.884  -10.939   42.088  I.00 49.00    C
ATOM  15634  O    GLY  D 417     31.439  -11.786   42.771  1.00 60.16    0
ATOM  15635  N    GLU  D 418     31.222  -10.653   40.837  1.00 49.83    N
ATOM  15636  CA   GLU  D 418     32.313  -11.301   40.142  1.00 48.88    C
ATOM  15637  C    GLU  D 418     33.673  -11.140   40.867  1.00 53.85    C
ATOM  15638  O    GLU  D 418     34.470  -12.073   40.919  1.00 58.33    0
ATOM  15639  CB   GLU  D 418     32.407  -10.765   38.702  1.00 45.07    C
ATOM  15640  CG   GLU  D 418     31.217  -11.120   37.805  I.00 40.95    C
ATOM  15641  CD   GLU  D 418     31.484  -10.849   36.320  1.00 42.83    C
ATOM  15642  OE1  GLU  D 418     32.621  -10.456   35.960  1.00 43.64    0
ATOM  15643  OE2  GLU  D 418     30.565  -11.046   35.495  I.00 38.22    0
ATOM  15644  N    LEU  D 419     33.945   -9.963   41.416  1.00 52.47    N
ATOM  15645  CA   LEU  D 419     35.220   -9.722   42.095  1.00 53.78    C
ATOM  15646  C    LEU  D 419     35.342  -10.546   43.370  I.00 57.24    C
ATOM  15647  O    LEU  D 419     36.348  -11.207   43.594  1.00 58.18    0
ATOM  15648  CB   LEU  D 419     35.388   -8.242   42.424  1.00 49.12    C
ATOM  15649  CG   LEU  D 419     36.489   -7.860   43.419  I.00 53.84    C
ATOM  15650  CD1  LEU  D 419     37.242   -6.643   42.930  1.00 47.71    C
ATOM  15651  CD2  LEU  D 419     35.886   -7.594   44.804  1.00 56.67    C
ATOM  15652  N    HIS  D 420     34.322  -10.451   44.211  1.00 51.11    N
ATOM  15653  CA   HI S D 420     34.155  -11.282   45.385  1.00 52.18    C
ATOM  15654  C    HIS  D 420     34.354  -12.768   45.008  1.00 64.64    C
ATOM  15655  O    HIS  D 420     35.176  -13.480   45.615  1.00 64.74    0
ATOM  15656  CB   HI S D 420     32.769  -11.003   45.977  I.00 49.09    C
ATOM  15657  CG   HIS  D 420     32.377  -11.884   47.124  1.00 58.34    C
ATOM  15658  ND1  HIS  D 420     33.062  -11.911   48.319  1.00 61.81    N
ATOM  15659  CD2  HI S D 420     31.333  -12.735   47.272  I.00 58.07    C
ATOM  15660  CE1  HI S D 420     32.472  -12.757   49.147  1.00 56.11    C
ATOM  15661  NE2  HIS  D 420     31.422  -13.274   48.534  1.00 59.09    N
ATOM  15662  N    ALA  D 421     33.643  -13.216   43.972  I.00 60.28    N
ATOM  15663  CA   ALA  D 421     33.722  -14.609   43.553  1.00 59.64    C
ATOM  15664  C    ALA  D 421     35.149  -14.971   43.180  1.00 60.70    C
ATOM  15665  O    ALA  D 421     35.647  -16.022   43.582  1.00 68.07    0
ATOM  15666  CB   ALA  D 421     32.779  -14.881   42.396  1.00 56.97    C
ATOM  15667  N    ILE  D 422     35.821  -14.099   42.436  1.00 60.12    N
ATOM  15668  CA   ILE  D 422     37.195  -14.390   42.022  1.00 59.68    C
ATOM  15669  C    ILE  D 422     38.070  -14.504   43.260  I.00 60.77    C
ATOM  15670  O    ILE  D 422     38.902  -15.402   43.364  1.00 70.30    0
ATOM  15671  CB   ILE  D 422     37.766  -13.320   41.074  1.00 55.01    C
ATOM  15672  CGI  ILE  D 422     37.210  -13.485   39.661  I.00 60.53    C
ATOM  15673  CG2  ILE  D 422     39.265  -13.402   40.982  1.00 50.43    C
ATOM  15674  CD1  ILE  D 422     37.839  -12.517   38.651  1.00 55.59    C
ATOM  15675  N    LEU  D 423     37.851  -13.621   44.220  I.00 60.04    N
ATOM  15676  CA   LEU  D 423     38.678  -13.613   45.414  1.00 65.64    C
ATOM  15677  C    LEU  D 423     38.477  -14.899   46.218  1.00 66.98    C
ATOM  15678  O    LEU  D 423     39.439  -15.485   46.700  I.00 59.78    0
ATOM  15679  CB   LEU  D 423     38.379  -12.385   46.292  1.00 57.47    C
ATOM  15680  CG   LEU  D 423     38.832  -11.023   45.758  1.00 59.93    C
ATOM  15681  CD1  LEU  D 423     38.204   -9.882   46.565  1.00 53.31    C
ATOM  15682  CD2  LEU  D 423     40.347  -10.908   45.735  1.00 57.54    C
ATOM  15683  N    AP.G D 424     37.223  -15.330   46.355  1.00 70.49    N
ATOM  15684  CA   ARG  D 424     36.914  -16.513   47.149  1.00 63.45    C
ATOM  15685  C    ARG  D 424     37.455  -17.767   46.476  I.00 67.76    C
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ATOM	15686	O	ARG	D	424	37.561	--18.810	47.110	1.00	71.25	O
ATOM	15687	CB	ARG	D	424	35.410	--16.643	47.379	1.00	57.65	C
ATOM	15688	N	ARG	D	425	37.818	-17.664	45.201	1.00	67.43	N
ATOM	15689	CA	ARG	D	425	38.358	--18.814	44.482	1.00	63.05	C
ATOM	15690	C	ARG	D	425	39.845	-18.950	44.657	1.00	66.51	C
ATOM	15691	O	ARG	D	425	40.361	-20.057	44.754	1.00	74.36	O
ATOM	15692	CB	ARG	D	425	38.051	-18.731	42.989	1.00	67.45	C
ATOM	15693	CG	ARG	D	425	36.570	-18.863	42.649	1.00	67.00	C
ATOM	15694	CD	ARG	D	425	36.049	-20.243	42.952	1.00	62.23	C
ATOM	15695	NE	ARG	D	425	35.528	-20.873	41.749	1.00	61.22	N
ATOM	15696	CZ	ARG	D	425	34.534	-21.753	41.735	1.00	60.41	C
ATOM	15697	NH1	ARG	D	425	33.947	-22.116	42.866	1.00	64.63	N
ATOM	15698	NH2	ARG	D	425	34.117	-22.264	40.584	1.00	60.79	N
ATOM	15699	N	GLN	D	426	40.545	-17.832	44.700	1.00	61.44	N
ATOM	15700	C	GLN	D	426	42.742	-17.433	45.818	1.00	67.75	C
ATOM	15701	CA	GLN	D	426	41.985	-17.901	44.587	1.00	63.08	C
ATOM	15702	O	GLN	D	426	43.983	-17.329	45.813	1.00	59.42	O
ATOM	15703	CB	GLN	D	426	42.402	-17.112	43.373	1.00	61.76	C
ATOM	15704	CG	GLN	D	426	42.117	-17.888	42.120	1.00	61.95	C
ATOM	15705	CD	GLN	D	426	43.376	-18.265	41.419	1.00	60.72	C
ATOM	15706	OE1	GLN	D	426	43.352	-18.666	40.266	1.00	60.23	0
ATOM	15707	ME 2	GLN	D	426	44.503	-18.127	42.108	1.00	61.07	N
ATOM	15708	O	GLU	D	427	44.497	-17.674	49.246	1.00	78.66	O
ATOM	15709	N	GLU	D	427	41.989	-17.172	46.878	1.00	67.13	N
ATOM	15710	CA	GLU	D	427	42.586	-16.762	48.132	1.00	70.64	C
ATOM	15711	C	GLU	D	427	43.429	-17.898	48.676	1.00	76.20	C
ATOM	15712	CB	GLU	D	427	41.514	-16.365	49.130	1.00	70.19	C
ATOM	15713	CG	GLU	D	427	40.365	-17.334	49.186	1.00	72.08	C
ATOM	15714	CD	GLU	D	427	39.279	-16.858	50.118	1.00	76.40	C
ATOM	15715	OE1	GLU	D	427	39.382	-15.709	50.605	1.00	73.06	0
ATOM	15716	OE2	GLU	D	427	38.325	-17.631	50.361	1.00	82.64	0
ATOM	15717	O	ASP	D	428	46.061	-20.361	48.944	1.00	79.40	0
ATOM	15718	N	ASP	D	428	42.940	-19.118	48.481	1.00	76.01	N
ATOM	15719	CA.	ASP	D	428	43.672	-20.311	48.871	1.00	78.67	C
ATOM	15720	C	ASP	D	428	45.064	-20.306	48.236	1.00	73.27	C
ATOM	15721	CB	ASP	D	428	42.885	-21.577	48.491	1.00	80.17	C
ATOM	15722	CG	ASP	D	428	41.638	-21.781	49.362	1.00	88.02	C
ATOM	15723	OD1	ASP	D	428	41.163	-20.802	49.987	1.00	86.64	0
ATOM	15724	OD2	ASP	D	428	41.131	-22.922	49.427	1.00	87.13	0
ATOM	15725	N	PHE	D	429	45.141	-20.192	46.915	1.00	69.33	N
ATOM	15726	CA	FHE	D	429	46.435	-20.243	46.238	1.00	67.29	C
ATOM	15727	C	PHE	D	429	47.314	-19.045	46.540	1.00	69.70	C
ATOM	15728	O	PHE	D	429	48.508	-19.045	46.236	1.00	72.24	0
ATOM	15729	CB	FHE	D	429	46.246	-20.360	44.729	1.00	65.11	C
ATOM	15730	CG	PHE	D	429	45.364	-21.490	44.334	1.00	71.37	C
ATOM	15731	CD1	PHE	D	429	45.873	-22.775	44.235	1.00	68.93	C
ATOM	15732	CD2	PHE	D	429	44.016	-21.281	44.103	1.00	66.12	C
ATOM	15733	CE1	PHE	D	429	45.060	-23.823	43.880	1.00	65.31	C
ATOM	15734	CE2	PHE	D	429	43.196	-22.329	43.755	1.00	68.42	C
ATOM	15735	CZ	PHE	D	429	43.714	-23.603	43.640	1.00	65.26	C
ATOM	15736	N	TYR	D	430	46.731	-18.017	47.137	1.00	74.87	N
ATOM	15737	CA	TYR	D	430	47.460	-16.776	47.312	1.00	70.08	C
ATOM	15738	C	TYR	D	430	47.103	-16.136	48.631	1.00	74.23	C
ATOM	15739	O	TYR	D	430	46.018	-15.583	48.791	1.00	75.77	0
ATOM	15740	CB	TYR	D	430	47.175	-15.823	46.165	1.00	62.05	C
ATOM	15741	CG	TYR	D	430	47.875	-16.147	44.870	1.00	54.61	C
ATOM	15742	CD1	TYR	D	430	49.181	-15.763	44.664	1.00	50.77	C
ATOM	15743	CD2	TYR	D	430	47.207	-16.787	43.830	1.00	53.44	C
ATOM	15744	CE1	TYR	D	430	49.832	-16.027	43.464	1.00	55.89	C
ATOM	15745	CE2	TYR	D	430	47.842	-17.048	42.613	1.00	52.35	C
ATOM	15746	CZ	TYR	D	430	49.160	-16.669	42.437	1.00	58.13	C
ATOM	15747	OH	TYR	D	430	49.817	-16.917	41.237	1.00	56.66	0
ATOM	15748	N	PRO	D	431	48.030	-16.223	49.588	1.00	81.41	N

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ATOM    15749    CA   PRO  D  431        47.919   --15.,726   50.,959   1,00  81.25          C
ATOM    15750    C    FRO  D  431        47,160   -14.404     51.,093   1,00  78..88          C
ATOM    157 51   O    PRO  D  431        46..046  -14,375     51..634   1,00  76,.44          0
ATOM    157 52   CB   PRO  D  431        49..377  --15.,552   51.,358   1,00  78..17          C
ATOM    15753    CG   PRO  D  431        50.,049  -16.713     50.,661   1,00  77,12           C
ATOM    157 54   CD   PRO  D  431        49..340  -16,857     49.342    1,00  78,.79          C
ATOM    15755    O    PHE  D  432        45..095  -10.,999     50..970   1,00  76,38           0
ATOM    15756    N    PHE  D  432        47,762   -13. 334     50.,585   1,00  76.,32          N
ATOM    157 57   CA   PHE  D  432        47.270   -11 ,975     50.,809   1,00  78..68          C
ATOM    15758    C    PHE  D  432        45..836  -11 ,736     50..328   1,00  76,72           C
ATOM    15759    CB   PHE  D  432        48.,213  -10.961     50.,153   I,00  77.53           C
ATOM    15760    CG   PHE  D  432        48.,193  -10.,981     48.,651   1,00  75..19          C
ATOM    15761    CD2  PHE  D  4.32       47.813    -9.,857     47.942    1,00  71 ,57          C
ATOM    15762    CD1  PHE  D  432        48.,589  -12.,101     47,951    1,00  70..78          C
ATOM    15763    CE2  PHE  D  432        47,811    -9..859     46.,564   1,00  67.72           C
ATOM    15764    CE1  PHE  D  4.32       48..589  -12.,111     46..578   1,00  70,.10          C
ATOM    15765    CZ   PHE  D  432        48.,197  -10.,990     45.,882   1,00  67.23           C
ATOM    15766    N    LEU  D  433        45,431   -12.375     49.,234   1,00  71,83           N
ATOM    15767    CA   LEU  D  4.33       44.073   -12.,195     48..738   1,00  69,.85          C
ATOM    15768    C    LEU  D  433        43..018  -12.,612     49..755   1,00  72,48           C
ATOM    15769    0    LEU  D  433        41,883   -12.153     49.,689   1,00  79.,38          0
ATOM    15770    CB   LEU  D  433        43,872   -12.,965     47,440    1,00  67.98           C
ATOM    15771    CG   LEU  D  433        44.855   -12.,534     46..362   1,00  65,.40          C
ATOM    157 72   CD1  LEU  D  433        44,683   -13..356     45.,091   I,00  56..50          C
ATOM    15773    CD2  LEU  D  433        44,657   -11 ,060     46.,096   1,00  63..87          C
ATOM    15774    N    LYS  D  4.34       43. 378   -13.,471     50. 699   1,00  73,54           N
ATOM    15775    CA   LYS  D  434        42.,441  -13.851     51.,761   I,00  75..80          C
ATOM    15776    C    LYS  D  434        42.,403  -12..756     52.,814   1,00  77.01           C
ATOM    15777    O    LYS  D  4.34       41..342  -12.,394     53. 338   1,00  76,69           O
ATOM    15778    CB   LYS  D  434        42.,837  -15.,183     52.,405   1,00  68..75          C
ATOM    15779    N    ASP  D  435        43.,587  -12..230     53.,106   1,00  73..69          N
ATOM    15780    CA   ASP  D  4.35       43..767  -11 ,232     54..144   1,00  78,.51          C
ATOM    15781    C    ASP  D  435        43.,064   -9 ,923     53.,772   1,00  79..33          C
ATOM    157 82   O    ASP  D  435        42.,309   -9. 370     54,571    1,00  82,08           0
ATOM    15783    CB   ASP  D  4.35       45..264  -11 ,003     54...393  1,00  78,.80          C
ATOM    15784    N    ASN  D  436        43..293   -9.,455     52..548   1,00  76,52           N
ATOM    157 85   CA.  ASM  D  436        42.,719   -8. 200     52.,069   1,00  75.,36          C
ATOM    15786    C    ASN  D  436        41,393    -8.,303     51.,295   1,00  73..11          C
ATOM    15787    O    ASN  D  4.36       41.074    -7,399     50. 535   1,00  69,60           O
ATOM    15788    CB   ASN  D  436        43.,733   -7.482     51.,169   I,00  71.67           C
ATOM    15789    CG   ASN  D  436        45.,070   -7.250     51.,850   1,00  72.04           C
ATOM    15790    OD1  ASN  D  4.36       45. 326   -6.,173     52. 396   1,00  68,90           0
ATOM    15791    ND2  ASN  D  436        45.,937   -8.,257     51.,808   1,00  70..14          N
ATOM    15792    N    ARG  D  437        40.,615   -9..365     51.,470   1,00  71.12           N
ATOM    15793    CA   ARG  D  4.37       39..394   -9.,486     50..667   1,00  72,10           C
ATOM    157 94   C    ARG  D  437        38.,447   -8.,316     50.,932   1,00  71.11           C
ATOM    157 95   O    ARG  D  437        .37.,900  -7.724      50.,003   1,00  69.,03          0
ATOM    15796    CB   ARG  D  4.37       38..665  -10.,811     50..932   1,00  64,08           C
ATOM    15797    N    GLU  D  438        38..266   -7,983      52..203   1,00  72,23           N
ATOM    157 98   CA.  GLU  D  438        .37.,278  -6. 991      52.,587   1,00  66.,46          C
ATOM    15799    C    GLU  D  438        37.,719   -5.,588     52.,166   1,00  65..12          C
ATOM    15800    O    GLU  D  438        36..881   -4,729      51..914   1,00  68,.01          O
ATOM    15801    CB   GLU  D  438        .37.,017  -7.056      54.,096   I,00  63..77          C
ATOM    15802    N    LYS  D  439        39.,030   -5.,375     52.,072   1,00  67.41           N
ATOM    15803    CA   LYS  D  4.39       39. 595   -4,076      51. 712   1,00  62,32           C
ATOM    15804    C    LYS  D  439        39,544    -3..825     50.,202   I,00  65..37          C
ATOM    15805    O    LYS  D  439        39.,241   -2.702      49.,771   1,00  68..33          O
ATOM    15806    CB   LYS  D  4.39       41.043    -3.,951     52. 209   1,00  53,77           C
ATOM    15807    N    ILE  D  440        39.,852   -4,856      49.,412   1,00  59..90          N
ATOM    15808    CA   ILE  D  440        39.,722   -4.829      47,949    1,00  54.56           C
ATOM    15809    C    ILE  D  440        38..286   -4,544      47.536    1,00  59,.44          C
ATOM    15810    O    ILE  D  440        38.,034   -3.,821     46.,571   1,00  56..18          0
ATOM    15811    CB   ILE  D  440        40.,163   -6. 178     47,301    1,00  57,56           C
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ATOM  15812  CGI  ILE  D 440    41.598  -6.518  47.687  1.00  59.38      C
ATOM  15813  CG2  ILE  D 440    40.047  -6.139  45.769  1.00  44.43      C
ATOM  15814  GD1  ILE  D 440    41.947  -7.993  47.504  1.00  59.64      C
ATOM  15815  N    GLU  D 441    37.339  -5.128  48.261  1.00  59.72      N
ATOM  15816  CA.  GLU  D 441    35.937  -4.873  47.981  I.00  60.26      C
ATOM  15817  C    GLU  D 441    35.556  -3.440  48.293  1.00  59.78      C
ATOM  15818  O    GLU  D 441    34.684  -2.887  47.638  1.00  58.30      O
ATOM  15819  CB   GLU  D 441    35.053  -5.818  48.770  I.00  59.35      C
ATOM  1582 0 CG   GLU  D 441    35.126  -7.225  48.246  1.00  72.05      C
ATOM  1582 1 CD   GLU  D 441    34.381  -8.178  49.126  1.00  75.04      C
ATOM  15822  OE1  GLU  D 441    33.546  -7.695  49.940  I.00  75.55      0
ATOM  1582 3 OE2  GLU  D 441    34.650  -9.392  49.006  1.00  70.11      0
ATOM  1582 4 N    LYS  D 442    36.208  -2.857  49.297  1.00  56.00      N
ATOM  1582 5 CA   LYS  D 442    35.979  -1.463  49.655  1.00  62.80      C
ATOM  1582 6 C    LYS  D 442    36.493  -0.513  48.575  1.00  57.08      C
ATOM  1582 7 O    LYS  D 442    35.888   0.517  48.329  1.00  57.96      0
ATOM  1582 8 CB   LYS  D 442    36.642  -1.126  50.989  1.00  61.20      C
ATOM  15829  CG   LYS  D 442    35.711  -1.180  52.175  I.00  65.49      C
ATOM  15830  CD   LYS  D 442    34.905   0.106  52.354  1.00  55.69      C
ATOM  15831  CE   LYS  D 442    33.525  -0.224  52.880  1.00  50.20      C
ATOM  15832  NZ   LYS  D 442    32.663   0.994  52.938  I.00  64.21      N
ATOM  15833  N    ILE  D 443    37.606  -0.855  47.935  1.00  55.78      N
ATOM  15834  CA   ILE  D 443    38.090  -0.028  46.845  1.00  56.05      C
ATOM  15835  C    ILE  D 443    37.018   0.060  45.759  I.00  57.02      C
ATOM  15836  O    ILE  D 443    36.824   1.117  45.176  1.00  55.28      0
ATOM  15837  CB   ILE  D 443    39.403  -0.557  46.242  1.00  54.97      C
ATOM  15838  CGI  ILE  D 443    40.450  -0.796  47.335  I.00  62.04      C
ATOM  15839  CG2  ILE  D 443    39.960   0.437  45.207  1.00  52.14      C
ATOM  15840  CD1  ILE  D 443    41.806  -1.371  46.813  1.00  57.49      C
ATOM  15841  N    LEU  D 444    36.308  -1.040  45.507  1.00  54.32      N
ATOM  15842  CA   LEU  D 444    35.187  -1.012  44.569  1.00  55.26      C
ATOM  15843  C    LEU  D 444    33.980  -0.218  45.084  1.00  53.37      C
ATOM  15844  O    LEU  D 444    33.372   0.543  44.339  1.00  54.48      0
ATOM  15845  CB   LEU  D 444    34.716  -2.433  44.229  I.00  48.41      C
ATOM  15846  CG   LEU  D 444    33.979  -2.625  42.889  1.00  44.70      C
ATOM  15847  CD1  LEU  D 444    34.075  -4.078  42.444  1.00  49.85      C
ATOM  15848  CD2  LEU  D 444    32.526  -2.268  42.960  I.00  47.28      C
ATOM  15849  N    THR  D 445    33.618  -0.429  46.341  1.00  47.43      N
ATOM  15850  CA   THR  D 445    32.286  -0.084  46.796  1.00  51.59      C
ATOM  15851  C    THR  D 445    32.181   1.239  47.535  I.00  54.81      C
ATOM  15852  O    THR  D 445    31.083   1.721  47.757  1.00  49.45      0
ATOM  15853  CB   THR  D 445    31.734  -1.140  47.737  1.00  52.66      C
ATOM  15854  OG1  THR  D 445    32.511  -1.130  48.937  1.00  55.35      0
ATOM  15855  CG2  THR  D 445    31.770  -2.521  47.087  1.00  53.08      C
ATOM  15856  N    PHE  D 446    33.314   1.790  47.954  1.00  55.82      N
ATOM  15857  CA   PHE  D 446    33.296   3.001  48.746  1.00  52.45      C
ATOM  15858  C    PHE  D 446    33.078   4.207  47.865  I.00  52.00      C
ATOM  15859  O    PHE  D 446    33.707   4.336  46.817  1.00  54.11      O
ATOM  15860  CB   PHE  D 446    34.598   3.190  49.522  1.00  54.44      C
ATOM  15861  CG   PHE  D 446    34.762   4.580  50.068  I.00  54.59      C
ATOM  15862  CD1  PHE  D 446    33.811   5.112  50.942  1.00  55.61      C
ATOM  15863  CD2  PHE  D 446    35.839   5.369  49.688  1.00  58.14      C
ATOM  15864  CE1  PHE  D 446    33.945   6.403  51.437  I.00  56.53      C
ATOM  15865  CE2  PHE  D 446    35.981   6.659  50.177  1.00  54.89      C
ATOM  15866  CZ   PHE  D 446    35.034   7.174  51.051  1.00  54.88      C
ATOM  15867  O    ARG  D 447    31.011   7.476  49.417  I.00  49.37      0
ATOM  15868  N    ARG  D 447    32.224   5.111  48.323  1.00  52.78      N
ATOM  15869  CA   ARG  D 447    31.911   6.308  47.560  1.00  52.55      C
ATOM  15870  C    ARG  D 447    31.801   7.507  48.486  1.00  49.21      C
ATOM  15871  CB   ARG  D 447    30.608   6.088  46.797  1.00  50.68      C
ATOM  15872  CG   ARG  D 447    30.037   7.296  46.150  1.00  49.57      C
ATOM  15873  CD   ARG  D 447    28.563   7.083  45.854  1.00  46.97      C
ATOM  15874  NE   ARG  D 447    28.089   8.093  44.927  I.00  53.47      N
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ATOM   15875  CZ   ARG  D 447     26..818   8..261   44.593   1.00  55..30      C
ATOM   15876  NH1  ARG  D 447     25,,888   7.481    45.,124  1,00  56..25      N
ATOM   15877  NH2  ARG  D 447     26..489   9,200    43..721  1,00  47,.33      N
ATOM   15878  O    ILE  D 448     30..605   10.,689  47,986   1.00  47.41       O
ATOM   15879  N    ILE  D 448     32.,601   8.543    48.,242  1,00  46..64      N
ATOM   15880  CA   ILE  D 448     32..545   9,756    49.049   1,00  46,.41      C
ATOM   15881  C    ILE  D 448     31..126   10.,338  49..046  1,00  47,.35      C
ATOM   15882  CB   ILE  D 448     33.,514   10.827   48.,534  1,00  46..67      C
ATOM   15883  CGI  ILE  D 448     34..844   10.,205  48.,136  1,00  48..50      C
ATOM   15884  CG2  ILE  D 448     33..721   11,910   49..575  1,00  49,.37      C
ATOM   15885  CDI  ILE  D 448     .35.,927  11.265   47,836   I,00  51.47       C
ATOM   15886  O    FRO  D 449     29..975   13..173  50.,178  1,00  49..21      0
ATOM   15887  N    PRO  D 449     30.479    10.,398  50.222   1,00  51,68       N
ATOM   15888  CA   PRO  D 449     29..115   10.,944  50.,285  1.00  47.97       C
ATOM   15889  C    FRO  D 449     29.,073   12..398  49.,851  1,00  43..02      C
ATOM   15890  CB   PRO  D 449     28..748   10.,795  51..760  1,00  54,.38      C
ATOM   15891  CG   PRO  D 449     29..650   9,683    52.,261  1.00  46..94      C
ATOM   15892  CD   PRO  D 449     30.,936   9.936    51,545   1,00  49..93      C
ATOM   15893  O    TYR  D 450     28...385  16.,313  49.298   1,00  48,.67      0
ATOM   15894  N    TYR  D 450     28..059   12.,748  49..075  1,00  44,.62      N
ATOM   15895  CA.  TYR  D 450     27.,958   14.099   48.,510  1,00  45..25      C
ATOM   15896  C    TYR  D 450     27..943   15.,201  49.,574  1,00  51.23       C
ATOM   15897  CB   TYR  D 450     26..701   14,212   4,..654  1,00  47,.20      C
ATOM   15898  CG   TYR  D 450     25.,450   14.163   48.,484  I,00  45..61      C
ATOM   15899  CD2  TYR  D 450     24..822   15..333  48.,897  1,00  53..24      C
ATOM   15900  GDI  TYR  D 450     24.901    12.,953  48.863   1,00  49,.48      C
ATOM   15901  CE2  TYR  D 450     23.,696   15.295   49.,671  I,00  52.34       C
ATOM   15902  CEl  TYR  D 450     23.,779   12..896  49.,627  1,00  53..76      C
ATOM   15903  CZ   TYR  D 450     23.173    14,077   50.034   1,00  60,.34      C
ATOM   15904  OH   TYR  D 450     22..037   14,034   50.,803  1.00  65..38      0
ATOM   15905  O    TYR  D 451     28.,790   16..779  53.,565  1,00  55..18      0
ATOM   15906  N    TYR  D 451     27.426    14,898   50..773  1,00  47,.33      N
ATOM   15907  CA   TYR  D 451     27..349   15.,879  51.,862  1.00  46..09      C
ATOM   15908  C    TYR  D 451     28.,686   16.042   52.,575  1,00  53..58      C
ATOM   15909  CB   TYR  D 451     26..279   15.,491  52..875  1,00  44,.93      C
ATOM   15910  CG   TYR  D 451     26..485   14,138   53..496  1,00  49,.75      C
ATOM   15911  CD2  TYR  D 451     25,742    13.046   53.,088  1,00  48..46      C
ATOM   15912  CD1  TYR  D 451     27..416   13.,952  54.,505  1,00  55..33      C
ATOM   15913  CE2  TYR  D 451     25.940    11,805   53.664   1,00  51,.60      C
ATOM   15914  CEl  TYR  D 451     27.,619   12.721   55.,078  I,00  51.79       C
ATOM   15915  CZ   TYR  D 451     26.,884   11.656   54.,654  1,00  53..26      C
ATOM   15916  OH   TYR  D 451     27.103    10.,432  55.237   1,00  66,.25      0
ATOM   15917  O    VAL  D 452     31..650   16.,002  50.,279  1.00  41.09       0
ATOM   15918  N    VAL  D 452     29.,697   15..334  52.,082  1,00  43..94      N
ATOM   15919  CA   VAL  D 452     31..058   15.,509  52..549  1,00  44,.87      C
ATOM   15920  C    VAL  D 452     31..806   16.,269  51.,475  1.00  47.13       C
ATOM   15921  CB   VAL  D 452     31.,758   14.137   52.,822  1,00  50.,39      C
ATOM   15922  CGI  VAL  D 452     33..234   14,337   53..203  1,00  48,.93      C
ATOM   15923  CG2  VAL  D 452     31..018   13.,338  53..893  1,00  44,.45      C
ATOM   15924  O    GLY  D 453     34.,317   15.764   50.,121  1,00  43..55      0
ATOM   15925  N    GLY  D 453     32..613   17,243   51.,854  1,00  48..26      N
ATOM   15926  CA   GLY  D 453     33..379   17,908   50..810  1,00  53,.19      C
ATOM   15927  C    GLY  D 453     .34.,252  16.982   49.,933  I,00  50..82      C
ATOM   15928  O    FRO  D 454     36.990    17.666   50.,812  1,00  51.18       0
ATOM   15929  N    PRO  D 454     34.931    17,567   48.949   1,00  47,.89      N
ATOM   15930  CA   PRO  D 454     36,242    17.003   48.,622  I,00  44.44       C
ATOM   15931  C    FRO  D 454     37.,107   16..866  49.,881  1,00  49..65      C
ATOM   15932  CB   PRO  D 454     36.840    18.,029  47.662   1,00  42,.22      C
ATOM   15933  CG   PRO  D 454     35.,851   19.,228  47,686   1.00  42.48       C
ATOM   15934  CD   FRO  D 454     34.,538   18..641  48.,029  1,00  38..52      C
ATOM   15935  O    LEU  D 455     41.110    16.,010  51..409  1,00  52,.71      0
ATOM   15936  N    LEU  D 455     37..982   15.,867  49.,918  1.00  50..90      N
ATOM   15937  CA.  LEU  D 455     38.,729   15.583   51,150   1,00  51.86       C
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ATOM   15938   C     LEU  D  455      39..963    16..487    51.,316    1 .00   55..35           C
ATOM   15939   CB    LEU  D  455      39,,122    14 .114    51.,176    1 ,00   43..42           C
ATOM   15940   CG    LEU  D  455      37..936    13.,227    50..792    1 ,00   50,.38           C
ATOM   15941   GDI   LEU  D  455      38..368    11 ,753    50..768    1 .00   49..05           C
ATOM   15942   CD2   LEU  D  455      36.,705    13. 429    51 ,694    1 ,00   40..83           C
ATOM   15943   O     ALA  D  456      41 .007    18.,453    53..775    1 ,00   50,,25           0
ATOM   15944   N     ALA  D  456      39..705    17 ,793    51..393    1 ,00   47 ,76           N
ATOM   15945   CA.   ALA  D  456      40.,760    18. 792    51 ,390    1 ,00   49..31           C
ATOM   15946   C     ALA  D  456      41 .438    18.,984    52.,743    1 ,00   52 .67           C
ATOM   15947   CB    ALA  D  456      40..204    20.,133    50..899    1 ,00   46,.55           C
ATOM   15948   O     ARG  D  457      44 ,634    22..100    53.,835    1 ,00   57 .22           0
ATOM   15949   N     ARG  D  457      42..523    19..750    52.,711    1 ,00   51 .34           N
ATOM   15950   CA    ARG  D  457      43. 226    20.,156    53. 918    1 ,00   57 ,31           C
ATOM   15951   C     ARG  D  457      43..482    21.,648    53.,835    1 .00   61 .41           C
ATOM   15952   CB    ARG  D  457      44 ,549    19..399    54.,099    1 ,00   62 .67           C
ATOM   15953   CG    ARG  D  457      45..089    19.,514    55..510    1 ,00   64 ,69           C
ATOM   15954   CD    ARG  D  457      46..554    19.,190    55.,580    1 .00   66..12           C
ATOM   15955   NE    ARG  D  457      46.,744    17.779     55.,859    1 ,00   70..54           N
ATOM   15956   CZ    ARG  D  457      47 .890    17 ,141    55..689    1 ,00   71 ,80           C
ATOM   15957   NH1   ARG  D  457      4,, .967   15.,841    55..958    1 ,00   72 ,13           N
ATOM   15958   NH2   ARG  D  457      48.,948    17.804     55.,228    1 ,00   69..71           N
ATOM   15959   O     GLY  D  458      43 .365    25.,753    52.,754    1 ,00   61 .48           O
ATOM   15960   N     GLY  D  458      42..392    22.,403    53..713    1 ,00   56,.90           N
ATOM   15961   CA    GLY  D  458      42.,443    23..842    53.,813    1 ,00   54 .09           C
ATOM   15962   C     GLY  D  458      43 .006    24..582    52.,624    1 ,00   57 .38           C
ATOM   15963   O     ASN  D  459      42 .833    24.,758    47 .975    1 ,00   43 ,77           O
ATOM   15964   N     ASM  D  459      43.,087    23..935    51.,469    1 ,00   52 .31           N
ATOM   15965   CA    ASM  D  459      43.,470    24 .676    50.,27 3   1 ,00   47 .15           C
ATOM   15966   C     ASN  D  459      42 .483    24.,549    49. 147    1 ,00   49 ,70           C
ATOM   15967   CB    ASN  D  459      44 .831    24.,253    49.,800    1 .00   56..87           C
ATOM   15968   CG    ASM  D  459      45.,904    24 .804    50.,655    1 ,00   66..31           C
ATOM   15969   OD1   ASN  D  459      46..237    24.,231    51..693    1 ,00   70,.96           0
ATOM   15970   ND2   ASN  D  459      46..441    25.,948    50..257    1 .00   69..59           N
ATOM   15971   O     SER  D  460      38.,425    25. 158    49..969    1 ,00   49..72           O
ATOM   15972   N     SEP. D  460      41 .242    24.,237    49 .514    1 ,00   47 ,11           N
ATOM   15973   CA    SER  D  460      40..143    24.,223    48..561    1 ,00   44 ,58           C
ATOM   15974   C     SER  D  460      39.,074    25. 264    48.,921    1 ,00   45..78           C
ATOM   15975   CB    SER  D  460      39..509    22.,837    48.,501    1 ,00   42 .67           C
ATOM   15976   OG    SER  D  460      38. 473    22.,804    47 .539    1 ,00   43 ,01           0
ATOM   15977   O     ARG  D  461      35.,450    27 .266    48.,516    1 ,00   47 .71           0
ATOM   15978   N     ARG  D  461      38.,853    26..238    48.,046    1 ,00   42 .46           N
ATOM   15979   CA    ARG  D  461      37. 803    27.,213    48. 310    1 ,00   40 ,01           C
ATOM   15980   C     ARG  D  461      36..416    26.,578    48.,250    1 .00   46..47           C
ATOM   15981   CB    ARG  D  461      37.,884    28..379    47 ,334    1 ,00   43..54           C
ATOM   15982   CG    ARG  D  461      37..183    28.,151    45..994    1 .00   46,.44           C
ATOM   15983   CD    ARG  D  461      37..548    29.,273    45.,049    1 .00   39..16           C
ATOM   15984   NE    ARG  D  461      37.,022    29. 114    43.,699    1 ,00   40..32           N
ATOM   15985   CZ    ARG  D  461      35..742    29.,22 9   43...354   1 .00   45,.51           C
ATOM   15986   NH1   ARG  D  461      34..799    29.,470    44 .255    1 ,00   50,.45           N
ATOM   15987   NH2   ARG  D  461      35.,399    29. 084    42.,090    1 ,00   48..15           N
ATOM   15988   O     FHE  D  462      33..640    23.,018    48.,910    1 ,00   47 .85           O
ATOM   15989   N     PHE  D  462      36..340    25.,271    4,, .939   1 ,00   42 ,44           N
ATOM   15990   CA    PHE  D  462      35.,082    24..526    47 ,738    1 ,00   41 .68           C
ATOM   15991   C     PHE  D  462      34.,734    23..579    48.,874    1 ,00   46..99           C
ATOM   15992   CB    PHE  D  462      35. 135    23.,655    46. 462    1 ,00   39 ,97           C
ATOM   15993   CG    PHE  D  462      35.,506    24..405    45.,211    1 ,00   47 .76           C
ATOM   15994   CD1   FHE  D  462      34.,560    25..206    44 ,542    1 ,00   43..06           C
ATOM   15995   CD2   PHE  D  462      36. 799    24.,333    44.708     1 ,00   38 ,07           C
ATOM   15996   CE1   PHE  D  462      34..914    25.,908    43.,394    1 .00   41 .75           C
ATOM   15997   CE2   FHE  D  462      37.,162    25..032    43.,555    1 ,00   36..14           C
ATOM   15998   CZ    PHE  D  462      36..216    25.,807    42 .893    1 .00   43,.93           C
ATOM   15999   O     ALA  D  463      35..036    23.,892    52.,331    1 .00   56..60           0
ATOM   16000   N     ALA  D  463      35 ,682    23.331     49.,768    1 ,00   46..51           N
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ATOM	16001	CA	ALA	D	463	35.511	22.229	50.700	1.00	43.65	C
ATOM	16002	C	ALA	D	463	34.946	22.716	52.017	1.00	46.58	C
ATOM	16003	CB	ALA	D	463	36.824	21.513	50.908	1.00	45.91	C
ATOM	16004	O	TRP	D	464	33.591	21.078	56.203	1.00	60.97	0
ATOM	16005	N	TRP	D	464	34.344	21.815	52.776	1.00	50.71	N
ATOM	16006	CA	TRP	D	464	33.772	22.150	54.074	1.00	52.93	C
ATOM	16007	C	TRP	D	464	34.002	21.014	55.049	1.00	48.32	C
ATOM	16008	CB	TRP	D	464	32.277	22.416	53.950	1.00	51.04	C
ATOM	16009	CG	TRP	D	464	31.522	21.221	53.465	1.00	48.93	C
ATOM	16010	CD1	TRP	D	464	31.018	20.209	54.218	1.00	48.78	C
ATOM	16011	CD2	TRP	D	464	31.188	20.923	52.116	1.00	45.10	C
ATOM	16012	ME 1	TRP	D	464	30.382	19.296	53.423	1.00	46.51	N
ATOM	16013	CE2	TRP	D	464	30.479	19.708	52.121	1.00	49.67	C
ATOM	16014	CE3	TRP	D	464	31.413	21.574	50.896	1.00	48.58	C
ATOM	16015	CZ2	TRP	D	464	29.991	19.119	50.953	1.00	47.01	C
ATOM	16016	Ca 3	TRP	D	464	30.926	20.994	49.743	1.00	46.79	C
ATOM	16017	CH2	TRP	D	464	30.226	19.770	49.781	1.00	43.69	C
ATOM	16018	0	MET	D	465	36.507	19.578	56.775	1.00	55.80	0
ATOM	16019	N	MET	D	465	34.652	19.971	54.563	1.00	50.07	N
ATOM	16020	CA	MET	D	465	34.808	18.716	55.307	1.00	54.07	C
ATOM	16021	C	MET	D	465	35.520	18.860	56.654	1.00	53.55	C
ATOM	16022	CB	MET	D	465	35.555	17.704	54.445	1.00	45.37	C
ATOM	16023	CG	MET	D	465	35.521	16.314	54.999	1.00	48.10	C
ATOM	16024	SD	MET	D	465	36.990	15.919	55.947	1.00	64.16	S
ATOM	16025	CE	MET	D	465	38.298	16.319	54.795	1.00	49.72	C
ATOM	16026	O	THR	D	466	35.551	15.784	59.401	1.00	63.01	0
ATOM	16027	N	THR	D	466	35.012	18.152	57.655	1.00	56.04	N
ATOM	16028	CA	THR	D	466	35.581	18.163	59.004	1.00	62.59	C
ATOM	16029	C	THR	D	466	36.225	16.821	59.397	1.00	59.58	C
ATOM	16030	CB	THR	D	466	34.491	18.505	60.041	1.00	60.11	C
ATOM	16031	OG1	THR	D	466	33.825	19.710	59.647	1.00	76.27	0
ATOM	16032	CG2	THR	D	466	35.085	18.664	61.421	1.00	60.74	C
ATOM	16033	O	ARG	D	467	38.054	16.215	62.501	1.00	69.53	0
ATOM	16034	N	ARG	D	467	37.508	16.838	59.751	1.00	59.38	N
ATOM	16035	CA	ARG	D	467	38.194	15.610	60.171	1.00	61.77	C
ATOM	16036	C	ARG	D	467	38.077	15.305	61.671	1.00	66.62	C
ATOM	16037	CB	ARG	D	467	39.673	15.679	59.798	1.00	64.82	C
ATOM	16038	CG	ARG	D	467	39.964	15.259	58.385	1.00	61.14	C
ATOM	16039	CD	ARG	D	467	41.439	15.296	58.086	1.00	63.64	C
ATOM	16040	NE	ARG	D	467	41.684	14.973	56.683	1.00	64.92	N
ATOM	16041	CZ	ARG	D	467	42.151	15.836	55.789	1.00	61.87	C
ATOM	16042	NH1	ARG	D	467	42.328	15.456	54.533	1.00	58.07	N
ATOM	16043	NH2	ARG	D	467	42.448	17.080	56.155	1.00	68.42	N
ATOM	16044	O	LYS	D	468	40.097	13.799	64.797	1.00	71.33	0
ATOM	16045	N	LYS	D	468	38.008	14.019	62.005	1.00	67.29	N
ATOM	16046	CA	LYS	D	468	38.165	13.551	63.385	1.00	65.86	C
ATOM	16047	C	LYS	D	468	39.643	13.374	63.735	1.00	70.00	C
ATOM	16048	CB	LYS	D	468	37.424	12.234	63.603	1.00	64.60	C
ATOM	16049	CG	LYS	D	468	36.052	12.397	64.181	1.00	64.63	C
ATOM	16050	CD	LYS	D	468	35.435	11.058	64.512	1.00	65.12	C
ATOM	16051	CE	LYS	D	468	35.180	10.263	63.267	1.00	64.41	C
ATOM	16052	NZ	LYS	D	468	34.424	9.016	63.566	1.00	65.34	N
ATOM	16053	O	SER	D	469	42.075	13.797	60.948	1.00	73.38	O
ATOM	16054	N	SEP.	D	469	40.397	12.737	62.846	1.00	71.04	N
ATOM	16055	CA	SER	D	469	41.840	12.647	63.035	1.00	70.28	C
ATOM	16056	C	SER	D	469	42.605	13.447	61.998	1.00	70.66	C
ATOM	16057	CB	SER	D	469	42.312	11.207	62.988	1.00	71.17	C
ATOM	16058	OG	SER	D	469	43.698	11.185	62.713	1.00	75.39	0
ATOM	16059	O	GLU	D	470	46.857	13.653	60.772	1.00	80.87	0
ATOM	16060	N	GLU	D	470	43.864	13.727	62.295	1.00	72.81	N
ATOM	16061	CA	GLU	D	470	44.683	14.496	61.376	1.00	75.06	C
ATOM	16062	C	GLU	D	470	45.636	13.571	60.618	1.00	77.93	C
ATOM	16063	CB	GLU	D	470	45.450	15.585	62.132	1.00	75.68	C

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ATOM   16064  CG   GLU  D 470      45.413  16.958  61.459  1.00  76.66         c
ATOM   16065  CD   GLU  D 470      44.000  17.455  61.160  1.00  73.31         C
ATOM   16066  OE1  GLU  D 470      43.845  18.215  60.183  1.00  75.01         0
ATOM   16067  OE2  GLU  D 470      43.050  17.098  61.895  1.00  70.82         0
ATOM   16068  O    GLU  D 471      44.118  12.185  57.290  I.00  67.03         0
ATOM   16069  M    GLU  D 471      45.056  12.688  59.807  1.00  69.51         M
ATOM   16070  CA   GLU  D 471      45.813  11.776  58.957  1.00  74.76         c
ATOM   16071  C    GLU  D 471      45.188  11.636  57.559  I.00  71.83         C
ATOM   16072  CB   GLU  D 471      45.909  10.398  59.621  1.00  70.15         c
ATOM   16073  CG   GLU  D 471      44.561   9.846  60.042  1.00  72.57         c
ATOM   16074  CD   GLU  D 471      44.617   8.381  60.436  I.00  78.85         c
ATOM   16075  OE1  GLU  D 471      43.955   7.993  61.427  1.00  78.18         0
ATOM   16076  OE2  GLU  D 471      45.314   7.610  59.742  1.00  80.67         0
ATOM   16077  O    THR  D 472      43.935   8.818  56.040  1.00  66.85         0
ATOM   16078  M    THR  D 472      45.852  10.874  56.689  1.00  72.97         M
ATOM   16079  CA   THR  D 472      45.367  10.599  55.335  1.00  62.82         c
ATOM   16080  c    THR  D 472      44.071   9.801  55.321  1.00  60.94         c
ATOM   16081  CB   THR  D 472      46.420   9.836  54.525  I.00  60.70         c
ATOM   16082  OG1  THR  D 472      47.442  10.748  54.108  1.00  64.33         0
ATOM   16083  CG2  THR  D 472      45.802   9.199  53.292  1.00  58.66         c
ATOM   16084  O    ILE  D 473      42.674   8.590  52.250  I.00  62.32         0
ATOM   16085  M    1LE  D 473      43.113  10.234  54.504  1.00  60.05         M
ATOM   16086  CA   ILE  D 473      41.864   9.501  54.336  1.00  57.33         c
ATOM   16087  C    ILE  D 473      41.993   8.418  53.267  I.00  62.51         c
ATOM   16088  CB   ILE  D 473      40.716  10.440  53.977  1.00  59.63         c
ATOM   16089  CGI  ILE  D 473      40.576  11.517  55.055  1.00  61.03         c
ATOM   16090  CG2  ILE  D 473      39.413   9.670  53.832  I.00  55.69         c
ATOM   16091  CD1  ILE  D 473      39.853  12.761  54.598  1.00  53.05         c
ATOM   16092  O    THR  D 474      39.182   5.906  53.384  1.00  55.91         0
ATOM   16093  N    THR  D 474      41.363   7.279  53.527  1.00  57.97         N
ATOM   16094  CA   THR  D 474      41.419   6.141  52.627  1.00  55.82         c
ATOM   16095  C    THR  D 474      40.031   5.559  52.560  1.00  57.79         c
ATOM   16096  CB   THR  D 474      42.418   5.032  53.107  1.00  57.51         c
ATOM   16097  OG1  THR  D 474      41.800   4.225  54.124  I.00  58.51         0
ATOM   16098  CG2  THR  D 474      43.706   5.632  53.631  1.00  50.82         c
ATOM   16099  O    PRO  D 475      37.157   2.994  53.279  1.00  58.72         0
ATOM   16100  N    PRO  D 475      39.792   4.661  51.592  I.00  56.05         M
ATOM   16101  CA   PRO  D 475      38.527   3.930  51.576  1.00  53.51         c
ATOM   16102  C    PRO  D 475      38.310   3.165  52.865  1.00  57.06         c
ATOM   16103  CB   PRO  D 475      38.689   2.980  50.396  I.00  52.69         c
ATOM   16104  CG   FRO  D 475      39.607   3.699  49.485  1.00  55.39         c
ATOM   16105  CD   PRO  D 475      40.569   4.441  50.361  1.00  53.73         c
ATOM   16106  O    TRP  D 476      38.259   2.360  56.748  1.00  59.50         0
ATOM   16107  M    TRP  D 476      39.405   2.752  53.507  1.00  57.55         M
ATOM   16108  CA   TRP  D 476      39.337   1.894  54.692  1.00  57.42         c
ATOM   16109  c    TRP  D 476      39.150   2.682  55.970  1.00  54.10         c
ATOM   16110  CB   TRP  D 476      40.592   1.018  54.777  I.00  57.05         c
ATOM   16111  CG   TRP  D 476      40.880   0.488  53.451  1.00  56.48         c
ATOM   16112  CD1  TRP  D 476      40.091  -0.350  52.719  1.00  55.06         c
ATOM   16113  CD2  TRP  D 476      41.995   0.811  52.631  I.00  58.11         c
ATOM   16114  ME1  TRP  D 476      40.662  --0.585  51.499  1.00  58.34         M
ATOM   16115  CE2  TRP  D 476      41.833   0.118  51.418  1.00  55.24         c
ATOM   16116  CE3  TRP  D 476      43.124   1.610  52.805  I.00  60.99         c
ATOM   16117  CZ2  TRP  D 476      42.762   0.191  50.390  1.00  60.01         c
ATOM   16118  CZ3  TRP  D 476      44.045   1.688  51.773  1.00  57.06         c
ATOM   16119  CH2  TRP  D 476      43.856   0.987  50.582  I.00  57.93         c
ATOM   16120  O    ASM  D 477      38.655   6.446  58.310  1.00  65.51         0
ATOM   16121  N    A.SM D 477      39.953   3.719  56.185  1.00  52.69         N
ATOM   16122  CA   ASN  D 477      39.804   4.533  57.406  1.00  57.39         c
ATOM   16123  C    ASM  D 477      38.744   5.661  57.368  1.00  61.65         c
ATOM   16124  CB   ASN  D 477      41.161   5.144  57.796  1.00  49.75         c
ATOM   16125  CG   ASN  D 477      41.658   6.207  56.812  1.00  59.79         c
ATOM   16126  OD1  ASM  D 477      40.935   6.646  55.920  I.00  61.83         0
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ATOM   16127  ND2 ASN D 477      42.902   6.634  56.992  1.00 57.12           N
ATOM   16128  O   FHE D 478      36.197   8.365  57.781  1.00 67.04           O
ATOM   16129  N   PHE D 478      37.944   5.743  56.305  1.00 60.45           N
ATOM   16130  CA  PHE D 478      37.072   6.916  56.092  1.00 62.49           C
ATOM   16131  C   PHE D 478      36.156   7.248  57.264  1.00 64.70           C
ATOM   16132  CB  PHE D 478      36.206   6.740  54.842  1.00 59.69           C
ATOM   16133  CG  PHE D 478      35.372   7.965  54.482  1.00 62.74           C
ATOM   16134  GDI PHE D 478      35.885   8.952  53.659  1.00 57.09           C
ATOM   16135  CD2 PHE D 478      34.064   8.107  54.946  1.00 61.79           C
ATOM   16136  CE1 PHE D 478      35.117  10.049  53.312  1.00 59.45           C
ATOM   16137  CE2 PHE D 478      33.302   9.202  54.607  1.00 63.34           C
ATOM   16138  CZ  PHE D 478      33.828  10.179  53.788  1.00 59.04           C
ATOM   16139  O   GUI D 479      34.215   7.387  60.961  1.00 68.14           0
ATOM   16140  N   GLU D 479      35.323   6.300  57.685  1.00 66.64           N
ATOM   16141  CA  GLU D 479      34.308   6.616  58.689  1.00 67.70           C
ATOM   16142  C   GLU D 479      34.907   6.906  60.066  1.00 69.45           C
ATOM   16143  CB  GLU D 479      33.288   5.489  58.791  1.00 70.81           C
ATOM   16144  CG  GLU D 479      31.906   5.981  59.179  1.00 81.58           C
ATOM   16145  CD  GLU D 479      30.786   5.095  58.638  1.00 92.76           C
ATOM   16146  OE1 GLU D 479      31.091   4.037  58.037  1.00 87.38           0
ATOM   16147  OE2 GLU D 479      29.599   5.465  58.815  1.00 95.20           0
ATOM   16148  O   GLU D 480      37.843   8.987  62.360  1.00 67.13           0
ATOM   16149  N   GLU D 480      36.200   6.632  60.223  1.00 68.69           N
ATOM   16150  CA  GLU D 480      36.915   6.946  61.459  1.00 68.07           C
ATOM   16151  C   GLU D 480      37.709   8.267  61.370  1.00 67.21           C
ATOM   16152  CB  GLU D 480      37.854   5.784  61.835  1.00 71.40           C
ATOM   16153  CG  GLU D 480      37.138   4.502  62.330  1.00 68.54           C
ATOM   16154  CD  GLU D 480      36.809   3.502  61.224  1.00 73.85           C
ATOM   16155  OE1 GLU D 480      37.639   3.326  60.302  1.00 76.48           0
ATOM   16156  OE2 GLU D 480      35.723   2.877  61.285  1.00 75.39           0
ATOM   16157  O   VAL D 481      38.377  12.141  60.064  1.00 64.59           0
ATOM   16158  N   VAL D 481      38.234   8.583  60.188  1.00 68.37           N
ATOM   16159  CA  VAL D 481      38.998   9.814  59.996  1.00 64.27           C
ATOM   16160  C   VAL D 481      38.083  11.008  59.698  1.00 66.26           C
ATOM   16161  CB  VAL D 481      40.011   9.661  58.865  1.00 61.72           C
ATOM   16162  CGI VAL D 481      40.795  10.944  58.670  1.00 66.13           C
ATOM   16163  CG2 VAL D 481      40.952   8.532  59.170  1.00 68.88           C
ATOM   16164  O   VAL D 482      34.192  11.033  59.919  1.00 66.07           0
ATOM   16165  N   VAL D 482      36.958  10.750  59.050  1.00 65.26           N
ATOM   16166  CA  VAL D 482      36.069  11.834  58.653  1.00 64.52           C
ATOM   16167  C   VAL D 482      34.923  11.988  59.641  1.00 65.40           C
ATOM   16168  CB  VAL D 482      35.505  11.605  57.222  1.00 64.25           C
ATOM   16169  CGI VAL D 482      34.287  12.481  56.963  1.00 60.36           C
ATOM   16170  CG2 VAL D 482      36.594  11.832  56.162  1.00 60.50           C
ATOM   16171  N   ASP D 483      34.758  13.193  60.174  1.00 63.87           N
ATOM   16172  CA  ASP D 483      33.601  13.456  61.012  1.00 62.69           C
ATOM   16173  C   ASP D 483      32.412  13.756  60.107  1.00 66.05           C
ATOM   16174  O   ASP D 483      32.179  14.905  59.744  1.00 66.03           0
ATOM   16175  CB  ASP D 483      33.855  14.614  61.977  1.00 58.53           C
ATOM   16176  CG  ASP D 483      32.740  14.774  62.999  1.00 61.68           C
ATOM   16177  OD1 ASP D 483      31.600  14.312  62.753  1.00 60.27           0
ATOM   16178  OD2 ASP D 483      33.000  15.375  64.061  1.00 70.00           0
ATOM   16179  N   LYS D 484      31.669  12.714  59.750  1.00 62.67           N
ATOM   16180  CA  LYS D 484      30.545  12.844  58.844  1.00 57.10           C
ATOM   16181  C   LYS D 484      29.526  13.829  59.394  1.00 63.55           C
ATOM   16182  O   LYS D 484      29.134  14.785  58.713  1.00 65.10           0
ATOM   16183  CB  LYS D 484      29.889  11.487  58.612  1.00 65.21           C
ATOM   16184  CG  LYS D 484      30.825  10.414  58.081  1.00 69.08           C
ATOM   16185  CD  LYS D 484      30.271   9.812  56.801  1.00 68.42           C
ATOM   16186  CE  LYS D 484      30.387   8.301  56.779  1.00 68.43           C
ATOM   16187  NZ  LYS D 484      29.373   7.688  57.677  1.00 74.69           N
ATOM   16188  N   GLY D 485      29.119  13.592  60.637  1.00 64.11           N
ATOM   16189  CA. GLY D 485      28.149  14.428  61.315  1.00 61.94           C
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ATOM   16190   C    GLY  D  485       28..462   15..894   61..128   1 .00  55..42          C
ATOM   16191   O    GLY  D  485       27.,672   16..620   60.,531   1,00   61 .64          O
ATOM   16192   N    ALA  D  486       29..633   16.,306   61..597   1 .00  52 ,.19         N
ATOM   16193   CA   ALA  D  486       30..074   17,682    61..481   1 .00  57 .24          C
ATOM   16194   C    ALA  D  486       .30.,116  18. 148   60.,028   1,00   62 .20          C
ATOM   16195   O    ALA  D  486       30..003   19.,343   59 .743    1 .00  65,.30          O
ATOM   16196   CB   ALA  D  486       31..431   17,852    62..121   1,00   60,.45          C
ATOM   16197   N    SER  D  487       .30.,266  17.210    59.,105   1,00   58..17          N
ATOM   16198   CA   SEP. D  487       30..347   17,577    57.,707   1,00   58..79          C
ATOM   16199   C    SER  D  487       28..951   17,728    57..115   1,00   58,.72          C
ATOM   16200   0    SER  D  487       28.,700   18.663    56,361    I,00   59..66          0
ATOM   162 01  CB   SER  D  487       31..178   16..558   56.,931   1,00   54 .73          C
ATOM   162 02  OG   SER  D  487       32.562    16.,762   57. 179   1,00   57,00           0
ATOM   16203   N    ALA  D  488       28..039   16.,833   57..474   1 .00  56..10          N
ATOM   16204   CA   ALA  D  488       26.,660   16..969   57.,043   1,00   51 .79          C
ATOM   162 05  C    ALA  D  488       26..075   18.,294   57..531   1.00   62 ,24          C
ATOM   16206   O    ALA  D  488       25..394   19.,001   56..786   1.00   63..89          0
ATOM   16207   CB   ALA  D  488       25,831    15. 822   57,542    1,00   55..91          C
ATOM   162 08  N    GLN  D  489       26...345  18.,637   58..780   1.00   58,.93          N
ATOM   16209   CA   GLN  D  489       25..803   19.,863   59..321   1,00   56,.64          C
ATOM   16210   C    GLN  D  489       26.,365   21.074    58.,581   1,00   58..55          C
ATOM   16211   O    GLN  D  489       25..608   21.,956   58..154   1,00   59..85          O
ATOM   16212   CB   GLN  D  489       26..091   19.,964   60..812   1,00   58,.97          C
ATOM   16213   CG   GLN  D  489       25.,528   21..219   61.,441   I,00   66..4.3         C
ATOM   16214   CD   GLN  D  489       25..083   21..014   62.,884   1,00   69..57          C
ATOM   16215   OE1  GLN  D  489       25. 426   20.,019   63. 526   1,00   64 ,78          0
ATOM   16216   NE2  GLN  D  489       24.,312   21..959   63.,397   I,00   67 .51          N
ATOM   16217   N    SER  D  490       27.,684   21 .112   58.,423   1,00   56..12          N
ATOM   16218   CA   SER  D  490       28. .339   22.,203   57. 711   1,00   53,86           C
ATOM   16219   C    SER  D  490       27..815   22.,325   56.,294   1.00   58..81          C
ATOM   16220   O    SER  D  490       27.,581   23..429   55.,806   1,00   61 .44          0
ATOM   16221   CB   SER  D  490       29..842   21.,995   57..671   1.00   57,27           C
ATOM   16222   OG   SER  D  490       30..456   22.,713   58..703   1.00   62 .16          0
ATOM   16223   N    PHE  D  491       27.,636   21 .175   55.,646   1,00   52 .26          N
ATOM   16224   CA   PHE  D  49.1      27.066    21.,103   54.. .308  1.00   52 ,61          C
ATOM   16225   C    PHE  D  491       25..812   21.,978   54..163   1,00   54 ,64          C
ATOM   16226   0    PHE  D  491       25,735    22.827    53.,274   1,00   53..13          0
ATOM   16227   CB   PHE  D  491       26..743   19.,640   53.,961   1,00   48..45          C
ATOM   16228   CG   PHE  D  491       26. 099   19.,448   52. 613   1,00   46,65           C
ATOM   16229   CD2  PHE  D  491       24.,843   18.874    52.,510   I,00   46..46          C
ATOM   16230   CD1  PHE  D  491       26.,765   19..788   51.,452   1,00   45..42          C
ATOM   16231   CE2  PHE  D  491       24.245    18.,671   51. 275   1,00   46,72           C
ATOM   16232   CE1  PHE  D  491       26.,175   19..577   50.,211   1.00   44 .31          C
ATOM   16233   CZ   PHE  D  491       24.,920   19..018   50.,126   1,00   45..51          C
ATOM   162 34  N    ILE  D  492       24..830   21.,765   55..028   1.00   54,89           N
ATOM   16235   CA   ILE  D  492       23..601   22.,547   54.,948   1.00   59..24          C
ATOM   16236   C    ILE  D  492       2.3.,774   23.964    55.,486   1,00   52 .44          C
ATOM   162 37  O    ILE  D  492       23...329  24.,917   54..859   1.00   59,.05          0
ATOM   16238   CB   ILE  D  492       22.457    21.,869   55..697   1,00   57,00           C
ATOM   16239   CGI  ILE  D  492       22.,197   20. 500   55.,071   1,00   60..11          C
ATOM   16240   CG2  ILE  D  492       21.,214   22.,720   55..613   1,00   54 .15          C
ATOM   16241   CD1  ILE  D  492       21.842    20.,595   53..598   1,00   54,51           C
ATOM   16242   N    GLU  D  493       24.,453   24..119   56,614    I,00   55..26          N
ATOM   16243   CA   GLU  D  493       24.,493   25..430   57.,260   1,00   56..90          C
ATOM   16244   C    GLU  D  49.3      25. 247   26.,482   56. 473   1,00   56,19           C
ATOM   16245   O    GLU  D  493       24.,956   27.662    56,618    I,00   56..20          0
ATOM   16246   CB   GLU  D  493       25.,082   25..327   58.,662   1,00   56..31          C
ATOM   16247   CG   GLU  D  49.3      24.110    24.,698   59. 624   1,00   62 ,85          C
ATOM   16248   CD   GLU  D  493       24..573   24.,763   61.,059   1.00   72 .22          C
ATOM   16249   OE1  GLU  D  493       25.,807   24.805    61.,278   1,00   67 .38          0
ATOM   162 50  OE2  GLU  D  49.3      23..694   24.,770   61.. 958   1.00   7.3,.91         0
ATOM   16251   N    ARG  D  494       26..198   26.,065   55.,636   1.00   57 .12          N
ATOM   16252   CA.  ARG  D  494       26.,971   27.009    54,823    1,00   53..72          C
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ATOM   16253   c    ARG  D  494      26..Ill   27..639   53..730   1 .00  53..09        c
ATOM   16254   0    ARG  D  494      26,,499   28..626   53.,095   1 ,00  49..10        0
ATOM   162 55  CB   ARG  D  494      28..195   26.,315   54..192   1 ,00  55,,36        c
ATOM   16256   CG   ARG  D  494      27..894   25.,057   53..352   1 .00  55..75        c
ATOM   16257   CD   ARG  D  494      29.,177   24.229    52.,977   1 ,00  51 .88        c
ATOM   162 58  KE   ARG  D  494      29..698   24.,662   51..683   1 ,00  50,.38        K
ATOM   16259   CZ   ARG  D  494      30..827   25.,338   51..532   1 ,00  50,.05        c
ATOM   16260   NH1  ARG  D  494      .31.,194  25. 726   50.,326   1 ,00  49..01        M
ATOM   162 61  KH2  ARG  D  494      31..591   25.,618   52.,581   1 ,00  49..77        K
ATOM   16262   N    MET  D  495      24 .933   27.,066   53..513   1 ,00  55,.98        M
ATOM   162 63  CA   MET  D  495      24.,097   27 .482   52.,400   1 ,00  52 .57        C
ATOM   162 64  C    MET  D  495      22..795   28..160   52.,801   1 ,00  47 .30        C
ATOM   162 65  O    MET  D  495      22.247    28.,907   52. 005   1 ,00  46 ,91        O
ATOM   16266   CB   MET  D  495      23..758   26.,284   51.,512   1 .00  50..42        c
ATOM   162 67  CG   MET  D  495      24.,955   25..631   50.,829   1 ,00  49..49        c
ATOM   162 68  SD   MET  D  495      24..419   24.,308   49 .742   1 .00  54 ,13        s
ATOM   16269   CE   MET  D  495      23..716   23.,175   50..916   1 .00  52 .73        c
ATOM   16270   O    TH.R D  496      21.,869   30. 517   55.,023   1 ,00  50..71        0
ATOM   16271   K    THR  D  496      22..287   27.,872   53..996   1 .00  47 ,19        K
ATOM   16272   CA   THR  D  496      20..954   28.,364   54..405   1 ,00  49,.32        c
ATOM   16273   C    TH.R D  496      20.,880   29. 883   54 ,683   1 ,00  46..86        c
ATOM   16274   CB   THR  D  496      20..444   27.,630   55.,659   1 ,00  51 .83        c
ATOM   16275   OG1  THR  D  496      21 .549   27.,304   56..512   1 ,00  55,.87        0
ATOM   16276   CG2  THR  D  496      19.,724   26...355  55.,274   1 ,00  49 .90        c
ATOM   16277   O    ASN  D  497      19..466   31..581   57.,077   1 ,00  52 .32        0
ATOM   16278   N    A SN D  497      19. 694   .30.,462  54. 532   1 ,00  51 ,48        N
ATOM   16279   CA   ASM  D  497      19.,542   31..905   54.,700   1 ,00  49 .45        c
ATOM   16280   C    ASM  D  497      19.,708   32..344   56.,141   1 ,00  51 .97        c
ATOM   16281   CB   A.SM D  497      18. 188   .32.,374  54. 181   1 ,00  46 ,08        c
ATOM   16282   CG   ASM  D  497      18..203   32.,680   52..702   1 .00  48..20        c
ATOM   16283   OD1  ASM  D  497      19.,156   33..254   52.,197   1 ,00  51 .15        0
ATOM   162 84  KD2  ASN  D  497      17 .142   .32.,299  52..000   1 .00  46,.40        K
ATOM   16285   O    PHE  D  498      18.,379   35.,523   56..250   1 .00  55..30        0
ATOM   16286   N    PH.E D  498      20.,174   33. 575   56.,298   1 ,00  54 .05        M
ATOM   162 87  CA   PHE  D  498      20 .006   .34.,321  57..535   1 .00  55,.40        c
ATOM   16288   c    PHE  D  498      18..757   35.,186   57..377   1 ,00  55,.72        c
ATOM   16289   CB   PH.E D  498      21.,244   35. 165   57 ,821   1 ,00  54 .94        c
ATOM   162 90  CG   PHE  D  498      22.,413   34..366   58.,305   1 ,00  55..90        c
ATOM   162 91  CD2  PHE  D  498      22.592    .34.,130  59. 655   1 ,00  55 ,31        c
ATOM   162 92  CD1  PHE  D  498      23.,325   33..825   57.,403   1 ,00  63..69        c
ATOM   16293   CE2  PHE  D  498      23.,668   33..381   60.,101   1 ,00  61 .93        c
ATOM   162 94  CE1  PHE  D  498      24.405    .33.,069  57. 840   1 ,00  55 ,51        c
ATOM   16295   CZ   PHE  D  498      24.,576   32.,847   59.,189   1 .00  58..74        c
ATOM   16296   O    ASP  D  499      18.,394   38..307   58.,384   1 ,00  58..46        0
ATOM   162 97  K    ASP  D  499      18..088   .35.,516  58..479   1 .00  63,.98        K
ATOM   16298   CA   ASP  D  499      16..926   36 ,421   58..415   1 .00  56..42        c
ATOM   16299   C    ASP  D  499      17 ,406   37. 765   57 ,888   1 ,00  57 .00        c
ATOM   16300   CB   ASP  D  499      16..267   3 6 ,580  59 .791   1 .00  57 ,42        c
ATOM   16301   CG   ASP  D  499      14 .852   37.,196   59..722   1 ,00  62 ,92        c
ATOM   16302   OD1  ASP  D  499      14 ,568   38. 059   58.,845   1 ,00  61 .52        0
ATOM   16303   OD2  ASP  D  499      14 ,013   36.,811   60.,567   1 ,00  58..46        0
ATOM   16304   O    LYS  D  500      17 .607   41 ,494   57..823   1 ,00  59,.85        0
ATOM   16305   N    LYS  D  500      16.,746   38..284   56.,858   1 ,00  51 .31        M
ATOM   16306   CA   LYS  D  500      17 ,060   39..627   56.,422   1 ,00  56..66        c
ATOM   16307   C    LYS  D  500      16. 795   40.,609   57. 568   1 ,00  60 ,19        c
ATOM   16308   CB   LYS  D  500      16.,253   40..020   55.,191   1 ,00  59..16        c
ATOM   16309   CG   LYS  D  500      16.,654   39..286   53.,941   1 ,00  61 .02        c
ATOM   16310   CD   LYS  D  500      15. 939   3 9 ,837  52. 731   1 ,00  57 ,28        c
ATOM   16311   CE   LYS  D  500      16.,115   38.,947   51.,529   1 .00  60..10        c
ATOM   16312   MZ   LYS  D  500      16.,077   39..743   50.,261   1 ,00  73..16        M
ATOM   16313   O    ASK  D  501      16..838   42.,408   60..853   1 .00  67 ,04        0
ATOM   16314   N    ASM  D  501      15..672   40 ,427   58..264   1 .00  59..60        M
ATOM   16315   CA.  ASM  D  501      15.,305   41.302    59.,382   1 ,00  61 .40        c
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ATOM   16316  c   ASN D 501      16.392  41.339  60.452  1.00 60.43           c
ATOM   16317  CB  ASM D 501      13.972  40.863  60.012  1.00 57.52           C
ATOM   16318  CG  ASN D 501      12.796  40.925  59.030  1.00 61.65           c
ATOM   16319  OD1 ASN D 501      12.127  39.920  58.782  1.00 67.49           0
ATOM   16320  ND2 ASN D 501      12.544  42.104  58.474  1.00 48.55           N
ATOM   16321  O   LEU D 502      18.883  37.944  61.046  1.00 61.46           0
ATOM   16322  N   LEU D 502      16.801  40.165  60.915  1.00 58.85           N
ATOM   16323  CA. LEU D 502      17.924  40.028  61.837  1.00 62.44           C
ATOM   16324  C   LEU D 502      19.007  39.176  61.157  1.00 66.51           C
ATOM   16325  CB  LEU D 502      17.466  39.404  63.153  1.00 64.31           c
ATOM   16326  CG  LEU D 502      16.230  40.079  63.765  1.00 64.97           c
ATOM   16327  CD1 LEU D 502      15.614  39.233  64.859  1.00 67.12           c
ATOM   16328  CD2 LEU D 502      16.598  41.452  64.306  1.00 62.15           c
ATOM   16329  O   PRO D 503      22.340  37.257  59.796  1.00 65.71           0
ATOM   16330  N   FRO D 503      20.054  39.845  60.656  1.00 67.47           N
ATOM   16331  CA  PRO D 503      21.081  39.258  59.787  1.00 65.74           C
ATOM   16332  c   PRO D 503      21.924  38.188  60.467  1.00 66.02           c
ATOM   16333  CB  PRO D 503      21.950  40.461  59.414  1.00 66.40           c
ATOM   16334  CG  PRO D 503      21.069  41.647  59.627  1.00 64.86           c
ATOM   16335  CD  PRO D 503      20.230  41.295  60.805  1.00 64.33           c
ATOM   16336  O   ASN D 504      22.815  35.247  63.501  1.00 63.39           0
ATOM   16337  N   ASN D 504      22.174  38.319  61.763  1.00 63.85           N
ATOM   16338  CA  ASN D 504      23.019  37.372  62.459  1.00 60.66           c
ATOM   16339  C   ASN D 504      22.261  36.138  62.877  1.00 65.08           C
ATOM   16340  CB  ASN D 504      23.641  38.016  63.685  1.00 65.96           C
ATOM   16341  CG  ASN D 504      25.140  37.857  63.713  1.00 80.98           C
ATOM   16342  OD1 ASN D 504      25.867  38.613  63.058  1.00 85.38           0
ATOM   16343  ND2 ASN D 504      25.619  36.864  64.461  1.00 74.67           N
ATOM   16344  O   GLU D 505      19.423  34.359  60.751  1.00 62.00           O
ATOM   16345  N   GLU D 505      20.983  36.092  62.537  1.00 66.08           N
ATOM   16346  CA  GLU D 505      20.126  34.996  62.971  1.00 64.84           C
ATOM   16347  C   GLU D 505      19.843  33.994  61.853  1.00 60.46           C
ATOM   16348  CB  GLU D 505      18.809  35.556  63.523  1.00 68.75           c
ATOM   16349  CG  GLU D 505      18.975  36.382  64.794  1.00 67.38           c
ATOM   16350  CD  GLU D 505      19.557  35.560  65.939  1.00 71.00           c
ATOM   16351  OE1 GLU D 505      19.161  34.379  66.088  1.00 70.74           0
ATOM   16352  OE2 GLU D 505      20.417  36.092  66.676  1.00 72.97           0
ATOM   16353  O   LYS D 506      17.543  31.565  61.977  1.00 62.73           0
ATOM   16354  N   LYS D 506      20.071  32.723  62.151  1.00 60.85           N
ATOM   16355  CA  LYS D 506      19.813  31.674  61.189  1.00 56.61           C
ATOM   16356  C   LYS D 506      18.318  31.517  61.022  1.00 56.81           C
ATOM   16357  CB  LYS D 506      20.470  30.352  61.623  1.00 60.46           C
ATOM   16358  CG  LYS D 506      21.128  29.566  60.478  1.00 57.96           c
ATOM   16359  CD  LYS D 506      21.948  30.461  59.547  1.00 55.84           c
ATOM   16360  CE  LYS D 506      23.072  29.704  58.840  1.00 57.59           c
ATOM   16361  NZ  LYS D 506      22.773  29.383  57.411  1.00 55.60           N
ATOM   16362  O   VAL D 507      16.699  29.021  60.385  1.00 62.24           O
ATOM   16363  N   VAL D 507      17.917  31.348  59.780  1.00 55.72           N
ATOM   16364  CA  VAL D 507      16.524  31.211  59.426  1.00 48.62           c
ATOM   16365  C   VAL D 507      15.944  29.916  59.995  1.00 55.57           c
ATOM   16366  CB  VAL D 507      16.405  31.255  57.910  1.00 54.07           c
ATOM   16367  CGI VAL D 507      16.312  29.837  57.314  1.00 54.31           c
ATOM   16368  CG2 VAL D 507      15.288  32.162  57.499  1.00 50.46           c
ATOM   16369  O   LEU D 508      13.680  27.743  58.386  1.00 55.03           0
ATOM   16370  N   LEU D 508      14.620  29.801  60.059  1.00 52.78           N
ATOM   16371  CA  LEU D 508      14.015  28.589  60.616  1.00 57.45           C
ATOM   16372  C   LEU D 508      13.745  27.488  59.589  1.00 55.40           C
ATOM   16373  CB  LEU D 508      12.696  28.924  61.313  1.00 54.38           C
ATOM   16374  CG  LEU D 508      12.656  29.243  62.807  1.00 59.86           c
ATOM   16375  CD1 LEU D 508      11.327  29.940  63.136  1.00 61.29           c
ATOM   16376  CD2 LEU D 508      12.833  28.022  63.684  1.00 48.20           c
ATOM   16377  O   PRO D 509      10.869  26.232  59.488  1.00 66.55           0
ATOM   16378  N   PRO D 509      13.563  26.253  60.069  1.00 51.82           N
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ATOM   16379  CA   PRO  D  509     12.984  25.200  59.219  1.00  57.39       c
ATOM   16380  C    FRO  D  509     11.599  25.603  58.729  1.00  62.80       C
ATOM   16381  CB   PRO  D  509     12.904  23.995  60.150  1.00  53.92       C
ATOM   16382  CG   PRO  D  509     14.011  24.220  61.118  1.00  57.55       c
ATOM   16383  CD   PRO  D  509     14.097  25.716  61.328  I.00  52.19       C
ATOM   16384  O    LYS  D  510      7.655  25.155  57.309  1.00  68.42       0
ATOM   16385  N    LYS  D  510     11.244  25.258  57.493  1.00  63.47       N
ATOM   16386  CA.  LYS  D  510      9.967  25.679  56.908  I.00  61.90       C
ATOM   16387  C    LYS  D  510      8.832  24.860  57.502  1.00  63.77       C
ATOM   16388  CB   LYS  D  510     10.009  25.544  55.385  1.00  61.86       c
ATOM   16389  CG   LYS  D  510      8.754  25.992  54.635  I.00  66.74       c
ATOM   16390  CD   LYS  D  510      8.562  27.510  54.587  1.00  60.85       c
ATOM   16391  CE   LYS  D  510      7.545  27.874  53.487  1.00  65.86       c
ATOM   16392  NZ   LYS  D  510      7.897  29.088  52.659  1.00  62.75       N
ATOM   16393  N    HIS  D  511      9.198  23.840  58.264  1.00  66.35       N
ATOM   16394  CA   HIS  D  511      8.213  22.926  58.810  1.00  67.40       C
ATOM   16395  c    HIS  D  511      8.184  23.018  60.326  1.00  68.04       c
ATOM   16396  O    HIS  D  511      7.461  22.273  60.982  I.00  69.77       0
ATOM   16397  CB   HIS  D  511      8.503  21.486  58.347  1.00  64.36       c
ATOM   16398  CG   HIS  D  511      8.179  21.241  56.906  1.00  62.38       c
ATOM   16399  ND1  HIS  D  511      6.892  21.041  56.455  I.00  63.84       N
ATOM   16400  CD2  HIS  D  511      8.972  21.181  55.811  1.00  66.32       C
ATOM   16401  CE1  HIS  D  511      6.902  20.878  55.146  1.00  63.57       c
ATOM   16402  NE2  HIS  D  511      8.154  20.955  54.730  I.00  73.64       N
ATOM   16403  N    SEP. D  512      8.977  23.937  60.874  1.00  67.88       N
ATOM   16404  CA   SER  D  512      8.979  24.200  62.315  1.00  66.81       C
ATOM   16405  C    SER  D  512      7.585  24.528  62.821  I.00  71.01       C
ATOM   16406  O    SER  D  512      6.820  25.209  62.139  1.00  74.14       O
ATOM   16407  CB   SER  D  512      9.925  25.348  62.650  1.00  65.09       c
ATOM   16408  OG   SER  D  512      9.640  25.873  63.933  1.00  67.24       0
ATOM   16409  O    LEU  D  513      4.587  26.291  64.390  1.00  72.08       0
ATOM   16410  N    LEU  D  513      7.252  24.052  64.017  1.00  74.01       N
ATOM   16411  CA   LEU  D  513      5.926  24.304  64.592  1.00  75.10       c
ATOM   16412  C    LEU  D  513      5.643  25.791  64.800  I.00  71.53       C
ATOM   16413  CB   LEU  D  513      5.780  23.557  65.915  1.00  78.75       C
ATOM   16414  CG   LEU  D  513      5.701  22.041  65.741  1.00  67.00       c
ATOM   16415  CD2  LEU  D  513      4.357  21.689  65.134  I.00  70.48       c
ATOM   16416  CD1  LEU  D  513      5.897  21.339  67.063  1.00  66.38       c
ATOM   16417  N    LEU  D  514      6.594  26.489  65.424  1.00  72.24       N
ATOM   16418  CA   LEU  D  514      6.470  27.930  65.695  I.00  68.55       c
ATOM   16419  C    LEU  D  514      6.345  28.717  64.408  1.00  68.90       c
ATOM   16420  O    LEU  D  514      5.586  29.688  64.328  1.00  72.81       0
ATOM   16421  CB   LEU  D  514      7.667  28.444  66.501  1.00  68.30       c
ATOM   16422  CG   LEU  D  514      7.583  28.219  68.015  1.00  74.81       c
ATOM   16423  CD1  LEU  D  514      8.947  28.263  68.672  1.00  82.56       c
ATOM   16424  CD2  LEU  D  514      6.662  29.252  68.646  1.00  82.14       c
ATOM   16425  N    TYR  D  515      7.091  28.290  63.399  I.00  69.58       N
ATOM   16426  CA   TYR  D  515      6.983  28.883  62.078  1.00  66.84       c
ATOM   16427  c    TYR  D  515      5.564  28.664  61.577  1.00  66.47       c
ATOM   16428  0    TYR  D  515      4.977  29.514  60.904  I.00  65.45       0
ATOM   16429  CB   TYR  D  515      8.013  28.275  61.105  1.00  61.81       c
ATOM   16430  CG   TYR  D  515      8.212  29.114  59.872  1.00  55.61       c
ATOM   16431  CD2  TYR  D  515      7.521  28.836  58.707  I.00  53.67       c
ATOM   16432  CD1  TYR  D  515      9.066  30.211  59.882  1.00  60.76       c
ATOM   16433  CF.2 TYR  D  515      7.673  29.619  57.573  1.00  52.80       c
ATOM   16434  CE1  TYR  D  515      9.231  31.008  58.744  I.00  57.49       c
ATOM   16435  CZ   TYR  D  515      8.529  30.698  57.595  1.00  54.15       c
ATOM   16436  OH   TYR  D  515      8.675  31.462  56.458  1.00  57.77       0
ATOM   16437  N    GLU  D  516      5.003  27.513  61.916  1.00  70.26       N
ATOM   16438  CA   GLU  D  516      3.707  27.161  61.377  1.00  71.45       c
ATOM   16439  C    GLU  D  516      2.611  27.859  62.164  1.00  70.01       c
ATOM   16440  O    GLU  D  516      1.604  28.263  61.593  1.00  71.92       0
ATOM   16441  CB   GLU  D  516      3.525  25.643  61.369  I.00  77.66       c
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ATOM   16442   CG   GLU  D  516       4.370   24.934   60.300   1.00  69.91           C
ATOM   16443   CD   GLU  D  516       3.889   23.524   60.010   1.00  75.36           C
ATOM   16444   OE1  GLU  D  516       3.578   22.794   60.975   1.00  79.99           0
ATOM   16445   OE2  GLU  D  516       3.806   23.149   58.820   1.00  75.98           0
ATOM   16446   N    TYR  D  517       2.825   28.028   63.467   1.00  72.20           M
ATOM   16447   CA   TYR  D  517       1.944   28.865   64.281   1.00  70.43           C
ATOM   16448   C    TYR  D  517       1.952   30.295   63.767   1.00  69.54           C
ATOM   16449   0    TYR  D  517       0.920   30.963   63.743   1.00  71.03           0
ATOM   164 50  CB   TYR  D  517       2.368   28.847   65.749   1.00  70.08           C
ATOM   16451   CG   TYR  D  517       2.050   27.570   66.486   1.00  65.58           C
ATOM   16452   CD1  TYR  D  517       0.873   26.871   66.242   1.00  68.50           C
ATOM   164 53  CD2  TYR  D  517       2.916   27.078   67.437   1.00  65.59           C
ATOM   164 54  CE1  TYR  D  517       0.580   25.710   66.919   1.00  68.12           C
ATOM   164 55  CE2  TYR  D  517       2.638   25.924   68.121   1.00  68.91           C
ATOM   16456   CZ   TYR  D  517       1.471   25.235   67.861   1.00  74.79           C
ATOM   164 57  OH   TYR  D  517       1.213   24.066   68.555   1.00  79.25           0
ATOM   164 58  N    PHE  D  518       3.132   30.757   63.368   1.00  66.55           M
ATOM   16459   CA.  PHE  D  518       3.295   32.088   62.808   1.00  64.65           C
ATOM   164 60  C    PHE  D  518       2. .38 9  .32 .294  61.613   1.00  67.88           C
ATOM   16461   O    PHE  D  518       1.599   33.250   61.565   1.00  69.88           0
ATOM   16462   CB   PHE  D  518       4.751   32. .335   62.383   1.00  64.28           C
ATOM   164 63  CG   PHE  D  518       4.974   33.675   61.700   1.00  68.99           C
ATOM   16464   CD2  PHE  D  518       4.680   33.852   60.351   1.00  66.98           C
ATOM   164 65  CD1  PHE  D  518       5.468   34.757   62.411   1.00  62. .32           C
ATOM   164 66  CE2  PHE  D  518       4.871   35.074   59.730   1.00  58.51           C
ATOM   164 67  CF.1 PHE  D  518       5.683   .35 .969  61.791   1.00  58.26           C
ATOM   164 68  CZ   PHE  D  518       5.376   36.129   60.448   1.00  59.98           C
ATOM   16469   N    THR  D  519       2.536   31.414   60.630   1.00  66.05           M
ATOM   16470   CA   THR  D  519       1.857   .31 .605  59. .357   1.00  66.34           C
ATOM   16471   C    THR  D  519       0.362   31.657   59.577   1.00  62.33           C
ATOM   16472   O    THR  D  519      -0.308   32.474   58.967   1.00  70.95           0
ATOM   16473   CB   THR  D  519       2.194   .30 .484  58. .302   1.00  69.36           C
ATOM   16474   OG1  THR  D  519       1.706   29.203   58.741   1.00  67.83           0
ATOM   16475   CG2  THR  D  519       3.699   30.413   58.028   1.00  62.16           C
ATOM   16476   K    VAL  D  520      -0.157   .30 .813  60.464   1.00  60.68           K
ATOM   16477   CA   VAL  D  520     --1 .605   30.690   60.619   1.00  71.95           C
ATOM   16478   C    VAL  D  520      -2.192   31.927   61.322   1.00  70.67           C
ATOM   16479   O    VAL  D  520      -3.183   32.498   60.856   1.00  67.48           0
ATOM   164 80  CB   VAL  D  520      -1.989   29.389   61. .37 4  1.00  73.40           C
ATOM   164 81  CGI  VAL  D  520      -3.338   29.540   62.073   1.00  77.99           C
ATOM   16482   CG2  VAL  D  520      -2.029   28.213   60.410   1.00  70.40           C
ATOM   164 83  N    TYR  D  521      -1.554   32.362   62.406   1.00  70.83           N
ATOM   16484   CA   TYR  D  521      ..2.001   33.557   63.117   1.00  68.66           C
ATOM   16485   C    TYR  D  521      -1.949   34.800   62.248   1.00  69.23           C
ATOM   16486   O    TYR  D  521      -2.905   .35 .565  62.219   1.00  71.15           0
ATOM   16487   CB   TYR  D  521     --1 .178   33.777   64.378   1.00  64.98           C
ATOM   164 88  CG   TYR  D  521     -.1 .678   32.951   65.533   1.00  70. .38           C
ATOM   16489   CD1  TYR  D  521      -2.881   .33 .266  66.157   1.00  75.30           C
ATOM   16490   CD2  TYR  D  521     --0 .961   31.855   66.001   1.00  74.18           C
ATOM   16491   CE1  TYR  D  521      -3.362   32.525   67.214   1.00  71.71           C
ATOM   16492   CE2  TYR  D  521      -1.430   31.101   67.064   1.00  78.87           C
ATOM   16493   CZ   TYR  D  521     --2 .639   31.445   67.665   1.00  81.17           C
ATOM   164 94  OH   TYR  D  521      -3.128   30.715   68.723   1.00  79.79           0
ATOM   164 95  K    ASN  D  522      -0.852   34.993   61.524   1.00  70.29           K
ATOM   164 96  CA   ASN  D  522      -0.725   3 6.177  60.684   1.00  68.73           C
ATOM   164 97  C    ASM  D  522      -1.851   36.280   59.663   1.00  63.90           C
ATOM   164 98  O    ASM  D  522      -2.234   37.369   59.263   1.00  67.55           0
ATOM   164 99  CB   A.SM D  522       0.623   3 6.197  59.961   1.00  65.57           C
ATOM   16500   CG   ASM  D  522       0.951   37.572   59.420   1.00  70.01           C
ATOM   16501   OD1  ASM  D  522       0.991   38.538   60.175   1.00  71.83           0
ATOM   16502   KD2  ASN  D  522       1.149   .37 .678  58.112   1.00  65.86           K
ATOM   16503   N    GLU  D  523      ..2.369   35.133   59.238   1.00  66.52           M
ATOM   16504   CA.  GLU  D  523      -3.461   35.081   58.268   1.00  66.59           C
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ATOM	16505	C	GLU	D	523	-4.791	35.169	59.008	1.00	67.50	C
ATOM	16506	O	GLU	D	523	-5.739	35.807	58.552	1.00	62.35	O
ATOM	16507	CB	GLU	D	523	-3.396	33.788	57.436	1.00	67.91	C
ATOM	16508	CG	GLU	D	523	-4.442	33.678	56.313	1.00	73.30	C
ATOM	16509	CD	GLU	D	523	-4.316	32.394	55.478	1.00	82.31	C
ATOM	16510	OE1	GLU	D	523	-5.228	32.130	54.655	1.00	76.14	0
ATOM	16511	OE2	GLU	D	523	-3.309	31.657	55.644	1.00	80.76	0
ATOM	16512	N	LEU	D	524	-4.837	34.520	60.164	1.00	66.40	N
ATOM	16513	CA	LEU	D	524	-6.024	34.520	60.996	1.00	73.13	C
ATOM	16514	C	LEU	D	524	-6.351	35.924	61.537	1.00	75.97	C
ATOM	16515	0	LEU	D	524	-7.510	36.336	61.524	1.00	71.92	0
ATOM	16516	CB	LEU	D	524	-5.846	33.536	62.147	1.00	72.24	C
ATOM	16517	CG	LEU	D	524	-7.112	32.900	62.720	1.00	77.26	C
ATOM	16518	CD1	LEU	D	524	-8.096	32.604	61.618	1.00	75.53	C
ATOM	16519	CD2	LEU	D	524	-6.738	31.621	63.452	1.00	79.49	C
ATOM	16520	N	THR	D	525	-5.325	36.659	61.972	1.00	70.54	N
ATOM	16521	CA	THR	D	525	-5.517	37.950	62.623	1.00	67.01	C
ATOM	16522	C	THR	D	525	-5.995	39.039	61.680	1.00	69.54	C
ATOM	16523	O	THR	D	525	-6.143	40.180	62.098	1.00	73.35	0
ATOM	16524	CB	THR	D	525	-4.221	38.448	63.288	1.00	69.38	C
ATOM	16525	OG1	THR	D	525	-4.511	39.582	64.113	1.00	72.05	0
ATOM	16526	CG2	THR	D	525	-3.203	38.855	62.235	1.00	71.06	C
ATOM	16527	N	LYS	D	526	-6.231	38.697	60.416	1.00	70.27	N
ATOM	16528	CA	LYS	D	526	-6.695	39.677	59.434	1.00	71.61	C
ATOM	16529	C	LYS	D	526	-7.979	39.205	58.760	1.00	73.57	C
ATOM	16530	O	LYS	D	526	-8.424	39.794	57.778	1.00	74.01	0
ATOM	16531	CB	LYS	D	526	-5.612	39.964	58.381	1.00	70.85	C
ATOM	16532	CG	LYS	D	526	-4.666	41.105	58.749	1.00	65.93	C
ATOM	16533	CD	LYS	D	526	-5.407	42.428	58.770	1.00	68.04	C
ATOM	16534	CE	LYS	D	526	-4.668	43.473	59.603	1.00	67.55	C
ATOM	16535	NZ	LYS	D	526	-5.226	44.854	59.428	1.00	66.43	N
ATOM	16536	N	VAL	D	527	-8.569	38.142	59.300	1.00	75.94	N
ATOM	16537	CA	VAL	D	527	-9.895	37.681	58.878	1.00	82.84	C
ATOM	16538	C	VAL	D	527	-11.020	38.390	59.649	1.00	83.22	C
ATOM	16539	O	VAL	D	527	-10.972	38.490	60.879	1.00	82.60	0
ATOM	16540	CB	VAL	D	527	-10.037	36.155	59.059	1.00	79.96	C
ATOM	16541	CG2	VAL	D	527	-9.382	35.421	57.890	1.00	82.12	C
ATOM	16542	CGI	VAL	D	527	-11.494	35.763	59.195	1.00	79.28	C
ATOM	16543	O	LYS	D	528	-14.721	38.486	58.071	1.00	87.18	0
ATOM	16544	N	LYS	D	528	-12.022	38.884	58.918	1.00	84.10	N
ATOM	16545	CA	LYS	D	528	-13.152	39.604	59.521	1.00	87.04	C
ATOM	16546	C	LYS	D	528	-14.509	38.963	59.189	1.00	89.37	C
ATOM	16547	CB	LYS	D	528	-13.166	41.075	59.068	1.00	84.09	C
ATOM	16548	CG	LYS	D	528	-12.032	41.935	59.613	1.00	79.80	C
ATOM	16549	CD	LYS	D	528	-12.449	43.401	59.805	1.00	80.76	C
ATOM	16550	CE	LYS	D	528	-12.762	44.104	58.480	1.00	85.35	C
ATOM	16551	NZ	LYS	D	528	-13.247	45.517	58.656	1.00	76.60	N
ATOM	16552	O	TYR	D	529	-17.682	40.400	61.091	1.00	83.47	O
ATOM	16553	N	TYR	D	529	-15.423	38.974	60.163	1.00	89.86	N
ATOM	16554	CA.	TYR	D	529	-16.785	38.456	59.988	1.00	86.58	C
ATOM	16555	C	TYR	D	529	-17.856	39.516	60.247	1.00	87.94	C
ATOM	16556	CB	TYR	D	529	-17.036	37.276	60.924	1.00	87.51	C
ATOM	16557	CG	TYR	D	529	-16.848	37.628	62.381	1.00	89.86	C
ATOM	16558	CD1	TYR	D	529	-15.623	37.437	63.002	1.00	91.02	C
ATOM	16559	CD2	TYR	D	529	-17.886	38.161	63.137	1.00	86.62	C
ATOM	16560	CE1	TYR	D	529	-15.438	37.755	64.331	1.00	89.33	C
ATOM	16561	CE2	TYR	D	529	-17.704	38.492	64.475	1.00	87.49	C
ATOM	16562	CZ	TYR	D	529	-16.476	38.282	65.066	1.00	91.72	C
ATOM	16563	OH	TYR	D	529	-16.266	38.591	66.393	1.00	92.50	0
ATOM	16564	O	VAL	D	530	-21.474	38.599	58.703	1.00	91.77	0
ATOM	16565	N	VAL	D	530	-18.973	39.402	59.535	1.00	84.05	N
ATOM	16566	CA	VAL	D	530	-20.113	40.266	59.757	1.00	86.45	C
ATOM	16567	C	VAL	D	530	-21.401	39.466	59.569	1.00	88.74	C

ATOM	16568	CB	VAL	D	530	-20.084	41.494	58.813	1.00	88.15	C
ATOM	16569	CG2	VAL	D	530	--21.100	42.549	59.257	1.00	87.80	C
ATOM	16570	CGI	VAL	D	5.30	-20.312	41.079	57.368	1.00	83.40	C
ATOM	16571	O	THR	D	531	-24.528	41.358	60.413	1.00	90.57	0
ATOM	16572	N	TH.R	D	531	-22.397	39.728	60.414	1.00	89.96	N
ATOM	16573	CA	THR	D	531	-23.711	39.092	60.289	1.00	92.67	C
ATOM	16574	C	THR	D	531	-24.816	40.165	60.288	1.00	91.02	C
ATOM	16575	CB	TH.R	D	531	-23.958	38.057	61.420	1.00	91.15	C
ATOM	16576	OG1	THR	D	531	-25.059	37.201	61.073	1.00	88.41	0
ATOM	16577	CG2	THR	D	531	-24.237	38.758	62.750	1.00	87.56	C
ATOM	16578	O	GLU	D	532	-27.506	42.956	60.510	1.00	98.64	0
ATOM	16579	N	GLU	D	532	-26.068	39.733	60.143	1.00	91.91	N
ATOM	16580	CA	GLU	D	532	-27.205	40.635	59.920	1.00	94.76	C
ATOM	16581	C	GLU	D	532	-27.318	41.805	60.914	1.00	97.43	C
ATOM	16582	CB	GLU	D	532	-28.505	39.830	59.938	1.00	95.39	C
ATOM	16583	CG	GLU	D	5.32	-29.724	40.601	59.447	1.00	99.12	C
ATOM	16584	CD	GLU	D	532	-30.970	39.735	59.372	1.00	103.87	C
ATOM	16585	OE1	GLU	D	532	-30.983	38.652	60.000	1.00	102.69	0
ATOM	16586	OE2	GLU	D	5.32	-31.932	40.136	58.680	1.00	105.14	0
ATOM	16587	O	GLY	D	533	-25.763	43.363	64.849	1.00	100.37	0
ATOM	16588	N	GLY	D	533	-27.202	41.513	62.206	1.00	91.25	N
ATOM	16589	CA	GLY	D	533	-27.320	42.539	63.225	1.00	91.88	C
ATOM	16590	C	GLY	D	533	-26.008	43.175	63.651	1.00	97.52	C
ATOM	16591	0	MET	D	534	-24.009	45.612	61.000	1.00	92.89	0
ATOM	16592	N	MET	D	534	-25.167	43.510	62.675	1.00	94.73	N
ATOM	16593	CA	MET	D	534	-23.888	44.168	62.949	1.00	91.67	C
ATOM	16594	C	MET	D	534	-23.738	45.512	62.206	1.00	91.40	C
ATOM	16595	CB	MET	D	534	-22.727	43.227	62.595	1.00	91.50	C
ATOM	16596	CG	MET	D	534	-22.625	41.999	63.502	1.00	88.22	C
ATOM	16597	SD	MET	D	534	-21.225	40.896	63.167	1.00	82.09	S
ATOM	16598	CE	MET	D	534	-19.830	41.932	63.617	1.00	83.55	C
ATOM	16599	O	AP.G	D	5.35	-22.015	48.622	60.387	1.00	90.77	0
ATOM	16600	N	ARG	D	535	-23.307	46.539	62.935	1.00	82.88	N
ATOM	16601	CA.	ARG	D	535	-23.152	47.876	62.373	1.00	86.13	C
ATOM	16602	C	AP.G	D	5.35	-21.988	47.913	61.397	1.00	89.82	C
ATOM	16603	CB	ARG	D	535	-22.941	48.909	63.486	1.00	88.06	C
ATOM	16604	O	LYS	D	536	-19.341	45.029	62.205	1.00	84.86	0
ATOM	16605	N	LYS	D	536	-20.958	47.144	61.724	1.00	92.28	N
ATOM	16606	CA	LYS	D	536	-19.795	46.980	60.867	1.00	84.85	C
ATOM	16607	C	LYS	D	536	-19.159	45.608	61.132	1.00	83.30	C
ATOM	16608	CB	LYS	D	536	-18.790	48.113	61.105	1.00	77.78	C
ATOM	16609	O	PRO	D	537	-15.886	45.051	61.457	1.00	81.34	0
ATOM	16610	N	PRO	D	537	-18.441	45.067	60.137	1.00	82.93	N
ATOM	16611	CA	FRO	D	537	-17.602	43.866	60.282	1.00	84.93	C
ATOM	16612	C	PRO	D	5.37	-16.501	43.992	61.345	1.00	77.93	C
ATOM	16613	CB	PRO	D	537	-16.983	43.708	58.888	1.00	84.76	C
ATOM	16614	CG	PRO	D	537	-17.290	45.025	58.157	1.00	78.64	C
ATOM	16615	CD	PRO	D	5.37	-18.564	45.477	58.730	1.00	77.76	C
ATOM	16616	O	ALA	D	538	-14.338	40.881	62.295	1.00	82.98	0
ATOM	16617	N	ALA	D	538	-16.251	42.926	62.103	1.00	78.27	N
ATOM	16618	CA	ALA	D	538	-15.233	42.958	63.153	1.00	80.58	C
ATOM	16619	C	ALA	D	538	-14.147	41.888	62.985	1.00	85.44	C
ATOM	16620	CB	ALA	D	538	-15.882	42.810	64.516	1.00	81.46	C
ATOM	16621	O	PHE	D	539	-13.325	39.756	64.917	1.00	90.75	0
ATOM	16622	N	PHE	D	539	-13.012	42.129	63.645	1.00	82.99	N
ATOM	16623	CA	PHE	D	539	-11.872	41.212	63.684	1.00	77.67	C
ATOM	16624	C	PHE	D	539	-12.185	39.974	64.520	1.00	82.01	C
ATOM	16625	CB	PHE	D	539	-10.635	41.907	64.273	1.00	74.30	C
ATOM	16626	CG	PHE	D	539	-9.928	42.849	63.327	1.00	69.73	C
ATOM	16627	CD2	PHE	D	539	-9.491	44.092	63.769	1.00	73.86	C
ATOM	16628	CD1	PHE	D	5.39	-9.677	42.491	62.018	1.00	72.52	C
ATOM	16629	CE2	PHE	D	539	-8.831	44.966	62.917	1.00	73.59	C
ATOM	16630	CE1	PHE	D	539	-9.017	43.355	61.158	1.00	70.55	C

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ATOM  16631  CZ   PHE D 539      -8.592  44.592  61.607  1.00 72.92           C
ATOM  16632  O    LEU D 540      -9.373  38.955  66.903  1.00 84.70           0
ATOM  16633  N    LEU D 540     -11.162  39.176  64.801  1.00 76.93           N
ATOM  16634  CA   LEU D 540     -11.283  38.078  65.754  1.00 85.02           c
ATOM  16635  C    LEU D 540     -10.464  38.399  66.997  I.00 86.52           c
ATOM  16636  CB   LEU D 540     -10.821  36.755  65.138  1.00 79.34           c
ATOM  16637  CG   LEU D 540     -11.646  36.269  63.946  1.00 80.33           c
ATOM  16638  GDI  LEU D 540     -10.836  35.351  63.054  I.00 86.01           c
ATOM  16639  CD2  LEU D 540     -12.861  35.548  64.446  1.00 83.43           c
ATOM  16640  O    SER D 541      -9.425  36.134  69.187  1.00 91.97           0
ATOM  16641  N    SER D 541     -10.997  38.059  68.163  I.00 89.93           N
ATOM  16642  CA   SER D 541     -10.306  38.342  69.412  1.00 89.66           c
ATOM  16643  C    SER D 541      -9.330  37.232  69.738  1.00 90.17           c
ATOM  16644  CB   SER D 541     -11.298  38.498  70.558  1.00 90.96           c
ATOM  16645  OG   SER D 541     -11.718  37.226  71.009  1.00 89.03           0
ATOM  16646  N    GLY D 542      -8.400  37.516  70.644  1.00 90.21           N
ATOM  16647  CA   GLY D 542      -7.470  36.508  71.116  1.00 86.84           c
ATOM  16648  C    GLY D 542      -8.245  35.316  71.639  I.00 91.54           c
ATOM  16649  O    GLY D 542      -7.811  34.173  71.494  1.00 89.51           0
ATOM  16650  N    GLU D 543      -9.404  35.598  72.235  1.00 92.65           N
ATOM  16651  CA.  GLU D 543     -10.311  34.566  72.721  I.00 91.72           C
ATOM  16652  C    GLU D 543     -10.775  33.694  71.565  1.00 87.41           c
ATOM  16653  O    GLU D 543     -10.660  32.472  71.619  1.00 91.13           0
ATOM  16654  CB   GLU D 543     -11.519  35.188  73.438  I.00 86.05           c
ATOM  16655  N    GLU D 544     -11.290  34.331  70.519  1.00 87.30           N
ATOM  16656  CA   GLN D 544     -11.766  33.617  69.342  1.00 85.92           C
ATOM  16657  C    GLN D 544     -10.583  32.940  68.664  I.00 91.98           C
ATOM  16658  O    GLN D 544     -10.675  31.791  68.239  1.00 91.88           0
ATOM  16659  CB   GLN D 544     -12.492  34.567  68.373  1.00 85.18           c
ATOM  16660  CG   GLN D 544     -13.774  35.177  68.946  1.00 86.10           c
ATOM  16661  CD   GLN D 544     -14.292  36.367  68.148  1.00 86.59           c
ATOM  16662  OE1  GLN D 544     -14.068  37.520  68.513  1.00 91.05           0
ATOM  16663  NE2  GLN D 544     -15.007  36.089  67.069  1.00 89.92           N
ATOM  16664  N    LYS D 545      -9.462  33.650  68.594  I.00 92.25           N
ATOM  16665  CA   LYS D 545      -8.265  33.135  67.941  1.00 90.16           c
ATOM  16666  c    LYS D 545      -7.848  31.780  68.516  1.00 87.25           c
ATOM  16667  0    LYS D 545      -7.779  30.796  67.783  I.00 87.47           0
ATOM  16668  CB   LYS D 545      -7.118  34.144  68.061  1.00 90.07           c
ATOM  16669  N    LYS D 546      -7.594  31.725  69.823  1.00 85.44           N
ATOM  16670  CA   LYS D 546      -7.181  30.478  70.468  I.00 84.32           C
ATOM  16671  C    LYS D 546      -8.217  29.394  70.249  1.00 87.23           C
ATOM  16672  O    LYS D 546      -7.889  28.216  70.185  1.00 88.07           O
ATOM  16673  CB   LYS D 546      -6.950  30.678  71.966  1.00 79.34           c
ATOM  16674  N    ALA D 547      -9.474  29.806  70.130  1.00 92.01           N
ATOM  16675  CA   ALA D 547     -10.561  28.869  69.882  1.00 90.20           C
ATOM  16676  c    ALA D 547     -10.494  28.320  68.465  1.00 88.51           c
ATOM  16677  O    ALA D 547     -10.397  27.115  68.283  I.00 91.88           0
ATOM  16678  CB   ALA D 547     -11.906  29.528  70.135  1.00 88.28           c
ATOM  16679  N    ILE D 548     -10.529  29.202  67.468  1.00 88.48           N
ATOM  16680  CA.  ILE D 548     -10.546  28.786  66.063  I.00 88.82           C
ATOM  16681  C    ILE D 548      -9.308  27.956  65.709  1.00 87.92           C
ATOM  16682  O    ILE D 548      -9.326  27.173  64.763  1.00 84.68           O
ATOM  16683  CB   ILE D 548     -10.630  30.001  65.116  I.00 83.29           C
ATOM  16684  CGI  ILE D 548     -11.727  30.954  65.568  1.00 86.79           c
ATOM  16685  CG2  ILE D 548     -10.920  29.568  63.688  1.00 85.43           c
ATOM  16686  CDI  ILE D 548     -11.715  32.250  64.835  I.00 87.54           c
ATOM  16687  N    VAL D 549      -8.242  28.128  66.483  1.00 84.18           N
ATOM  16688  CA   VAL D 549      -7.023  27.368  66.282  1.00 87.02           C
ATOM  16689  c    VAL D 549      -7.107  26.009  66.977  1.00 92.14           c
ATOM  16690  O    VAL D 549      -6.801  24.975  66.373  1.00 92.85           0
ATOM  16691  CB   VAL D 549      -5.777  28.127  66.802  1.00 88.99           c
ATOM  16692  CGI  VAL D 549      -4.543  27.221  66.765  1.00 84.61           c
ATOM  16693  CG2  VAL D 549      -5.534  29.396  65.989  I.00 85.13           c
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ATOM   16694   N    ASP  D  550        --7.516   26.013   68.245   1.00 92.88            N
ATOM   16695   CA   ASP  D  550        -7.617    24.777   69.030   1.00 93.93            C
ATOM   16696   C    ASP  D  550        -8.7.18   23.863   68.502   1.00 91.65            C
ATOM   16697   O    ASP  D  550        --8.698    22.651   68.715   1.00 93.79            0
ATOM   166 98  CB   ASP  D  550        -7.877    25.093   70.508   1.00 96.72            C
ATOM   16699   CG   ASP  D  550        -6.598    25.380   71.283   1.00100.41            C
ATOM   16700   OD1  ASP  D  550        --5.534    24.844   70.884   1.00 95.63            0
ATOM   16701   OD2  ASP  D  550        -6.665    26.133   72.291   1.00 94.42            0
ATOM   16702   N    LEU  D  551        -y.666    24.463   67.794   1.00 90.55            N
ATOM   16703   CA   LEU  D  551        --10.854   23.771   67.318   1.00 90.96            C
ATOM   167 04  C    LEU  D  551        -10.688   23.240   65.905   1.00 94.13            C
ATOM   167 05  O    LEU  D  551        --10.915   22.060   65.645   1.00 98.24            O
ATOM   16706   CB   LEU  D  551        -12.058   24.713   67.363   1.00 94.36            C
ATOM   167 07  CG   LEU  D  551        -13.427   24.055   67.386   1.00 93.27            C
ATOM   16708   CD1  LEU  D  551        -13.536   23.198   68.638   1.00 93.09            C
ATOM   16709   CD2  LEU  D  551        -14.5.18   25.110   67..337   1.00 88.63            C
ATOM   16710   N    LEU  D  552        -10.294   24.116   64.991   1.00 90.44            N
ATOM   16711   CA.  LEU  D  552        -10.262   23.757   63.583   1.00 91.4.1            C
ATOM   16712   C    LEU  D  552        -8.862    23.310   63.104   1.00 96.90            C
ATOM   16713   O    LEU  D  552        -8.689    22.168   62.647   1.00 97.51            O
ATOM   16714   CB   LEU  D  552        -10.780   24.929   62.738   1.00 91.50            C
ATOM   16715   CG   LEU  D  552        -12.303   25.042   62.542   1.00 94.80            C
ATOM   16716   CD1  LEU  D  552        -13.040   25.182   63.862   1.00 98.04            C
ATOM   16717   CD2  LEU  D  552        -12.682   26.194   61.614   1.00 94.15            C
ATOM   16718   N    PHE  D  553        -7.871    24.191   63.221   1.00 91.54            N
ATOM   16719   CA   PHE  D  553        -6.535    23.920   62.692   1.00 88.79            C
ATOM   16720   C    PHE  D  553        -5.832    22.730   63.354   1.00 92.76            C
ATOM   16721   O    PHE  D  553        -5.071    22.007   62.694   1.00 90.43            0
ATOM   167 22  CB   PHE  D  553        -5.660    25.163   62.823   1.00 86.52            C
ATOM   16723   CG   PHE  D  553        -6.068    26.274   61.919   1.00 86.91            C
ATOM   16724   CD1  PHE  D  553        -g.962    27.232   62.345   1.00 83.10            C
ATOM   16725   CD2  PHE  D  553        -5.564    26.360   60.637   1.00 84.55            C
ATOM   16726   CE1  PHE  D  553        -7.348    28.252   61.512   1.00 81.39            C
ATOM   16727   CE2  PHE  D  553        -5.949    27.387   59.802   1.00 83.69            C
ATOM   16728   CZ   PHE  D  553        -6.843    28.331   60.243   1.00 79.36            C
ATOM   16729   N    LYS  D  554        -6.080    22.525   64.646   1.00 89.24            N
ATOM   167 30  CA.  LYS  D  554        -5.435    21.432   65.363   1.00 91.00            C
ATOM   16731   C    LYS  D  554        -6.194    20.116   65.214   1.00 93.57            C
ATOM   16732   O    LYS  D  554        -5.824    19.110   65.820   1.00 93.85            0
ATOM   167 33  CB   LYS  D  554        -5.273    21.780   66.837   1.00 88.75            C
ATOM   16734   CG   LYS  D  554        -4.128    22.730   67.103   1.00 87.29            C
ATOM   16735   CD   LYS  D  554        -3.8.15    22.825   68.584   1.00 89.99            C
ATOM   16736   CE   LYS  D  554        -2.478    23.512   68.816   1.00 86.52            C
ATOM   167 37  NZ   LYS  D  554        -2.115    23.606   70.257   1.00 84.81            N
ATOM   167 38  N    THR  D  555        -7.244    20.126   64..395   1.00 96.92            N
ATOM   16739   CA   THR  D  555        -8.001    18.909   64.100   1.00 98.92            C
ATOM   16740   C    THR  D  555        -8.088    18.627   62.595   1.00 98.78            C
ATOM   16741   O    THR  D  555        -7.890    17.490   62.162   1.00 99.10            O
ATOM   16742   CB   THR  D  555        -9.426    18.979   64.663   1.00 95.70            C
ATOM   16743   OG1  THR  D  555        -10.165   19.966   63.941   1.00 99.10            0
ATOM   16744   CG2  THR  D  555        -y.409    19.332   66.146   1.00 94.53            C
ATOM   16745   N    ASN  D  556        -8.392    19.654   61.804   1.00 96.20            N
ATOM   16746   CA   ASM  D  556        -8.421    19.504   60.349   1.00 95.87            C
ATOM   16747   C    ASN  D  556        -7.086    19.874   59.713   1.00 94.62            C
ATOM   16748   O    ASN  D  556        -6.524    20.931   59.998   1.00 93.93            O
ATOM   16749   CB   ASN  D  556        -9.540    20..349   59.734   1.00 97.42            C
ATOM   16750   CG   ASN  D  556        -10.915   19.755   59.965   1.00 95.63            C
ATOM   167 51  OD1  ASN  D  556        -11.126   19.019   60.925   1.00100.65            O
ATOM   167 52  ND2  ASN  D  556        -11.858   20.071   59.084   1.00 93.14            N
ATOM   16753   O    ARG  D  557        -4.421    21.324   57.597   1.00 86.49            O
ATOM   167 54  N    ARG  D  557        -6.580    18.977   58.871   1.00 99.20            N
ATOM   16755   CA   ARG  D  557        -5.313    19.160   58.161   1.00 94.95            C
ATOM   16756   C    ARG  D  557        -5.308    20.495   57.420   1.00 89.93            C
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ATOM	16757	CB	ARG	D	557	-5.089	17.996	57.185	1.00	91.68	C
ATOM	16758	CG	ARG	D	557	-3.665	17.834	56.695	1.00	91.98	C
ATOM	16759	CD	ARG	D	557	-2.927	16.719	57.437	1.00	91.48	C
ATOM	16760	NE	ARG	D	557	-1.489	16.982	57.499	1.00	92.43	N
ATOM	16761	CZ	ARG	D	557	-0.598	16.228	58.141	1.00	87.42	C
ATOM	16762	NH1	ARG	D	557	-0.969	15.130	58.792	1.00	83.34	N
ATOM	16763	NH2	ARG	D	557	0.676	16.582	58.129	1.00	79.73	N
ATOM	16764	O	LYS	D	558	-8.627	21.819	57.064	1.00	94.06	O
ATOM	16765	N	LYS	D	558	-6.319	20.693	56.589	1.00	89.93	N
ATOM	16766	CA	LYS	D	558	-6.528	21.972	55.942	1.00	88.59	C
ATOM	16767	C	LYS	D	558	-7.810	22.558	56.518	1.00	92.20	C
ATOM	16768	CB	LYS	D	558	-6.620	21.807	54.424	1.00	87.31	C
ATOM	16769	CG	LYS	D	558	-6.070	22.990	53.632	1.00	86.20	C
ATOM	16770	O	VAL	D	559	-9.399	26.183	55.221	1.00	91.02	0
ATOM	16771	N	VAL	D	559	-7.988	23.873	56.416	1.00	92.18	N
ATOM	16772	CA	VAL	D	559	-9.202	24.503	56.930	1.00	87.26	C
ATOM	16773	C	VAL	D	559	-9.962	25.301	55.871	1.00	90.34	C
ATOM	16774	CB	VAL	D	559	-8.882	25.416	58.105	1.00	84.86	C
ATOM	16775	CGI	VAL	D	559	-10.125	26.185	58.518	1.00	90.78	C
ATOM	16776	CG2	VAL	D	559	-8.344	24.588	59.266	1.00	87.60	C
ATOM	16777	O	TH.R	D	560	-12.931	27.021	56.491	1.00	94.65	0
ATOM	16778	N	THR	D	560	-11.245	24.979	55.712	1.00	93.82	N
ATOM	16779	CA	THR	D	560	-12.114	25.624	54.725	1.00	95.80	C
ATOM	16780	C	THR	D	560	-12.775	26.878	55.276	1.00	96.58	C
ATOM	16781	CB	THR	D	560	-13.244	24.679	54.257	1.00	96.41	C
ATOM	16782	OG1	THR	D	560	-12.825	23.317	54.403	1.00	98.47	0
ATOM	16783	CG2	THR	D	560	-13.666	24.970	52.815	1.00	94.03	C
ATOM	16784	N	VAL	D	561	-13.176	27.773	54.377	1.00	98.21	N
ATOM	16785	CA	VAL	D	561	-14.055	28.877	54.742	1.00	98.03	C
ATOM	16786	C	VAL	D	561	-15.459	28.313	54.939	1.00	102.59	C
ATOM	16787	O	VAL	D	561	-16.212	28.761	55.812	1.00	102.24	0
ATOM	16788	CB	VAL	D	561	-14.058	29.982	53.674	1.00	97.26	C
ATOM	16789	CGI	VAL	D	561	-15.109	31.045	53.987	1.00	96.94	C
ATOM	16790	CG2	VAL	D	561	-12.681	30.603	53.571	1.00	94.56	C
ATOM	16791	N	LYS	D	562	-15.793	27.309	54.130	1.00	104.51	N
ATOM	16792	CA	LYS	D	562	-17.031	26.559	54.301	1.00	103.19	C
ATOM	16793	C	LYS	D	562	-17.014	25.804	55.629	1.00	102.69	C
ATOM	16794	O	LYS	D	562	-18.060	25.519	56.196	1.00	105.23	0
ATOM	16795	CB	LYS	D	562	-17.242	25.589	53.136	1.00	104.29	C
ATOM	16796	N	GLN	D	563	-15.823	25.487	56.127	1.00	102.42	N
ATOM	16797	CA	GLN	D	563	-15.691	24.822	57.420	1.00	100.53	C
ATOM	16798	C	GLN	D	563	-15.660	25.834	58.564	1.00	101.32	C
ATOM	16799	O	GLN	D	563	-16.155	25.566	59.647	1.00	103.05	0
ATOM	16800	CB	GLN	D	563	-14.432	23.951	57.457	1.00	92.96	C
ATOM	16801	N	LEU	D	564	-15.071	26.998	58.334	1.00	99.26	N
ATOM	16802	CA	LEU	D	564	-15.032	28.023	59.371	1.00	101.42	C
ATOM	16803	C	LEU	D	564	-16.418	28.629	59.603	1.00	105.01	C
ATOM	16804	O	LEU	D	564	-16.832	28.846	60.749	1.00	101.53	O
ATOM	16805	CB	LEU	D	564	-14.046	29.130	59.002	1.00	101.63	C
ATOM	16806	CG	LEU	D	564	-14.151	30.378	59.884	1.00	95.64	C
ATOM	16807	CD1	LEU	D	564	-13.489	30.126	61.237	1.00	91.79	C
ATOM	16808	CD2	LEU	D	564	-13.578	31.607	59.182	1.00	84.35	C
ATOM	16809	N	LYS	D	565	-17.114	28.906	58.500	1.00	102.81	N
ATOM	16810	CA	LYS	D	565	-18.452	29.477	58.537	1.00	97.33	C
ATOM	16811	C	LYS	D	565	-19.452	28.540	59.212	1.00	99.96	C
ATOM	16812	O	LYS	D	565	-20.167	28.939	60.125	1.00	99.36	0
ATOM	16813	CB	LYS	D	565	-18.920	29.814	57.120	1.00	96.29	C
ATOM	16814	N	GLU	D	566	-19.488	27.284	58.784	1.00	102.64	N
ATOM	16815	CA	GLU	D	566	-20.515	26.358	59.262	1.00	104.30	C
ATOM	16816	C	GLU	D	566	-20.203	25.672	60.603	1.00	101.02	C
ATOM	16817	O	GLU	D	566	-21.117	25.320	61.348	1.00	97.05	0
ATOM	16818	CB	GLU	D	566	-20.785	25.301	58.184	1.00	104.50	C
ATOM	16819	CG	GLU	D	566	-21.547	25.855	56.971	1.00	110.38	C

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ATOM  16820  CD   GLU D 566    -20.948  25.438  55.632  1.00115.21      C
ATOM  16821  OE1  GLU D 566    -20.939  26.273  54.694  1.00109.20      O
ATOM  16822  OE2  GLU D 566    -20.486  24.279  55.520  1.00115.50      O
ATOM  16823  N    ASP D 567    -18.926  25.501  60.924  1.00102.65      N
ATOM  16824  CA.  ASP D 567    -18.552  24.686  62.078  I.00103.96      C
ATOM  16825  C    ASP D 567    -18.278  25.486  63.340  1.00106.78      C
ATOM  16826  O    ASP D 567    -18.610  25.041  64.434  1.00111.62      O
ATOM  16827  CB   ASP D 567    -17.319  23.844  61.757  I.00108.41      C
ATOM  16828  CG   ASP D 567    -17.240  22.590  62.589  1.00110.14      C
ATOM  16829  OD1  ASP D 567    -17.943  22.505  63.617  1.00109.68      O
ATOM  16830  OD2  ASP D 567    -16.473  21.684  62.208  I.00115.10      0
ATOM  16831  N    TYR D 568    -17.661  26.654  63.202  1.00106.86      N
ATOM  16832  CA   TYR D 568    -17.279  27.425  64.381  1.00103.41      C
ATOM  16833  C    TYR D 568    -18.481  28.045  65.102  1.00105.93      C
ATOM  16834  O    TYR D 568    -18.535  28.069  66.334  1.00103.46      0
ATOM  16835  CB   TYR D 568    -16.288  28.520  64.007  1.00100.47      C
ATOM  16836  CG   TYR D 568    -15.920  29.370  65.194  1.00 97.65      C
ATOM  16837  CD1  TYR D 568    -15.115  28.865  66.204  I.00 93.49      C
ATOM  16838  CD2  TYR D 568    -16.394  30.669  65.319  1.00100.43      C
ATOM  16839  CE1  TYR D 568    -14.782  29.632  67.301  1.00 92.41      C
ATOM  16840  CE2  TYR D 568    -16.068  31.447  66.413  I.00 97.58      C
ATOM  16841  CZ   TYR D 568    -15.260  30.922  67.402  1.00 92.89      C
ATOM  16842  OH   TYR D 568    -14.927  31.685  68.496  1.00 87.33      0
ATOM  16843  N    PHE D 569    -19.444  28.545  64.334  I.00105.50      N
ATOM  16844  CA   PHE D 569    -20.620  29.178  64.915  1.00102.96      C
ATOM  16845  C    PHE D 569    -21.748  28.171  65.156  1.00106.70      C
ATOM  16846  O    PHE D 569    -21.697  27.365  66.091  I.00101.65      0
ATOM  16847  CB   PHE D 569    -21.100  30.305  64.005  1.00103.07      C
ATOM  16848  CG   PHE D 569    -19.987  31.183  63.487  1.00104.91      C
ATOM  16849  CD2  PHE D 569    -19.585  31.110  62.164  1.00102.06      C
ATOM  16850  CD1  PHE D 569    -19.353  32.093  64.319  1.00108.38      C
ATOM  16851  CE2  PHE D 569    -18.567  31.923  61.677  1.00 99.52      C
ATOM  16852  CE1  PHE D 569    -18.334  32.911  63.839  1.00105.63      C
ATOM  16853  CZ   PHE D 569    -17.940  32.820  62.515  I.00100.60      C
ATOM  16854  0    VAL D 578    -21.695  33.901  56.726  1.00 92.10      0
ATOM  16855  N    VAL D 578    -24.253  34.649  58.039  1.00 92.98      N
ATOM  16856  CA.  VAL D 578    -22.904  35.043  58.435  I.00 93.58      C
ATOM  16857  C    VAL D 578    -21.898  34.960  57.299  1.00 91.60      C
ATOM  16858  CB   VAL D 578    -22.373  34.172  59.571  1.00 93.39      C
ATOM  16859  CGI  VAL D 578    -20.950  34.596  59.920  I.00 91.40      C
ATOM  16860  CG2  VAL D 578    -23.304  34.251  60.783  1.00 97.15      C
ATOM  16861  O    GLU D 579    -18.575  36.738  57.524  1.00 90.95      0
ATOM  16862  N    GLU D 579    -21.247  36.074  56.994  1.00 92.99      N
ATOM  16863  CA   GLU D 579    -20.270  36.102  55.913  1.00 96.43      C
ATOM  16864  C    GLU D 579    -18.825  36.263  56.409  1.00 98.25      C
ATOM  16865  CB   GLU D 579    -20.614  37.215  54.928  1.00 96.17      C
ATOM  16866  CG   GLU D 579    -21.472  36.755  53.769  I.00 99.19      C
ATOM  16867  CD   GLU D 579    -20.742  36.856  52.443  1.00110.77      C
ATOM  16868  OE1  GLU D 579    -20.612  37.986  51.920  1.00116.95      0
ATOM  16869  OE2  GLU D 579    -20.289  35.810  51.930  I.00113.62      0
ATOM  16870  O    1LE D 580    -15.888  36.636  53.672  1.00 92.17      0
ATOM  16871  N    ILE D 580    -17.882  35.848  55.563  1.00 97.44      N
ATOM  16872  CA   ILE D 580    -16.460  35.876  55.892  I.00 90.37      C
ATOM  16873  C    ILE D 580    -15.647  36.693  54.880  1.00 92.50      C
ATOM  16874  CB   ILE D 580    -15.881  34.458  55.959  1.00 91.56      C
ATOM  16875  CGI  ILE D 580    -16.798  33.548  56.777  I.00 94.39      C
ATOM  16876  CG2  ILE D 580    -14.487  34.482  56.551  1.00 91.71      C
ATOM  16877  CD1  ILE D 580    -16.955  33.981  58.222  1.00 98.27      C
ATOM  16878  O    SER D 581    -12.048  37.294  55.882  1.00 84.54      0
ATOM  16879  N    SEP. D 581    -14.683  37.453  55.390  1.00 93.33      N
ATOM  16880  CA   SER D 581    -13.805  38.263  54.558  1.00 89.37      C
ATOM  16881  C    SER D 581    -12.337  37.947  54.880  1.00 84.76      C
ATOM  16882  CB   SER D 581    -14.107  39.749  54.772  I.00 84.45      C
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ATOM  16883  OG   SER D 581     -13.585  40.544  53.723  1.00 83.89           O
ATOM  16884  O    GLY D 582      -8.663  36.292  54.792  1.00 85.79           O
ATOM  16885  N    GLY D 582     -11.418  38.404  54.032  1.00 84.51           N
ATOM  16886  CA   GLY D 582      -9.997  38.209  54.264  1.00 81.46           C
ATOM  16887  C    GLY D 582      -9.582  36.757  54.120  1.00 83.58           C
ATOM  16888  O    VAL D 583     -12.077  34.883  51.778  1.00 88.83           O
ATOM  16889  N    VAL D 583     -10.273  36.048  53.237  1.00 85.21           N
ATOM  16890  CA.  VAL D 583     -10.024  34.633  52.975  1.00 89.17           C
ATOM  16891  C    VAL D 583     -11.057  34.212  51.933  1.00 91.94           C
ATOM  16892  CB   VAL D 583     -10.132  33.772  54.257  1.00 85.05           C
ATOM  16893  CGI  VAL D 583     -11.553  33.743  54.748  1.00 87.15           C
ATOM  16894  CG2  VAL D 583      -9.610  32.374  54.024  1.00 85.34           C
ATOM  16895  O    GUI D 584     -13.521  31.322  50.527  1.00102.09           0
ATOM  16896  N    GLU D 584     -10.805  33.120  51.215  1.00 95.68           N
ATOM  16897  CA   GLU D 584     -11.644  32.761  50.070  1.00 94.19           C
ATOM  16898  C    GLU D 584     -12.335  31.397  50.191  1.00 97.84           C
ATOM  16899  CB   GLU D 584     -10.808  32.803  48.794  1.00 95.88           c
ATOM  16900  CG   GLU D 584     -10.253  34.179  48.465  1.00 97.30           C
ATOM  16901  CD   GLU D 584     -11.134  34.946  47.507  1.00 95.59           C
ATOM  16902  OE1  GLU D 584     -10.584  35.697  46.671  1.00 94.93           0
ATOM  16903  OE2  GLU D 584     -12.372  34.793  47.584  1.00 96.18           0
ATOM  16904  O    ASP D 585     -12.426  27.759  52.044  1.00 92.04           0
ATOM  16905  N    ASP D 585     -11.617  30.318  49.896  1.00 96.64           N
ATOM  16906  CA   ASP D 585     -12.216  28.989  49.991  1.00 94.83           C
ATOM  16907  C    ASP D 585     -11.675  28.266  51.209  1.00 93.37           C
ATOM  16908  CB   ASP D 585     -11.940  28.168  48.731  1.00 96.52           C
ATOM  16909  CG   ASP D 585     -11.883  29.021  47.480  1.00 97.56           C
ATOM  16910  OD1  ASP D 585     -11.220  30.076  47.502  1.00 93.36           0
ATOM  16911  OD2  ASP D 585     -12.499  28.632  46.470  1.00103.86           0
ATOM  16912  O    ARG D 586      -8.142  29.388  52.074  1.00 85.03           0
ATOM  16913  N    ARG D 586     -10.353  28.221  51.288  1.00 94.33           N
ATOM  16914  CA   ARG D 586      -9.665  27.585  52.394  1.00 91.41           C
ATOM  16915  C    ARG D 586      -8.555  28.510  52.833  1.00 87.92           c
ATOM  16916  CB   ARG D 586      -9.106  26.221  51.988  1.00 82.68           C
ATOM  16917  O    PHE D 587      -5.488  27.343  53.581  1.00 78.93           0
ATOM  16918  N    PHE D 587      -8.078  28.327  54.057  1.00 85.46           N
ATOM  16919  CA.  PHE D 587      -6.907  29.061  54.502  1.00 86.30           C
ATOM  16920  C    PHE D 587      -5.660  28.557  53.777  1.00 84.99           C
ATOM  16921  CB   PHE D 587      -6.724  28.942  56.018  1.00 88.60           C
ATOM  16922  CG   PHE D 587      -7.711  29.752  56.814  1.00 89.08           C
ATOM  16923  CD1  PHE D 587      -7.690  31.133  56.768  1.00 84.58           C
ATOM  16924  CD2  PHE D 587      -8.654  29.129  57.614  1.00 89.48           C
ATOM  16925  CE1  PHE D 587      -8.597  31.872  57.499  1.00 85.98           c
ATOM  16926  CE2  PHE D 587      -9.558  29.864  58.349  1.00 80.37           C
ATOM  16927  CZ   PHE D 587      -9.527  31.234  58.291  1.00 81.43           C
ATOM  16928  O    ASN D 588      -1.885  27.529  53.369  1.00 75.65           0
ATOM  16929  N    ASM D 588      -4.812  29.504  53.368  1.00 82.60           N
ATOM  16930  CA   ASN D 588      -3.500  29.215  52.789  1.00 79.41           C
ATOM  16931  C    ASN D 588      -2.572  28.473  53.754  1.00 77.23           C
ATOM  16932  CB   ASN D 588      -2.821  30.511  52.347  1.00 75.29           C
ATOM  16933  CG   ASN D 588      -3.624  31.277  51.313  1.00 71.60           C
ATOM  16934  OD1  ASN D 588      -4.272  30.690  50.450  1.00 70.37           0
ATOM  16935  ND2  ASN D 588      -3.564  32.601  51.387  1.00 72.12           N
ATOM  16936  O    ALA D 589      -3.524  26.940  56.645  1.00 78.43           0
ATOM  16937  N    ALA D 589      -2.552  28.909  55.009  1.00 76.07           N
ATOM  16938  CA   ALA D 589      -1.673  28.316  56.012  1.00 76.41           C
ATOM  16939  C    ALA D 589      -2.308  27.107  56.683  1.00 73.83           C
ATOM  16940  CB   ALA D 589      -1.296  29.354  57.054  1.00 72.39           C
ATOM  16941  O    SER D 590       0.276  25.029  58.934  1.00 74.48           O
ATOM  16942  N    SER D 590      -1.476  26.279  57.305  1.00 72.65           N
ATOM  16943  CA   SER D 590      -1.929  25.079  57.998  1.00 68.67           C
ATOM  16944  C    SER D 590      -0.868  24.584  58.969  1.00 73.62           C
ATOM  16945  CB   SER D 590      -2.280  23.977  57.000  1.00 79.41           C
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ATOM	16946	OG	SER	D	590	-1.337	23.925	55.941	1.00	80.15	O
ATOM	16947	N	LEU	D	591	-1,251	23.659	59,840	1,00	76.95	N
ATOM	16948	CA	LEU	D	591	-0.344	23,148	60.855	1,00	76,47	C
ATOM	16949	c	LEU	D	591	0.159	21.749	60.513	1.00	82.87	c
ATOM	16950	O	LEU	D	591	0,082	20.835	61,345	1,00	83,71	0
ATOM	16951	CB	LEU	D	591	-1.030	23,133	62.218	1,00	78,81	c
ATOM	16952	CG	LEU	D	591	-1.503	24,500	62.715	1,00	86,24	c
ATOM	16953	GDI	LEU	D	591	-2,056	24.391	64,128	1,00	88.85	c
ATOM	16954	CD2	LEU	D	591	-0.374	25.531	62.647	1,00	80.55	c
ATOM	16955	N	GLY	D	592	0.682	21,598	59.296	1,00	75,87	N
ATOM	16956	CA	GLY	D	592	1,161	20.318	58,802	I,00	79.55	C
ATOM	16957	C	GLY	D	592	1.922	19.479	59.811	1,00	77.59	C
ATOM	16958	O	GLY	D	592	1.531	18,357	60.103	1,00	79,49	O
ATOM	16959	N	THR	D	593	2.988	20.044	60.365	1.00	76.99	N
ATOM	16960	CA	THR	D	593	3,871	19.326	61,273	1,00	74.14	C
ATOM	16961	C	THR	D	593	3.180	18,907	62.562	1,00	77,84	C
ATOM	16962	O	THR	D	593	3.511	17.882	63.146	1.00	79.38	O
ATOM	16963	CB	THR	D	593	5,094	20.184	61,628	1,00	75.33	C
ATOM	16964	OG1	THR	D	593	5.603	20,803	60.440	1,00	74,22	O
ATOM	16965	CG2	THR	D	593	6.187	19,344	62.279	1,00	74,16	c
ATOM	16966	N	TYR	D	594	2,225	19.705	63,015	1,00	78.93	N
ATOM	16967	CA	TYR	D	594	1.479	19.364	64.216	1,00	81.00	C
ATOM	16968	c	TYR	D	594	0.662	18,080	63.999	1,00	83,55	c
ATOM	16969	0	TYR	D	594	0,679	17.175	64,839	I,00	84.19	0
ATOM	16970	CB	TYR	D	594	0.583	20.534	64.619	1,00	81.66	c
ATOM	16971	CG	TYR	D	594	-0.325	20,294	65.807	1,00	82,17	c
ATOM	16972	CD1	TYR	D	594	0,090	20.608	67,097	I,00	83.37	c
ATOM	16973	CD2	TYR	D	594	-1,618	19.792	65,633	1,00	83.63	c
ATOM	16974	CE1	TYR	D	594	-0.747	20,415	68.190	1,00	84,05	c
ATOM	16975	CE2	TYR	D	594	-2.464	19.589	66.715	1.00	86.56	c
ATOM	16976	CZ	TYR	D	594	-2,023	19.906	67,992	1,00	90.17	c
ATOM	16977	OH	TYR	D	594	-2.854	19,712	69.074	1,00	89,55	0
ATOM	16978	N	HIS	D	595	-0.036	17.996	62,869	1.00	80.90	N
ATOM	16979	CA.	HI S	D	595	-0,802	16.796	62,534	1,00	82.76	c
ATOM	16980	C	HIS	D	595	0.098	15,604	62.199	1,00	83,97	c
ATOM	16981	O	HIS	D	595	-0.221	14,475	62.563	1,00	86,04	0
ATOM	16982	CB	HI S	D	595	-1,748	17.067	61,363	1,00	82.50	c
ATOM	16983	CG	HI S	D	595	-2.940	17.891	61.730	1,00	87.34	c
ATOM	16984	ND1	HIS	D	595	-4.164	17,745	61.112	1,00	94,49	N
ATOM	16985	CD2	HIS	D	595	-3,097	18.874	62,646	I,00	86.92	c
ATOM	16986	CEl	HI S	D	595	-5,022	18.603	61,633	1,00	91.58	c
ATOM	16987	NE2	HIS	D	595	-4.400	19,300	62.566	1,00	91,46	N
ATOM	16988	N	ASP	D	596	1.200	15.854	61.489	1.00	81.81	N
ATOM	16989	CA	ASP	D	596	2,212	14.822	61,243	1,00	83.17	c
ATOM	16990	C	ASP	D	596	2.622	14,175	62.542	1,00	84,55	c
ATOM	16991	O	ASP	D	596	2.587	12.957	62.687	1.00	91.34	0
ATOM	16992	CB	ASP	D	596	3,467	15.393	60,580	1,00	79.20	c
ATOM	16993	CG	ASP	D	596	3.275	15,682	59.120	1,00	78,87	c
ATOM	16994	OD2	ASP	D	596	4.001	16,561	58.593	1,00	74,38	0
ATOM	16995	OD1	ASP	D	596	2,392	15.039	58,505	1,00	79.87	0
ATOM	16996	N	LEU	D	597	3.016	15.015	63.485	1,00	83.57	N
ATOM	16997	CA	LEU	D	597	3.529	14,549	64.752	1,00	84,84	c
ATOM	16998	C	LEU	D	597	2,424	13.989	65,638	I,00	88.18	c
ATOM	16999	O	LEU	D	597	2.670	13.099	66.449	1,00	91.01	0
ATOM	17000	CB	LEU	D	597	4.271	15,686	65.449	1,00	8.3,73	c
ATOM	17001	CG	LEU	D	597	5,563	16.053	64,719	I,00	81.89	c
ATOM	17002	CD1	LEU	D	597	6,154	17.324	65,275	1,00	79.27	c
ATOM	17003	CD2	LEU	D	597	6.570	14,914	64.799	1,00	79,32	c
ATOM	17004	N	LEU	D	598	1.204	14.488	65.469	1.00	87.19	N
ATOM	17005	CA	LEU	D	598	0,072	13.994	66,256	1,00	92.51	c
ATOM	17006	C	LEU	D	598	-0.152	12,502	65.991	1,00	87,86	c
ATOM	17007	O	LEU	D	598	-0.535	11.760	66.888	1.00	88.12	0
ATOM	17008	CB	LEU	D	598	-1,201	14.800	65,950	1,00	90.22	c

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ATOM   17009  CG   LEU D 598      -2.272  14.987  67.029  1.00 83.55           c
ATOM   17010  GDI  LEU D 598      -3.343  15.911  66.507  1.00 85.58           C
ATOM   17011  CD2  LEU D 598      -2.901  13.676  67.463  1.00 91.67           c
ATOM   17012  N    LYS D 599       0.092  12.055  64.766  1.00 87.76           N
ATOM   17013  CA.  LYS D 599       0.043  10.621  64.506  I.00 93.95           C
ATOM   17014  C    LYS D 599       1.271   9.933  65.099  1.00 88.99           C
ATOM   17015  O    LYS D 599       1.161   8.860  65.680  1.00 90.47           O
ATOM   17016  CB   LYS D 599      -0.062  10.316  63.005  I.00 92.01           c
ATOM   17017  CG   LYS D 599      -0.028   8.810  62.684  1.00 92.80           c
ATOM   17018  CD   LYS D 599     --0.418   8.519  61.241  1.00 88.06           c
ATOM   17019  CE   LYS D 599      -1.851   8.950  60.972  I.00 89.52           c
ATOM   17020  NZ   LYS D 599      -2.221   8.803  59.536  1.00 94.44           N
ATOM   17021  N    ILE D 600       2.430  10.573  64.973  1.00 89.23           N
ATOM   17022  CA   ILE D 600       3.711   9.958  65.336  1.00 91.07           c
ATOM   17023  C    ILE D 600       3.854   9.693  66.840  1.00 90.56           C
ATOM   17024  O    ILE D 600       4.559   8.774  67.238  1.00 91.32           O
ATOM   17025  CB   ILE D 600       4.913  10.833  64.845  1.00 90.38           c
ATOM   17026  CGI  ILE D 600       4.891  10.974  63.316  I.00 89.23           c
ATOM   17027  CG2  ILE D 600       6.259  10.272  65.318  1.00 86.18           c
ATOM   17028  CD1  ILE D 600       6.111  10.411  62.606  1.00 91.13           c
ATOM   17029  N    ILE D 601       3.181  10.469  67.684  I.00 91.73           N
ATOM   17030  CA   ILE D 601       3.337  10.264  69.126  1.00 92.53           C
ATOM   17031  c    ILE D 601       2.024  10.314  69.908  1.00 93.37           c
ATOM   17032  0    ILE D 601       2.015  10.119  71.131  I.00 93.68           0
ATOM   17033  CB   ILE D 601       4.313  11.298  69.730  1.00 93.72           c
ATOM   17034  CGI  ILE D 601       4.367  12.554  68.854  1.00 92.00           c
ATOM   17035  CG2  ILE D 601       5.705  10.690  69.875  I.00 91.12           c
ATOM   17036  CD1  ILE D 601       5.375  13.589  69.296  1.00 94.23           c
ATOM   17037  N    LYS D 602       0.926  10.549  69.193  1.00 93.53           N
ATOM   17038  CA   LYS D 602     --0.392  10.756  69.799  1.00 96.62           c
ATOM   17039  C    LYS D 602      -0.332  11.909  70.815  1.00101.78           c
ATOM   17040  O    LYS D 602      -0.343  13.080  70.417  1.00 99.50           0
ATOM   17041  CB   LYS D 602     --0.901   9.471  70.454  1.00 98.20           c
ATOM   17042  CG   LYS D 602      -0.579   8.196  69.674  I.00 94.33           c
ATOM   17043  CD   LYS D 602      -1.025   8.281  68.222  1.00 93.73           c
ATOM   17044  CE   LYS D 602     --2.528   8.457  68.091  1.00 93.38           c
ATOM   17045  NZ   LYS D 602      -2.955   8.279  66.673  I.00 93.13           N
ATOM   17046  O    ASP D 603       0.431  14.857  73.185  1.00 94.23           0
ATOM   17047  N    ASP D 603      -0.283  11.564  72.105  1.00101.32           N
ATOM   17048  CA   ASP D 603      -0.025  12.497  73.217  I.00 95.45           c
ATOM   17049  C    ASP D 603      -0.403  13.974  73.005  1.00 94.97           c
ATOM   17050  CB   ASP D 603       1.460  12.420  73.585  1.00 90.78           c
ATOM   17051  CG   ASP D 603       1.683  12.397  75.077  1.00 95.18           c
ATOM   17052  OD1  ASP D 603       0.818  12.932  75.804  1.00 95.41           0
ATOM   17053  OD2  ASP D 603       2.714  11.839  75.523  1.00 95.51           0
ATOM   17054  O    LYS D 604     --1.714  17.835  73.132  1.00 90.92           0
ATOM   17055  N    LYS D 604     --1.657  14.246  72.653  I.00 95.61           N
ATOM   17056  CA   LYS D 604      -2.060  15.606  72.277  1.00 97.16           c
ATOM   17057  c    LYS D 604     --1.801  16.631  73.390  1.00 94.46           c
ATOM   17058  CB   LYS D 604      -3.540  15.644  71.873  I.00 92.66           c
ATOM   17059  CG   LYS D 604      -3.927  16.913  71.127  1.00 91.07           c
ATOM   17060  CD   LYS D 604     --5.426  17.176  71.157  1.00 91.73           c
ATOM   17061  CE   LYS D 604      -5.736  18.597  70.697  I.00 89.66           c
ATOM   17062  NZ   LYS D 604      -5.000  19.598  71.524  1.00 90.11           N
ATOM   17063  O    ASP D 605       0.306  18.819  75.402  1.00 90.58           0
ATOM   17064  N    ASP D 605      -1.682  16.149  74.622  I.00 92.84           N
ATOM   17065  CA   ASP D 605      -1.244  16.997  75.723  1.00 93.17           c
ATOM   17066  C    ASP D 605       0.125  17.595  75.406  1.00 93.74           c
ATOM   17067  CB   ASP D 605     --1.183  16.202  77.030  1.00 92.34           c
ATOM   17068  CG   ASP D 605      -2.534  16.063  77.690  1.00 96.36           c
ATOM   17069  OD1  ASP D 605      -3.304  17.046  77.680  1.00103.48           0
ATOM   17070  OD2  ASP D 605      -2.831  14.971  78.218  1.00100.82           0
ATOM   17071  O    PHE D 606       3.518  18.965  73.863  I.00 80.95           0
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ATOM   17072   N    PHE  D  606        1..071    16.. 703    75.. 121    1 .00  90..98          M
ATOM   17073   CA   FHE  D  606        2 ,462    17 .048     74 ,854     1 ,00  84 .06          C
ATOM   17074   C    PHE  D  606        2 .645    18.,106     73..761     1 ,00  83,.47          C
ATOM   17075   CB   PHE  D  606        3 .224    15.. 779    74 ..473    1 .00  84 .03          C
ATOM   17076   CG   PHE  D  606        4 „689    15. 967     74 ,405     1 ,00  77 ,51          C
ATOM   17077   CD2  PHE  D  606        5 ..298   16.,299     73..213     1 ,00  77 ,92          C
ATOM   17078   CD1  PHE  D  606        5 ..460   15.,826     75 .537     1 ,00  74 ,92          C
ATOM   1707 9  CE2  PHE  D  606        6 „655    16. 488     73 ,153     1 ,00  76.,49          C
ATOM   17080   CE1  PHE  D  606        6 .816    16.. 014    75.. 490    1 ,00  75..89          C
ATOM   17081   CZ   PHE  D  606        7 .420    16.,344     74 .295     1 ,00  76 ,69          C
ATOM   17082   O    LEU  D  607        1 „744    21..299     71 ,188     1 ,00  86..79          0
ATOM   17083   N    LEU  D  607        1 ..822   18.. 033    72.. 720    1 ,00  85..30          M
ATOM   17084   CA   LEU  D  607        1 .922    18.,938     71 .573     1 ,00  85 ,67          C
ATOM   17085   c    LEU  D  607        1 ..432   20.. 338    71 ..901    1 .00  89..04          C
ATOM   17086   CB   LEU  D  607        1 ,118    18..400     70 ,384     1 ,00  89..16          C
ATOM   17087   CG   LEU  D  607        1 .755    17 ,461     69...35 9   1 ,00  81 ,37          C
ATOM   17088   CD1  LEU  D  607        2 ..238   16.. 179    70.. 012    1 .00  85..96          C
ATOM   17089   CD2  LEU  D  607        0 „757    17.146      68.,251     1 ,00  86.,94          C
ATOM   17090   O    ASP  D  608        0 ..998   23.,563     74 .595     1 ,00  83,.97          0
ATOM   17091   N    ASP  D  608        0 ..638   20.,438     72 .967     1 ,00  90,.56          M
ATOM   17092   CA.  ASP  D  608        0 „067    21 .707     73 ,396     1 ,00  85.,03          C
ATOM   17093   C    ASP  D  608        0 .890    22.. 338    74 ..517    1 ,00  83..43          C
ATOM   17094   CB   ASP  D  608       --1 .384   21.,513     73 .849     1 ,00  85,.97          C
ATOM   17095   CG   ASP  D  608       -2,,316    21..149     72.,704     1 ,00  88..25          C
ATOM   17096   OD2  ASP  D  608       -3.. 542   21.. 069    72.. 934    1 ,00  89..43          0
ATOM   170 97  OD1  ASP  D  608       -1 .826    20.,932     71 .578     1 ,00  89 ,55          0
ATOM   17098   O    ASM  D  609        4 „506    22..476     75.,846     1 ,00  80..01          0
ATOM   17099   N    ASM  D  609        1 ,467    21 .506     75 ,381     1 ,00  78..47          M
ATOM   17100   CA   A.SM D  609        2 .254    22.,008     76 .510     1 ,00  79 ,90          C
ATOM   17101   c    ASM  D  609        3 .381    22.. 924    76.. 062    1 .00  78..76          C
ATOM   17102   CB   ASM  D  609        2 ,832    20..848     77 ,329     1 ,00  78..25          C
ATOM   17103   CG   ASN  D  609        3 ..633   21.,314     78..542     1 ,00  77 ,39          C
ATOM   17104   OD1  ASM  D  609        3 .659    22.. 502    78.. 875    1 .00  79..84          0
ATOM   17105   ND2  ASM  D  609        4 „27 6   20. 367     79.,219     1 ,00  74 ,29          M
ATOM   17106   O    GLU  D  610        6 ..326   25.,843     75..918     1 ,00  80,.55          0
ATOM   17107   N    GLU  D  610        3 ..077   24.,213     75 .963     1 ,00  78,.61          M
ATOM   17108   CA.  GLU  D  610        4 „040    25. 223     75 ,539     1 ,00  80.,31          C
ATOM   17109   C    GLU  D  610        5 .377    25.. 159    76.. 292    1 ,00  77 .58          C
ATOM   17110   CB   GLU  D  610        3 .425    26.,624     75 .684     1 ,00  75 ,97          C
ATOM   17111   O    GLU  D  611        8 „861    23..282     77 ,278     1 ,00  77 .23          O
ATOM   17112   N    GLU  D  611        5 „458    24 .346     77 ,341     1 ,00  75..69          M
ATOM   17113   CA   GLU  D  611        6 .736    24.,105     78 .006     1 ,00  79 ,21          C
ATOM   17114   c    GLU  D  611        7 ..645   23.. 237    77 ..139    1 .00  78..05          C
ATOM   17115   CB   GLU  D  611        6 ,530    23.. 447    79.,375     1 ,00  80..70          C
ATOM   17116   O    ASN  D  612        9 .260    21.,535     73..494     1 ,00  78,.39          0
ATOM   17117   N    ASM  D  612        7 ..043   22.. 460    76.. 240    1 .00  79..26          M
ATOM   17118   CA.  ASM  D  612        7 „773    21 .525     75 ,378     1 ,00  77 ,49          C
ATOM   17119   C    ASK  D  612        8 ..415   22.,157     74 .143     1 ,00  78,.47          C
ATOM   17120   CB   ASM  D  612        6 ..843   20.,404     74 .901     1 ,00  74 ,15          C
ATOM   17121   CG   ASM  D  612        6 „342    19. 529     76 ,029     1 ,00  74 ,62          C
ATOM   17122   OD1  ASN  D  612        7 ..042   19.. 291    77 ..014    1 ,00  75..24          0
ATOM   17123   ND2  ASM  D  612        5 ..125   19.,025     75 .879     1 ,00  75,.4           M
ATOM   17124   O    GLU  D  613       10,,144    23..617     70.,978     1 ,00  78..68          O
ATOM   17125   N    GLU  D  613        8 .004    23.. 381    73.. 818    1 ,00  80..12          M
ATOM   17126   CA   GLU  D  613        8 .384    24.,027     72 .557     1 ,00  83 ,07          C
ATOM   17127   C    GLU  D  613        9 „848    23..848     72.,149     1 ,00  81 .09          C
ATOM   17128   CB   GLU  D  613        8 „073    25..521     72.,618     1 ,00  81 .88          C
ATOM   17129   CG   GLU  D  613        6 .590    25 ,832     72 .643     1 ,00  84 ,62          C
ATOM   17130   CD   GLU  D  613        6 .306    27.. 262    72.. 239    1 .00  89..51          C
ATOM   17131   OE1  GLU  D  613        7 ,269    28..067     72.,197     1 ,00  92 .29          0
ATOM   17132   OE2  GLU  D  613        5 ..128   27.,573     71 .950     1 ,00  89,.23          0
ATOM   17133   N    ASP  D  614       10.. 754   23.. 950    73.. 113    1 .00  77 .95          M
ATOM   17134   CA.  ASP  D  614       12,,173    23.860      72.,815     1 ,00  82 ,02          C
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ATOM   17135  C    ASP  D  614      12.538  22.541  72.150  1.00  79.20          C
ATOM   17136  O    ASP  D  614      12.982  22.545  71.004  1.00  78.65          O
ATOM   17137  CB   ASP  D  614      13.002  24.065  74.081  1.00  84.96          C
ATOM   17138  CG   ASP  D  614      13.169  25.527  74.421  1.00  88.51          C
ATOM   17139  OD1  ASP  D  614      14.199  26.111  74.020  I.00  86.51          0
ATOM   17140  OD2  ASP  D  614      12.259  26.096  75.066  1.00  95.60          0
ATOM   17141  N    ILE  D  615      12.333  21.420  72.839  1.00  80.22          N
ATOM   17142  CA.  ILE  D  615      12.715  20.120  72.278  I.00  77.79          C
ATOM   17143  C    ILE  D  615      11.886  19.800  71.017  1.00  75.29          C
ATOM   17144  O    ILE  D  615      12.349  19.064  70.152  1.00  74.62          O
ATOM   17145  CB   ILE  D  615      12.598  18.964  73.339  I.00  75.99          C
ATOM   17146  CGI  ILE  D  615      13.103  17.609  72.784  1.00  76.14          C
ATOM   17147  CG2  ILE  D  615      11.177  18.853  73.874  1.00  74.61          C
ATOM   17148  CD1  ILE  D  615      14.642  17.472  72.608  1.00  72.93          C
ATOM   17149  N    LEU  D  616      10.693  20.376  70.874  1.00  72.35          N
ATOM   17150  CA   LEU  D  616       9.942  20.169  69.636  1.00  69.05          C
ATOM   17151  C    LEU  D  616      10.588  20.904  68.463  1.00  71.10          C
ATOM   17152  O    LEU  D  616      10.544  20.435  67.332  I.00  68.78          0
ATOM   17153  CB   LEU  D  616       8.488  20.609  69.788  1.00  74.20          C
ATOM   17154  CG   LEU  D  616       7.634  19.703  70.675  1.00  77.24          C
ATOM   17155  CD1  LEU  D  616       6.165  19.992  70.482  I.00  67.73          C
ATOM   17156  CD2  LEU  D  616       7.936  18.249  70.369  1.00  76.39          C
ATOM   17157  N    GLU  D  617      11.190  22.057  68.735  1.00  72.66          N
ATOM   17158  CA   GLU  D  617      11.936  22.777  67.710  I.00  69.45          C
ATOM   17159  C    GLU  D  617      13.254  22.068  67.418  1.00  69.78          C
ATOM   17160  O    GLU  D  617      13.645  21.925  66.271  1.00  70.91          O
ATOM   17161  CB   GLU  D  617      12.203  24.225  68.138  I.00  73.75          C
ATOM   17162  CG   GLU  D  617      11.000  25.154  67.994  1.00  72.71          C
ATOM   17163  CD   GLU  D  617      10.476  25.220  66.566  1.00  74.46          C
ATOM   17164  OE1  GLU  D  617      11.282  25.051  65.617  1.00  79.01          0
ATOM   17165  OE2  GLU  D  617       9.255  25.434  66.381  1.00  70.26          0
ATOM   17166  N    ASP  D  618      13.928  21.629  68.472  1.00  67.43          N
ATOM   17167  CA   ASP  D  618      15.174  20.904  68.362  1.00  66.26          C
ATOM   17168  C    ASP  D  618      14.975  19.622  67.551  I.00  69.35          C
ATOM   17169  O    ASP  D  618      15.881  19.145  66.877  1.00  66.96          0
ATOM   17170  CB   ASP  D  618      15.716  20.604  69.762  1.00  70.28          C
ATOM   17171  CG   ASP  D  618      16.637  19.395  69.801  I.00  75.12          C
ATOM   17172  OD2  ASP  D  618      17.875  19.579  69.761  1.00  73.34          0
ATOM   17173  OD1  ASP  D  618      16.117  18.261  69.906  1.00  78.28          0
ATOM   17174  N    ILE  D  619      13.771  19.082  67.591  I.00  66.09          N
ATOM   17175  CA   ILE  D  619      13.498  17.867  66.861  1.00  67.85          C
ATOM   17176  C    ILE  D  619      13.223  18.179  65.390  1.00  67.58          C
ATOM   17177  O    ILE  D  619      13.806  17.565  64.503  1.00  66.20          0
ATOM   17178  CB   ILE  D  619      12.333  17.099  67.503  1.00  69.08          C
ATOM   17179  CGI  ILE  D  619      12.863  16.244  68.659  1.00  70.96          C
ATOM   17180  CG2  ILE  D  619      11.649  16.210  66.503  1.00  71.83          C
ATOM   17181  CD1  ILE  D  619      11.780  15.581  69.464  I.00  65.58          C
ATOM   17182  N    VAL  D  620      12.366  19.156  65.124  1.00  69.34          N
ATOM   17183  CA   VAL  D  620      12.065  19.511  63.744  1.00  64.63          C
ATOM   17184  C    VAL  D  620      13.315  20.075  63.072  I.00  63.16          C
ATOM   17185  O    VAL  D  620      13.472  19.981  61.862  1.00  64.00          0
ATOM   17186  CB   VAL  D  620      10.902  20.498  63.673  1.00  60.02          C
ATOM   17187  CGI  VAL  D  620      10.572  20.861  62.231  I.00  64.25          C
ATOM   17188  CG2  VAL  D  620       9.695  19.879  64.327  1.00  66.59          C
ATOM   17189  N    LEU  D  621      14.223  20.628  63.864  1.00  62.81          N
ATOM   17190  CA   LEU  D  621      15.493  21.096  63.335  I.00  63.44          C
ATOM   17191  C    LEU  D  621      16.346  19.924  62.816  1.00  71.44          C
ATOM   17192  O    LEU  D  621      16.808  19.923  61.667  1.00  70.07          0
ATOM   17193  CB   LEU  D  621      16.267  21.857  64.398  1.00  63.36          C
ATOM   17194  CG   LEU  D  621      17.539  22.527  63.902  1.00  64.09          C
ATOM   17195  CD1  LEU  D  621      17.150  23.702  63.033  1.00  66.76          C
ATOM   17196  CD2  LEU  D  621      18.384  22.975  65.061  1.00  63.19          C
ATOM   17197  N    TH.R D  622      16.562  18.936  63.674  I.00  68.23          N
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ATOM	17198	CA	THR	D	622	17.330	17.748	63..299	1,00	68..42	C
ATOM	17199	C	THR	D	622	16,,749	17.066	62,,053	1,00	67.12	C
ATOM	17200	O	THR	D	622	17.477	16,,745	61..120	1,00	72,61	0
ATOM	17201	CB	THR	D	622	17.390	16..741	64..470	1,00	63..24	c
ATOM	17202	OG1	THR	D	622	18,,235	17.263	65,,505	1,00	62,92	0
ATOM	17203	CG2	THR	D	622	17.933	15,,400	64..005	1,00	76,.41	C
ATOM	17204	N	LEU	D	623	15..436	16,,873	62..032	1,00	65,.03	N
ATOM	17205	CA.	LEU	D	623	14,762	16. 248	60,,897	1,00	70.,22	C
ATOM	17206	C	LEU	D	623	14.918	17.009	59..579	1,00	69..29	C
ATOM	172 07	O	LEU	D	623	14.695	16,,452	58..511	1,00	72,62	0
ATOM	17208	CB	LEU	D	623	13,,268	16..094	61,,189	1,00	71.4.3	C
ATOM	17209	CG	LEU	D	623	12..876	15..302	62..431	1,00	72.33	C
ATOM	17210	GDI	LEU	D	62.3	11.369	15,,211	62. 524	1,00	70,77	C
ATOM	17211	CD2	LEU	D	623	13..511	13..922	62..405	1,00	71.63	c
ATOM	17212	N	THR	D	624	15,,270	18..286	59,,649	1,00	67.16	N
ATOM	17213	CA	THR	D	624	15..404	19,,082	58..443	1,00	61,80	C
ATOM	17214	C	THR	D	624	16..874	19..211	58..045	1,00	66..10	c
ATOM	17215	0	THR	D	624	17,185	19. 533	56,,906	1,00	72,30	0
ATOM	17216	CB	THR	D	624	14.778	20,,476	58..623	1,00	66,.11	C
ATOM	17217	OG1	THR	D	624	13..503	20,,355	59..268	1,00	61,88	0
ATOM	17218	CG2	THR	D	624	14,572	21.139	57,287	1,00	64,92	C
ATOM	17219	N	LEU	D	625	17.771	18..917	58..981	1,00	67.62	N
ATOM	17220	CA	LEU	D	625	19..208	19,,064	58..781	1,00	65,.88	c
ATOM	17221	C	LEU	D	625	19,,888	17.799	58,,224	1,00	68..01	C
ATOM	17222	O	LEU	D	625	20..860	17.892	57..460	1,00	64.11	0
ATOM	17223	CB	LEU	D	625	19. 863	19,,464	60. 101	1,00	61,08	C
ATOM	17224	CG	LEU	D	625	20,,914	20.575	60,,171	1,00	63..40	C
ATOM	17225	CD1	LEU	D	625	20,,604	21.765	59,,282	1,00	63..97	C
ATOM	17226	CD2	LEU	D	625	21.012	21,,047	61. 606	1,00	61,56	C
ATOM	17227	N	PHE	D	626	19..393	16..623	58..609	1,00	68..16	N
ATOM	17228	CA	FHE	D	626	20,,008	15..359	58,,183	1,00	65..07	C
ATOM	17229	C	PHE	D	626	19.037	14,440	57..468	1,00	71,36	C
ATOM	17230	O	PHE	D	626	17.820	14.568	57..606	1,00	72.57	0
ATOM	172 31	CB	PHE	D	626	20,,596	14.604	59,,373	1,00	67,41	C
ATOM	17232	CG	PHE	D	626	21..424	15,,452	60..273	1,00	62,54	C
ATOM	17233	CD1	PHE	D	626	22.761	15,,661	60..004	1,00	57,09	c
ATOM	17234	CD.2	PHE	D	626	20,,860	16. 044	61,,396	1,00	62,98	C
ATOM	17235	CE1	PHE	D	626	23..524	16..456	60..833	1,00	63..19	C
ATOM	17236	CE2	PHE	D	626	21.617	16,,833	62. 230	1,00	65,01	C
ATOM	17237	CZ	PHE	D	626	22,,949	17.045	61,,952	1,00	66..61	C
ATOM	17238	O	GLU	D	627	18,,491	10..135	56,,214	1,00	81.77	0
ATOM	17239	N	GLU	D	627	19. 591	13,,496	56. 717	1,00	74,35	N
ATOM	17240	CA	GLU	D	627	18..781	12..516	56..015	1,00	78..95	c
ATOM	17241	C	GLU	D	627	19,,249	11.099	56,,337	1,00	81.64	C
ATOM	17242	CB	GLU	D	627	18..824	12,,764	54..507	1,00	82,90	C
ATOM	17243	CG	GLU	D	627	20..189	12..550	53..866	1,00	86..16	c
ATOM	17244	CD	GLU	D	627	20,,085	12.107	52,,405	1,00	92,67	C
ATOM	17245	OE1	GLU	D	627	19.113	11,396	52..058	1,00	92,54	0
ATOM	17246	OE2	GLU	D	627	20..973	12,,469	51..601	1,00	83,.87	0
ATOM	17247	O	ASP	D	628	20,,404	9.923	59,,422	1,00	85.,37	0
ATOM	17248	N	ASP	D	628	20..503	10..982	56..755	1,00	80..10	N
ATOM	17249	CA	ASP	D	628	21.061	9,694	57..136	1,00	80,.19	c
ATOM	17250	C	ASP	D	628	20,,429	9.198	58,,428	1,00	86..78	C
ATOM	17251	CB	ASP	D	628	22..572	9..790	57..309	1,00	80..83	C
ATOM	172 52	CG	ASP	D	628	23.212	8,435	57. 538	1,00	86,38	C
ATOM	17253	OD1	ASP	D	628	22,,789	7.470	56,867	1,00	89..15	0
ATOM	172 54	OD2	ASP	D	628	24,,128	8..331	58,,385	1,00	85..28	0
ATOM	172 55	O	A.P.G	D	629	19. 590	7,665	61. 937	1,00	85,06	0
ATOM	17256	N	ARG	D	629	19..937	7.961	58..415	1,00	88..33	N
ATOM	172 57	CA	ARG	D	629	19,,276	7.369	59,,578	1,00	84.92	C
ATOM	172 58	C	ARG	D	629	20.121	7,425	60..858	1,00	84,01	C
ATOM	17259	CB	ARG	D	629	18..884	5..915	59..274	1,00	90..23	c
ATOM	17260	CG	ARG	D	629	19,,409	4.881	60,,275	1,00	95.,94	C

ATOM	17261	CD	ARG	D	629	18.769	3.511	60.096	1.00	94.90	c
ATOM	17262	NE	ARG	D	629	19,544	2.643	59,219	1,00	93.72	N
ATOM	17263	CZ	ARG	D	629	19.419	2,625	57.896	1,00	103,09	C
ATOM	17264	NH1	ARG	D	629	18.549	3;437	57.299	1.00	97.98	N
ATOM	17265	NH2	ARG	D	629	20,163	1.797	57,168	1,00	102.20	N
ATOM	17266	O	GLU	D	6.30	22.467	8,611	63.846	1,00	86,11	O
ATOM	17267	N	GLU	D	630	21.430	7,229	60.746	1,00	79,80	N
ATOM	17268	CA.	GLU	D	630	22,261	7.149	61,943	1,00	83.97	C
ATOM	17269	C	GLU	D	630	22.456	8.512	62,614	1,00	85.94	C
ATOM	17270	CB	GLU	D	630	23.623	6,533	61.612	1,00	81,77	c
ATOM	17271	O	MET	D	631	21,638	12.070	64,043	I,00	80.92	0
ATOM	17272	N	MET	D	631	22,624	9.552	61:799	1,00	84.50	N
ATOM	17273	CA	MET	D	631	22.818	10,913	62.295	1,00	81,59	C
ATOM	17274	C	MET	D	631	21,564	11;400	63,010	1.00	80.47	c
ATOM	17275	CB	MET	D	631	23,170	11.864	61,145	1,00	79.50	C
ATOM	17276	CG	MET	D	631	24.555	11,669	60.560	1,00	81,04	C
ATOM	17277	SD	MET	D	631	24.895	12,730	59.145	1.00	74.82	s
ATOM	17278	CE	MET	D	631	26,443	12.051	58,593	1,00	68.72	C
ATOM	17279	O	ILE	D	6.32	18.983	11,562	65.444	1,00	84,44	0
ATOM	17280	N	ILE	D	632	20.418	11,064	62.430	1,00	77,43	N
ATOM	17281	CA.	ILE	D	632	19,135	11.307	63,049	1,00	79.28	C
ATOM	17282	C	ILE	D	632	19;133	10.800	64,489	1,00	83.31	C
ATOM	17283	CB	ILE	D	632	18.017	10,617	62.263	1,00	80,22	c
ATOM	17284	CGI	ILE	D	632	17,930	11.186	60,846	I,00	77.71	C
ATOM	17285	CG2	ILE	D	632	16;696	10.763	62,991	1,00	81.85	C
ATOM	17286	GDI	ILE	D	632	17.056	12,405	60.721	1,00	72,57	C
ATOM	17287	O	GLU	D	633	19,831	9.567	68,102	I,00	87.59	0
ATOM	17288	N	GLU	D	633	19,345	9.500	64,622	1,00	85.98	N
ATOM	17289	CA	GLU	D	633	19.251	8,816	65.897	1,00	83,71	C
ATOM	17290	C	GLU	D	633	20;229	9;347	66,960	1.00	83.77	c
ATOM	17291	CB	GLU	D	633	19,460	7.320	65,661	1,00	89.56	C
ATOM	17292	CG	GLU	D	6.33	18.455	6,723	64.672	1,00	87,59	C
ATOM	17293	CD	GLU	D	633	18.838	5;318	64.222	1.00	91.63	c
ATOM	17294	OE1	GLU	D	633	19,946	4.864	64,577	1,00	92.98	0
ATOM	17295	OE2	GLU	D	6.33	18.033	4,672	63.514	1,00	88,39	0
ATOM	17296	O	GLU	D	634	22.400	11,678	69.303	1,00	87,92	0
ATOM	17297	N	GLU	D	634	21,491	9.553	66,592	1,00	81.81	N
ATOM	17298	CA	GLU	D	634	22;499	10;031	67;542	1,00	79.91	C
ATOM	17299	C	GLU	D	634	22.127	11,392	68.129	1,00	89,33	C
ATOM	17300	CB	GLU	D	634	23,871	10.119	66,875	I,00	77.04	C
ATOM	17301	O	ARG	D	635	19,171	14.720	68,512	1,00	87.20	0
ATOM	17302	N	ARG	D	635	21.491	12,220	67.303	1,00	86,68	N
ATOM	17303	CA	ARG	D	635	21;119	13;572	67.695	1.00	84.31	c
ATOM	17304	C	ARG	D	635	19,685	13.635	68,215	1,00	87.90	C
ATOM	17305	CB	ARG	D	6.35	21.291	14,538	66.518	1,00	79,47	C
ATOM	17306	CG	ARG	D	635	22.501	15;447	66.647	1.00	76.10	c
ATOM	17307	CD	ARG	D	635	22,536	16.466	65,529	1,00	77.99	C
ATOM	17308	NE	ARG	D	6.35	21..325	17,284	65.494	1,00	77,01	N
ATOM	17309	CZ	ARG	D	635	21.319	18,615	65.511	1,00	77,20	c
ATOM	17310	NH1	ARG	D	635	20,162	19.286	65,488	1,00	69,37	N
ATOM	17311	NH2	ARG	D	635	22;474	19;276	65;550	1,00	73.88	N
ATOM	17312	O	LEU	D	636	16.402	11,011	70.325	1,00	90,21	O
ATOM	17313	N	LEU	D	636	19,050	12.471	68,332	I,00	85.81	N
ATOM	17314	CA	LEU	D	636	17;669	12.378	68;796	1,00	82.34	C
ATOM	17315	C	LEU	D	636	17.521	11,416	69.985	1,00	92,26	C
ATOM	17316	CB	LEU	D	636	16,772	11.923	67,651	I,00	79.24	C
ATOM	17317	CG	LEU	D	636	15,353	12.467	67,613	1,00	80.77	C
ATOM	17318	GDI	LEU	D	636	15.370	13,987	67.667	1,00	81,28	C
ATOM	17319	CD2	LEU	D	636	14,665	11;986	66,357	1.00	84.94	c
ATOM	17320	O	LYS	D	637	17,308	9.285	73,433	1,00	94.88	0
ATOM	17321	N	LYS	D	6.37	18.652	11,065	70.606	1,00	90,07	N
ATOM	17322	CA	LYS	D	637	18.723	10;006	71.617	1.00	87.65	c
ATOM	17323	C	LYS	D	637	17,839	10.238	72,858	1,00	92.83	C

ATOM	17324	CB	LYS	D	637	20.182	9.815	72.057	1.00	85.51	c
ATOM	17325	O	THR	D	638	14.699	11.831	73.589	1.00	92.90	O
ATOM	17326	N	THR	D	638	17.669	11.493	73.262	1.00	89.95	N
ATOM	17327	CA	THR	D	638	16.926	11.799	74.485	1.00	91.01	c
ATOM	17328	C	THR	D	638	15.454	11.383	74.451	1.00	93.10	C
ATOM	17329	CB	THR	D	638	16.983	13.297	74.798	1.00	91.34	C
ATOM	17330	OG1	THR	D	638	17.910	13.937	73.909	1.00	91.54	O
ATOM	17331	CG2	THR	D	638	17.414	13.519	76.239	1.00	87.14	C
ATOM	17332	O	TYR	D	639	12.197	9.447	77.380	1.00	84.64	O
ATOM	17333	N	TYR	D	639	15.056	10.537	75.404	1.00	98.20	N
ATOM	17334	CA	TYR	D	639	13.646	10.186	75.598	1.00	98.33	C
ATOM	17335	C	TYR	D	639	13.357	9.539	76.958	1.00	93.12	C
ATOM	17336	CB	TYR	D	639	13.176	9.260	74.483	1.00	93.63	C
ATOM	17337	CG	TYR	D	639	11.918	9.750	73.804	1.00	94.76	c
ATOM	17338	CD1	TYR	D	639	11.900	10.963	73.121	1.00	93.21	c
ATOM	17339	CD2	TYR	D	639	10.753	8.999	73.832	1.00	95.98	c
ATOM	17340	CE1	TYR	D	639	10.750	11.417	72.484	1.00	91.42	c
ATOM	17341	CE2	TYR	D	639	9.596	9.438	73.200	1.00	99.11	c
ATOM	17342	CZ	TYR	D	639	9.602	10.651	72.528	1.00	94.90	c
ATOM	17343	OH	TYR	D	639	8.461	11.097	71.905	1.00	89.94	0
ATOM	17344	O	ASP	D	644	10.310	5.587	71.685	1.00	100.02	0
ATOM	17345	N	ASP	D	644	9.967	6.260	74.446	1.00	92.70	N
ATOM	17346	CA	ASP	D	644	9.184	5.231	73.773	1.00	96.51	c
ATOM	17347	C	ASP	D	644	9.850	4.770	72.479	1.00	96.01	C
ATOM	17348	CB	ASP	D	644	7.774	5.734	73.477	1.00	93.25	c
ATOM	17349	CG	ASP	D	644	6.840	4.611	73.082	1.00	95.47	c
ATOM	17350	OD1	ASP	D	644	6.009	4.211	73.923	1.00	94.78	0
ATOM	17351	OD2	ASP	D	644	6.954	4.109	71.942	1.00	88.79	0
ATOM	17352	N	ASP	D	645	9.869	3.459	72.258	1.00	97.58	N
ATOM	17353	CA	ASP	D	645	10.636	2.868	71.161	1.00	96.15	c
ATOM	17354	C	ASP	D	645	9.897	2.868	69.813	1.00	96.64	c
ATOM	17355	O	ASP	D	645	10.487	3.208	68.788	1.00	95.08	0
ATOM	17356	CB	ASP	D	645	11.048	1.437	71.526	1.00	96.20	c
ATOM	17357	CG	ASP	D	645	12.265	0.957	70.741	1.00	106.87	c
ATOM	17358	OD1	ASP	D	645	13.072	0.182	71.302	1.00	114.09	0
ATOM	17359	OD2	ASP	D	645	12.421	1.353	69.564	1.00	106.37	0
ATOM	17360	N	LYS	D	646	8.624	2.477	69.797	1.00	95.99	N
ATOM	17361	CA	LYS	D	646	7.860	2.479	68.547	1.00	90.17	c
ATOM	17362	C	LYS	D	646	7.672	3.905	68.049	1.00	94.94	c
ATOM	17363	O	LYS	D	646	7.514	4.137	66.850	1.00	96.68	0
ATOM	17364	CB	LYS	D	646	6.502	1.806	68.724	1.00	84.13	c
ATOM	17365	O	VAL	D	647	9.074	7.265	66.955	1.00	87.27	0
ATOM	17366	N	VAL	D	647	7.685	4.858	68.978	1.00	96.02	N
ATOM	17367	CA	VAL	D	647	7.655	6.274	68.624	1.00	94.27	C
ATOM	17368	C	VAL	D	647	9.008	6.695	68.044	1.00	91.10	c
ATOM	17369	CB	VAL	D	647	7.313	7.162	69.840	1.00	92.13	c
ATOM	17370	O	MET	D	648	12.679	6.637	66.256	1.00	92.70	0
ATOM	17371	N	MET	D	648	10.083	6.389	68.766	1.00	90.39	N
ATOM	17372	CA	MET	D	648	11.437	6.725	68.316	1.00	92.36	c
ATOM	17373	C	MET	D	648	11.818	6.104	66.955	1.00	94.08	c
ATOM	17374	CB	MET	D	648	12.461	6.311	69.375	1.00	89.68	c
ATOM	17375	CG	MET	D	648	13.876	6.835	69.131	1.00	93.19	c
ATOM	17376	SD	MET	D	648	14.075	8.604	69.480	1.00	91.44	s
ATOM	17377	CE	MET	D	648	12.967	8.760	70.867	1.00	94.01	c
ATOM	17378	N	LYS	D	649	11.200	4.983	66.583	1.00	95.03	N
ATOM	17379	CA	LYS	D	649	11.360	4.464	65.227	1.00	90.63	c
ATOM	17380	C	LYS	D	649	10.590	5.355	64.268	1.00	90.77	c
ATOM	17381	O	LYS	D	649	11.161	5.917	63.339	1.00	95.63	0
ATOM	17382	CB	LYS	D	649	10.875	3.017	65.106	1.00	91.04	c
ATOM	17383	CG	LYS	D	649	11.951	1.973	65.325	1.00	91.21	c
ATOM	17384	CD	LYS	D	649	11.472	0.586	64.922	1.00	96.70	c
ATOM	17385	CE	LYS	D	649	12.573	-0.459	65.099	1.00	92.56	c
ATOM	17386	NZ	LYS	D	649	12.090	-1.834	64.782	1.00	92.29	N

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ATOM  17387  N    GLN  D  650    9.292   5.487  64.509  1.00  87.72   N
ATOM  17388  CA   GLN  D  650    8.419   6.308  63.673  1.00  91.56   C
ATOM  17389  C    GLN  D  650    8.899   7.760  63.510  1.00  95.36   C
ATOM  17390  O    GLN  D  650    8.609   8.419  62.502  1.00  92.93   0
ATOM  17391  CB   GLN  D  650    7.008   6.305  64.256  1.00  90.05   c
ATOM  17392  CG   GLN  D  650    6.181   5.098  63.901  1.00  90.89   c
ATOM  17393  CD   GLN  D  650    5.253   5.375  62.746  1.00  94.42   c
ATOM  17394  OE1  GLN  D  650    5.217   6.489  62.224  1.00  93.68   0
ATOM  17395  ME 2 GLN  D  650    4.492   4.366  62.338  1.00  96.36   N
ATOM  17396  N    LEU  D  651    9.623   8.251  64.513  1.00  95.16   N
ATOM  17397  CA   LEU  D  651   10.086   9.635  64.537  1.00  91.46   C
ATOM  17398  C    LEU  D  651   11.390   9.779  63.763  1.00  87.06   C
ATOM  17399  O    LEU  D  651   11.592  10.762  63.050  1.00  80.30   O
ATOM  17400  CB   LEU  D  651   10.261  10.107  65.988  1.00  90.45   c
ATOM  17401  CG   LEU  D  651   10.835  11.496  66.289  1.00  86.44   c
ATOM  17402  CD1  LEU  D  651    9.788  12.572  66.055  1.00  80.67   c
ATOM  17403  CD2  LEU  D  651   11.372  11.551  67.713  1.00  78.22   c
ATOM  17404  O    LYS  D  652   14.369   9.146  60.999  1.00  86.06   0
ATOM  17405  N    LYS  D  652   12.260   8.780  63.897  1.00  87.18   N
ATOM  17406  CA   LYS  D  652   13.561   8.774  63.226  1.00  85.70   c
ATOM  17407  C    LYS  D  652   13.428   8.797  61.708  1.00  85.82   c
ATOM  17408  CB   LYS  D  652   14.380   7.547  63.645  1.00  84.47   c
ATOM  17409  O    ARG  D  653   11.862  10.052  58.127  1.00  78.99   0
ATOM  17410  N    ARG  D  653   12.259   8.417  61.211  1.00  85.67   N
ATOM  17411  CA   ARG  D  653   12.053   8.351  59.779  1.00  83.78   c
ATOM  17412  C    ARG  D  653   11.500   9.652  59.224  1.00  77.66   c
ATOM  17413  CB   ARG  D  653   11.127   7.186  59.435  1.00  86.30   c
ATOM  17414  CG   ARG  D  653   11.533   5.880  60.079  1.00  81.74   c
ATOM  17415  CD   ARG  D  653   10.596   4.755  59.686  1.00  87.59   c
ATOM  17416  NE   ARG  D  653   11.045   3.487  60.240  1.00  87.21   N
ATOM  17417  CZ   ARG  D  653   10.240   2.483  60.566  1.00  84.35   C
ATOM  17418  NH1  ARG  D  653    8.932   2.596  60.388  1.00  78.14   N
ATOM  17419  NH2  ARG  D  653   10.751   1.366  61.078  1.00  87.63   N
ATOM  17420  O    ARG  D  654   11.389  13.485  59.940  1.00  82.16   O
ATOM  17421  N    ARG  D  654   10.628  10.311  59.982  1.00  82.33   N
ATOM  17422  CA   ARG  D  654    9.990  11.552  59.521  1.00  85.07   c
ATOM  17423  C    ARG  D  654   10.999  12.646  59.124  1.00  82.68   c
ATOM  17424  CB   ARG  D  654    9.040  12.100  60.595  1.00  83.71   c
ATOM  17425  CG   ARG  D  654    8.399  13.449  60.256  1.00  75.86   c
ATOM  17426  CD   ARG  D  654    7.250  13.307  59.280  1.00  78.23   c
ATOM  17427  NE   ARG  D  654    7.550  13.923  57.993  1.00  78.40   N
ATOM  17428  CZ   ARG  D  654    6.677  14.037  56.998  1.00  78.48   C
ATOM  17429  NH1  ARG  D  654    5.439  13.577  57.137  1.00  80.24   N
ATOM  17430  NH2  ARG  D  654    7.043  14.619  55.866  1.00  76.03   N
ATOM  17431  O    ARG  D  655   10.342  14.836  56.584  1.00  71.43   O
ATOM  17432  N    ARG  D  655   11.415  12.623  57.862  1.00  80.44   N
ATOM  17433  CA.  ARG  D  655   12.300  13.642  57.327  1.00  74.97   C
ATOM  17434  C    ARG  D  655   11.518  14.896  56.952  1.00  73.73   C
ATOM  17435  CB   ARG  D  655   13.052  13.120  56.104  1.00  71.57   c
ATOM  17436  O    TYR  D  656   13.933  17.833  55.979  1.00  68.79   0
ATOM  17437  N    TYR  D  656   12.178  16.037  57.069  1.00  68.24   N
ATOM  17438  CA   TYR  D  656   11.656  17.262  56.489  1.00  70.03   c
ATOM  17439  C    TYR  D  656   12.744  17.910  55.653  1.00  70.41   c
ATOM  17440  CB   TYR  D  656   11.157  18.236  57.561  1.00  63.23   c
ATOM  17441  CG   TYR  D  656    9.832  17.859  58.177  1.00  62.05   c
ATOM  17442  CD1  TYR  D  656    8.653  18.053  57.487  1.00  61.36   c
ATOM  17443  CD2  TYR  D  656    9.765  17.313  59.452  1.00  67.14   c
ATOM  17444  CE1  TYR  D  656    7.448  17.717  58.038  1.00  64.06   c
ATOM  17445  CE2  TYR  D  656    8.557  16.964  60.013  1.00  67.58   c
ATOM  17446  CZ   TYR  D  656    7.397  17.175  59.300  1.00  70.34   c
ATOM  17447  OH   TYR  D  656    6.177  16.842  59.848  1.00  76.12   0
ATOM  17448  O    THR  D  657   11.463  20.933  53.926  1.00  62.38   0
ATOM  17449  N    TH.R D  657   12.320  18.526  54.560  1.00  65.40   N
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ATOM	17450	CA	THR	D	657	13.198	19.319	53.723	1.00	65.79	c
ATOM	17451	C	THR	D	657	12.654	20.742	53.718	1.00	58.31	c
ATOM	17452	CB	THR	D	657	13.263	18.763	52.287	1.00	65.82	c
ATOM	17453	OG1	THR	D	657	13.722	19.792	51.407	1.00	74.94	0
ATOM	17454	CG2	THR	D	657	11.880	18.325	51.816	1.00	59.93	c
ATOM	17455	O	GLY	D	658	13.595	23.650	55.607	1.00	61.00	0
ATOM	17456	N	GLY	D	658	13.510	21.729	53.485	1.00	59.66	N
ATOM	17457	CA.	GLY	D	658	13.052	23.105	53.333	1.00	56.28	C
ATOM	17458	C	GLY	D	658	13.443	24.053	54.462	1.00	59.18	C
ATOM	17459	O	TRP	D	659	12.299	27.726	53.839	1.00	56.11	0
ATOM	17460	N	TRP	D	659	13.624	25.322	54.127	1.00	54.68	N
ATOM	17461	CA	TRP	D	659	13.838	26.353	55.128	1.00	57.20	C
ATOM	17462	C	TRP	D	659	12.877	27.546	54.918	1.00	60.28	C
ATOM	17463	CB	TRP	D	659	15.301	26.801	55.116	1.00	53.01	c
ATOM	17464	CG	TRP	D	659	16.191	25.658	55.448	1.00	56.69	c
ATOM	17465	CD1	TRP	D	659	16.709	24.732	54.573	1.00	54.12	c
ATOM	17466	*CD2*	TRP	D	659	16.639	25.275	56.746	1.00	58.67	c
ATOM	17467	NE1	TRP	D	659	17.452	23.811	55.251	1.00	55.83	N
ATOM	17468	CE2	TRP	D	659	17.431	24.112	56.587	1.00	58.17	C
ATOM	17469	CE3	TRP	D	659	16.451	25.794	58.029	1.00	54.19	c
ATOM	17470	CZ2	TRP	D	659	18.040	23.468	57.661	1.00	55.76	c
ATOM	17471	CZ3	TRP	D	659	17.063	25.152	59.101	1.00	56.52	c
ATOM	17472	CI-I2	TRP	D	659	17.847	24.000	58.908	1.00	59.11	c
ATOM	17473	0	GLY	D	660	13.654	30.771	55.515	1.00	58.03	0
ATOM	17474	N	GLY	D	660	12.693	28.334	55.971	1.00	55.23	N
ATOM	17475	CA	GLY	D	660	11.744	29.433	55.950	1.00	55.08	c
ATOM	17476	C	GLY	D	660	12.453	30.752	55.748	1.00	54.77	c
ATOM	17477	O	ARG	D	661	13.215	35.079	56.544	1.00	52.96	0
ATOM	17478	N	AR.G	D	661	11.724	31.858	55.833	1.00	53.61	N
ATOM	17479	CA	ARG	D	661	12.313	33.140	55.482	1.00	52.26	c
ATOM	17480	C	ARG	D	661	12.661	33.992	56.694	1.00	50.62	c
ATOM	17481	CB	ARG	D	661	11.375	33.898	54.562	1.00	50.79	c
ATOM	17482	CG	ARG	D	661	11.014	33.138	53.298	1.00	56.48	c
ATOM	17483	CD	ARG	D	661	12.014	33.405	52.174	1.00	58.79	c
ATOM	17484	NE	ARG	D	661	12.403	34.813	52.122	1.00	59.60	N
ATOM	17485	CZ	ARG	D	661	13.371	35.308	51.358	1.00	58.74	c
ATOM	17486	NH1	ARG	D	661	14.075	34.514	50.557	1.00	60.23	N
ATOM	17487	NH2	ARG	D	661	13.653	36.600	51.415	1.00	58.91	N
ATOM	17488	O	LEU	D	662	12.805	32.231	60.432	1.00	56.83	0
ATOM	17489	N	LEU	D	662	12.369	33.487	57.895	1.00	52.90	N
ATOM	17490	CA	LEU	D	662	12.600	34.247	59.134	1.00	57.82	c
ATOM	17491	C	LEU	D	662	13.146	33.400	60.299	1.00	55.01	c
ATOM	17492	CB	LEU	D	662	11.290	34.934	59.578	1.00	57.43	c
ATOM	17493	CG	LEU	D	662	10.417	35.536	58.468	1.00	48.91	c
ATOM	17494	CD1	LEU	D	662	8.940	35.496	58.823	1.00	48.51	c
ATOM	17495	*CD2*	LEU	D	662	10.888	36.943	58.179	1.00	57.63	c
ATOM	17496	N	SER	D	663	13.966	34.012	61.152	1.00	54.03	N
ATOM	17497	CA	SEP.	D	663	14.529	33.342	62.323	1.00	55.39	C
ATOM	17498	c	SER	D	663	13.567	33.237	63.496	1.00	58.88	c
ATOM	17499	0	SER	D	663	12.599	33.993	63.587	1.00	57.93	0
ATOM	17500	CB	SER	D	663	15.765	34.081	62.792	1.00	59.22	c
ATOM	17501	OG	SER	D	663	15.394	35.350	63.287	1.00	58.14	0
ATOM	17502	N	ARG	D	664	13.856	32.322	64.416	1.00	56.13	N
ATOM	17503	CA	ARG	D	664	13.067	32.208	65.633	1.00	59.64	C
ATOM	17504	C	ARG	D	664	13.085	33.518	66.457	1.00	63.29	c
ATOM	17505	O	ARG	D	664	12.044	33.971	66.922	1.00	61.43	0
ATOM	17506	CB	ARG	D	664	13.561	31.049	66.496	1.00	57.66	c
ATOM	17507	CG	ARG	D	664	12.549	30.583	67.530	1.00	60.88	c
ATOM	17508	CD	ARG	D	664	13.140	29.565	68.503	1.00	66.97	c
ATOM	17509	NE	ARG	D	664	12.191	29.194	69.558	1.00	73.86	N
ATOM	17510	CZ	ARG	D	664	12.365	28.195	70.425	1.00	80.30	c
ATOM	17511	NH1	ARG	D	664	13.457	27.437	70.368	1.00	78.85	N
ATOM	17512	NH2	ARG	D	664	11.438	27.945	71.346	1.00	82.04	N

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ATOM   17513  N    LYS D 665      14.260  34.122  66.616  1.00 60.84           M
ATOM   17514  CA   LYS D 665      14.407  35.306  67.445  1.00 58.65           C
ATOM   17515  C    LYS D 665      13.464  36.428  66.972  1.00 65.35           C
ATOM   17516  O    LYS D 665      12.880  37.159  67.770  1.00 67.18           0
ATOM   17517  CB   LYS D 665      15.868  35.764  67.445  I.00 63.85           C
ATOM   17518  CG   LYS D 665      16.082  37.154  67.998  1.00 67.98           C
ATOM   17519  CD   LYS D 665      17.506  37.379  68.450  1.00 66.68           C
ATOM   17520  CE   LYS D 665      17.590  38.607  69.360  I.00 75.58           C
ATOM   17521  NZ   LYS D 665      18.958  38.876  69.909  1.00 79.10           M
ATOM   17522  M    LEU D 666      13.272  36.526  65.670  1.00 62.85           M
ATOM   17523  CA   LEU D 666      12.393  37.538  65.131  I.00 59.32           C
ATOM   17524  C    LEU D 666      10.928  37.251  65.450  1.00 60.34           C
ATOM   17525  O    LEU D 666      10.157  38.142  65.812  1.00 68.82           O
ATOM   17526  CB   LEU D 666      12.570  37.636  63.619  1.00 58.85           C
ATOM   17527  CG   LEU D 666      11.597  38.602  62.945  1.00 61.81           C
ATOM   17528  CD1  LEU D 666      12.142  40.019  63.002  1.00 65.23           C
ATOM   17529  CD2  LEU D 666      11.315  38.197  61.522  1.00 61.63           C
ATOM   17530  N    ILE D 667      10.539  36.000  65.299  I.00 59.48           M
ATOM   17531  CA   ILE D 667       9.136  35.650  65.349  1.00 57.42           C
ATOM   17532  C    ILE D 667       8.652  35.503  66.790  1.00 65.78           C
ATOM   17533  0    ILE D 667       7.514  35.873  67.119  I.00 65.42           0
ATOM   17534  CB   ILE D 667       8.877  34.374  64.547  1.00 55.65           C
ATOM   17535  CGI  ILE D 667       8.959  34.699  63.055  1.00 54.19           C
ATOM   17536  CG2  ILE D 667       7.527  33.782  64.882  I.00 61.34           C
ATOM   17537  CD1  ILE D 667       8.612  33.535  62.154  1.00 57.07           C
ATOM   17538  N    A.SM D 668      9.526  35.011  67.659  1.00 60.01           N
ATOM   17539  CA   ASM D 668       9.138  34.790  69.039  I.00 60.52           C
ATOM   17540  C    ASM D 668      10.341  34.819  69.969  1.00 61.80           C
ATOM   17541  O    A.SM D 668     10.551  33.913  70.773  1.00 65.57           0
ATOM   17542  CB   ASM D 668       8.385  33.469  69.160  1.00 64.21           C
ATOM   17543  CG   ASM D 668       7.508  33.406  70.389  1.00 69.39           C
ATOM   17544  OD1  ASN D 668       7.633  32.496  71.212  1.00 68.37           0
ATOM   17545  ND2  ASM D 668       6.613  34.376  70.524  1.00 65.43           M
ATOM   17546  N    GLY D 669      11.140  35.868  69.830  I.00 60.48           M
ATOM   17547  CA   GLY D 669      12.201  36.158  70.769  1.00 64.63           C
ATOM   17548  C    GLY D 669      12.142  37.640  71.089  1.00 68.69           C
ATOM   17549  0    GLY D 669      11.867  38.043  72.233  I.00 70.16           0
ATOM   17550  0    ILE D 670       9.984  40.095  70.435  1.00 65.17           0
ATOM   17551  N    ILE D 670      12.386  38.447  70.059  1.00 64.10           N
ATOM   17552  CA   ILE D 670      12.395  39.902  70.167  I.00 66.16           C
ATOM   17553  C    ILE D 670      11.112  40.438  70.830  1.00 66.91           C
ATOM   17554  CB   ILE D 670      12.597  40.542  68.768  1.00 62.22           C
ATOM   17555  CGI  ILE D 670      14.070  40.527  68.410  1.00 69.20           C
ATOM   17556  CG2  ILE D 670      12.179  41.984  68.762  1.00 74.66           C
ATOM   17557  CD1  ILE D 670      14.927  41.335  69.368  1.00 71.70           C
ATOM   17558  O    ARG D 671      11.018  44.062  72.530  1.00 63.18           0
ATOM   17559  N    ARG D 671      11.291  41.259  71.860  I.00 65.83           M
ATOM   17560  CA   ARG D 671      10.148  41.817  72.575  1.00 64.25           C
ATOM   17561  C    ARG D 671      10.032  43.326  72.393  1.00 62.38           C
ATOM   17562  CB   ARG D 671      10.239  41.481  74.064  I.00 65.11           C
ATOM   17563  CG   ARG D 671      10.272  39.995  74.362  1.00 67.90           C
ATOM   17564  CD   ARG D 671      10.123  39.709  75.845  1.00 62.10           C
ATOM   17565  ME   ARG D 671      10.222  38.279  76.125  I.00 72.93           M
ATOM   17566  CZ   ARG D 671       9.231  37.407  75.942  1.00 73.61           C
ATOM   17567  NH1  ARG D 671       8.055  37.813  75.471  1.00 70.19           N
ATOM   17568  NH2  ARG D 671       9.417  36.126  76.229  I.00 70.15           M
ATOM   17569  O    ASP D 672       8.242  45.045  74.529  1.00 65.64           0
ATOM   17570  N    ASP D 672       8.828  43.789  72.080  1.00 61.66           N
ATOM   17571  CA   ASP D 672       8.545  45.215  72.154  1.00 64.01           C
ATOM   17572  C    ASP D 672       8.708  45.704  73.597  1.00 64.15           C
ATOM   17573  CB   ASP D 672       7.146  45.521  71.644  1.00 62.57           C
ATOM   17574  CG   ASP D 672       6.733  46.946  71.928  1.00 61.69           C
ATOM   17575  OD1  ASP D 672       7.240  47.874  71.253  I.00 59.94           0
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ATOM   17576   OD2  ASP  D  672        5 ..901    47 .125    72.. 835    1 .00   65..14         O
ATOM   17577   O    LYS  D  673        8 „570     46..757    77 ,142     1 ,00   73..93         O
ATOM   17578   N    LYS  D  673        9 .377     46.,839    73..779     1 ,00   53,.56         N
ATOM   17579   CA   LYS  D  673        9 ..772    47 ..284   75..115     1 .00   66..15         C
ATOM   17580   C    LYS  D  673        8 „612     47 .422    76 ,103     1 ,00   68.,51         C
ATOM   17581   CB   LYS  D  673       10 ..514    48.,622    75..027     1 ,00   70,.31         C
ATOM   17582   O    GLN  D  674        5 ..357    47 ,112    78 .109     1 ,00   77 ,21         O
ATOM   17583   N    GLN  D  674        7 ,672     48. 293    75 ,776     1 ,00   73.,49         N
ATOM   17584   CA   GLN  D  674        6 ..559    48.. 584   76.. 663    1 ,00   69..05         C
ATOM   17585   c    GLN  D  674        5 ..682    47 ,375    76 .961     1 ,00   70,.66         c
ATOM   17586   CB   GLN  D  674        5 ,722     49 .698    76.,066     I ,00   73..23         c
ATOM   17587   CG   GLN  D  674        6 ..118    51.. 056   76.. 592    1 ,00   75..03         c
ATOM   17588   CD   GLN  D  674        6 .067     52.,096    75 .526     1 ,00   72 ,37         c
ATOM   17589   OE1  GLN  D  674        5 ..817    51.. 784   74 ..360    1 .00   83..79         0
ATOM   17590   NE2  GLN  D  674        6 ,315     53..341    75 ,900     1 ,00   65..74         N
ATOM   17591   O    SER. D  675        4 .456     43.,473    77 ...309   1 ,00   62 ,.93        O
ATOM   17592   N    SER  D  675        5 ..308    46.. 631   75..935     1 .00   66..06         N
ATOM   17593   CA.  SER  D  675        4 ,366     45. 547    76 ,131     1 ,00   60.,94         C
ATOM   17594   C    SER  D  675        5 ..049    44 ,274    76..589     1 ,00   67 ,24         C
ATOM   17595   CB   SER  D  675        3 ..593    45.,291    74 .844     1 ,00   68,.21         c
ATOM   17596   OG   SER  D  675        4 ,472     45. 005    73 ,770     1 ,00   68.,76         0
ATOM   17597   O    GLY  D  676        7 .070     40.. 588   75.. 786    1 ,00   70..06         0
ATOM   17598   N    GLY  D  676        6 ..298    44 ,089    76 .164     1 ,00   66,.20         N
ATOM   17599   CA   GLY  D  676        7 ,033     42 .867    76.,447     I ,00   67 .65         C
ATOM   17600   C    GLY  D  676        6 ..599    41 .693    75.. 590    1 ,00   64 .06         C
ATOM   17601   O    LYS  D  677        6 . 668    41 ,608    71 .983     1 ,00   63 ,19         O
ATOM   17602   N    LYS  D  677        5 ,697     41 .949    74 ,645     I ,00   66..64         N
ATOM   17603   CA   LYS  D  677        5 ,166     40..936    73 ,741     1 ,00   63..74         C
ATOM   17604   C    LYS  D  677        6 .088     40.,676    72 .555     1 ,00   67 ,35         C
ATOM   17605   CB   LYS  D  677        3 ..794    41 ..347   73.. 204    1 .00   63..19         c
ATOM   17606   CG   LYS  D  677        2 ,878     41 .963    74 ,240     1 ,00   68..42         c
ATOM   17607   CD   LYS  D  677        1 .492     41 ,344    74 .218     1 ,00   70,.19         c
ATOM   17608   CE   LYS  D  677        0 ..650    41 ..836   73..049     1 .00   71 .42         c
ATOM   17609   NZ   LYS  D  677       -0.,706     41 .191    73 ,031     1 ,00   70.,68         N
ATOM   17610   N    THR  D  678        6 ..203    .39.,404   72 .184     1 ,00   64 ,47         N
ATOM   17611   CA   THR  D  678        6 ..874    39.,027    70 .951     1 ,00   61 ,83         c
ATOM   17612   C    THR  D  678        5 ,979     39. 317    69.,770     1 ,00   62 ,74         c
ATOM   17613   O    THR  D  678        4 .797     39..643    69.. 940    1 ,00   62 .40         0
ATOM   17614   CB   THR  D  678        7 .223     .37.,541   70 .913     1 ,00   63 ,69         c
ATOM   17615   OG1  THR  D  678        6 ,049     36..790    70.,566     I ,00   58..93         0
ATOM   17616   CG2  THR  D  678        7 ,770     37 .077    72.,258     1 ,00   65..01         c
ATOM   17617   N    ILE  D  679        6 .533     3 9 ,169   68. 572     1 ,00   59 ,60         N
ATOM   17618   CA   ILE  D  679        5 ..744    39.. 319   67.. 361    1 .00   64 .56         c
ATOM   17619   C    ILE  D  679        4 ,634     38..249    67.,320     1 ,00   64 .55         C
ATOM   17620   O    ILE  D  679        3 ..534    .38.,504   66..825     1 ,00   66,.83         O
ATOM   17621   CB   ILE  D  679        6 ..642    39.. 264   66..090     1 .00   64 .33         c
ATOM   17622   CGI  ILE  D  679        7 ,349     40. 608    65.,903     1 ,00   58.,51         c
ATOM   17623   CG2  ILE  D  679        5 ..829    .38.,953   64..839     1 ,00   58,.56         c
ATOM   17624   CD1  ILE  D  679        7 .925     40.,803    64..529     1 ,00   58,.18         c
ATOM   17625   N    LEU  D  680        4 ,885     37. 074    67.,884     1 ,00   62 ,62         N
ATOM   17626   CA   LEU  D  680        3 ..874    36.. 026   67.. 829    1 ,00   64 .76         C
ATOM   17627   c    LEU  D  680        2 .805     36.,244    68..886     1 ,00   63,.18         c
ATOM   17628   0    LEU  D  680        1 ,646     35..874    68.,691     I ,00   67 .34         0
ATOM   17629   CB   LEU  D  680        4 .500     34..635    67.. 989    1 ,00   69..91         c
ATOM   17630   CG   LEU  D  680        3 .520     .33.,476   67. 745     1 ,00   65 ,95         c
ATOM   17631   CDI  LEU  D  680        2 ,838     33..603    66.,381     I ,00   60..90         c
ATOM   17632   CD2  LEU  D  680        4 ,206     32..137    67.,900     1 ,00   61 .42         c
ATOM   17633   N    ASP  D  681        3 .197     3 6 ,845   70 .002     1 ,00   67 ,65         N
ATOM   17634   CA   ASP  D  681        2 ..239    37.. 283   71 ..015    1 .00   65..85         c
ATOM   17635   C    ASP  D  681        1 ,191     38..237    70 ,424     1 ,00   62 .61         C
ATOM   17636   O    ASP  D  681       -0..006     .38.,025   70..596     1 ,00   68,.85         0
ATOM   17637   CB   ASP  D  681        2 .975     37.. 933   72..181     1 .00   58..73         c
ATOM   17638   CG   ASP  D  681        3 ,658     36. 918    73 ,064     1 ,00   62 ,38         c
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ATOM   17639   OD1  ASP  D  681       3.069    35.836    73.290    1.00  67.15            O
ATOM   17640   OD2  ASP  D  681       4.786    37.188    73.532    1.00  66.71            O
ATOM   17641   N    PHE  D  682       1.637    39.254    69.695    1.00  61.76            N
ATOM   17642   CA   PHE  D  682       0.717    40.189    69.052    1.00  64.08            C
ATOM   17643   C    PHE  D  682      -0.192    39.514    68.040    1.00  65.08            C
ATOM   17644   O    PHE  D  682      -1..336   39.927    67.853    1.00  65.49            0
ATOM   17645   CB   PHE  D  682       1.474    41.324    68.355    1.00  66.11            C
ATOM   17646   CG   PHE  D  682       1.830    42.465    69.262    1.00  62.93            C
ATOM   17647   GDI  PHE  D  682       0.862    43.380    69.659    1.00  69.67            C
ATOM   17648   CD2  PHE  D  682       3.130    42.633    69.712    1.00  58.98            C
ATOM   17649   CE1  PHE  D  682       1.188    44.436    70.498    1.00  63.52            C
ATOM   17650   CE2  PHE  D  682       3.465    43.681    70.543    1.00  61.43            C
ATOM   17651   CZ   PHE  D  682       2.494    44.588    70.939    1.00  65.49            C
ATOM   17652   N    LEU  D  683       0.315    38.489    67.365    1.00  70.24            N
ATOM   17653   CA   LEU  D  683      -0.495    37.786    66.371    1.00  67.92            C
ATOM   17654   C    LEU  D  683      -1.524    36.892    67.073    1.00  70.35            C
ATOM   17655   O    LEU  D  683      -2.622    36.661    66.554    1.00  67.00            0
ATOM   17656   CB   LEU  D  683       0.395    36.974    65.425    1.00  70.54            C
ATOM   17657   CG   LEU  D  683       1..375   .37.779   64.563    1.00  69.00            C
ATOM   17658   CD1  LEU  D  683       2.227    36.845    63.743    1.00  63.98            C
ATOM   17659   CD2  LEU  D  683       0.660    38.801    63.669    1.00  63.81            C
ATOM   17660   N    LYS  D  684      -1.163    36.399    68.256    1.00  70.54            N
ATOM   17661   CA   LYS  D  684     --2.117    35.709    69.115    1.00  70.96            C
ATOM   17662   C    LYS  D  684      -3.200    36.681    69.611    1.00  74.87            C
ATOM   17663   O    LYS  D  684      -4.393    36.403    69.490    1.00  79.21            0
ATOM   17664   CB   LYS  D  684      -1..399   .35.053   70.292    1.00  71.39            C
ATOM   17665   CG   LYS  D  684      -0.511    33.865    69.905    1.00  71.02            C
ATOM   17666   CD   LYS  D  684       0.276    33.327    71.107    1.00  72.65            C
ATOM   17667   CE   LYS  D  684       0.905   .31.958    70.804    1.00  70.93            C
ATOM   17668   NZ   LYS  D  684       1.675    31.377    71.947    1.00  75.29            N
ATOM   17669   N    SEP. D  685      -2.790    37.832    70.139    1.00  70.96            N
ATOM   17670   CA   SEP. D  685      -3.748   .38.806    70.674    1.00  71.94            C
ATOM   17671   C    SER  D  685     --3.306    40.263    70.521    1.00  68.93            C
ATOM   17672   O    SER  D  685      -2.329    40.691    71.139    1.00  70.04            0
ATOM   17673   CB   SER  D  685      -4.001   .38.528    72.155    1.00  76.33            C
ATOM   17674   OG   SER  D  685     --2.834    38.810    72.916    1.00  77.12            0
ATOM   17675   O    ASP  D  686      -5.064    44.438    69.273    1.00  71.55            0
ATOM   17676   N    ASP  D  686      -4.042    41.031    69.725    1.00  63.65            N
ATOM   17677   CA   ASP  D  686      -3.727    42.441    69.527    1.00  65.41            C
ATOM   17678   C    ASP  D  686      -4.934    43..347   69.837    1.00  70..35            C
ATOM   17679   CB   ASP  D  686      -3.244    42.663    68.093    1.00  68.25            C
ATOM   17680   CG   ASP  D  686      -2.589    44.021    67.889    1.00  72.53            C
ATOM   17681   OD2  ASP  D  686      -2.518    44.472    66.716    1.00  69.48            0
ATOM   17682   OD1  ASP  D  686      -2.146    44.629    68.899    1.00  72.59            0
ATOM   17683   O    GLY  D  687      -8.484    42.979    69..306   1.00  77.30            0
ATOM   17684   N    GLY  D  687     --5.812    42.892    70.732    1.00  69.79            N
ATOM   17685   CA.  GLY  D  687      -7.010    43.638    71.090    1.00  72.00            C
ATOM   17686   C    GLY  D  687      -7.964    43.904    69.934    1.00  73.34            C
ATOM   17687   O    PHE  D  688     --8.705    45.950    66.204    1.00  69.80            0
ATOM   17688   N    PHE  D  688      -8.210    45.178    69.653    1.00  72.46            N
ATOM   17689   CA   PHE  D  688      -y.071    45.547    68.530    1.00  75.69            C
ATOM   17690   C    PHE  D  688     --8.222    45.936    67.325    1.00  69.07            C
ATOM   17691   CB   PHE  D  688     -10.022    46.700    68.906    1.00  77.54            C
ATOM   17692   CG   PHE  D  688    --11.029    46.350    69.985    1.00  81.62            C
ATOM   17693   GDI  PHE  D  688     -11.459    45.041    70.168    1.00  77.77            C
ATOM   17694   CD2  PHE  D  688     -11.551    47..341   70.818    1.00  81..32            C
ATOM   17695   CEl  PHE  D  688     -12.389    44.725    71.165    1.00  83.02            C
ATOM   17696   CF.2 PHE  D  688     -12.486    47.031    71.8.10   1.00  74.83            C
ATOM   17697   CZ   PHE  D  688     -12.901    45.724    71.987    1.00  77.85            C
ATOM   17698   O    ALA  D  689      -6.066    45.769    64.265    1.00  63.61            0
ATOM   17699   N    ALA  D  689      -6.953    46.247    67.573    1.00  71.25            N
ATOM   17700   CA   ALA  D  689      -6.008    46.624    66.523    1.00  69.14            C
ATOM   17701   C    ALA  D  689      -5.834    45.524    65.457    1.00  68.95            C
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ATOM	17702	CB	ALA	D	689	-4.661	46..980	67..144	1.00	67.10	C
ATOM	17703	O	ASM	D	690	-4,528	43..248	62.,705	1,00	62.66	O
ATOM	17704	N	ASN	D	690	-5..430	44,330	65..900	1.00	66,.68	N
ATOM	17705	CA	ASN	D	690	-5..192	43,163	65..034	1.00	67.10	C
ATOM	17706	C	ASM	D	690	-4„213	43. 417	63.,884	1,00	64.47	C
ATOM	17707	CB	ASN	D	690	-6..511	42.,637	64..480	1.00	67,74	C
ATOM	17708	CG	ASN	D	690	-7.059	41,487	65..296	1,00	68,.71	C
ATOM	17709	OD1	ASN	D	690	-6„902	41.443	66.,515	1,00	71.72	0
ATOM	17710	ND2	ASN	D	690	-7.678	40.,533	64.,625	1,00	66..65	N
ATOM	17711	O	ARG	D	691	-1.027	41,942	63..692	1,00	61,84	O
ATOM	17712	N	ARG	D	691	-.3.,014	43..829	64.,254	1,00	62.34	N
ATOM	17713	CA	ARG	D	691	-1.987	44.118	63.,283	1,00	63..80	C
ATOM	17714	C	ARG	D	691	-1.293	42.,814	62. 856	1,00	61,87	C
ATOM	17715	CB	ARG	D	691	-0..989	45.,127	63.,867	1.00	66..49	C
ATOM	17716	CG	ARG	D	691	-1,640	46.. 441	64.,330	1,00	65..33	C
ATOM	17717	CD	ARG	D	69.1	-0..743	47,292	65..247	1.00	57,69	C
ATOM	17718	NE	ARG	D	691	-0..623	46.,714	66..580	1.00	65..00	N
ATOM	17719	CZ	ARG	D	691	-0„247	47..381	67.,671	1,00	64.32	C
ATOM	17720	NH1	ARG	D	69.1	0..054	48.,668	67..606	1.00	61,09	N
ATOM	17721	NH2	ARG	D	691	-0..178	46.,756	68..837	1,00	62,48	N
ATOM	17722	O	ASN	D	692	1„573	42.901	61.,573	1,00	57.27	O
ATOM	17723	N	ASN	D	692	-1,050	42.,667	61.,552	1,00	57.38	N
ATOM	17724	CA	ASN	D	692	-0..296	41,523	61..053	1,00	61,37	C
ATOM	17725	C	ASN	D	692	1„188	41.813	61.,139	1,00	58..45	C
ATOM	17726	CB	ASN	D	692	-0,701	41.170	59.,618	1,00	60..53	C
ATOM	17727	CG	ASN	D	692	-0.495	42.,316	58. 628	1,00	59,06	C
ATOM	17728	OD1	ASN	D	692	0„245	43..267	58.,882	1,00	63..38	O
ATOM	17729	ND2	ASN	D	692	-1,142	42..209	57.,478	1,00	55..28	N
ATOM	17730	O	PHE	D	69.3	4.949	42.,829	60. 561	1,00	54,50	O
ATOM	17731	N	PHE	D	693	2,005	40,853	60.,711	1.00	59..16	N
ATOM	17732	CA	PHE	D	693	3„470	40..952	60.,760	1,00	52..42	C
ATOM	17733	C	PRE	D	69.3	4.034	42.,173	60..042	1.00	54,93	C
ATOM	17734	CB	PHE	D	693	4.110	39.,682	60..172	1.00	60..28	C
ATOM	17735	CG	PHE	D	693	5„602	39. 791	59.,980	1,00	57.72	C
ATOM	17736	CD1	PHE	D	69.3	6..454	39,765	61..070	1.00	54,79	C
ATOM	17737	CD2	PHE	D	693	6..148	39.,934	58..711	1,00	55,.16	C
ATOM	17738	CE1	PHE	D	693	7„829	39. 877	60.,901	1,00	59..69	C
ATOM	17739	CE2	PHE	D	693	7,519	40.,045	58..539	1,00	55..08	C
ATOM	17740	CZ	PHE	D	69.3	8.361	40.,022	59. 635	1,00	49,85	C
ATOM	17741	O	MET	D	694	4„394	45..876	58.,807	1,00	59..29	0
ATOM	17742	N	MET	D	694	3„510	42..464	58.,848	1,00	54.29	N
ATOM	17743	CA	MET	D	694	3.925	4.3.,651	58. 098	1,00	56,11	C
ATOM	17744	C	MET	D	694	3,616	44.931	58.,855	1.00	57.96	C
ATOM	17745	CB	MET	D	694	3„251	43..715	56.,720	1,00	56..37	C
ATOM	17746	CG	MET	D	694	4.047	4.3.,118	55..577	1.00	54,77	C
ATOM	17747	SD	MET	D	694	5..593	43,974	55..178	1.00	64.34	S
ATOM	17748	CE	MET	D	694	6„773	43. 050	56.,126	1,00	58..55	C
ATOM	17749	O	GLN	D	695	3..434	47,384	61..909	1.00	61,78	0
ATOM	17750	N	GLN	D	695	2.482	44,974	59..546	1,00	53,.31	N
ATOM	17751	CA.	GLN	D	695	2„154	46. 178	60.,300	1,00	59..99	C
ATOM	17752	C	GLN	D	695	2,995	46..289	61.,565	1,00	58..91	C
ATOM	17753	CB	GLN	D	695	0..656	46.,230	60..635	1,00	60,.47	C
ATOM	17754	CG	GLN	D	695	-0„224	46..562	59.,441	1,00	56..2.3	C
ATOM	17755	CD	GLN	D	695	-1,695	46..403	59.,763	1,00	62.52	C
ATOM	17756	OE1	GLN	D	695	-2.071	45,542	60. 553	1,00	59,62	0
ATOM	17757	NE2	GLN	D	695	-2„535	47.248	59.,166	1,00	58..50	N
ATOM	17758	O	LEU	D	696	5„992	46..305	64.,288	1,00	60..97	0
ATOM	17759	N	LEU	D	696	3.235	45,165	62. 238	1,00	51,85	N
ATOM	17760	CA	LEU	D	696	4,008	45.,167	63.,488	1.00	57.39	C
ATOM	17761	C	LEU	D	696	5„454	45..685	63.,354	1,00	63..79	C
ATOM	17762	CB	LEU	D	696	4.048	4.3.,761	64..086	1.00	52,54	C
ATOM	17763	CG	LEU	D	696	2.761	43,092	64..556	1.00	62.51	C
ATOM	17764	CD1	LEU	D	696	.3.,038	41.627	64.,955	1,00	58..47	C

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ATOM  17765  CD2  LEU  D  696      2.113   43.879   65.709   1.00  58.69        C
ATOM  17766  O    ILE  D  697      8.787   47.570   61.042   1.00  62.31        O
ATOM  17767  N    ILE  D  697      6.093   45.425   62.211   1.00  63.64        N
ATOM  17768  CA   ILE  D  697      7.493   45.822   62.039   1.00  58.59        C
ATOM  17769  C    ILE  D  697      7.663   47.160   61.318   I.00  61.58        C
ATOM  17770  CB   ILE  D  697      8.293   44.755   61.266   1.00  61.54        C
ATOM  17771  CGI  ILE  D  697      7.817   44.665   59.812   1.00  55.91        C
ATOM  17772  CG2  ILE  D  697      8.210   43.415   61.970   I.00  55.50        C
ATOM  17773  GDI  ILE  D  697      8.455   43.557   59.042   1.00  61.67        C
ATOM  17774  O    HIS  D  698      6.092   51.412   61.179   1.00  62.89        0
ATOM  17775  N    HIS  D  698      6.554   47.829   61.007   I.00  59.46        N
ATOM  17776  CA   HIS  D  698      6.602   49.179   60.447   1.00  62.72        C
ATOM  17777  C    HIS  D  698      6.030   50.207   61.417   1.00  60.73        C
ATOM  17778  CB   HIS  D  698      5.828   49.255   59.123   1.00  63.65        C
ATOM  17779  CG   HIS  D  698      6.578   48.707   57.947   1.00  62.80        C
ATOM  17780  ND1  HIS  D  698      6.554   47.374   57.602   1.00  60.63        N
ATOM  17781  CD2  HIS  D  698      7.373   49.316   57.035   1.00  64.50        C
ATOM  17782  CE1  HIS  D  698      7.303   47.181   56.533   I.00  59.74        C
ATOM  17783  NE2  HIS  D  698      7.812   48.344   56.167   1.00  66.66        N
ATOM  17784  O    ASP  D  699      6.502   50.918   64.924   1.00  59.16        0
ATOM  17785  N    ASP  D  699      5.451   49.720   62.503   I.00  61.38        N
ATOM  17786  CA   ASP  D  699      4.681   50.570   63.401   1.00  61.81        C
ATOM  17787  C    ASP  D  699      5.586   51.424   64.276   1.00  60.31        C
ATOM  17788  CB   ASP  D  699      3.763   49.706   64.261   I.00  63.00        C
ATOM  17789  CG   ASP  D  699      2.811   50.519   65.096   1.00  62.73        C
ATOM  17790  OD2  ASP  D  699      2.297   49.974   66.092   1.00  67.44        0
ATOM  17791  OD1  ASP  D  699      2.565   51.696   64.760   I.00  66.71        0
ATOM  17792  O    ASP  D  700      6.840   53.934   67.350   1.00  66.00        0
ATOM  17793  N    ASP  D  700      5.328   52.727   64.305   1.00  62.01        N
ATOM  17794  CA   ASP  D  700      6.196   53.626   65.063   1.00  59.06        C
ATOM  17795  C    ASP  D  700      5.961   53.571   66.580   1.00  58.92        C
ATOM  17796  CB   ASP  D  700      6.048   55.050   64.540   1.00  63.65        C
ATOM  17797  CG   ASP  D  700      6.822   55.274   63.241   1.00  67.55        C
ATOM  17798  OD2  ASP  D  700      6.319   56.001   62.352   I.00  66.33        0
ATOM  17799  OD1  ASP  D  700      7.942   54.725   63.118   1.00  57.64        0
ATOM  17800  N    SER  D  701      4.796   53.087   66.999   1.00  64.87        N
ATOM  17801  CA.  SER  D  701      4.479   52.894   68.414   I.00  61.32        C
ATOM  17802  C    SER  D  701      5.041   51.576   68.949   1.00  56.69        C
ATOM  17803  O    SER  D  701      4.934   51.262   70.130   1.00  58.38        0
ATOM  17804  CB   SER  D  701      2.965   52.931   68.617   I.00  62.79        C
ATOM  17805  OG   SER  D  701      2.362   51.785   68.049   1.00  60.45        0
ATOM  17806  N    LEU  D  702      5.633   50.787   68.072   1.00  61.59        N
ATOM  17807  CA   LEU  D  702      6.305   49.576   68.531   1.00  58.95        C
ATOM  17808  C    LEU  D  702      7.815   49.696   68.327   1.00  58.57        C
ATOM  17809  O    LEU  D  702      8.276   50.471   67.480   1.00  59.60        0
ATOM  17810  CB   LEU  D  702      5.745   48.371   67.805   1.00  58.27        C
ATOM  17811  CG   LEU  D  702      4.281   48.174   68.151   I.00  55.89        C
ATOM  17812  CD1  LEU  D  702      3.686   47.045   67.345   1.00  57.02        C
ATOM  17813  CD2  LEU  D  702      4.193   47.868   69.611   1.00  54.49        C
ATOM  17814  N    TH.R D  703      8.592   48.949   69.103   I.00  56.89        N
ATOM  17815  CA   THR  D  703     10.039   49.055   68.978   1.00  56.54        C
ATOM  17816  C    THR  D  703     10.649   48.067   67.967   1.00  60.94        C
ATOM  17817  0    THR  D  703     11.857   48.138   67.706   I.00  61.11        0
ATOM  17818  CB   THR  D  703     10.746   48.870   70.347   1.00  57.50        C
ATOM  17819  OG1  THR  D  703     10.041   47.909   71.133   1.00  62.20        0
ATOM  17820  CG2  THR  D  703     10.779   50.173   71.098   I.00  53.30        C
ATOM  17821  N    PHE  D  704      9.831   47.180   67.387   1.00  57.32        N
ATOM  17822  CA   PHE  D  704     10.340   46.148   66.458   1.00  63.93        C
ATOM  17823  C    PHE  D  704     11.109   46.770   65.289   1.00  59.84        C
ATOM  17824  O    PHE  D  704     12.246   46.400   65.020   1.00  60.85        0
ATOM  17825  CB   PHE  D  704      9.200   45.269   65.917   1.00  55.35        C
ATOM  17826  CG   PHE  D  704      8.511   44.451   66.973   1.00  55.46        C
ATOM  17827  CD1  PHE  D  704      9.254   43.682   67.871   I.00  52.91        C
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ATOM   17828  CD2  PHE  D  704       7.111   44.471   67.086   1.00  54.68            c
ATOM   17829  CEl  PHE  D  704       8.630   42.934   68.853   1.00  54.25            C
ATOM   17830  CE2  PHE  D  704       6.467   43.726   68.058   1.00  52.72            c
ATOM   17831  CZ   PHE  D  704       7.224   42.955   68.952   1.00  60.32            c
ATOM   17832  N    LYS  D  705      10.468   47.718   64.618   I.00  55.86            N
ATOM   17833  CA   LYS  D  705      11.078   48.540   63.581   1.00  62.29            c
ATOM   17834  c    LYS  D  705      12.476   49.039   63.969   1.00  65.37            c
ATOM   17835  0    LYS  D  705      13.413   49.008   63.165   I.00  66.25            0
ATOM   17836  CB   LYS  D  705      10.157   49.725   63.277   1.00  56.61            c
ATOM   17837  CG   LYS  D  705      10.581   50.631   62.141   1.00  56.12            c
ATOM   17838  CD   LYS  D  705       9.424   51.577   61.787   I.00  55.39            c
ATOM   17839  CE   LYS  D  705       9.910   52.824   61.083   1.00  48.91            c
ATOM   17840  NZ   LYS  D  705       8.866   53.406   60.224   1.00  61.43            N
ATOM   17841  N    GLU  D  706      12.616   49.478   65.211   1.00  63.85            N
ATOM   17842  CA   GLU  D  706      13.892   49.984   65.685   1.00  68.04            C
ATOM   17843  C    GLU  D  706      14.950   48.875   65.856   1.00  64.14            c
ATOM   17844  O    GLU  D  706      16.085   49.032   65.413   1.00  66.86            0
ATOM   17845  CB   GLU  D  706      13.696   50.742   67.005   I.00  56.74            c
ATOM   17846  N    ASP  D  707      14.581   47.774   66.504   1.00  59.83            N
ATOM   17847  CA   ASP  D  707      15.513   46.669   66.731   1.00  67.63            c
ATOM   17848  C    ASP  D  707      15.972   46.035   65.415   I.00  65.61            C
ATOM   17849  O    ASP  D  707      17.117   45.589   65.290   1.00  68.47            O
ATOM   17850  CB   ASP  D  707      14.873   45.606   67.631   1.00  68.14            c
ATOM   17851  CG   ASP  D  707      14.870   46.005   69.099   I.00  68.72            c
ATOM   17852  OD1  ASP  D  707      14.886   47.217   69.374   1.00  67.52            0
ATOM   17853  OD2  ASP  D  707      14.860   45.111   69.978   1.00  76.05            0
ATOM   17854  N    ILE  D  708      15.061   46.002   64.445   I.00  61.78            N
ATOM   17855  CA   ILE  D  708      15.336   45.494   63.102   1.00  62.53            C
ATOM   17856  C    ILE  D  708      16.326   46.378   62.350   1.00  65.03            c
ATOM   17857  O    ILE  D  708      17.308   45.894   61.811   1.00  64.66            0
ATOM   17858  CB   ILE  D  708      14.041   45.372   62.276   1.00  55.32            c
ATOM   17859  CGI  ILE  D  708      13.193   44.209   62.780   1.00  53.12            c
ATOM   17860  CG2  ILE  D  708      14.337   45.166   60.823   1.00  54.14            c
ATOM   17861  CD1  ILE  D  708      11.872   44.067   62.059   I.00  57.52            c
ATOM   17862  N    GLN  D  709      16.075   47.681   62.326   1.00  71.59            N
ATOM   17863  CA   GLN  D  709      16.979   48.605   61.650   1.00  70.11            c
ATOM   17864  C    GLN  D  709      18.324   48.682   62.376   I.00  69.66            C
ATOM   17865  O    GLN  D  709      19.354   48.931   61.758   1.00  72.87            0
ATOM   17866  CB   GLN  D  709      16.341   49.994   61.538   1.00  72.08            c
ATOM   17867  CG   GLN  D  709      17.167   51.007   60.744   I.00  80.82            c
ATOM   17868  CD   GLN  D  709      17.461   50.576   59.300   1.00  88.53            c
ATOM   17869  OE1  GLN  D  709      16.765   49.730   58.724   1.00  89.87            0
ATOM   17870  NE2  GLN  D  709      18.495   51.171   58.709   1.00  88.92            N
ATOM   17871  N    LYS  D  710      18.313   48.449   63.684   1.00  64.14            N
ATOM   17872  CA   LYS  D  710      19.531   48.466   64.462   1.00  59.82            c
ATOM   17873  c    LYS  D  710      20.356   47.206   64.183   1.00  70.33            c
ATOM   17874  O    LYS  D  710      21.543   47.132   64.517   I.00  62.05            0
ATOM   17875  CB   LYS  D  710      19.212   48.574   65.954   1.00  66.68            c
ATOM   17876  N    ALA  D  711      19.720   46.215   63.563   1.00  71.18            N
ATOM   17877  CA.  ALA  D  711      20.348   44.915   63.374   I.00  64.75            C
ATOM   17878  C    ALA  D  711      21.236   44.852   62.122   1.00  67.05            C
ATOM   17879  O    ALA  D  711      22.196   44.090   62.094   1.00  72.26            O
ATOM   17880  CB   ALA  D  711      19.287   43.825   63.332   I.00  67.28            C
ATOM   17881  N    GLN  D  712      20.946   45.644   61.096   1.00  62.50            N
ATOM   17882  CA   GLN  D  712      21.862   45.689   59.967   1.00  68.02            C
ATOM   17883  C    GLN  D  712      23.090   46.555   60.274   I.00  66.76            C
ATOM   17884  O    GLN  D  712      24.165   46.357   59.698   1.00  75.23            0
ATOM   17885  CB   GLN  D  712      21.149   46.193   58.715   1.00  74.61            c
ATOM   17886  CG   GLN  D  712      20.146   45.203   58.133   1.00  72.96            c
ATOM   17887  CD   GLN  D  712      18.771   45.371   58.722   1.00  68.17            c
ATOM   17888  OE1  GLN  D  712      18.463   46.418   59.289   1.00  76.22            0
ATOM   17889  NE2  GLN  D  712      17.930   44.352   58.588   1.00  61.08            N
ATOM   17890  O    ASP  D  718      33.262   47.863   51.123   I.00103.64            O
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ATOM   17891   N    ASP  D  718       31..856    46..661    53..339    1 .00107..98         N
ATOM   17892   CA   ASP  D  718       32.,921    45..985    52.,601    1 ,00106..92         C
ATOM   17893   C    ASP  D  718       33..200    46.,635    51..233    1 ,00103,.34         C
ATOM   17894   CB   ASP  D  718       32..583    44 ,499    52.,426    1 .00106..30         C
ATOM   17895   CG   ASP  D  718       3.1.,257   44 .272    51 ,715    1 ,00106.,45         C
ATOM   17896   OD2  ASP  D  718       31..262    44 ,145    50..469    1 ,00101,.66         0
ATOM   17897   OD1  ASP  D  718       30..215    44 ,209    52..403    1 ,00104,.81         0
ATOM   17898   N    SER  D  719       33.,375    45. 811    50.,199    1 ,00  98.,84        N
ATOM   17899   CA   SEP. D  719       33..780    46..309    48.,882    1 ,00  95..58        C
ATOM   17900   C    SER  D  719       32..725    46.,109    47 .798    1 ,00  88,.33        C
ATOM   17901   0    SER  D  719       31.,857    45..234    47 ,899    I ,00  86..63        0
ATOM   17902   CB   SER  D  719       35..087    45..638    48.,433    1 ,00  95..23        C
ATOM   17903   OG   SER  D  719       35. 387     45 ,937    47 .077    1 ,00  89 ,71        0
ATOM   17904   N    LEU  D  720       32..821    46.,941    46.,764    1 .00  84 .27        N
ATOM   17905   CA   LEU  D  720       32.,018    46..802    45.,556    1 ,00  76..84        C
ATOM   17906   C    LEU  D  720       32..165    45.,394    44 .997    1 ,00  79,.89        C
ATOM   17907   O    LEU  D  720       31..197    44 ,621    44 ,948    1 .00  70..16        0
ATOM   17908   CB   LEU  D  720       32.,452    47 .826    44 ,512    1 ,00  68.,86        C
ATOM   17909   CG   LEU  D  720       31..704    47 ,795    43..186    1 ,00  6.3,.97        C
ATOM   17910   CD1  LEU  D  720       30..223    47 ,877    43.. 472   1 ,00  59,.09        C
ATOM   17911   CD2  LEU  D  720       32.,156    48. 931    42.,267    1 ,00  58.,04        C
ATOM   17912   N    HIS  D  721       33..400    45.,078    44 ,599    1 ,00  80..94        N
ATOM   17913   CA   HIS  D  721       33..745    43.,785    44 .025    1 ,00  80,.24        C
ATOM   17914   C    HIS  D  721       .3.3.,231  42 .680    44 ,914    I ,00  78..39        C
ATOM   17915   O    HIS  D  721       32..678    41 ,691    44 ,436    1 ,00  72 .55        0
ATOM   17916   CB   HIS  D  721       35. 254    43.,658    43. 833    1 ,00  85 ,26        C
ATOM   17917   CG   HIS  D  721       35.,805    44 .564    42.,776    I ,00  87 .90        C
ATOM   17918   ND1  HIS  D  721       35.,528    45..914    42.,731    1 ,00  88..91        N
ATOM   17919   CD2  HIS  D  721       36. 622    44 ,314    41 .726    1 ,00  87 ,13        C
ATOM   17920   CE1  HIS  D  721       36.,147    46.,454    41 ,695    1 .00  87 .66        C
ATOM   17921   NE2  HIS  D  721       36.,818    45..505    41 ,070    1 ,00  85..03        N
ATOM   17922   N    GLU  D  722       33...385    42.,872    46..218    1 ,00  81 ,12        N
ATOM   17923   CA   GLU  D  722       32..868    41 ,910    47 .177    1 .00  84 .05        C
ATOM   17924   C    GLU  D  722       3.1.,346   41 .807    47 ,076    1 ,00  80.,93        C
ATOM   17925   O    GLU  D  722       30..834    40.,730    46..802    1 ,00  78,.05        0
ATOM   17926   CB   GLU  D  722       33..298    42.,274    48..602    1 ,00  91 ,19        C
ATOM   17927   CG   GLU  D  722       34.,776    41 .989    48.,889    1 ,00  93.,57        C
ATOM   17928   CD   GLU  D  722       35.,037    41 ,623    50.,346    1 ,00  98..54        C
ATOM   17929   OE1  GLU  D  722       34. 426    42.,245    51. 241    1 ,00106,.59         0
ATOM   17930   OE2  GLU  D  722       35.,845    40..704    50.,598    I ,00  95..90        0
ATOM   17931   N    HIS  D  723       30.,638    42..923    47 ,262    1 ,00  81 .03        N
ATOM   17932   CA   HIS  D  723       29. 170    42.,917    47 .251    1 ,00  82 ,36        C
ATOM   17933   C    HIS  D  723       28..579    42.,171    46.,056    1 .00  78..49        C
ATOM   17934   O    HIS  D  723       27.,683    41 .334    46.,219    1 ,00  75..25        0
ATOM   17935   CB   HIS  D  723       28..604    44 ,347    47 .264    1 ,00  74 ,38        C
ATOM   17936   CG   HIS  D  723       27..119    44 ,398    47 .058    1 .00  74 .67        C
ATOM   17937   ND1  HIS  D  723       26.,219    44 .037    48.,035    1 ,00  79.,3.1       N
ATOM   17938   CD2  HIS  D  723       26...377    44 ,740    45..977    1 ,00  80,.76        C
ATOM   17939   CE1  HIS  D  723       24 .988    44 ,169    47 .574    1 ,00  80,.09        C
ATOM   17940   NE2  HIS  D  723       25 ,055    44 .593    46.,325    1 ,00  78.,10        N
ATOM   17941   N    ILE  D  724       29.,098    42.,479    44 ,866    1 ,00  75..01        N
ATOM   17942   CA   ILE  D  724       28..529    41 ,990    43..615    1 ,00  73,.26        C
ATOM   17943   C    ILE  D  724       28..758    40..485    4.3.,451   I ,00  76..24        C
ATOM   17944   O    ILE  D  724       27.,898    39.,763    42..937    1 ,00  74 .99        0
ATOM   17945   CB   ILE  D  724       29. 108    42.,762    42 .389    1 ,00  68 ,92        C
ATOM   17946   CGI  ILE  D  724       28.,616    44 .219    42.,386    I ,00  67 .22        C
ATOM   17947   CG2  ILE  D  724       28.,698    42..107    41 ,085    1 ,00  63..49        C
ATOM   17948   GD1  ILE  D  724       29. 114    45 ,046    41 .211    1 ,00  51 ,92        C
ATOM   17949   N    ALA  D  725       29..904    40 ,003    43..913    1 .00  77 .22        N
ATOM   17950   CA   ALA  D  725       30.,272    38..613    43.,680    1 ,00  75..52        C
ATOM   17951   C    ALA  D  725       29...324    .37.,654   44 .401    1 ,00  77 ,91        C
ATOM   17952   O    ALA  D  725       28..800    36 ,725    43..791    1 .00  77 .29        O
ATOM   17953   CB   ALA  D  725       3.1.,707   38. 373    44 ,105    1 ,00  68.,57        C
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ATOM  17954  N    ASN D 726      29..075  37..883  45..686  1.00 77.33       N
ATOM  17955  CA   ASM D 726      28,,209  36..961  46..416  1,00 83..32      C
ATOM  17956  C    ASN D 726      26..750  .37.,379 46...321 1,00 77,94       C
ATOM  17957  O    ASN D 726      25..906  36,880   47.064   1.00 77.54       0
ATOM  17958  CB   ASN D 726      28.,640  36. 824  47,883   1,00 82.51       C
ATOM  17959  CG   ASN D 726      29..333  .38.,062 48..405  1,00 85,,97      C
ATOM  17960  OD1  ASN D 726      29..181  39.,143  47.844   1,00 85,.08      0
ATOM  17961  ND2  ASN D 726      30.,101  37. 912  49.,486  1,00 87.16       N
ATOM  17962  O    LEU D 727      25..189  36.,697  43,430   1,00 82.88       0
ATOM  17963  N    LEU D 727      26..459  38.,294  45..403  1,00 76,83       N
ATOM  17964  CA   LEU D 727      25.,081  38..493  44,988   I,00 80..96      C
ATOM  17965  C    LEU D 727      24..608  37..186  44,403   1,00 84.57       C
ATOM  17966  CB   LEU D 727      24.936   39.,594  43. 946   1,00 76,19       C
ATOM  17967  CG   LEU D 727      25..231  41,030   44,345   1.00 80..75      C
ATOM  17968  CD2  LEU D 727      24.,445  41.405   45.,589  1,00 84.56       C
ATOM  17969  CD1  LEU D 727      24..926  41,963   43..179  1,00 73,.25      C
ATOM  17970  O    ALA D 728      22..202  36,715   42..608  1.00 82.21       0
ATOM  17971  N    ALA D 728      23.,574  36. 610  45,002   1,00 87.00       N
ATOM  17972  CA   ALA D 728      22..981  .35.,401 44.459   1,00 82,87       C
ATOM  17973  c    ALA D 728      22.656   35.,637  42..981  1,00 81,20       C
ATOM  17974  CB   ALA D 728      21.,741  35. 013  45,250   1,00 75..70      C
ATOM  17975  O    GLY D 729      24..858  33.,590  40,639   1,00 64.95       0
ATOM  17976  N    GLY D 729      22.932   34.,634  42..151  1,00 82,49       N
ATOM  17977  CA   GLY D 729      22.,744  34..717  40.,712  I,00 72.97       C
ATOM  17978  C    GLY D 729      23..893  34..026  39.,996  1,00 66..43      C
ATOM  17979  O    SER D 730      25. 612  .35.,726 37. 624   1,00 56,05       O
ATOM  17980  N    SER D 730      23.,783  33..908  .38.,673 I,00 60..78      N
ATOM  17981  CA   SER D 730      24.,882  33..431  37.,831  1,00 54.68       C
ATOM  17982  C    SER D 730      25. 936  .34.,527 37. 627   1,00 60,52       C
ATOM  17983  CB   SER D 730      24..351  32.,976  36.,483  1.00 55..89      C
ATOM  17984  OG   SER D 730      23.,422  33..934  36.,000  1,00 68..36      0
ATOM  17985  O    PRO D 731      28..842  .36.,821 35..759  1,00 59,.30      0
ATOM  17986  N    PRO D 731      27..206  34.,122  37..455  1.00 58..74      N
ATOM  17987  CA.  PRO D 731      28.,285  35. 104  .37.,324 1,00 50..79      C
ATOM  17988  C    PRO D 731      28..220  .35.,784 35..964  1,00 52,88       C
ATOM  17989  CB   PRO D 731      29..558  34.,254  37.478   1,00 53,.26      C
ATOM  17990  CG   PRO D 731      29.,096  32. 978  .38.,134 1,00 48..52      C
ATOM  17991  CD   PRO D 731      27.,737  32.,753  37.,543  1,00 55..78      C
ATOM  17992  O    ALA D 732      27.108   .38.,004 32. 932   1,00 61,92       0
ATOM  17993  N    ALA D 732      27.,453  35..195  .35.,055 I,00 46..23      N
ATOM  17994  CA   ALA D 732      27.,250  35..754  33.,738  1,00 52..70      C
ATOM  17995  C    ALA D 732      26. 738  .37.,214 33. 780   1,00 55,32       C
ATOM  17996  CB   ALA D 732      26.,289  34.,879  32.,950  1.00 48..35      C
ATOM  17997  O    ILE D 733      26.,059  41.132   35.,461  1,00 62.95       0
ATOM  17998  N    ILE D 733      25.917   .37.,586 34..757  1,00 57,20       N
ATOM  17999  CA   ILE D 733      25..361  38.,956  34..767  1.00 57.57       C
ATOM  18000  C    ILE D 733      26.,189  39. 920  .35.,597 1,00 54.52       C
ATOM  18001  CB   ILE D 733      23..905  .39.,006 35...303 1,00 57,16       C
ATOM  18002  CGI  ILE D 733      23..873  38.,744  36..812  1,00 60,.50      C
ATOM  18003  CG2  ILE D 733      23.,015  38. 038  .34.,558 1,00 57.25       C
ATOM  18004  CD1  ILE D 733      22.,482  38.,771  37.,395  1,00 57.09       C
ATOM  18005  O    LYS D 734      28..961  42.,295  37.246   1,00 59,.02      0
ATOM  18006  N    LYS D 734      27.,044  39..380  .36.,451 I,00 59..04      N
ATOM  18007  CA   LYS D 734      27.,819  40..198  37.,384  1,00 63..02      C
ATOM  18008  C    LYS D 734      28. 658  41,255   36. 670   1,00 58,03       C
ATOM  18009  CB   LYS D 734      28.,726  39..306  .38.,262 I,00 49.66       C
ATOM  18010  N    LYS D 735      29.,019  40..983  35.,417  1,00 56..73      N
ATOM  18011  CA   LYS D 735      29. 877  41,861   34. 614   1,00 52,14       C
ATOM  18012  c    LYS D 735      29.,133  43,111   34.,105  1.00 56..86      C
ATOM  18013  O    LYS D 735      29.,732  44.174   33.,911  1,00 50..76      0
ATOM  18014  CB   LYS D 735      30..447  41,079   33..437  1,00 47,72       C
ATOM  18015  CG   LYS D 735      31..316  41,867   32..470  1.00 50..07      C
ATOM  18016  CD   LYS D 735      31.,568  41.055   .31.,169 1,00 44.07       C
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ATOM   18017   CE   LYS  D  735      32..830   41,510   30.,487   1.00  47.58        C
ATOM   18018   NZ   LYS  D  735      32.,948   41.047   29.,089   1,00  39..67       N
ATOM   18019   N    GLY  D  7.36     27.832    42.,976  33..876   1,00  52,29        N
ATOM   18020   CA   GLY  D  736      27..027   44,102   33.,451   1.00  46..13       C
ATOM   18021   C    GLY  D  736      26.,893   45. 080  .34.,599  1,00  50..47       C
ATOM   18022   O    GLY  D  7.36     27.248    46.,237  34..485   1,00  53,.45       O
ATOM   18023   N    ILE  D  737      26..379   44,586   35..710   1,00  51,00        N
ATOM   18024   CA.  ILE  D  737      26.,307   45. .333 36,941    1,00  51.25        C
ATOM   18025   C    ILE  D  737      27..560   46.,150  37.,227   1,00  52.57        C
ATOM   18026   O    ILE  D  737      27.488    47,366   37.404    1,00  50,.71       O
ATOM   18027   CB   ILE  D  737      26.,057   44..387  .38.,108  I,00  51.04        C
ATOM   18028   CGI  ILE  D  737      24..777   43.,593  37.,844   1,00  55..80       C
ATOM   18029   CG2  ILE  D  7.37     25. 966   45,169   39. 405   1,00  56,93        C
ATOM   18030   CD1  ILE  D  737      24..621   42.,360  38.,700   1.00  58..73       C
ATOM   18031   N    LEU  D  738      28.,700   45..469  37.,239   1,00  49..25       N
ATOM   18032   CA   LEU  D  7.38     29..982   46.,059  37..608   1,00  48,.60       C
ATOM   18033   C    LEU  D  738      30..476   47,129   36.,639   1.00  47.73        C
ATOM   18034   O    LEU  D  738      31,068    48. 119  .37.,054  1,00  50..87       0
ATOM   18035   CB   LEU  D  7.38     31..055   44,961   37..723   1,00  50,.80       C
ATOM   18036   CG   LEU  D  738      32..455   45.,468  38..057   1,00  52,38        C
ATOM   18037   CD1  LEU  D  738      .32.,410  46. 167  39,415    1,00  53..18       C
ATOM   18038   CD2  LEU  D  738      33..523   44,365   38.,052   1,00  60..92       C
ATOM   18039   N    GLN  D  739      30..287   46.,924  35..346   1,00  47,25        N
ATOM   18040   CA   GLN  D  739      .30.,748  47.908   .34.,384  I,00  46..78       C
ATOM   18041   C    GLN  D  739      29..885   49.,189  34.,467   1,00  51.79        C
ATOM   18042   O    GLN  D  7.39     30. .363  50.,296  34. 176   1,00  44,93        O
ATOM   18043   CB   GLN  D  739      .30.,725  47.332   .32.,965  I,00  48..55       C
ATOM   18044   CG   GLN  D  739      31.,669   46..124  32.,758   1,00  47.58        C
ATOM   18045   CD   GLN  D  7.39     33. 128   46.,518  32. 718   1,00  51,17        C
ATOM   18046   OE1  GLN  D  739      33..565   47,223   31.,816   1.00  53..75       0
ATOM   18047   NE2  GLN  D  739      33.,890   46..072  33.,705   1,00  55..97       N
ATOM   18048   N    THR  D  740      28..623   49.,031  34..856   1,00  45,.75       N
ATOM   18049   CA   THR  D  740      27..734   50.,175  34.,955   1.00  46..35       C
ATOM   18050   C    THR  D  740      28.,200   51. 116  36,049    1,00  47.97        C
ATOM   18051   O    THR  D  740      28..462   52.,297  35..804   1,00  46,.30       O
ATOM   18052   CB   THR  D  740      26..306   49.,768  35..256   1,00  47,20        C
ATOM   18053   OG1  THR  D  740      25,821    48. 906  .34.,219  1,00  44.98        0
ATOM   18054   CG2  THR  D  740      25..446   51.,017  35.,351   1,00  47.74        C
ATOM   18055   N    VAL  D  741      28. .318  50.,566  37. 253   1,00  49,41        N
ATOM   18056   CA   VAL  D  741      28.,833   51..286  .38.,405  I,00  45..40       C
ATOM   18057   C    VAL  D  741      30.,185   51..919  38.,089   1,00  49..78       C
ATOM   18058   O    VAL  D  741      30. 463   53.,031  38. 527   1,00  55,41        O
ATOM   18059   CB   VAL  D  741      28..954   50.,368  39.,619   1.00  47.18        C
ATOM   18060   CGI  VAL  D  741      29.,525   51..121  40.,789   1,00  50..01       C
ATOM   18061   CG2  VAL  D  741      27.606    49.,776  39.962    1,00  46,.88       C
ATOM   18062   N    LYS  D  742      31..017   51.,247  37.,298   1.00  48..93       N
ATOM   18063   CA.  LYS  D  742      .32.,318  51. 834  36,995    1,00  49..63       C
ATOM   18064   C    LYS  D  742      32..180   53.,005  36..043   1,00  47,44        C
ATOM   18065   O    LYS  D  742      32..957   53.,952  36..122   1,00  49,.58       O
ATOM   18066   CB   LYS  D  742      .33.,307  50. 791  36,432    1,00  49..13       C
ATOM   18067   CG   LYS  D  742      33..737   49.,757  37.,494   1,00  52.39        C
ATOM   18068   CD   LYS  D  742      34..888   48.,792  37.097    1,00  61,69        C
ATOM   18069   CE   LYS  D  742      .35.,515  49.079   .35.,734  I,00  57.40        C
ATOM   18070   NZ   LYS  D  742      36.694    48.,210  35.,518   1,00  69..04       N
ATOM   18071   N    VAL  D  743      31. 205   52.,939  35. 141   1,00  47,56        N
ATOM   18072   CA   VAL  D  743      .30.,893  54..068  .34.,283  I,00  45..38       C
ATOM   18073   C    VAL  D  743      30.,469   55..262  35.,153   1,00  50..77       C
ATOM   18074   O    VAL  D  743      30. 957   56.,372  35. 001   1,00  45,73        O
ATOM   18075   CB   VAL  D  743      29.,752   53.,768  33.,291   1.00  47.74        C
ATOM   18076   CGI  VAL  D  743      29.,145   55..101  32.,772   1,00  43..88       C
ATOM   18077   CG2  VAL  D  743      30..245   52.,928  32..147   1,00  43,.61       C
ATOM   18078   N    VAL  D  744      29.,566   55.,003  36.,080   1.00  46..31       N
ATOM   18079   CA.  VAL  D  744      29.,021   56. 064  36,869    1,00  48..97       C
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ATOM    18080   C     VAL  D  744        30..118    56..717    37..680    1 .00  52 .41          C
ATOM    18081   O     VAL  D  744        30,,265    57..944    37.,663    1 ,00  48..09          O
ATOM    18082   CB    VAL  D  744        27 .919    55.,565    37.. 774   1 ,00  47 ,56          C
ATOM    18083   CGI   VAL  D  744        27..543    56.,663    38.,745    1 .00  47 .82          C
ATOM    18084   CG2   VAL  D  744        26.,738    55. 125    3 6 ,918   1 ,00  46..07          C
ATOM    18085   N     ASP  D  745        30..922    55.,891    38.. .34 6 1 ,00  56,.35          N
ATOM    18086   CA    ASP  D  745        32..014    56.,407    39.. 172   1 ,00  50,.69          C
ATOM    18087   C     ASP  D  745        33.,005    57. 224    .38.,344   1 ,00  54 .90          C
ATOM    18088   O     ASP  D  745        33..516    58.,225    38.,832    1 ,00  63..27          0
ATOM    18089   CB    ASP  D  745        32..735    55.,271    39.. 906   1 ,00  53,.67          C
ATOM    18090   CG    ASP  D  745        31.,940    54..751    41 ,118    1 ,00  65..49          C
ATOM    18091   OD1   ASP  D  745        30..924    55..385    41 ,497    1 ,00  67 .85          0
ATOM    18092   OD2   ASP  D  745        32 .334    53.,711    41 .699    1 ,00  70 ,40          0
ATOM    18093   N     GLU  D  746        33..257    56.,841    37.,091    1 .00  46..53          N
ATOM    18094   CA    GLU  D  746        34.,107    57..680    36.,24 3   1 ,00  48..24          C
ATOM    180 95  C     GLU  D  746        33..453    59 ,061    35.. 992   1 ,00  54 ,09          C
ATOM    18096   O     GLU  D  746        34..107    60.,090    36.,088    1 .00  61 .00          0
ATOM    180 97  CB    GLU  D  746        34.,409    56. 987    .34.,920   1 ,00  44 .94          C
ATOM    18098   CG    GLU  D  746        35..279    57.,766    33.. 918   1 ,00  44 ,08          C
ATOM    18099   CD    GLU  D  746        36..393    56.,902    33.. 293   1 ,00  53,.59          C
ATOM    18100   OE1   GLU  D  746        36.,509    56. 846    .32.,044   1 ,00  51 .48          0
ATOM    18101   OE2   GLU  D  746        37..169    56.,289    34.,064    1 ,00  52 .31          0
ATOM    18102   N     LEU  D  747        32..164    59.,063    35.. 679   1 ,00  47 ,29          N
ATOM    18103   CA    LEU  D  747        31.,471    60.. 255   .35.,247   1 ,00  53..70          C
ATOM    18104   C     LEU  D  747        31..491    61.,290    36 ,375    1 ,00  59..84          C
ATOM    18105   O     LEU  D  747        31. 739    62.,474    36. 152    1 ,00  55 ,82          0
ATOM    18106   CB    LEU  D  747        30.,037    59 .912    .34.,826   1 ,00  45..81          C
ATOM    18107   CG    LEU  D  747        29.,950    59.. 088   33.,544    1 ,00  46..85          C
ATOM    18108   CD1   LEU  D  747        28. 509    58.,781    33. 169    1 ,00  44 ,80          C
ATOM    18109   CD2   LEU  D  747        30..676    59.,791    32.,419    1 .00  50..38          C
ATOM    18110   N     VAL  D  748        31.,274    60.. 801   37.,589    1 ,00  58..63          N
ATOM    18111   CA    VAL  D  748        31...335   61.,607    38.. 785   1 ,00  54 ,73          C
ATOM    18112   C     VAL  D  748        32..693    62.,274    38.,977    1 .00  60..58          C
ATOM    18113   0     VAL  D  748        32.,755    63. 385    3 9 ,500   1 ,00  67 .95          0
ATOM    18114   CB    VAL  D  748        30..990    60.,761    40.. 002   1 ,00  55,.36          C
ATOM    18115   CGI   VAL  D  748        31..067    61.,582    41 .276    1 ,00  63,.39          C
ATOM    18116   CG2   VAL  D  748        29.,603    60. 183    3 9 ,829   1 ,00  52 .69          C
ATOM    18117   N     LYS  D  749        33.,771    61.,629    38.,535    1 ,00  59..82          N
ATOM    18118   CA    LYS  D  749        35. 116    62.,222    38. 641    1 ,00  62 ,52          C
ATOM    18119   C     LYS  D  749        35.,338    63.. 217   .37.,523   1 ,00  61 .65          C
ATOM    18120   O     LYS  D  749        36.,141    64.. 141   37.,645    1 ,00  67 .83          0
ATOM    18121   CB    LYS  D  749        36. 237    61.,169    38. 574    1 ,00  63 ,75          C
ATOM    18122   CG    LYS  D  749        36.,302    60.,154    39.,698    1 .00  66..80          C
ATOM    18123   CD    LYS  D  749        37.,626    59.. 381   39.,657    1 ,00  64 .14          C
ATOM    18124   CE    LYS  D  749        37..948    58.,811    38.. 262   1 ,00  68,.40          C
ATOM    18125   NZ    LYS  D  749        37..272    57.,502    37.,926    1 .00  62 .56          N
ATOM    1812 6  N     VAL  D  750        34.,663    62. 995    3 6 ,407   1 ,00  58..52          N
ATOM    18127   CA    VAL  D  750        34..761    63.,917    35.. 286   1 ,00  6.3,.77         C
ATOM    18128   C     VAL  D  750        34..009    65.,216    35.. 631   1 ,00  62 ,57          C
ATOM    1812 9  0     VAL  D  750        34.,378    66. 294    .35.,176   1 ,00  62 .68          0
ATOM    18130   CB    VAL  D  750        34.,212    63.,275    33.,993    1 ,00  62 .60          C
ATOM    18131   CGI   VAL  D  750        34..293    64.,24 6   32.. 810   1 ,00  57 ,84          C
ATOM    18132   CG2   VAL  D  750        34.,976    61.. 991   .3.3.,687  1 ,00  51 .92          C
ATOM    18133   O     MET  D  751        31.,959    66.,812    39.,286    1 ,00  71 .54          0
ATOM    18134   N     MET  D  751        32. 976    65.,094    36. 462    1 ,00  60 ,05          N
ATOM    18135   CA    MET  D  751        32.,244    66.. 246   3 6 ,969   1 ,00  63..55          C
ATOM    18136   C     MET  D  751        32.,750    66.. 659   38.,351    1 ,00  68..41          C
ATOM    18137   CB    MET  D  751        30. 745    65.,947    37. 041    1 ,00  63 ,49          C
ATOM    18138   CG    MET  D  751        30.,128    65.,392    35.,773    1 .00  63..29          C
ATOM    18139   SD    MET  D  751        29.,589    66.. 623   34.,581    1 ,00  65..71          S
ATOM    18140   CE    MET  D  751        31..114    66.,985    33.. 737   1 ,00  58,.90          C
ATOM    18141   O     GLY  D  752        34..158    67.,474    41 ,989    1 .00  78..89          0
ATOM    18142   N     GLY  D  752        34.,066    66. 807    .38.,478   1 ,00  63...30         N
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ATOM  18143  CA   GLY  D 752    34.686  67:360  39:668  1.00  62.13   C
ATOM  18144  C    GLY  D 752    34,222  66.768  40,983  1,00  72.40   C
ATOM  18145  O    AP.G D 753    31.726  64,893  43.804  1,00  71,42   0
ATOM  18146  N    ARG  D 753    33.900  65:475  40:972  1.00  72.42   N
ATOM  18147  CA.  ARG  D 753    33,455  64.744  42,166  1,00  72.24   C
ATOM  18148  C    ARG  D 753    32.077  65,169  42.667  1,00  69,00   C
ATOM  18149  CB   ARG  D 753    34.465  64,882  43.313  1,00  74,58   C
ATOM  18150  CG   ARG  D 753    35,369  63.679  43,516  1,00  77.55   C
ATOM  18151  CD   ARG  D 753    36.702  63:854  42:810  1,00  72.81   C
ATOM  18152  NE   ARG  D 753    37.461  62,611  42.799  1,00  79,02   N
ATOM  18153  CZ   ARG  D 753    38,607  62.438  42,148  I,00  82.11   C
ATOM  18154  NH1  ARG  D 753    39.131  63:441  41:454  1,00  78.31   N
ATOM  18155  NH2  ARG  D 753    39.227  61,262  42.191  1,00  79,09   N
ATOM  18156  O    HIS  D 754    28.984  64:443  40:856  1.00  70.75   O
ATOM  18157  N    HI S D 754    31,285  65.822  41,827  1,00  70.20   N
ATOM  18158  CA   HIS  D 754    29.924  66,157  42.229  1,00  73,15   C
ATOM  18159  C    HIS  D 754    28.985  64:990  41,953  1.00  69.35   C
ATOM  18160  CB   HI S D 754    29,420  67.406  41,495  1,00  75,39   C
ATOM  18161  CG   HIS  D 754    30.280  68,616  41.688  1,00  78,82   C
ATOM  18162  ND1  HIS  D 754    30:172  69,737  40.891  1,00  84,38   N
ATOM  18163  CD2  HI S D 754    31,260  68.883  42,585  1,00  76.14   C
ATOM  18164  CE1  HI S D 754    31:047  70:644  41:292  1,00  88.60   C
ATOM  18165  NE2  HIS  D 754    31.723  70,148  42.314  1,00  81,12   N
ATOM  18166  O    LYS  D 755    26,113  65.611  41,517  I,00  66.60   O
ATOM  18167  N    LYS  D 755    28:195  64:600  42:946  1,00  64.91   N
ATOM  18168  CA   LYS  D 755    27.045  63,742  42.694  1,00  64,03   C
ATOM  18169  C    LYS  D 755    26,125  64.392  41,653  I,00  64.69   C
ATOM  18170  CB   LYS  D 755    26,266  63.482  43,980  1,00  59.68   C
ATOM  18171  CG   LYS  D 755    27.080  62,848  45.074  1,00  64,43   C
ATOM  18172  CD   LYS  D 755    26:371  61:646  45:631  1.00  63.52   C
ATOM  18173  CE   LYS  D 755    26,885  61.303  46,995  1,00  64.02   C
ATOM  18174  NZ   LYS  D 755    26.501  62,393  47.925  1,00  67,46   N
ATOM  18175  0    PRO  D 756    22:805  63:919  41:785  1.00  62.40   O
ATOM  18176  N    PRO  D 756    25,372  63.573  40,901  1,00  62.46   N
ATOM  18177  CA   PRO  D 756    24..339 64,042  39.966  1,00  63,92   C
ATOM  18178  C    PRO  D 756    23.012  64,384  40.666  1,00  60,19   C
ATOM  18179  CB   PRO  D 756    24,152  62.843  39,036  1,00  56.26   C
ATOM  18180  CG   PRO  D 756    24:429  61:673  39:918  1,00  61.64   C
ATOM  18181  CD   PRO  D 756    25.567  62,114  40.808  1,00  61,51   C
ATOM  18182  O    GLU  D 757    19,611  63.592  41,631  I,00  59.25   0
ATOM  18183  N    GLU  D 757    22,132  65.153  40,022  1,00  56.51   N
ATOM  18184  CA   GLU  D 757    20.819  65,429  40.609  1,00  61,58   C
ATOM  18185  C    GLU  D 757    20:052  64:108  40:600  1.00  59.25   C
ATOM  18186  CB   GLU  D 757    20,054  66.563  39,848  1,00  66.95   C
ATOM  18187  CG   GLU  D 757    20.070  66,518  38.274  1,00  70,15   C
ATOM  18188  CD   GLU  D 757    19:206  67:613  37:531  1.00  78.92   C
ATOM  18189  OE1  GLU  D 757    18,493  68.413  38,194  1,00  74.31   0
ATOM  18190  OE2  GLU  D 757    19.245  67,661  36.260  1,00  70,44   0
ATOM  18191  N    ASN  D 758    19.927  63,544  39.411  1,00  62,27   N
ATOM  18192  CA.  ASM  D 758    19,256  62.271  39,247  1,00  61.01   C
ATOM  18193  C    ASN  D 758    20:091  61:295  38:418  1,00  51.84   C
ATOM  18194  O    ASN  D 758    20.998  61,691  37.666  1,00  47,37   0
ATOM  18195  CB   ASN  D 758    17,890  62.477  38,577  I,00  63.60   C
ATOM  18196  CG   ASN  D 758    17:175  63:734  39:062  1,00  64.84   C
ATOM  18197  OD1  ASN  D 758    17.426  64,825  38.561  1,00  63,68   0
ATOM  18198  ND2  ASN  D 758    16,278  63.580  40,036  I,00  65.66   N
ATOM  18199  N    ILE  D 759    19,743  60.025  38,546  1,00  52.76   N
ATOM  18200  CA   ILE  D 759    20.279  58,956  37.703  1,00  45,73   C
ATOM  18201  C    ILE  D 759    19,100  58:194  37:126  1.00  46.99   C
ATOM  18202  O    ILE  D 759    18,347  57.561  37,873  1,00  48.26   O
ATOM  18203  CB   ILE  D 759    21.173  57,970  38.495  1,00  49,22   C
ATOM  18204  CGI  ILE  D 759    22:397  58:686  39:075  1.00  45.74   C
ATOM  18205  CG2  ILE  D 759    21,590  56.786  37,601  1,00  43.02   C
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ATOM   18206   GDI  ILE  D  759      22.970   57.989   40.279   1.00  50.04        C
ATOM   18207   N    VAL  D  760      18.911   58.256   35.817   1.00  40.24        N
ATOM   18208   CA   VAL  D  760      17.773   57.553   35.239   1.00  46.00        C
ATOM   18209   C    VAL  D  760      18.188   56.250   34.550   1.00  42.60        C
ATOM   18210   O    VAL  D  760      19.027   56.242   .33.657  I.00  39.29        0
ATOM   18211   CB   VAL  D  760      17.001   58.453   34.216   1.00  44.76        C
ATOM   18212   CGI  VAL  D  760      15.666   57.846   33.915   1.00  44.11        C
ATOM   18213   CG2  VAL  D  760      16.806   59.868   .34.779  I.00  53.56        C
ATOM   18214   N    ILE  D  761      17.563   55.158   34.958   1.00  48.98        N
ATOM   18215   CA   ILE  D  761      17.853   53.856   34.374   1.00  46.55        C
ATOM   18216   C    ILE  D  761      16.658   53.253   .33.641  I.00  48.61        C
ATOM   18217   O    ILE  D  761      15.644   52.923   34.241   1.00  55.49        O
ATOM   18218   CB   ILE  D  761      18..313   52.835   35.445   1.00  48.64        C
ATOM   18219   CGI  ILE  D  761      19.393   53.429   36.350   1.00  47.68        C
ATOM   18220   CG2  ILE  D  761      18.858   51.575   34.777   1.00  45.98        C
ATOM   18221   CD1  ILE  D  761      19.740   52.548   37.542   1.00  49.60        C
ATOM   18222   N    GLU  D  762      16.790   53.070   32.341   1.00  45.90        N
ATOM   18223   CA.  GLU  D  762      15.773   52..340   31.595   I.00  55.25        C
ATOM   18224   C    GLU  D  762      15.581   50.872   32.031   1.00  58.61        C
ATOM   18225   O    GLU  D  762      16.542   50.190   32.418   1.00  56.83        O
ATOM   18226   CB   GLU  D  762      16.113   52..387   .30.109  I.00  51.16        C
ATOM   18227   CG   GLU  D  762      15.043   51.814   29.228   1.00  58.86        C
ATOM   18228   CD   GLU  D  762      15.401   51.906   27.768   1.00  66.48        C
ATOM   18229   OE1  GLU  D  762      16.581   51.659   27.445   I.00  71.15        0
ATOM   18230   OE2  GLU  D  762      14.506   52.228   26.947   1.00  73.75        0
ATOM   18231   O    MET  D  763      12.814   47.415   30.622   1.00  75.85        0
ATOM   18232   N    MET  D  763      14.328   50.411   31.973   I.00  59.26        N
ATOM   18233   CA   MET  D  763      13.972   48.996   32.056   1.00  56.30        C
ATOM   18234   C    MET  D  763      13.455   48.478   30.706   1.00  65.44        C
ATOM   18235   CB   MET  D  763      12.915   48.773   33.124   1.00  59.82        C
ATOM   18236   CG   MET  D  763      12.899   49.845   34.178   1.00  66.70        C
ATOM   18237   SD   MET  D  763      14.216   49.660   35.391   1.00  88.06        S
ATOM   18238   CE   MET  D  763      13.840   48.023   36.048   1.00  78.47        C
ATOM   18239   O    ARG  D  919      18.630   36..376   29.528   I.00  81.88        0
ATOM   18240   N    AP.G D  919      16.635   .34.352   27.266   1.00  88.74        N
ATOM   18241   CA   ARG  D  919      17.122   34.738   28.588   1.00  87.53        C
ATOM   18242   C    ARG  D  919      17.996   35.999   28.538   I.00  85.43        C
ATOM   18243   CB   ARG  D  919      17.892   33.583   29.236   1.00  84.24        C
ATOM   18244   CG   ARG  D  919      19.182   .33.191   28.535   1.00  85.35        C
ATOM   18245   CD   ARG  D  919      19.893   32.098   29.327   I.00  86.97        C
ATOM   18246   NE   ARG  D  919      19.156   30.831   29.326   1.00  82.88        N
ATOM   18247   CZ   ARG  D  919      19.191   29.932   30..312   1.00  79.19        C
ATOM   18248   NHl  ARG  D  919      19.921   30.157   31.401   1.00  74.61        N
ATOM   18249   NH2  ARG  D  919      18.491   28.805   30.213   1.00  75.33        N
ATOM   18250   O    GLN  D  920      18.472   39.490   29.069   1.00  81.35        O
ATOM   18251   N    GLN  D  920      18.015   36.658   27.385   1.00  83.59        N
ATOM   18252   CA.  GLN  D  920      18.723   37.921   27.260   I.00  83.23        C
ATOM   18253   C    GLN  D  920      17.986   39.025   28.035   1.00  84.49        C
ATOM   18254   CB   GLN  D  920      18.888   38.303   25.787   1.00  85.66        C
ATOM   18255   CG   GLN  D  920      19.770   37..349   24.987   I.00  91.08        C
ATOM   18256   CD   GLN  D  920      19.891   37.757   23.528   1.00  97.89        C
ATOM   18257   OE1  GLN  D  920      20.142   38.925   23.219   1.00100 .43        0
ATOM   18258   NE2  GLN  D  920      19.704   36.797   22.622   I.00  93.23        N
ATOM   18259   O    LEU  D  921      14.981   40.797   30.363   1.00  73.21        O
ATOM   18260   N    LEU  D  921      16.811   39.434   27.556   1.00  82.52        N
ATOM   18261   CA   LEU  D  921      16.060   40.496   28.221   I.00  82.10        C
ATOM   18262   C    LEU  D  921      15.519   40.016   29.581   1.00  79.68        C
ATOM   18263   CB   LEU  D  921      14.922   41.006   27.316   1.00  88.00        C
ATOM   18264   CG   LEU  D  921      15.272   41.891   26.094   1.00  87.01        C
ATOM   18265   CD1  LEU  D  921      14.049   42.155   25.200   1.00  78.44        C
ATOM   18266   CD2  LEU  D  921      15.909   43.218   26.501   1.00  77.89        C
ATOM   18267   O    VAL  D  922      16.166   38.978   33.320   1.00  69.92        0
ATOM   18268   N    VAL  D  922      15.683   38.730   29.867   I.00  78.65        N
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ATOM	18269	CA	VAL	D	922	15.367	38.199	31.189	1,00	76.98	C
ATOM	18270	C	VAL	D	922	16,455	38.574	32,200	1,00	71.82	C
ATOM	18271	CB	VAL	D	922	15.208	36,658	31:160	1,00	80,78	C
ATOM	18272	CG2	VAL	D	922	14.280	36:222	30:020	1,00	71.18	C
ATOM	18273	CGI	VAL	D	922	14,709	36.150	.32,507	1,00	81,78	C
ATOM	18274	O	GLU	D	923	I9.921	40,739	33:435	1,00	64,38	0
ATOM	18275	N	GLU	D	923	17.711	38,420	31.795	1,00	74,73	N
ATOM	18276	CA.	GLU	D	923	18,846	38.733	.32,649	1,00	69,71	C
ATOM	18277	C	GLU	D	923	19.133	40.229	32.628	1,00	67.91	C
ATOM	18278	CB	GLU	D	923	20.085	37,943	32.204	1,00	63,06	C
ATOM	18279	O	THR	D	924	18,441	43:950	33,411	I,00	67.57	0
ATOM	18280	N	THR	D	924	18.494	40:926	31:691	1,00	71.61	N
ATOM	18281	CA	THR	D	924	18.606	42,384	31.608	1,00	69,16	C
ATOM	18282	C	THR	D	924	17.918	43:013	32,808	1,00	65.90	C
ATOM	18283	CB	THR	D	924	17,995	42.947	30,309	1,00	69.97	C
ATOM	18284	OG1	THR	D	924	18.873	42,684	29:205	1,00	70,98	0
ATOM	18285	CG2	THR	D	924	17.813	44.428	30.416	1,00	63.37	C
ATOM	18286	O	ARG	D	925	16,967	43.772	36,400	1,00	73,58	0
ATOM	18287	N	AP.G	D	925	16.760	42,475	33:176	1,00	66,09	N
ATOM	18288	CA	ARG	D	925	16.026	43,005	34.317	1,00	67,03	C
ATOM	18289	C	ARG	D	925	16,856	42.845	35,595	1,00	67,62	C
ATOM	18290	CB	ARG	D	925	14.670	42.314	34.459	1,00	63.05	C
ATOM	18291	O	GLN	D	926	19.613	42,906	38.215	1,00	64,81	0
ATOM	18292	N	GLN	D	926	17,459	41:679	35,766	I,00	57.45	N
ATOM	18293	CA	GLN	D	926	18.224	41.397	36:971	1,00	66.41	C
ATOM	18294	C	GLN	D	926	19.361	42,401	37.122	1,00	65,51	C
ATOM	18295	CB	GLN	D	926	18,782	39:963	36,945	I,00	56.31	C
ATOM	18296	N	ILE	D	927	20,044	42.683	36,019	1,00	62.79	N
ATOM	18297	CA	ILE	D	927	21.138	43,641	36.024	1,00	58,45	C
ATOM	18298	C	ILE	D	927	20.619	45:042	36.388	1,00	61.81	C
ATOM	18299	O	ILE	D	927	21,248	45.769	37,147	1,00	60.84	0
ATOM	18300	CB	ILE	D	927	21.841	43,679	34:654	1,00	54,17	C
ATOM	18301	CGI	ILE	D	927	22.416	42:309	34.301	1,00	56.42	C
ATOM	18302	CG2	ILE	D	927	22,940	44.720	34,625	1,00	51.42	C
ATOM	18303	CD1	ILE	D	927	23.022	42,232	32:910	1,00	52,96	C
ATOM	18304	N	THR	D	928	19.454	45,410	35.871	1,00	56,90	N
ATOM	18305	CA.	THR	D	928	18,971	46.777	36,077	1,00	64.69	C
ATOM	18306	C	THR	D	928	18:530	46:978	37.522	1,00	63.81	C
ATOM	18307	O	THR	D	928	18.850	47,995	38.132	1,00	58,68	O
ATOM	18308	CB	THR	D	928	17,801	47.160	35,138	I,00	60.34	C
ATOM	18309	OG1	THR	D	928	18,259	47.297	33,788	1,00	52.55	0
ATOM	18310	CG2	THR	D	928	17.288	48,488	35.541	1,00	68,45	C
ATOM	18311	N	LYS	D	929	17.817	46:000	38:068	1,00	60.55	N
ATOM	18312	CA	LYS	D	929	17,444	46.045	39,473	1,00	61.63	C
ATOM	18313	C	LYS	D	929	18.690	46,140	40:366	1,00	64,83	C
ATOM	18314	O	LYS	D	929	18.743	46:948	41.297	1,00	65.12	O
ATOM	18315	CB	LYS	D	929	16,612	44.824	39,843	1,00	56.45	C
ATOM	18316	N	HIS	D	9.30	19.710	45,342	40:061	1,00	67,77	N
ATOM	18317	CA	HIS	D	930	20.944	45,369	40.843	1,00	66,67	C
ATOM	18318	C	HIS	D	930	21,660	46.694	40,761	1,00	58.31	C
ATOM	18319	O	HIS	D	930	22,205	47.166	41.755	1,00	59.52	0
ATOM	18320	CB	HIS	D	930	21.906	44,272	40.395	1,00	65,67	C
ATOM	18321	CG	HIS	D	930	21,592	42.944	40,982	I,00	71.32	C
ATOM	18322	ND1	HIS	D	930	21.660	42.704	42.336	1,00	72.44	N
ATOM	18323	CD2	HIS	D	9.30	21.182	41,789	40.409	1,00	70,58	C
ATOM	18324	CE1	HIS	D	930	21,308	41.454	42,571	I,00	76.28	C
ATOM	18325	NE2	HIS	D	930	21,009	40.878	41,420	1,00	74.11	N
ATOM	18326	N	VAL	D	9.31	21.699	47,258	39.560	1,00	56,11	N
ATOM	18327	CA	VAL	D	931	22.385	48:522	39.354	1,00	60.24	C
ATOM	18328	C	VAL	D	931	21,670	49.615	40,150	1,00	58.67	C
ATOM	18329	O	VAL	D	931	22..318	50,444	40:789	1,00	53,73	O
ATOM	18330	CB	VAL	D	931	22.454	48:896	37.868	1,00	55.91	C
ATOM	18331	CGI	VAL	D	931	23,015	50.290	37,703	1,00	45.27	C

ATOM	18332	CG2	VAL	D	931	23.314	47,891	37,115	1.00	52.36	C
ATOM	18333	N	ALA	D	932	20,336	49.575	40,138	1,00	57.75	N
ATOM	18334	CA	ALA	D	9.32	19.529	50,508	40:917	1,00	61.,22	C
ATOM	18335	C	ALA	D	932	19.863	50,397	42,413	1.00	65.68	C
ATOM	18336	0	ALA	D	932	20,204	51.400	43,048	1,00	63.31	0
ATOM	18337	CB	ALA	D	9.32	18.036	50,270	40:676	1,00	56,76	C
ATOM	18338	N	GLN	D	933	19.789	49,187	42.970	1,00	61,28	N
ATOM	18339	CA.	GLN	D	933	20,069	49.015	44,394	1,00	60.94	C
ATOM	18340	C	GLN	D	933	21.472	49,518	44,753	1,00	59.31	C
ATOM	18341	O	GLN	D	933	21.661	50,141	45:783	1,00	57,75	O
ATOM	18342	CB	GLN	D	933	19,891	47.551	44,807	1,00	55.50	C
ATOM	18343	CG	GLN	D	933	20.257	47,223	46,278	1,00	62.05	C
ATOM	18344	CD	GLN	D	933	21.718	46,740	46.476	1.,00	75,38	C
ATOM	18345	OE1	GLN	D	933	22.157	45,742	45,879	1.00	80.14	0
ATOM	18346	NE2	GLN	D	933	22,462	47.446	47.327	1.00	73.62	N
ATOM	18347	N	ILE	D	9.34	22.456	49,259	43:900	1,00	64,93	N
ATOM	18348	CA	ILE	D	934	23,837	49,604	44,245	1.00	61.09	C
ATOM	18349	C	ILE	D	934	24,037	51.1.12	44,171	1,00	61,40	C
ATOM	18350	O	ILE	D	9.34	24.574	51,715	45:097	1,00	59,43	O
ATOM	18351	CB	ILE	D	934	24.861	48,881	43.335	1,00	59,00	C
ATOM	18352	CGI	ILE	D	934	25,062	47.444	43,816	1,00	64.76	C
ATOM	18353	CG2	ILE	D	934	26,202	49,581	43,354	1,00	54.31	C
ATOM	18354	CD1	ILE	D	934	25.417	46,451	42.720	1,00	62,92	C
ATOM	18355	N	LEU	D	935	23,598	51.720	43,075	1,00	61.59	N
ATOM	18356	CA	LEU	D	935	23,738	53,163	42,915	1,00	63.95	C
ATOM	18357	C	LEU	D	935	23.060	53,911	44.069	1.,00	61.,36	C
ATOM	18358	O	LEU	D	935	23,649	54:816	44,632	1,00	60.22	0
ATOM	18359	CB	LEU	D	935	23,183	53:619	41,562	1,00	57.31	C
ATOM	18360	CG	LEU	D	935	24.039	53,137	40.389	1.,00	58,15	C
ATOM	18361	CD2	LEU	D	935	25,534	53,048	40,767	1.00	51.98	c
ATOM	18362	CD1	LEU	D	935	23,824	54.003	39,164	1,00	53.65	C
ATOM	18363	O	ASP	D	936	22.096	55,103	47.505	1,00	69,36	0
ATOM	18364	N	ASP	D	936	21,861	53,482	44,453	1.00	64.01	N
ATOM	18365	CA.	ASP	D	936	21,133	54.1.02	45,558	1,00	61.77	C
ATOM	18366	C	ASP	D	936	21.885	54,062	46:867	1,00	67,72	C
ATOM	18367	CB	ASP	D	936	19.783	53,430	45.792	1,00	68,66	C
ATOM	18368	CG	ASP	D	936	18,897	54.240	46,734	1,00	67.72	C
ATOM	18369	OD1	ASP	D	936	18,806	55,462	46,521	1,00	68.11	0
ATOM	18370	OD2	ASP	D	936	18.317	53,672	47.682	1.,00	67,24	0
ATOM	18371	N	SER	D	937	22,258	52:854	47,280	1,00	60.23	N
ATOM	18372	CA	SEP.	D	937	22,974	52.669	48,534	1,00	61.50	C
ATOM	18373	C	SER	D	937	24.331	53,340	48.471	1.,00	60,57	C
ATOM	18374	O	SER	D	937	24,914	53,668	49,495	1.00	65.56	0
ATOM	18375	CB	SER	D	937	23,131	51:182	48,861	1,00	64.89	C
ATOM	18376	OG	SER	D	9.37	24.082	50,565	48:014	1,00	67,83	0
ATOM	18377	N	ARG	D	938	24,825	53,550	47,261	1.00	62.28	N
ATOM	18378	CA.	ARG	D	938	26,117	54.1.78	47,075	1,00	63.75	C
ATOM	18379	C	ARG	D	9.38	25.992	55,665	47:297	1,00	62,74	C
ATOM	18380	O	ARG	D	938	26.651	56,237	48.160	1,00	66,22	O
ATOM	18381	CB	ARG	D	938	26,660	53.895	45,672	1,00	66.74	C
ATOM	18382	CG	ARG	D	938	28,149	53,651	45,629	1,00	67.09	C
ATOM	18383	CD	ARG	D	938	28.466	52,315	44.991	1,00	61,82	C
ATOM	18384	NE	ARG	D	938	29,772	51:815	45,416	1,00	65.40	N
ATOM	18385	CZ	ARG	D	938	30,918	52,152	44,842	1,00	63.79	C
ATOM	18386	NH1	ARG	D	938	30.928	52,992	43.816	1.,00	64,97	N
ATOM	18387	NH2	ARG	D	938	.32,054	51:648	45,289	1,00	70.37	N
ATOM	18388	N	MET	D	939	25,119	56:281	46,514	1,00	64.97	N
ATOM	18389	CA	MET	D	939	24.915	57,722	46.542	1.,00	66,98	C
ATOM	18390	C	MET	D	939	24,274	58,260	47,816	1.00	68.07	c
ATOM	18391	O	MET	D	939	24,541	59.389	48,197	1,00	68.46	0
ATOM	18392	CB	MET	D	939	24.063	58,136	45:.350	1,00	59,47	C
ATOM	18393	CG	MET	D	939	24,623	57,723	44,025	1.00	58.18	C
ATOM	1.8394	SD	MET	D	939	25,889	58.799	43,342	1,00	67.48	s

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ATOM  18395  CE   MET  D 939    27.311  58.473  44.386  1.00  62.37      C
ATOM  18396  O    ASM  D 940    22.400  56.213  51.189  1.00  71.97      O
ATOM  18397  N    ASN  D 940    23.431  57.460  48.462  1.00  68.63      N
ATOM  18398  CA   ASN  D 940    22.605  57.958  49.563  1.00  69.15      C
ATOM  18399  C    ASM  D 940    22.912  57.288  50.885  1.00  72.35      C
ATOM  18400  CB   ASN  D 940    21.120  57.772  49.242  1.00  65.45      C
ATOM  18401  CG   ASN  D 940    20.732  58.387  47.915  1.00  69.01      C
ATOM  18402  OD1  ASN  D 940    21.256  59.430  47.524  1.00  72.21      0
ATOM  18403  ND2  ASN  D 940    19.813  57.742  47.210  1.00  66.45      N
ATOM  18404  O    THR  D 941    23.822  57.315  55.281  1.00  85.84      O
ATOM  18405  N    THR  D 941    23.718  57.951  51.696  1.00  78.38      N
ATOM  18406  CA   THR  D 941    24.215  57.326  52.907  1.00  78.27      C
ATOM  18407  C    THR  D 941    23.736  57.959  54.235  1.00  83.39      C
ATOM  18408  CB   THR  D 941    25.748  57.314  52.878  1.00  78.15      C
ATOM  18409  OG1  THR  D 941    26.250  57.081  54.199  1.00  91.56      0
ATOM  18410  CG2  THR  D 941    26.273  58.643  52.349  1.00  76.65      C
ATOM  18411  O    LYS  D 942    20.568  59.355  55.122  1.00  79.91      0
ATOM  18412  N    LYS  D 942    23.223  59.191  54.203  1.00  81.46      N
ATOM  18413  CA   LYS  D 942    22.882  59.902  55.442  1.00  78.72      C
ATOM  18414  C    LYS  D 942    21.452  59.624  55.921  1.00  76.51      C
ATOM  18415  CB   LYS  D 942    23.086  61.405  55.259  1.00  68.26      C
ATOM  18416  O    TYR  D 943    19.843  61.624  58.843  1.00  79.64      0
ATOM  18417  N    TYR  D 943    21.226  59.695  57.228  1.00  76.33      N
ATOM  18418  CA   TYR  D 943    19.892  59.451  57.777  1.00  78.37      C
ATOM  18419  C    TYR  D 943    19.200  60.723  58.297  1.00  83.20      C
ATOM  18420  CB   TYR  D 943    19.969  58.409  58.895  1.00  83.48      C
ATOM  18421  CG   TYR  D 943    20.376  57.031  58.414  1.00  84.45      C
ATOM  18422  CD1  TYR  D 943    19.420  56.069  58.108  1.00  86.15      C
ATOM  18423  CD2  TYR  D 943    21.710  56.696  58.254  1.00  81.03      C
ATOM  18424  CE1  TYR  D 943    19.786  54.810  57.666  1.00  86.89      C
ATOM  18425  CE2  TYR  D 943    22.084  55.450  57.821  1.00  86.28      C
ATOM  18426  CZ   TYR  D 943    21.121  54.508  57.521  1.00  91.33      C
ATOM  18427  OH   TYR  D 943    21.502  53.261  57.081  1.00  86.51      0
ATOM  18428  O    ASP  D 944    17.734  61.388  60.753  1.00  91.00      0
ATOM  18429  N    ASP  D 944    17.878  60.770  58.115  1.00  88.83      N
ATOM  18430  CA   ASP  D 944    17.032  61.895  58.523  1.00  83.65      C
ATOM  18431  C    ASP  D 944    17.076  62.130  60.018  1.00  89.75      C
ATOM  18432  CB   ASP  D 944    15.579  61.655  58.100  1.00  84.04      C
ATOM  18433  O    GUI  D 945    16.604  61.757  63.487  1.00  89.24      0
ATOM  18434  N    GLU  D 945    16.366  63.167  60.457  1.00  93.00      N
ATOM  18435  CA   GLU  D 945    16.273  63.500  61.871  1.00  95.36      C
ATOM  18436  C    GLU  D 945    15.873  62.248  62.624  1.00  94.43      C
ATOM  18437  CB   GLU  D 945    15.268  64.635  62.107  1.00  91.88      C
ATOM  18438  O    ASN  D 946    13.819  58.336  61.972  1.00  92.57      0
ATOM  18439  N    ASK  D 946    14.725  61.708  62.236  1.00  95.51      N
ATOM  18440  CA   ASN  D 946    14.159  60.529  62.868  1.00  94.66      C
ATOM  18441  C    ASN  D 946    14.612  59.245  62.195  1.00  91.86      C
ATOM  18442  CB   ASK  D 946    12.644  60.628  62.849  1.00  94.50      C
ATOM  18443  CG   ASN  D 946    12.137  61.184  61.546  1.00  98.77      C
ATOM  18444  OD1  ASN  D 946    12.738  60.953  60.494  1.00  98.07      0
ATOM  18445  ND2  ASN  D 946    11.048  61.945  61.603  1.00100.16      N
ATOM  18446  O    ASP  D 947    16.005  56.064  60.079  1.00  86.15      O
ATOM  18447  N    ASP  D 947    15.892  59.203  61.847  1.00  94.58      N
ATOM  18448  CA   ASP  D 947    16.562  57.973  61.444  1.00  92.38      C
ATOM  18449  C    ASP  D 947    15.972  57.294  60.202  1.00  90.69      C
ATOM  18450  CB   ASP  D 947    16.566  56.995  62.616  1.00  91.85      C
ATOM  18451  CG   ASP  D 947    17.898  56.305  62.784  1.00  95.50      C
ATOM  18452  OD2  ASP  D 947    18.463  56.363  63.899  1.00  95.30      0
ATOM  18453  OD1  ASP  D 947    18.386  55.720  61.791  1.00  92.42      0
ATOM  18454  O    LYS  D 948    16.702  59.091  57.002  1.00  84.05      0
ATOM  18455  N    LYS  D 948    15.450  58.100  59.282  1.00  86.90      N
ATOM  18456  CA   LYS  D 948    15.073  57.615  57.959  1.00  84.50      C
ATOM  18457  C    LYS  D 948    16.164  57.989  56.945  1.00  83.55      C
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ATOM   18458   CB   LYS  D  948       13.720   58.203   57.542   1.00  87.81            C
ATOM   18459   O    LEU  D  949       15.938   58.818   53.911   1.00  76.08            0
ATOM   18460   N    LEU  D  949       16.498   57.092   56.021   1.00  80.34            N
ATOM   18461   CA   LEU  D  949       17.530   57.402   55.024   1.00  79.81            C
ATOM   18462   C    LEU  D  949       17.123   58.603   54.161   I.00  74.97            C
ATOM   18463   CB   LEU  D  949       17.815   56.179   54.140   1.00  71.84            C
ATOM   18464   CG   LEU  D  949       19.252   56.036   53.619   1.00  78.06            C
ATOM   18465   GDI  LEU  D  949       19.648   54.559   53.476   I.00  86.78            C
ATOM   18466   CD2  LEU  D  949       19.443   56.762   52.299   1.00  74.75            C
ATOM   18467   O    ILE  D  950       19.385   59.811   51.212   1.00  72.87            0
ATOM   18468   N    ILE  D  950       18.103   59.387   53.723   I.00  71.41            N
ATOM   18469   CA   ILE  D  950       17.838   60.552   52.883   1.00  72.53            C
ATOM   18470   C    ILE  D  950       18.276   60.297   51.453   1.00  76.85            C
ATOM   18471   CB   ILE  D  950       18.564   61.808   53.392   1.00  74.64            C
ATOM   18472   CGI  ILE  D  950       18.315   62.004   54.886   1.00  77.35            C
ATOM   18473   CG2  ILE  D  950       18.110   63.023   52.627   1.00  71.21            C
ATOM   18474   CD1  ILE  D  950       19.305   62.920   55.549   1.00  77.61            C
ATOM   18475   O    ARG  D  951       17.358   62.318   47.709   I.00  71.63            0
ATOM   18476   N    AP.G D  951       17.407   60.632   50.505   1.00  76.93            N
ATOM   18477   CA   ARG  D  951       17.697   60.392   49.097   1.00  76.63            C
ATOM   18478   C    ARG  D  951       18.130   61.683   48.433   I.00  68.96            C
ATOM   18479   CB   ARG  D  951       16.481   59.802   48.361   1.00  74.96            C
ATOM   18480   CG   ARG  D  951       15.866   58.572   49.016   1.00  77.40            C
ATOM   18481   CD   ARG  D  951       16.473   57.239   48.554   I.00  73.12            C
ATOM   18482   ME   ARG  D  951       15.719   56.116   49.122   1.00  70.79            N
ATOM   18483   CZ   ARG  D  951       16.268   55.046   49.689   1.00  76.89            C
ATOM   18484   NH1  ARG  D  951       15.501   54.090   50.187   I.00  81.88            N
ATOM   18485   NH2  ARG  D  951       17.584   54.925   49.763   1.00  77.54            N
ATOM   18486   N    GLU  D  952       19.373   62.060   48.681   1.00  67.09            N
ATOM   18487   CA   GLU  D  952       19.970   63.223   48.042   1.00  69.76            C
ATOM   18488   C    GLU  D  952       20.067   63.086   46.513   1.00  70.77            C
ATOM   18489   O    GLU  D  952       19.774   64.036   45.778   1.00  71.14            0
ATOM   18490   CB   GLU  D  952       21.349   63.460   48.643   1.00  75.52            C
ATOM   18491   CG   GLU  D  952       22.143   64.554   47.985   I.00  81.34            C
ATOM   18492   CD   GLU  D  952       23.467   64.774   48.680   1.00  84.10            C
ATOM   18493   OE1  GLU  D  952       24.318   63.859   48.640   1.00  79.79            0
ATOM   18494   OE2  GLU  D  952       23.645   65.860   49.276   I.00  90.46            0
ATOM   18495   N    VAL  D  953       20.497   61.914   46.040   1.00  70.52            N
ATOM   18496   CA   VAL  D  953       20.527   61.622   44.602   1.00  68.55            C
ATOM   18497   C    VAL  D  953       19.360   60.704   44.280   I.00  64.64            C
ATOM   18498   O    VAL  D  953       19.170   59.708   44.968   1.00  62.47            0
ATOM   18499   CB   VAL  D  953       21.844   60.939   44.162   1.00  67.47            C
ATOM   18500   CG2  VAL  D  953       23.038   61.769   44.548   1.00  66.58            C
ATOM   18501   CGI  VAL  D  953       21.847   60.699   42.666   1.00  61.71            C
ATOM   18502   N    LYS  D  954       18.585   61.025   43.245   1.00  60.70            N
ATOM   18503   CA   LYS  D  954       17.393   60.227   42.920   1.00  57.36            C
ATOM   18504   C    LYS  D  954       17.619   59.222   41.773   I.00  52.59            C
ATOM   18505   O    LYS  D  954       18.007   59.584   40.650   1.00  50.46            O
ATOM   18506   CB   LYS  D  954       16.222   61.150   42.575   1.00  62.06            C
ATOM   18507   CG   LYS  D  954       16.401   62.566   43.089   I.00  63.04            C
ATOM   18508   CD   LYS  D  954       15.069   63.251   43.212   1.00  67.06            C
ATOM   18509   CE   LYS  D  954       15.199   64.774   43.330   1.00  72.24            C
ATOM   18510   NZ   LYS  D  954       13.849   65.424   43.268   I.00  62.83            N
ATOM   18511   N    VAL  D  955       17.362   57.954   42.062   1.00  48.50            N
ATOM   18512   CA   VAL  D  955       17.598   56.930   41.065   1.00  56.22            C
ATOM   18513   C    VAL  D  955       16.260   56.626   40.461   I.00  57.90            C
ATOM   18514   O    VAL  D  955       15.389   56.015   41.094   1.00  57.03            O
ATOM   18515   CB   VAL  D  955       18.252   55.648   41.640   1.00  56.39            C
ATOM   18516   CGI  VAL  D  955       18.407   54.617   40.555   1.00  54.04            C
ATOM   18517   CG2  VAL  D  955       19.600   55.965   42.264   1.00  47.07            C
ATOM   18518   N    ILE  D  956       16.101   57.097   39.233   1.00  50.81            N
ATOM   18519   CA   ILE  D  956       14.828   57.027   38.561   1.00  55.56            C
ATOM   18520   C    ILE  D  956       14.798   55.889   37.559   I.00  60.13            C
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ATOM	18521	O	ILE	D	956	15.690	55.745	36.707	1.00	58.63	O
ATOM	18522	CB	ILE	D	956	14.503	58.359	37.873	1.00	59.28	C
ATOM	18523	CGI	ILE	D	956	14.313	59.437	38.944	1.00	59.36	C
ATOM	18524	CG2	ILE	D	956	13.258	58.216	37.050	1.00	61.10	C
ATOM	18525	GDI	ILE	D	956	14.784	60.819	38.530	1.00	63.75	c
ATOM	18526	N	THR	D	957	13.757	55.078	37.683	1.00	61.92	N
ATOM	18527	CA	THR	D	957	13.604	53.877	36.890	1.00	57.09	C
ATOM	18528	C	THR	D	957	12.415	53.986	35.934	1.00	59.60	c
ATOM	18529	O	THR	D	957	11.270	53.839	36.352	1.00	59.27	0
ATOM	18530	CB	THR	D	957	13.420	52.694	37.816	1.00	60.20	C
ATOM	18531	OG1	THR	D	957	12.188	52.857	38.519	1.00	68.68	0
ATOM	18532	CG2	THR	D	957	14.530	52.685	38.837	1.00	62.51	c
ATOM	18533	N	LEU	D	958	12.693	54.256	34.660	1.00	58.97	N
ATOM	18534	CA	LEU	D	958	11.656	54.436	33.629	1.00	56.44	C
ATOM	18535	C	LEU	D	958	11.364	53.167	32.830	1.00	64.46	c
ATOM	18536	O	LEU	D	958	12.293	52.480	32.363	1.00	61.47	0
ATOM	18537	CB	LEU	D	958	12.081	55.515	32.639	1.00	57.45	C
ATOM	18538	CG	LEU	D	958	11.544	56.940	32.591	1.00	56.13	c
ATOM	18539	CD1	LEU	D	958	11.660	57.599	33.925	1.00	55.40	c
ATOM	18540	CD2	LEU	D	958	12.372	57.674	31.573	1.00	52.03	C
ATOM	18541	N	LYS	D	959	10.083	52.868	32.637	1.00	64.32	N
ATOM	18542	CA	LYS	D	959	9.713	51.809	31.709	1.00	61.22	c
ATOM	18543	c	LYS	D	959	10.228	52.214	30.340	1.00	63.64	C
ATOM	18544	0	LYS	D	959	10.219	53.397	29.993	1.00	60.16	0
ATOM	18545	CB	LYS	D	959	8.202	51.587	31.685	1.00	65.95	c
ATOM	18546	N	SER	D	960	10.706	51.249	29.565	1.00	65.92	N
ATOM	18547	CA	SER	D	960	11.310	51.580	28.283	1.00	61.87	c
ATOM	18548	C	SER	D	960	10.279	52.078	27.272	1.00	54.26	c
ATOM	18549	O	SER	D	960	10.611	52.854	26.385	1.00	58.52	0
ATOM	18550	CB	SER	D	960	12.058	50.368	27.720	1.00	63.70	C
ATOM	18551	OG	SER	D	960	11.168	49.292	27.492	1.00	72.13	0
ATOM	18552	N	LYS	D	961	9.034	51.631	27.393	1.00	54.98	N
ATOM	18553	CA	LYS	D	961	8.003	52.045	26.438	1.00	59.70	C
ATOM	18554	C	LYS	D	961	7.888	53.567	26.370	1.00	59.50	c
ATOM	18555	O	LYS	D	961	7.700	54.124	25.288	1.00	58.26	0
ATOM	18556	CB	LYS	D	961	6.648	51.431	26.790	1.00	58.76	C
ATOM	18557	N	LEU	D	962	8.060	54.222	27.519	1.00	56.52	N
ATOM	18558	CA	LEU	D	962	7.941	55.675	27.639	1.00	61.24	c
ATOM	18559	C	LEU	D	962	8.890	56.438	26.731	1.00	61.86	c
ATOM	18560	O	LEU	D	962	8.459	57.297	25.960	1.00	65.39	0
ATOM	18561	CB	LEU	D	962	8.164	56.108	29.087	1.00	60.56	c
ATOM	18562	CG	LEU	D	962	6.998	55.760	30.021	1.00	62.36	c
ATOM	18563	CD1	LEU	D	962	7.197	56.346	31.396	1.00	58.88	C
ATOM	18564	CD2	LEU	D	962	5.680	56.245	29.425	1.00	68.48	c
ATOM	18565	N	VAL	D	963	10.178	56.140	26.823	1.00	57.60	N
ATOM	18566	CA	VAL	D	963	11.171	56.774	25.956	1.00	54.98	C
ATOM	18567	C	VAL	D	963	10.918	56.341	24.522	1.00	58.68	c
ATOM	18568	O	VAL	D	963	11.146	57.082	23.588	1.00	58.76	0
ATOM	18569	CB	VAL	D	963	12.613	56.392	26.385	1.00	57.26	C
ATOM	18570	CGI	VAL	D	963	13.657	56.760	25.311	1.00	52.44	c
ATOM	18571	CG2	VAL	D	963	12.942	57.022	27.705	1.00	56.30	c
ATOM	18572	N	SER	D	964	10.425	55.120	24.371	1.00	58.45	N
ATOM	18573	CA	SER	D	964	10.154	54.546	23.070	1.00	51.17	c
ATOM	18574	C	SER	D	964	8.912	55.191	22.450	1.00	65.77	c
ATOM	18575	O	SER	D	964	8.837	55.396	21.231	1.00	65.11	0
ATOM	18576	CB	SER	D	964	9.978	53.045	23.210	1.00	54.85	c
ATOM	18577	OG	SER	D	964	9.903	52.442	21.951	1.00	65.25	0
ATOM	18578	N	ASP	D	965	7.938	55.523	23.296	1.00	63.11	N
ATOM	18579	CA	ASP	D	965	6.784	56.304	22.846	1.00	62.21	C
ATOM	18580	C	ASP	D	965	7.247	57.700	22.479	1.00	59.15	c
ATOM	18581	O	ASP	D	965	6.817	58.270	21.471	1.00	61.83	0
ATOM	18582	CB	ASP	D	965	5.691	56.375	23.919	1.00	57.62	C
ATOM	18583	CG	ASP	D	965	4.895	55.082	24.042	1.00	57.46	c

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ATOM   18584  OD1 ASP D 965      4.904   54..277  23..088  1.00  53..47          O
ATOM   18585  OD2 ASP D 965      4,245   54..880  25.,096  1,00  66..21          O
ATOM   18586  N   PHE D 966      8..134  58.,238  23...306 1,00  57,41           N
ATOM   18587  CA  PHE D 966      8..612  59..608  23..153  1.00  58..33          C
ATOM   18588  C   PHE D 966      9„305   59. 762  21.,809  1,00  62,48           C
ATOM   18589  O   PHE D 966      9.157   60.,776  21..147  1,00  67,60           O
ATOM   18590  CB  PHE D 966      9..550  59.,966  24.309   1,00  57,68           C
ATOM   18591  CG  PHE D 966      9„974   61. 416  24.,357  1,00  60.,78          C
ATOM   18592  CD2 PHE D 966      9.425   62..280  25..301  1,00  64.31           C
ATOM   18593  CD1 PHE D 966     10..948  61.,906  23..506  1,00  60,.13          C
ATOM   18594  CE2 PHE D 966      9„827   63..605  25.,385  1,00  57.12           C
ATOM   18595  CE1 PHE D 966     11.351   63..233  23..580  1,00  63..17          C
ATOM   18596  CZ  PHE D 966     10. 788  64.,084  24.523   1,00  59,79           C
ATOM   18597  N   ARG D 967     10..058  58..743  21..411  1.00  62.82           N
ATOM   18598  CA  ARG D 967     10.,793  58..776  20.,153  1,00  65..75          C
ATOM   18599  C   ARG D 967      9..841  58.,836  18..946  1,00  64,06           C
ATOM   18600  O   ARG D 967     10..099  59..544  17.969   1.00  60..92          0
ATOM   18601  CB  ARG D 967     11,717   57. 547  20.,031  1,00  59..46          C
ATOM   18602  CG  ARG D 967     12.808   57.,446  21..094  1,00  61,92           C
ATOM   18603  CD  ARG D 967     13..730  56.,257  20..819  1,00  58,.97          C
ATOM   18604  NE  ARG D 967     14,597   56. 596  19.,716  1,00  56..61          N
ATOM   18605  CZ  ARG D 967     15..888  56..827  19..831  1,00  56..56          C
ATOM   18606  NH1 ARG D 967     16..475  56.,672  20..999  1,00  53,.15          N
ATOM   18607  NH2 ARG D 967     16.,590  57..174  18.,764  1,00  61.85           N
ATOM   18608  N   LYS D 968      8.762   58..059  19..013  1,00  65..13          N
ATOM   18609  CA  LYS D 968      7.824   57,930   17.906   1,00  62,66           C
ATOM   18610  C   LYS D 968      6,866   59.112   17,880   1,00  61.99           C
ATOM   18611  O   LYS D 968      6,570   59..655  16.,819  1,00  59..18          O
ATOM   18612  CB  LYS D 968      7.051   56.,612  18. 001  1,00  62,57           C
ATOM   18613  N   ASP D 969      6.409   59..533  19..050  1.00  61.98           N
ATOM   18614  CA  ASP D 969      5,514   60..677  19.,104  1,00  61.41           C
ATOM   18615  C   ASP D 969      6.210   61.,949  18..636  1,00  61,64           C
ATOM   18616  O   ASP D 969      5.548   62..860  18..174  1.00  64.78           0
ATOM   18617  CB  ASP D 969      4,942   60. 862  20.,511  1,00  62.07           C
ATOM   18618  CG  ASP D 969      3.978   59.,752  20.895   1,00  65,.60          C
ATOM   18619  OD1 ASP D 969      3.923   58.,729  20..177  1,00  67,93           0
ATOM   18620  OD2 ASP D 969      3,279   59. 889  21.,915  1,00  68..46          0
ATOM   18621  N   PHE D 970      7.536   62..023  18..702  1,00  62.45           N
ATOM   18622  CA  PHE D 970      8.186   63.,259  18. 246  1,00  60,97           C
ATOM   18623  C   PHE D 970      9,294   63..052  17,220   1,00  60..58          C
ATOM   18624  O   PHE D 970     10.,149  63..914  17,033   1,00  63..63          0
ATOM   18625  CB  PHE D 970      8.706   64.,038  19. 444  1,00  57,08           C
ATOM   18626  CG  PHE D 970      7.649   64..298  20..469  1.00  66..51          C
ATOM   18627  CD1 PHE D 970      6,659   65..238  20.,232  1,00  69..70          C
ATOM   18628  CD2 PHE D 970      7.615   63.,586  21..650  1,00  64,82           C
ATOM   18629  CE1 PHE D 970      5.682   65..472  21..162  1.00  71.94           C
ATOM   18630  CE2 PHE D 970      6,632   63. 816  22.,580  1,00  66..65          C
ATOM   18631  CZ  PHE D 970      5.665   64.,755  22...336 1,00  70,.63          C
ATOM   18632  N   GLN D 971      9.236   61.,917  16..532  1,00  61,78           N
ATOM   18633  CA. GLN D 971     10.,098  61. 630  15.,389  1,00  65..53          C
ATOM   18634  C   GLN D 971     11..593  61..687  15..663  1,00  61.19           C
ATOM   18635  O   GLN D 971     12..365  62.,162  14.832   1,00  57,14           0
ATOM   18636  CB  GLN D 971      9,759   62..569  14,238   1,00  68..63          C
ATOM   18637  CG  GLN D 971      8.704   61..980  13..322  1,00  72.49           C
ATOM   18638  CD  GLN D 971      8.047   63.,009  12.424   1,00  85,49           C
ATOM   18639  OE1 GLN D 971      8,541   64..137  12.,279  1,00  86..83          0
ATOM   18640  NE2 GLN D 971      6,918   62..630  11,819   1,00  79..47          N
ATOM   18641  O   PHE D 972     13. 486  58.,589  17.860   1,00  59,32           0
ATOM   18642  N   PHE D 972     11..989  61..197  16..830  1.00  62.37           N
ATOM   18643  CA  PHE D 972     13.,383  60..854  17,074   1,00  62.47           C
ATOM   18644  C   PHE D 972     13.501   59.,344  16..889  1,00  62,50           C
ATOM   18645  CB  PHE D 972     13..831  61..269  18..474  1.00  57.52           C
ATOM   18646  CG  PHE D 972     13.,578  62. 713  18.,803  1,00  59..01          C
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ATOM	18647	GDI	PHE	D	972	14.224	63.727	18.106	1.00	63.54	C
ATOM	18648	CD2	PHE	D	972	12.719	63.062	19.836	1.00	61.67	C
ATOM	18649	CE1	PHE	D	972	14.004	65.070	18.429	1.00	62.42	C
ATOM	18650	CE2	PHE	D	972	12.491	64.402	20.166	1.00	54.36	C
ATOM	18651	CZ	PHE	D	972	13.135	65.401	19.467	I.00	55.22	C
ATOM	18652	0	TYR	D	973	15.928	57.276	15.355	1.00	57.03	0
ATOM	18653	N	TYR	D	973	13.572	58.894	15.642	1.00	57.96	N
ATOM	18654	CA.	TYR	D	973	13.518	57.460	15.393	I.00	61.21	C
ATOM	18655	C	TYR	D	973	14.850	56.756	15.656	1.00	64.76	C
ATOM	18656	CB	TYR	D	973	13.063	57.189	13.961	1.00	68.30	C
ATOM	18657	CG	TYR	D	973	11.672	57.697	13.684	I.00	68.87	C
ATOM	18658	GDI	TYR	D	973	10.637	57.437	14.566	1.00	67.03	C
ATOM	18659	CD2	TYR	D	973	11.398	58.451	12.554	1.00	67.81	C
ATOM	18660	CE1	TYR	D	973	9.373	57.895	14.329	1.00	68.17	C
ATOM	18661	CE2	TYR	D	973	10.131	58.919	12.310	1.00	68.79	C
ATOM	18662	CZ	TYR	D	973	9.125	58.639	13.200	1.00	70.96	C
ATOM	18663	OH	TYR	D	973	7.856	59.096	12.962	1.00	73.03	0
ATOM	18664	O	LYS	D	974	15.090	53.159	14.860	I.00	61.40	0
ATOM	18665	N	LYS	D	974	14.752	55.562	16.232	1.00	64.64	N
ATOM	18666	CA	LYS	D	974	15.913	54.712	16.428	1.00	58.12	C
ATOM	18667	C	LYS	D	974	16.048	53.828	15.215	I.00	55.57	C
ATOM	18668	CB	LYS	D	974	15.761	53.862	17.695	1.00	59.31	C
ATOM	18669	CG	LYS	D	974	17.060	53.289	18.255	1.00	55.13	C
ATOM	18670	CD	LYS	D	974	16.782	52.135	19.204	I.00	58.38	C
ATOM	18671	CE	LYS	D	974	15.748	52.533	20.242	1.00	60.45	C
ATOM	18672	NZ	LYS	D	974	15.416	51.439	21.198	1.00	65.63	N
ATOM	18673	O	VAL	D	975	19.962	52.500	13.739	I.00	58.93	0
ATOM	18674	N	VAL	D	975	17.214	53.827	14.569	1.00	58.51	N
ATOM	18675	CA	VAL	D	975	17.542	52.750	13.620	1.00	57.56	C
ATOM	18676	C	VAL	D	975	18.864	52.022	14.007	1.00	57.54	C
ATOM	18677	CB	VAL	D	975	17.640	53.266	12.168	1.00	56.60	C
ATOM	18678	CGI	VAL	D	975	17.764	52.087	11.218	1.00	54.66	C
ATOM	18679	CG2	VAL	D	975	16.425	54.094	11.806	1.00	58.20	C
ATOM	18680	O	ARG	D	976	22.095	49.571	14.636	I.00	59.15	0
ATOM	18681	N	AP.G	D	976	18.725	50.854	14.625	1.00	55.77	N
ATOM	18682	CA	ARG	D	976	19.835	50.117	15.216	1.00	51.32	C
ATOM	18683	C	ARG	D	976	20.938	49.701	14.239	I.00	57.11	C
ATOM	18684	CB	ARG	D	976	19.307	48.865	15.901	1.00	48.68	C
ATOM	18685	CG	ARG	D	976	18.802	49.067	17.283	1.00	50.94	C
ATOM	18686	CD	ARG	D	976	17.986	47.859	17.722	I.00	65.01	C
ATOM	18687	NE	ARG	D	976	17.362	48.042	19.039	1.00	73.50	N
ATOM	18688	CZ	ARG	D	976	16.110	48.463	19.238	1.00	81.11	C
ATOM	18689	NH1	ARG	D	976	15.644	48.583	20.477	1.00	85.05	N
ATOM	18690	NH2	ARG	D	976	15.320	48.769	18.207	1.00	69.77	N
ATOM	18691	O	GLU	D	977	23.491	49.613	10.770	1.00	57.36	O
ATOM	18692	N	GLU	D	977	20.593	49.480	12.978	1.00	55.27	N
ATOM	18693	CA.	GLU	D	977	21.560	48.938	12.026	I.00	54.41	C
ATOM	18694	C	GLU	D	977	22.568	49.972	11.510	1.00	57.38	C
ATOM	18695	CB	GLU	D	977	20.837	48.306	10.828	1.00	55.82	C
ATOM	18696	CG	GLU	D	977	19.933	47.096	11.149	I.00	61.00	C
ATOM	18697	CD	GLU	D	977	18.521	47.490	11.629	1.00	65.85	C
ATOM	18698	OE1	GLU	D	977	17.732	46.583	12.000	1.00	63.85	0
ATOM	18699	OE2	GLU	D	977	18.198	48.701	11.635	I.00	63.83	0
ATOM	18700	O	1LE	D	978	25.622	52.453	11.239	1.00	58.87	0
ATOM	18701	N	ILE	D	978	22.403	51.240	11.895	1.00	48.01	N
ATOM	18702	CA	ILE	D	978	23.207	52.322	11.318	I.00	51.82	C
ATOM	18703	C	ILE	D	978	24.602	52.388	11.930	1.00	55.64	C
ATOM	18704	CB	ILE	D	978	22.530	53.711	11.514	1.00	51.34	C
ATOM	18705	CGI	ILE	D	978	21.128	53.720	10.926	1.00	56.79	C
ATOM	18706	CG2	ILE	D	978	23.360	54.811	10.886	1.00	51.11	C
ATOM	18707	CD1	ILE	D	978	21.111	53.691	9.432	1.00	60.09	C
ATOM	18708	O	ASN	D	979	24.292	51.717	15.723	1.00	45.48	0
ATOM	18709	N	ASM	D	979	24.606	52.409	13.251	I.00	52.16	N

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ATOM  18710  CA   ASN  D  979    25..794   52.. 537   14..050   1.00   44.90      C
ATOM  18711  C    ASM  D  979    25,,401   52.. 222   15.,476   1,00   47.56      C
ATOM  18712  CB   ASN  D  979    26..408   53.,925    13..947   1,00   48,.02      C
ATOM  18713  CG   ASN  D  979    25..456   55.. 052   14..412   1.00   53..03      C
ATOM  18714  OD1  ASN  D  979    25,044    55. 112    15.,575   1,00   48.,61      0
ATOM  18715  ND2  ASN  D  979    25.139    55.,959    13..497   1,00   44,52       N
ATOM  18716  O    ASN  D  980    25..338   53.,167    19.. 864  1,00   50,.42      O
ATOM  18717  N    ASN  D  980    26.,299   52. 512    16.. 409  1,00   44.35      N
ATOM  18718  CA   ASN  D  980    26..034   52.. 193   17..801   1,00   46..91      C
ATOM  18719  C    ASN  D  980    25..588   53.,365    18.. 671  1,00   47,48       C
ATOM  18720  CB   ASN  D  980    27.,275   51.. 565   18.,425   I,00   44.58       C
ATOM  18721  CG   ASN  D  980    27.. 487  50.. 152   17..973   1,00   44.95       C
ATOM  18722  OD1  ASN  D  980    26. 738   49.,271    18. 347   1,00   46,38       0
ATOM  18723  ND2  ASN  D  980    28.. 514  49.. 927   17..172   1.00   41.05       N
ATOM  18724  N    TYR  D  981    25.,503   54.. 569   18.. 094  1,00   45..55      N
ATOM  18725  C    TYR  D  981    23.. 770  55.,610    I9..533   1,00   43,.79      C
ATOM  18726  CA   TYR  D  981    25.. 146  55.. 765   18.. 862  1.00   46..49      C
ATOM  18727  O    TYR  D  981    23.,495   56. 230    20.,559   1,00   48..95      0
ATOM  18728  CB   TYR  D  981    25..134   57.,019    17..985   1,00   51,48       C
ATOM  18729  CG   TYR  D  981    26.. 463  57.,487    17..399   1,00   52,27       C
ATOM  18730  CD2  TYR  D  981    26.,628   58. 805    16.,964   1,00   46..65      C
ATOM  18731  CD1  TYR  D  981    27.. 544  56.. 625   17..272   1,00   50..15      C
ATOM  18732  CE2  TYR  D  981    27..842   59.,242    16.. 421  1,00   55,.32      C
ATOM  18733  CE1  TYR  D  981    28.,757   57.. 049   16.,723   I,00   47.16       C
ATOM  18734  CZ   TYR  D  981    28.. 907  58.. 344   16.. 297  1,00   52.76       C
ATOM  18735  OH   TYR  D  981    30. 118    58.,744    15. 764   1,00   49,95       0
ATOM  18736  N    HIS  D  982    22.,930   54.. 741   18.,979   I,00   44.43       N
ATOM  18737  C    HIS  D  982    21.,589   54.. 128   20.,957   1,00   50..36      C
ATOM  18738  CA   HIS  D  982    21.584    54,560    19. 499   1,00   43,22       C
ATOM  18739  O    HIS  D  982    20.. 632  54.. 411   21.. 675  1.00   47.37       0
ATOM  18740  CB   HIS  D  982    20.,787   53.. 559   18.,650   1,00   42.71       C
ATOM  18741  CG   HIS  D  982    21.. 233  52.,132    18..795   1,00   47,36       C
ATOM  18742  ND1  HIS  D  982    21.. 939  51.. 466   17..814   1.00   46..41      N
ATOM  18743  CD2  HIS  D  982    21.,039   51. 235    19.,792   1,00   48..82      C
ATOM  18744  CE1  HIS  D  982    22..172   50.,226    18..208   1,00   48,.21      C
ATOM  18745  NE2  HIS  D  982    21.640    50.,061    19.. 405  1,00   46,.70      N
ATOM  18746  N    HIS  D  983    22.,650   53. 443    21.,398   1,00   47.97       N
ATOM  18747  C    HIS  D  983    22.. 883  54.. 316   23.. 673  1,00   39..40      C
ATOM  18748  CA   HIS  D  983    22.753    53.,057    22.804    1,00   44,52       C
ATOM  18749  O    HIS  D  983    22.,336   54.. 404   24.,751   I,00   42.39       O
ATOM  18750  CB   HIS  D  983    23.,971   52.. 131   23.,063   1,00   45..92      C
ATOM  18751  CG   HIS  D  983    23.920    50.,803    22.372    1,00   48,95       C
ATOM  18752  ND1  HIS  D  983    23.. 055  49.. 795   22.. 745  1.00   55..56      N
ATOM  18753  CD2  HIS  D  983    24.,666   50.. 298   21.,358   1,00   49..89      C
ATOM  18754  CE1  HIS  D  983    23.. 260  48.,733    21.. 984  1,00   46,.28      C
ATOM  18755  NE2  HIS  D  983    24.. 231  49.. 014   21.. 131  1.00   48..59      N
ATOM  18756  N    ALA  D  984    23.,661   55. 273    23.,201   1,00   41.88       N
ATOM  18757  C    ALA  D  984    22.. 755  57.,418    23.. 897  1,00   48,.40      C
ATOM  18758  CA   ALA  D  984    23.. 955  56.,466    23.. 974  1,00   42,42       C
ATOM  18759  O    ALA  D  984    22.,295   57. 928    24.,917   1,00   49..04      0
ATOM  18760  CB   ALA  D  984    25.. 229  57.. 137   23.. 456  1,00   41.47       C
ATOM  18761  N    HIS  D  985    22..249   57.,626    22..680   1,00   45,.96      N
ATOM  18762  C    HIS  D  985    19.,908   57.. 852   23.,414   I,00   49.46       C
ATOM  18763  CA   HIS  D  985    20.. 993  58.. 349   22.. 478  1,00   48..71      C
ATOM  18764  O    HIS  D  985    19. 200    58.,645    24.040    1,00   51,97       O
ATOM  18765  CB   HIS  D  985    20.,508   58.. 191   21.,056   I,00   46..59      C
ATOM  18766  CG   HIS  D  985    21.,410   58.. 798   20.,045   1,00   37.91       C
ATOM  18767  ND1  HIS  D  985    22.409    59.,675    20. 383   1,00   41,20       N
ATOM  18768  CD2  HIS  D  985    21.. 446  58.. 679   18.. 701  1.00   36..43      C
ATOM  18769  CEl  HIS  D  985    23.,038   60.. 064   19.,289   1,00   50..04      C
ATOM  18770  NE2  HIS  D  985    22.. 478  59.,468    18..255   1,00   42,79       N
ATOM  18771  N    ASP  D  986    19.. 799  56.. 532   23.. 517  1.00   43..55      N
ATOM  18772  C    ASP  D  986    18.,990   56. 369    25,827    1,00   55..33      C
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ATOM  18773  CA   ASP  D 986    18.805  55.926  24.382  1.00 49.89      c
ATOM  18774  O    ASP  D 986    18.017  56.561  26.540  1.00 52.99      O
ATOM  18775  CB   ASP  D 986    18.867  54.408  24.298  1.00 45.97      c
ATOM  18776  CG   ASP  D 986    17.887  53.841  23.299  1.00 52.15      c
ATOM  18777  OD1  ASP  D 986    17.414  54.601  22.428  1.00 56.08      0
ATOM  18778  OD2  ASP  D 986    17.574  52.635  23.392  1.00 62.99      0
ATOM  18779  N    ALA  D 987    20.243  56.539  26.248  1.00 51.69      N
ATOM  18780  C    ALA  D 987    20.192  58.360  27.909  1.00 49.85      C
ATOM  18781  CA   ALA  D 987    20.527  56.899  27.633  1.00 51.01      C
ATOM  18782  O    ALA  D 987    19.686  58.694  28.983  1.00 48.97      0
ATOM  18783  CB   ALA  D 987    22.000  56.623  27.976  1.00 46.47      c
ATOM  18784  N    TYR  D 988    20.543  59.209  26.950  1.00 48.85      N
ATOM  18785  CA   TYR  D 988    20.218  60.632  26.962  1.00 53.09      C
ATOM  18786  c    TYR  D 988    18.711  60.849  27.107  1.00 56.27      c
ATOM  18787  O    TYR  D 988    18.243  61.445  28.077  1.00 54.05      0
ATOM  18788  CB   TYR  D 988    20.719  61.275  25.676  1.00 52.09      c
ATOM  18789  CG   TYR  D 988    20.331  62.734  25.481  1.00 63.83      c
ATOM  18790  CD1  TYR  D 988    21.027  63.745  26.128  1.00 62.08      c
ATOM  18791  CD2  TYR  D 988    19.305  63.101  24.614  1.00 65.43      c
ATOM  18792  CE1  TYR  D 988    20.711  65.057  25.945  1.00 58.62      c
ATOM  18793  CE2  TYR  D 988    18.971  64.435  24.417  1.00 63.93      c
ATOM  18794  CZ   TYR  D 988    19.681  65.411  25.092  1.00 67.76      c
ATOM  18795  OH   TYR  D 988    19.380  66.752  24.924  1.00 61.19      0
ATOM  18796  N    LEU  D 989    17.969  60.309  26.143  1.00 55.15      N
ATOM  18797  CA   LEU  D 989    16.524  60.380  26.124  1.00 50.69      c
ATOM  18798  C    LEU  D 989    15.890  59.902  27.415  1.00 52.78      c
ATOM  18799  O    LEU  D 989    14.803  60.343  27.777  1.00 58.09      0
ATOM  18800  CB   LEU  D 989    15.982  59.590  24.941  1.00 52.48      c
ATOM  18801  CG   LEU  D 989    16.125  60.298  23.593  1.00 52.89      c
ATOM  18802  CD1  LEU  D 989    15.608  59.445  22.476  1.00 56.70      c
ATOM  18803  CD2  LEU  D 989    15.382  61.627  23.600  1.00 58.18      c
ATOM  18804  N    ASN  D 990    16.559  59.017  28.133  1.00 54.38      N
ATOM  18805  CA   ASN  D 990    16.038  58.630  29.436  1.00 54.29      c
ATOM  18806  C    ASM  D 990    16.342  59.667  30.496  1.00 55.66      c
ATOM  18807  O    ASN  D 990    15.563  59.849  31.437  1.00 50.90      0
ATOM  18808  CB   ASN  D 990    16.591  57.289  29.868  1.00 47.51      c
ATOM  18809  CG   ASN  D 990    15.737  56.142  29.385  1.00 56.31      c
ATOM  18810  OD1  ASN  D 990    14.856  55.668  30.099  1.00 58.77      0
ATOM  18811  ND2  ASN  D 990    15.964  55.712  28.156  1.00 58.55      N
ATOM  18812  N    ALA  D 991    17.487  60.322  30.357  1.00 53.60      N
ATOM  18813  CA   ALA  D 991    17.853  61.365  31.295  1.00 57.30      C
ATOM  18814  C    ALA  D 991    16.820  62.488  31.193  1.00 54.46      C
ATOM  18815  O    ALA  D 991    16.265  62.908  32.191  1.00 54.86      0
ATOM  18816  CB   ALA  D 991    19.250  61.883  31.024  1.00 49.85      c
ATOM  18817  N    VAL  D 992    16.555  62.926  29.968  1.00 56.32      N
ATOM  18818  CA   VAL  D 992    15.609  64.003  29.692  1.00 55.49      c
ATOM  18819  C    VAL  D 992    14.202  63.701  30.191  1.00 56.50      C
ATOM  1882 0 O    VAL  D 992    13.697  64.398  31.052  1.00 60.20      O
ATOM  1882 1 CB   VAL  D 992    15.539  64.275  28.210  1.00 53.90      c
ATOM  18822  CGI  VAL  D 992    14.462  65.299  27.920  1.00 61.80      c
ATOM  1882 3 CG2  VAL  D 992    16.903  64.713  27.690  1.00 52.48      c
ATOM  1882 4 N    VAL  D 993    13.579  62.655  29.659  1.00 54.02      N
ATOM  1882 5 CA   VAL  D 993    12.256  62.251  30.106  1.00 54.88      C
ATOM  1882 6 C    VAL  D 993    12.232  62.006  31.627  1.00 61.68      C
ATOM  1882 7 O    VAL  D 993    11.210  62.204  32.297  1.00 61.13      O
ATOM  1882 8 CB   VAL  D 993    11.782  60.986  29.336  1.00 54.58      C
ATOM  1882 9 CGI  VAL  D 993    10.478  60.437  29.899  1.00 47.37      C
ATOM  18830  CG2  VAL  D 993    11.609  61.309  27.863  1.00 54.13      c
ATOM  18831  N    GLY  D 994    13.370  61.595  32.180  1.00 60.29      N
ATOM  18832  CA   GLY  D 994    13.476  61.368  33.613  1.00 54.25      C
ATOM  18833  C    GLY  D 994    13.426  62.677  34.386  1.00 60.11      c
ATOM  18834  O    GLY  D 994    12.591  62.870  35.257  1.00 58.88      0
ATOM  18835  N    TH.R D 995    14.348  63.564  34.045  1.00 56.23      N
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ATOM   18836  CA   THR  D  995      14 .511   64.,852   34..675   1 .00  59..58          C
ATOM   18837  C    THR  D  995      13,,268   65..728   34,,473   1 ,00  66..76          C
ATOM   18838  O    THR  D  995      12 .832   66.,436   35...379  1 ,00  64 ,40          0
ATOM   18839  CB   THR  D  995      15..731   65.,578   34..092   1 .00  65..52          C
ATOM   18840  OG1  THR  D  995      16,,862   64. 699   .34,,102  1 ,00  67 ,92          0
ATOM   18841  CG2  THR  D  995      16 .047   66.,844   34..891   1 ,00  68,,50          C
ATOM   18842  N    ALA  D  996      12..713   65,,667   33..268   1 ,00  63,.34          N
ATOM   18843  CA.  ALA  D  996      11 „513   66. 410   .32,,939  1 ,00  69.,49          C
ATOM   18844  C    ALA  D  996      10..386   66.,021   33.,886   1 ,00  67 .67          C
ATOM   18845  O    ALA  D  996       9 ..921  66,,838   34..679   1 ,00  69,.04          0
ATOM   18846  CB   ALA  D  996      11 ,116   66.. 167  31.,492   I ,00  64 .32          C
ATOM   18847  N    LEU  D  997       9 .982   64.,763   33.,816   1 ,00  59..26          N
ATOM   18848  CA   LEU  D  997       8 .867   64,,258   34. 601   1 ,00  61 ,41          C
ATOM   18849  C    LEU  D  997       8 ..975  64.,609   36.,083   1 .00  70..55          C
ATOM   18850  O    LEU  D  997       8 „053   65.. 171  36,,672   1 ,00  72 .09          0
ATOM   18851  CB   LEU  D  997       8 ..757  62.,743   34..441   1 ,00  61 ,96          C
ATOM   18852  CG   LEU  D  997       7 .783   62.,186   33..404   1 .00  59..31          C
ATOM   18853  CD1  LEU  D  997       8 „335   60. 906   .32,,786  1 ,00  61 ,21          C
ATOM   18854  CD2  LEU  D  997       6 ..473  61.,899   34..083   1 ,00  59,.24          C
ATOM   18855  N    ILE  D  998      10..109   64,,287   36..687   1 ,00  70,.45          N
ATOM   18856  CA.  ILE  D  998      10,,270   64. 492   .38,,119  1 ,00  65.,47          C
ATOM   18857  C    ILE  D  998      10.,129   65.,975   38.,519   1 ,00  68..02          C
ATOM   18858  O    ILE  D  998       9 ..769  66,,287   39..652   1 ,00  64 ,08          0
ATOM   18859  CB   ILE  D  998      11 ,618   63..956   .38.,589  I ,00  55..83          C
ATOM   18860  CGI  ILE  D  998      11 ,570   63.,651   40 ,075   1 ,00  56..70          C
ATOM   188 61  CG2  ILE  D  998      12 .739   64,,917   38. 250   1 ,00  56 ,20          C
ATOM   18862  CD1  ILE  D  998      12.,741   62..849   40.,549   I ,00  66..67          C
ATOM   18863  O    LYS  D  999       8 „543   69..895   37,,156   1 ,00  74 .23          0
ATOM   188 64  N    LYS  D  999      10. 404   66,,868   37. 570   1 ,00  68 ,45          N
ATOM   18865  CA   LYS  D  999      10.,261   68.,304   37.,761   1 .00  71 .94          C
ATOM   18866  C    LYS  D  999       8 „808   68.. 744  37,,494   1 ,00  76..88          C
ATOM   18867  CB   LYS  D  999      11 .220   69.,056   36..843   1 ,00  70,.30          C
ATOM   18868  CG   LYS  D  999      12.,647   69.,149   37..328   1 .00  65..63          C
ATOM   18869  CD   LYS  D  999      13,,519   69. 640   36 „179   1 ,00  66.,68          C
ATOM   18870  CE   LYS  D  999      14 .913   70.,040   36..622   1 ,00  69,.51          C
ATOM   18871  NZ   LYS  D  999      15.. 721  70 „493   35..448   1 ,00  74 ,13          N
ATOM   18872  O    LYS  D1000       4 „732   66. .394   .37,,650  1 ,00  76.,50          0
ATOM   18873  N    LYS  D1000       7 ,886   67..793   37.,624   1 ,00  75..87          N
ATOM   18874  CA   LYS  D1000       6 .464   68,,045   37. 532   1 ,00  72 ,63          C
ATOM   18875  C    LYS  D1000       5 ,724   66..880   .38.,190  I ,00  72 .11          C
ATOM   18876  CB   LYS  D1000       6 „028   68..227   36,,073   1 ,00  72 .97          C
ATOM   18877  O    TYR  D1001       7 .260   65,,561   41 .842   1 ,00  80 ,73          0
ATOM   18878  N    TYR  D1001       6 ,218   66.,441   39.,353   1 .00  75..45          N
ATOM   18879  CA   TYR  D1001       5 „574   65..368   40,,128   1 ,00  79..11          C
ATOM   18880  C    TYR  D1001       6 .184   65.,067   41 .504   1 ,00  80,.87          C
ATOM   18881  CB   TYR  D1001       5 ,581   64.,064   39..326   1 .00  82 .88          C
ATOM   18882  O    PRO  D1002       5 ,983   61. 660   41 „815   1 ,00  76.,13          0
ATOM   18883  N    PRO  D1002       5 .454   64.,275   42 .312   1 ,00  85,.73          N
ATOM   18884  CA   PRO  D1002       5 .912   63,,424   43..425   1 ,00  83,.01          C
ATOM   18885  C    PRO  D1002       6 „321   62. 011   42,,944   1 ,00  79.,60          C
ATOM   18886  CB   PRO  D1002       4 ,682   63.,352   44 ,351   1 ,00  86..66          C
ATOM   18887  CG   PRO  D1002       3 .729   64,,410   43..865   1 ,00  80,.52          C
ATOM   18888  CD   PRO  D1002       4 ,005   64..540   42.,401   I ,00  88..90          C
ATOM   18889  O    LYS  D1003       6 ,997   58..095   44 ,628   1 ,00  65..85          0
ATOM   188 90  N    LYS  D1003       6 .978   61,,218   43. 803   1 ,00  88 ,09          N
ATOM   188 91  CA   LYS  D1003       7 „797   60..049   43.,398   I ,00  73..77          C
ATOM   18892  C    LYS  D1003       7 „180   58..638   43,,528   1 ,00  72 .84          C
ATOM   188 93  CB   LYS  D1003       9 .100   60,,084   44 .189   1 ,00  70 ,28          C
ATOM   18894  CG   LYS  D1003       9 ,604   61.,506   44 .404   1 .00  73..34          C
ATOM   18895  CD   LYS  D1003      10,,421   61..627   45,,678   1 ,00  77 .52          C
ATOM   18896  CE   LYS  D1003      10 ..365  63.,037   46..251   1 ,00  61 ,92          C
ATOM   18897  NZ   LYS  D1003      10.,937   64.,049   45..329   1 .00  63..91          N
ATOM   18898  O    LEU  D1004       7 „717   54. 713   41 „440   1 ,00  66.,18          0
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ATOM   18899   N    LEU  D1004        6.889   58.069   42.362   1.00  71.15           N
ATOM   18900   CA   LEU  D1004        6.496   56.676   42.161   1.00  66.77           C
ATOM   18901   C    LEU  D1004        7.676   55.941   41.5.15  1.00  70.18           C
ATOM   18902   CB   LEU  D1004        5.264   56.612   41.246   1.00  66.82           C
ATOM   18903   CG   LEU  D.1004       4.464   55.402   40.723   1.00  73.29           C
ATOM   18904   CD2  LEU  D1004        3.665   54.775   41.857   1.00  81.10           C
ATOM   18905   CD1  LEU  D1004        5.238   54.333   39.890   1.00  70.83           C
ATOM   18906   O    GLU  D.1005      12.070   56.451   40.049   1.00  68.9.3          0
ATOM   18907   N    GLU  D100 5       8.635   56.725   41.039   1.00  71.46           N
ATOM   18908   CA   GLU  D1005        9.686   56.236   40.156   1.00  72.41           C
ATOM   18909   C    GLU  D1005       11.070   56.457   40.764   1.00  68..34          C
ATOM   18910   CB   GLU  D100 5       9.586   56.945   38.793   1.00  70.56           C
ATOM   18911   CG   GLU  D1005        9.647   58.473   38.925   1.00  67.82           C
ATOM   18912   CD   GLU  D1005        9.772   59.195   37.595   1.00  72.39           C
ATOM   18913   OE1  GLU  D1005        9.175   58.737   36.600   1.00  74.44           0
ATOM   18914   OE2  GLU  D1005       10.473   60.230   37.549   1.00  68.76           0
ATOM   18915   O    SER  D100 6      11.755   55.088   44.262   1.00  78.13           0
ATOM   18916   N    SER  D.1006       1..118   56.694   42.073   1.00  68.52           N
ATOM   18917   CA   SER  D100 6      12..392   56.846   42.773   1.00  69.44           C
ATOM   18918   C    SER  D1006       12.659   55.605   43.603   1.00  77.23           C
ATOM   18919   CB   SER  D.1006      12.403   58.088   4.3.652  1.00  72.58           C
ATOM   18920   OG   SER  D100 6      13.446   58.960   43.254   1.00  74.18           0
ATOM   18921   O    GLU  D1007       13.161   51.934   44.903   1.00  77.13           0
ATOM   18922   N    GLU  D1.007      13.915   55.168   4.3.593  1.00  71.99           N
ATOM   18923   CA   GLU  D1007       14.273   53.777   43.851   1.00  72.87           C
ATOM   18924   C    GLU  D1007       13.617   5.3.072  45.041   1.00  75.67           C
ATOM   18925   CB   GLU  D1.007      15.783   53.665   4.3.989  1.00  72.73           C
ATOM   18926   CG   GLU  D1007       16.307   52.374   43.404   1.00  70.56           C
ATOM   18927   CD   GLU  D1007       16.190   51.218   44..358   1.00  72.04           C
ATOM   18928   OE1  GLU  D1007       16.510   51.414   45.562   1.00  68.49           0
ATOM   18929   OE2  GLU  D1007       15.784   50.121   43.903   1.00  72.25           0
ATOM   18930   O    PHE  D1008       12.4.14  54.642   49.043   1.00  77.05           0
ATOM   18931   N    PHE  D1008       13.573   53.701   46.206   1.00  75.79           N
ATOM   18932   CA.  PHE  D1008       12.815   53.085   47.295   1.00  77.16           C
ATOM   18933   C    PHE  D1008       11.976   54.105   48.034   1.00  77.93           C
ATOM   18934   CB   PHE  D1008       13.747   52.371   48.269   1.00  77.67           C
ATOM   18935   O    VAL  D1009        8.389   54.469   46.286   1.00  82.87           0
ATOM   18936   N    VAL  D100 9      10.781   54.362   47.496   1.00  82.43           N
ATOM   18937   CA   VAL  D100 9       9.743   55.229   48.072   1.00  74.82           C
ATOM   18938   C    VAL  D1.00 9      8.425   54.733   47.486   1.00  78.99           C
ATOM   18939   CB   VAL  D1009        9.954   56.716   47.716   1.00  73.35           C
ATOM   18940   CGI  VAL  D100 9       8.656   57.497   47.851   1.00  7.3.94          C
ATOM   18941   CG2  VAL  D100 9      11.067   57.341   48.561   1.00  77.29           C
ATOM   18942   O    TYR  D1010        4.802   53.578   49.717   1.00  83.80           0
ATOM   18943   N    TYR  D1010        7..357   54.587   48.281   1.00  78.17           N
ATOM   18944   CA   TYR  D1010        6.089   54.076   47.715   1.00  80.19           C
ATOM   18945   C    TYR  D1010        4.808   54.096   48.595   1.00  81..39          C
ATOM   18946   CB   TYR  D1010        6..309   52.623   47.234   1.00  76.06           C
ATOM   18947   CG   TYR  D1010        5.794   52.378   45.838   1.00  67.84           C
ATOM   18948   CD2  TYR  D1010        4.565   51.762   45.627   1.00  70.85           C
ATOM   18949   CD1  TYR  D1010        6.521   52.791   44.733   1.00  66.08           C
ATOM   18950   CE2  TYR  D1010        4.074   51.555   44.349   1.00  69.11           C
ATOM   18951   CE1  TYR  D1.010       6.046   52.597   4.3.462  1.00  71.51           C
ATOM   18952   CZ   TYR  D1010        4.825   51.972   43.270   1.00  77.53           C
ATOM   18953   OH   TYR  D1010        4..364   51.769   41.986   1.00  90.44           0
ATOM   18954   O    GLY  DI011        1.328   54.903   46.594   1.00  97.2.1          0
ATOM   18955   N    GLY  D1011        3.716   54.646   48.050   1.00  75.90           N
ATOM   18956   CA   GLY  D1011        2.4.12   54.578   48.693   1.00  8.3.14          C
ATOM   18957   C    GLY  D1011        1.239   55.000   47.815   1.00  91.93           C
ATOM   18958   O    ASP  D1012       -2.438   54.771   46.118   1.00  96.97           0
ATOM   18959   N    ASP  D1012        0.156   55.470   48.444   1.00  87.12           N
ATOM   18960   CA   ASP  D1012      --1.075   55.937   47.771   1.00  92.05           C
ATOM   18961   C    ASP  D1012      -.1.357   55..323   46.379   1.00  99.07           C
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ATOM   18962   CB   ASP  D1012      -1.063   57..475   47.657   1.00   80..22          C
ATOM   18963   CG   ASP  D1012       0„177   58..016   46.,950   1,00   84.71           C
ATOM   18964   OD1  ASP  D1012       0..259   57.,914   45..701   1,00   86,.87          0
ATOM   18965   OD2  ASP  D1012       1.061   58..566   47.641   1.00   76..50          0
ATOM   18966   N    TYR  D1039      0„072    56. 192   .32.,701   1,00   82.84           N
ATOM   18967   CA   TYR  D103 9     1.436    56.,729   32..690   1,00   81,33           C
ATOM   18968   C    TYR  D1039      1.776    57.,398   31..358   1,00   78,.56          C
ATOM   18969   0    TYR  D1039      2„518    58. 385   31.,320   1,00   72..35          0
ATOM   18970   CB   TYR  D103 9     2..467   55..638   33..015   1,00   71.18           C
ATOM   18971   CG   TYR  D1039      3..545   56.,131   33..975   1,00   72,83           C
ATOM   18972   CD2  TYR  D103 9     3„836    55..440   .35.,153   I,00   73..62          C
ATOM   18973   GDI  TYR  D103 9     4.237    57..318   33..729   1,00   76..68          C
ATOM   18974   CE2  TYR  D1039      4.810    55.,904   36. 050   1,00   68,13           C
ATOM   18975   CE1  TYR  D1039      5..211   57..789   34..618   1.00   74.92           C
ATOM   18976   CZ   TYR  D1039      5„491    57..074   35.,775   1,00   69..95          C
ATOM   18977   OH   TYR  D103 9     6..443   57.,530   36..664   1,00   68,.38          0
ATOM   18978   N    SER  D104 0     1.220    56..870   30..271   1.00   74.87           N
ATOM   18979   CA.  SER  D1040      1„349    57. 528   28.,979   1,00   74.59           C
ATOM   18980   C    SER  D104 0     0..405   58.,718   28..932   1,00   81,48           C
ATOM   18981   O    SER  D1040      0..522   59.,594   28..066   1,00   77,73           0
ATOM   18982   CB   SER  D1040      1„058    56. 560   27.,835   1,00   71.04           C
ATOM   18983   OG   SER  D104 0     2..221   55..806   27..509   1,00   86..22          0
ATOM   18984   N    ASN  D1041     -0..533   58.,733   29..876   1,00   79,.70          N
ATOM   18985   CA   ASM  D1041     -1„426    59.868    .30.,050   I,00   86..71          C
ATOM   18986   C    ASN  D1041     -0..680   61..067   30..622   1,00   82.02           C
ATOM   18987   O    ASN  D1041     -0.928    62.,200   30. 248   1,00   79,69           0
ATOM   18988   CB   ASN  D1041     -2„592    59.489    .30.,960   I,00   91.54           C
ATOM   18989   CG   ASN  D1041     -3„798    60..373   30.,751   1,00   95..64          C
ATOM   18990   OD1  ASN  D1041     -3.670    61.,574   30. 501   1,00   96,67           0
ATOM   18991   ND2  ASN  D1041     -4.982    59..781   30..838   1.00   98..81          N
ATOM   18992   N    ILE  D1042      0„247    60..792   31.,528   1,00   82.39           N
ATOM   18993   CA   ILE  D104 2     1.062    61.,817   32..165   1,00   78,.06          C
ATOM   18994   C    ILE  D104 2     2.128    62..345   31..214   1.00   77.77           C
ATOM   18995   O    ILE  D1042      2„507    63. 513   31.,263   1,00   80..50          0
ATOM   18996   CB   ILE  D104 2     1.731    61.,268   33..426   1,00   75,.94          C
ATOM   18997   CGI  ILE  D1042      0..673   60.,853   34..456   1,00   81,11           C
ATOM   18998   CG2  ILE  D1042      2„682    62. 292   .34.,013   1,00   82.67           C
ATOM   18999   CD1  ILE  D104 2     0..102   59..449   34..276   1,00   84.04           C
ATOM   19000   N    MET  D104 3     2.600    61.,464   30. .339   1,00   80,95           N
ATOM   19001   CA   MET  D104 3     3„552    61..825   29.,291   I,00   81.68           C
ATOM   19002   C    MET  D104 3     2,948    62..862   28.,354   1,00   81.15           C
ATOM   19003   O    MET  D104 3     3.651    63.,686   27.758   1,00   77,57           O
ATOM   19004   CB   MET  D1043      3..975   60..581   28..509   1.00   75..57          C
ATOM   19005   CG   MET  D104 3     4,994    59..715   29.,239   1,00   76..47          C
ATOM   19006   SD   MET  D104 3     6..600   60.,517   29..242   1,00   73,.78          S
ATOM   19007   CE   MET  D1043      6..925   60..610   27..480   1.00   63..32          C
ATOM   19008   N    ASN  D1044      1„628    62. 795   28.,232   1,00   80..80          N
ATOM   19009   C    ASN  D104 4     1.089    65.,187   28..024   1,00   84,86           C
ATOM   19010   CA   ASN  D1044      0..864   63.,785   27.493   1,00   85,.34          C
ATOM   19011   O    ASN  D1044      1„498    66. 095   27.,289   1,00   79...38         0
ATOM   19012   CB   ASN  D104 4    -0..619   63..457   27..568   1,00   80..16          C
ATOM   19013   CG   ASN  D1044     -1.232    63.,284   26..226   1,00   83,.30          C
ATOM   19014   OD1  ASN  D104 4    -0„707    63..786   25.,226   I,00   85..21          0
ATOM   19015   ND2  ASN  D104 4    -2.356    62..575   26..176   1,00   87.14           N
ATOM   19016   O    PHE  D104 5     1.970    68.,544   29. 227   1,00   97,38           O
ATOM   19017   N    PHE  D104 5     0„828    65...329  29.,323   I,00   89..62          N
ATOM   19018   CA   PHE  D104 5     0„751    66..629   29.,982   1,00   95..36          C
ATOM   19019   C    PHE  D104 5     2.019    67.,420   29. 714   1,00   90,82           C
ATOM   19020   CB   PHE  D1045      0.518    66..469   31..496   1.00   93..92          C
ATOM   19021   CG   PHE  D104 5    -0„806    65..825   31..856   1,00   94.47           C
ATOM   19022   CD2  PHE  D104 5    -1.008    65.,287   33..123   1,00   93,.83          C
ATOM   19023   CD1  PHE  D1045     -1.847    65..761   30..934   1.00   91.96           C
ATOM   19024   CE2  PHE  D1045     -2„220    64. 694   .33.,463   1,00   97.54           C
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ATOM   19025  CE1  PHE  D1045      --3.058   65.164   31.266   1.00  99.19         c
ATOM   19026  CZ   PHE  D1045      -3.246   64.633   32.534   1.00  99.46         c
ATOM   19027  O    PHE  D1046       4.344   68.895   27.860   1.00  85.71         0
ATOM   19028  N    PHE  D1046       3.153   66.807   30.008   1.00  93.60         N
ATOM   19029  CA.  PHE  D1046       4.435   67.449   29.792   1.00  93.43         C
ATOM   19030  C    PHE  D1046       4.576   67.754   28.281   1.00  91.74         C
ATOM   19031  CB   PHE  D1046       5.564   66.563   30.419   1.00  84.59         c
ATOM   19032  CG   PHE  D1046       6.788   66.320   29.543   1.00  92.16         c
ATOM   19033  GDI  PHE  D1046       7.791   67.271   29.426   1.00  92.31         c
ATOM   19034  CD2  PHE  D1046       6.966   65.097   28.896   1.00  87.31         c
ATOM   19035  CE1  PHE  D1046       8.914   67.021   28.637   1.00  85.92         c
ATOM   19036  CE2  PHE  D1046       8.077   64.856   28.116   1.00  77.09         c
ATOM   19037  CZ   PHE  D1046       9.045   65.814   27.983   1.00  79.71         c
ATOM   19038  O    LYS  D1047       4.928   68.569   24.473   1.00  74.93         0
ATOM   19039  N    LYS  D1047       4.838   66.741   27.463   1.00  88.93         N
ATOM   19040  CA   LYS  D1047       5.461   66.971   26.162   1.00  84.40         c
ATOM   19041  c    LYS  D1047       4.553   67.591   25.110   1.00  75.29         c
ATOM   19042  CB   LYS  D1047       6.030   65.652   25.614   1.00  79.29         c
ATOM   19043  O    THR  D1048       2.122   69.461   22.899   1.00  71.64         0
ATOM   19044  N    THR  D1048       3.375   67.009   24.922   1.00  72.67         N
ATOM   19045  CA.  THR  D1048       2.584   67.260   23.720   1.00  76.11         C
ATOM   19046  C    THR  D1048       1.857   68.601   23.740   1.00  73.09         C
ATOM   19047  CB   THR  D1048       1.556   66.132   23.493   1.00  80.29         c
ATOM   19048  OG1  THR  D1048       1.265   65.483   24.738   1.00  81.79         0
ATOM   19049  CG2  THR  D1048       2.104   65.095   22.524   1.00  76.60         c
ATOM   19050  O    THR  D1065       6.115   74.262   31.943   1.00  72.70         0
ATOM   19051  N    THR  D1065       5.129   72.832   29.776   1.00  78.70         N
ATOM   19052  CA   THR  D1065       4.238   73.211   30.863   1.00  70.22         c
ATOM   19053  C    THR  D1065       5.016   73.717   32.086   1.00  73.92         c
ATOM   19054  CB   THR  D1065       3.348   72.045   31.246   1.00  65.88         c
ATOM   19055  OG1  THR  D1065       4.091   71.121   32.042   1.00  77.51         0
ATOM   19056  CG2  THR  D1065       2.838   71.354   29.976   1.00  67.08         c
ATOM   19057  O    ASN  D1066       4.184   72.377   35.804   1.00  77.01         0
ATOM   19058  N    ASM  D1066       4.452   73.552   33.281   1.00  70.47         N
ATOM   19059  CA   ASN  D1066       5.025   74.191   34.463   1.00  75.79         c
ATOM   19060  c    ASN  D1066       4.999   73.306   35.707   1.00  78.04         c
ATOM   19061  CB   ASN  D1066       4.296   75.515   34.753   1.00  78.46         c
ATOM   19062  O    GLY  D1067       5.101   71.911   39.817   1.00  83.07         0
ATOM   19063  N    GLY  D1067       5.881   73.618   36.661   1.00  77.53         N
ATOM   19064  CA   GLY  D1067       6.114   72.780   37.831   1.00  84.50         C
ATOM   19065  C    GLY  D1067       5.000   72.691   38.860   1.00  88.22         C
ATOM   19066  O    GUI  D1068       2.160   73.605   41.834   1.00  89.42         O
ATOM   19067  N    GLU  D1068       3.959   73.507   38.675   1.00  93.30         N
ATOM   19068  CA   GLU  D1068       2.736   73.465   39.495   1.00  95.08         C
ATOM   19069  C    GLU  D1068       2.973   73.887   40.947   1.00  95.45         C
ATOM   19070  CB   GLU  D1068       2.115   72.063   39.459   1.00  90.83         c
ATOM   19071  O    THR  D1069       6.108   76.265   43.696   1.00  94.89         0
ATOM   19072  N    THR  D1069       4.092   74.566   41.173   1.00  93.53         N
ATOM   19073  CA   THR  D1069       4.461   75.042   42.497   1.00  88.09         c
ATOM   19074  C    THR  D1069       5.505   76.165   42.629   1.00  92.40         c
ATOM   19075  CB   THR  D1069       5.013   73.891   43.339   1.00  93.63         c
ATOM   19076  OG1  THR  D1069       5.385   74.389   44.631   1.00  90.19         0
ATOM   19077  CG2  THR  D1069       6.247   73.273   42.652   1.00  94.43         c
ATOM   19078  O    GLY  D1070       7.472   77.814   39.692   1.00  85.88         0
ATOM   19079  N    GLY  D1070       5.779   76.991   41.615   1.00  88.04         N
ATOM   19080  CA   GLY  D1070       5.384   76.848   40.230   1.00  87.54         C
ATOM   19081  C    GLY  D1070       6.703   76.874   39.514   1.00  85.47         c
ATOM   19082  O    GLU  D1071       7.531   74.958   36.068   1.00  77.26         0
ATOM   19083  N    GLU  D1071       6.992   75.841   38.733   1.00  91.87         N
ATOM   19084  CA   GLU  D1071       8.348   75.678   38.218   1.00  86.64         c
ATOM   19085  C    GLU  D1071       8.435   75.494   36.708   1.00  82.11         c
ATOM   19086  CB   GLU  D1071       9.024   74.501   38.917   1.00  85.10         c
ATOM   19087  O    ILE  D1072      11.734   74.495   34.399   1.00  81.19         0
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ATOM   19088   N     ILE  D1072       9.563   75.930   36.160   1.00  84.26          N
ATOM   19089   CA    ILE  D1072       9.802   75.939   34.722   1.00  85.28          C
ATOM   19090   C     ILE  D107 2     10.527   74.678   34.205   1.00  88.51          C
ATOM   19091   CB    ILE  D1072      10.603   77.182   34.348   1.00  89.44          C
ATOM   19092   CGI   ILE  D1072      11.735   77.394   35.361   I.00  85.75          C
ATOM   190 93  CG2   ILE  D107 2      9.681   78.399   34.352   1.00  93.62          C
ATOM   19094   CD1   ILE  D107 2     12.653   78.546   35.028   1.00  83.56          C
ATOM   19095   O     VAL  D1073      11.781   72.465   31.243   I.00  82.83          0
ATOM   19096   N     VAL  D107 3      9.774   73.825   33.522   1.00  87.83          N
ATOM   19097   CA    VAL  D1073      10.270   72.522   33.108   1.00  86.88          C
ATOM   19098   C     VAL  D107 3     10.610   72.428   31.624   I.00  85.73          C
ATOM   19099   CB    VAL  D107 3      9.248   71.430   33.414   1.00  85.57          C
ATOM   19100   CGI   VAL  D107 3      9.956   70.095   33.534   1.00  83.78          C
ATOM   19101   CG2   VAL  D107 3      8.473   71.766   34.682   1.00  79.70          C
ATOM   19102   N     TRP  D1074       9.578   72.306   30.791   1.00  85.60          N
ATOM   19103   CA    TP.P D107 4      9.774   71.987   29.377   1.00  86.69          C
ATOM   19104   C     TRP  D107 4      9.271   73.055   28.398   1.00  86.62          C
ATOM   19105   0     TRP  D1074       8.089   73.079   28.030   I.00  85.23          0
ATOM   19106   CB    TRP  D107 4      9.098   70.651   29.052   1.00  85.08          C
ATOM   19107   CG    TRP  D1074       9.408   70.174   27.680   1.00  81.93          C
ATOM   19108   CD1   TRP  D1074       8.600   70.237   26.585   I.00  82.42          C
ATOM   19109   CD2   TRP  D107 4     10.627   69.574   27.246   1.00  83.50          C
ATOM   19110   NE1   TRP  D1074       9.241   69.710   25.492   1.00  81.17          N
ATOM   19111   CE2   TRP  D107 4     10.488   69.290   25.874   I.00  82.98          C
ATOM   19112   CE3   TRP  D107 4     11.824   69.236   27.887   1.00  81.82          C
ATOM   191 13  CZ2   TRP  D107 4     11.500   68.689   25.131   1.00  77.09          C
ATOM   19114   CZ3   TRP  D107 4     12.825   68.644   27.149   I.00  70.46          C
ATOM   19115   CH2   TRP  D1074      12.658   68.376   25.787   1.00  71.65          C
ATOM   191 16  O     ASP  D107 5     10.831   74.069   24.890   1.00  73.58          0
ATOM   19117   N     ASP  D107 5     10.176   73.927   27.959   1.00  86.88          N
ATOM   19118   CA    ASP  D1075       9.848   74.889   26.914   1.00  85.34          C
ATOM   19119   C     ASP  D107 5      9.803   74.201   25.559   1.00  79.86          C
ATOM   19120   CB    ASP  D107 5     10.858   76.036   26.875   1.00  85.96          C
ATOM   19121   CG    ASP  D1075      10.687   76.913   25.647   I.00  89.97          C
ATOM   19122   OD2   ASP  D107 5     11.711   77.364   25.092   1.00  91.61          0
ATOM   19123   OD1   ASP  D1075       9.525   77.129   25.229   1.00  92.82          0
ATOM   19124   O     LYS  D1076       8.581   73.360   21.544   I.00  76.52          0
ATOM   19125   N     LYS  D107 6      8.602   73.807   25.138   1.00  78.12          N
ATOM   19126   CA    LYS  D107 6      8.421   73.045   23.905   1.00  73.85          C
ATOM   19127   C     LYS  D107 6      8.871   73.792   22.657   I.00  72.17          C
ATOM   19128   CB    LYS  D107 6      6.954   72.621   23.743   1.00  62.68          C
ATOM   19129   O     GLY  D107 7     11.694   74.768   20.184   1.00  93.11          0
ATOM   19130   N     GLY  D107 7      9.586   74.898   22.832   1.00  75.86          N
ATOM   19131   CA    GLY  D107 7     10.065   75.661   21.699   1.00  82.06          C
ATOM   19132   C     GLY  D107 7     11.463   75.252   21.297   1.00  88.34          C
ATOM   19133   N     ARG  D107 8     12.394   75.429   22.229   1.00  87.86          N
ATOM   19134   CA.   ARG  D1078      13.817   75.287   21.945   I.00  87.94          C
ATOM   19135   C     ARG  D107 8     14.452   74.061   22.625   1.00  82.45          C
ATOM   19136   O     ARG  D1078      15.643   73.797   22.447   1.00  79.49          O
ATOM   19137   CB    ARG  D1078      14.557   76.560   22.373   I.00  84.63          C
ATOM   19138   CG    ARG  D107 8     14.430   76.854   23.857   1.00  90.11          C
ATOM   19139   c D   ARG  D107 8     15.613   77.643   24.390   1.00  92.97          C
ATOM   19140   NE    ARG  D107 8     15.488   77.893   25.823   I.00  90.94          N
ATOM   19141   CZ    ARG  D107 8     16.273   78.718   26.514   1.00  97.38          C
ATOM   19142   NH1   ARG  D107 8     17.255   79.382   25.907   1.00  94.29          N
ATOM   19143   NH2   ARG  D107 8     16.072   78.883   27.818   I.00  97.11          N
ATOM   19144   N     ASP  D1079      13.664   73.332   23.412   1.00  76.78          N
ATOM   19145   CA    ASP  D107 9     14.137   72.105   24.034   1.00  72.41          C
ATOM   19146   C     ASP  D1079      14.172   70.990   22.975   1.00  75.30          C
ATOM   19147   O     ASP  D1079      15.251   70.546   22.571   1.00  70.13          0
ATOM   19148   CB    ASP  D107 9     13.256   71.730   25.225   1.00  73.53          C
ATOM   19149   CG    ASP  D1079      13.597   72.527   26.470   1.00  75.30          C
ATOM   19150   OD1   ASP  D1079      14.689   73.138   26.487   I.00  75.16          0
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ATOM   19151   OD2  ASP  D1079      12.789   72.533   27.430   1.00  74.76         O
ATOM   19152   N    PHE  D1080      13.003   70.586   22.480   1.00  70.94         N
ATOM   19153   CA   PHE  D1080      12.913   69.764   21.275   1.00  68.10         C
ATOM   19154   c    PHE  D1080      13.984   70.115   20.226   1.00  68.93         c
ATOM   19155   O    PHE  D1080      14.340   69.296   19.383   1.00  74.96         0
ATOM   19156   CB   PHE  D1080      11.526   69.898   20.636   1.00  7.1.08        c
ATOM   19157   CG   PHE  D1080      10.464   69.017   21.248   1.00  72.52         c
ATOM   19158   GDI  PHE  D1080      10.524   67.632   21.122   1.00  70.04         c
ATOM   19159   CD2  PHE  D1080       9.376   69.577   21.905   1.00  70.41         c
ATOM   19160   CE1  PHE  D1080       9.532   66.821   21.672   1.00  73.13         c
ATOM   19161   CE2  PHE  D1.080       8.376   68.778   22.453   1.00  71.42         c
ATOM   19162   CZ   PHE  D1080       8.447   67.400   22.337   1.00  74.84         c
ATOM   19163   N    ALA  D1081      14.501   71.332   20.285   1.00  68.86         N
ATOM   19164   CA   ALA  D1081      15.540   71.770   19.374   1.00  70.29         c
ATOM   19165   C    ALA  D1081      16.881   71.231   19.811   1.00  68.80         c
ATOM   19166   O    ALA  D108.1     17.631   70.694   18.990   1.00  68.76         0
ATOM   19167   CB   ALA  D1081      15.584   73.290   19.301   1.00  72.58         c
ATOM   19168   N    TH.R D1082      17.194   71.391   21.098   1.00  64.18         N
ATOM   19169   CA   THR  D1082      18.491   70.941   21.610   1.00  74.60         c
ATOM   19170   c    THR  D1082      18.573   69.400   21.556   1.00  68.12         c
ATOM   19171   0    TH.R D1082      19.561   68.852   21.081   1.00  61.66         0
ATOM   19172   CB   THR  D1082      18.771   71.463   23.049   1.00  77.12         c
ATOM   19173   OG1  THR  D1082      17.567   71.448   23.823   1.00  79.02         0
ATOM   19174   CG2  THR  D1082      19.309   72.899   2.3.009   1.00  65.90         c
ATOM   19175   N    VAL  D1083      17.509   68.732   22.006   1.00  64.79         N
ATOM   19176   CA   VAL  D1083      17.362   67.295   21.855   1.00  65.90         c
ATOM   19177   C    VAL  D.1083     17.624   66.875   20.414   1.00  68.49         c
ATOM   19178   O    VAL  D1083      18.310   65.882   20.173   1.00  69.97         0
ATOM   19179   CB   VAL  D1083      15.965   66.805   22.294   1.00  62.18         c
ATOM   19180   CGI  VAL  D1083      15.736   65.370   21.862   1.00  59.83         c
ATOM   19181   CG2  VAL  D1083      15.824   66.905   23.793   1.00  63.27         c
ATOM   19182   N    AP.G D1084      17.117   67.629   19.451   1.00  67.06         N
ATOM   19183   CA   ARG  D1084      17.452   67.313   18.068   1.00  67.16         c
ATOM   19184   C    ARG  D1084      18.946   67.501   17.887   1.00  65.20         c
ATOM   19185   O    AP.G D1084      19.593   66.729   17.181   1.00  66.67         0
ATOM   19186   CB   ARG  D1084      16.673   68.182   17.073   1.00  64.17         c
ATOM   19187   N    LYS  D1085      19.500   68.512   18.551   1.00  66.68         N
ATOM   19188   CA   LYS  D108 5     20.897   68.859   18.324   1.00  68.76         c
ATOM   19189   C    LYS  D1085      21.824   67.753   18.858   1.00  67.50         c
ATOM   19190   O    LYS  D1.085     22.744   67.298   18.153   1.00  61.29         0
ATOM   19191   CB   LYS  D1085      21.221   70.209   18.966   1.00  61.74         c
ATOM   19192   N    VAL  D108 6     21.549   67.327   20.092   1.00  62.84         N
ATOM   19193   CA   VAL  D1086      22.317   66.299   20.785   1.00  63.31         c
ATOM   19194   C    VAL  D108 6     22.347   64.959   20.045   1.00  61.35         c
ATOM   19195   O    VAL  D108 6     23.408   64.378   19.883   1.00  59.85         0
ATOM   19196   CB   VAL  D108 6     21.769   66.077   22.202   1.00  64.89         c
ATOM   19197   CGI  VAL  D108 6     22.194   64.712   22.741   1.00  61.95         c
ATOM   19198   CG2  VAL  D108 6     22.227   67.207   23.117   1.00  56.55         c
ATOM   19199   O    LEU  D1087      21.567   62.624   16.516   1.00  60.57         0
ATOM   19200   N    LEU  D1087      21.190   64.492   19.572   1.00  61.47         N
ATOM   19201   CA   LEU  D1087      21.117   63.274   18.766   1.00  56.65         c
ATOM   19202   c    LEU  D1087      21.726   63.473   17.391   1.00  58.24         c
ATOM   19203   CB   LEU  D.1087     19.674   62.791   18.589   1.00  53.98         c
ATOM   19204   CG   LEU  D1087      18.707   62.724   19.770   1.00  60.18         c
ATOM   19205   GDI  LEU  D1087      17.412   62.033   19..345   1.00  60.88         c
ATOM   19206   CD2  LEU  D.1087     19.314   62.020   20.971   1.00  52.10         c
ATOM   192 07  N    SEP. D1088      22.425   64.582   17.190   1.00  56.04         N
ATOM   192 08  CA   SER  D1088      23.014   64.851   15.889   1.00  55.98         c
ATOM   19209   c    SER  D1088      24.511   65.093   15.990   1.00  57.03         c
ATOM   19210   O    SER  D1088      25.195   65.195   14.961   1.00  57.33         0
ATOM   19211   CB   SER  D1088      22..325   66.058   15.250   1.00  66.28         c
ATOM   19212   OG   SER  D1088      20.998   66.163   15.736   1.00  71.37         0
ATOM   19213   N    MET  D108 9     25.005   65.224   17.223   1.00  55.13         N
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ATOM  19214  CA   MET  D1089   26.447  65.261  17.478  1.00  56.25   C
ATOM  19215  C    MET  D1089   27.127  64.106  16.760  1.00  59.64   C
ATOM  19216  O    MET  D1089   26.800  62.947  17.005  1.00  56.83   0
ATOM  19217  CB   MET  D1089   26.747  65.175  18.975  1.00  56.78   C
ATOM  19218  CG   MET  D1089   26.473  66.445  19.758  I.00  58.49   C
ATOM  19219  SD   MET  D1089   26.267  66.140  21.519  1.00  70.85   S
ATOM  19220  CE   MET  D1089   25.730  67.738  22.114  1.00  68.24   C
ATOM  19221  O    PRO  D1090   30.200  61.517  15.639  I.00  57.03   0
ATOM  19222  N    FRO  D1090   28.057  64.420  15.854  1.00  60.02   N
ATOM  19223  CA   PRO  D1090   28.791  63.390  15.118  1.00  61.68   C
ATOM  19224  C    PRO  D1090   29.769  62.594  16.017  I.00  59.43   C
ATOM  19225  CB   PRO  D1090   29.548  64.203  14.068  1.00  60.94   C
ATOM  19226  CG   PRO  D1090   29.809  65.494  14.753  1.00  63.91   C
ATOM  19227  CD   PRO  D1090   28.568  65.768  15.560  1.00  60.92   C
ATOM  19228  O    GLN  D1091   29.920  62.734  20.250  1.00  54.39   0
ATOM  19229  N    GLK  D1091   30.082  63.140  17.188  1.00  60.32   N
ATOM  19230  CA   GLN  D1091   31.038  62.581  18.132  1.00  56.85   C
ATOM  19231  C    GLN  D1091   30.348  61.991  19.355  I.00  58.82   C
ATOM  19232  CB   GLN  D1091   32.014  63.665  18.593  1.00  60.16   C
ATOM  19233  CG   GLN  D1091   33.272  63.173  19.309  1.00  59.76   C
ATOM  19234  CD   GLN  D1091   33.087  62.849  20.770  I.00  56.74   C
ATOM  19235  OE1  GLN  D1091   32.393  63.558  21.496  1.00  59.23   0
ATOM  19236  NE2  GLN  D1091   33.705  61.762  21.211  1.00  57.77   N
ATOM  19237  O    VAL  D1092   31.568  58.377  20.120  I.00  50.74   O
ATOM  19238  N    VAL  D1092   30.267  60.658  19.389  1.00  57.62   N
ATOM  19239  CA   VAL  D1092   29.801  59.903  20.557  1.00  55.07   C
ATOM  19240  C    VAL  D1092   30.914  58.945  20.975  I.00  52.53   C
ATOM  19241  CB   VAL  D1092   28.498  59.119  20.259  1.00  55.81   C
ATOM  19242  CGI  VAL  D1092   28.224  58.107  21.333  1.00  52.68   C
ATOM  19243  CG2  VAL  D1092   27.326  60.076  20.138  1.00  53.20   C
ATOM  19244  O    ASM  D1093   31.322  55.875  23.751  1.00  48.59   0
ATOM  19245  N    ASN  D1093   31.145  58.805  22.280  1.00  53.59   N
ATOM  19246  CA   ASN  D1093   32.181  57.927  22.815  1.00  47.63   C
ATOM  19247  C    ASM  D1093   31.826  56.440  22.764  I.00  51.00   C
ATOM  19248  CB   ASK  D1093   32.470  58.273  24.270  1.00  51.07   C
ATOM  19249  CG   ASN  D1093   33.033  59.642  24.440  1.00  49.29   C
ATOM  19250  OD1  ASN  D1093   33.942  60.050  23.726  I.00  52.09   0
ATOM  19251  ND2  ASN  D1093   32.493  60.373  25.397  1.00  53.31   N
ATOM  19252  O    ILE  D1094   34.004  53.639  21.251  1.00  45.78   O
ATOM  19253  N    ILE  D1094   32.083  55.782  21.645  I.00  49.41   N
ATOM  19254  CA   ILE  D1094   31.759  54.371  21.618  1.00  47.62   C
ATOM  19255  C    ILE  D1094   33.000  53.581  21.942  1.00  44.22   C
ATOM  19256  CB   ILE  D1094   31.135  53.973  20.305  1.00  50.50   C
ATOM  19257  CGI  ILE  D1094   29.699  54.485  20.337  1.00  46.98   C
ATOM  19258  CG2  ILE  D1094   31.134  52.446  20.111  1.00  41.03   C
ATOM  19259  CD1  ILE  D1094   29.008  54.284  19.091  1.00  49.89   C
ATOM  19260  O    VAL  D1095   32.783  50.066  24.166  I.00  41.19   0
ATOM  19261  N    VAL  D1095   32.913  52.902  23.071  1.00  41.19   N
ATOM  19262  CA   VAL  D1095   33.995  52.089  23.553  1.00  44.11   C
ATOM  19263  C    VAL  D1095   33.699  50.585  23.495  I.00  45.18   C
ATOM  19264  CB   VAL  D1095   34.340  52.483  24.964  1.00  45.83   C
ATOM  19265  CGI  VAL  D1095   35.315  51.465  25.568  1.00  46.40   C
ATOM  19266  CG2  VAL  D1095   34.916  53.889  24.945  I.00  47.84   C
ATOM  19267  O    LYS  D1096   36.668  48.038  23.559  1.00  41.53   0
ATOM  19268  N    LYS  D1096   34.470  49.901  22.656  1.00  44.89   N
ATOM  19269  CA   LYS  D1096   34.476  48.442  22.653  I.00  43.73   C
ATOM  19270  C    LYS  D1096   35.451  47.921  23.721  1.00  43.02   C
ATOM  19271  CB   LYS  D1096   34.847  47.929  21.278  1.00  40.81   C
ATOM  19272  CG   LYS  D1096   34.979  46.424  21.232  1.00  48.37   C
ATOM  19273  CD   LYS  D1096   33.667  45.754  21.646  1.00  49.52   C
ATOM  19274  CE   LYS  D1096   33.595  44.325  21.114  1.00  47.57   C
ATOM  19275  NZ   LYS  D1096   32.673  43.514  21.942  1.00  49.34   N
ATOM  19276  O    LYS  D1097   36.481  44.908  24.775  I.00  44.96   O
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ATOM	19277	N	LYS	D1097	34.914	47.394	24.818	1.00	36.19	N
ATOM	19278	CA	LYS	D1097	35,734	46.909	25,940	1,00	38.78	C
ATOM	19279	C	LYS	D1097	36.789	45,836	25:524	1,00	46,22	C
ATOM	19280	CB	LYS	D1097	34.827	46;345	27.022	1.00	44.25	C
ATOM	19281	CG	LYS	D1097	35,537	45.942	28,271	1,00	42.88	C
ATOM	19282	CD	LYS	D1097	34.636	45,118	29:148	1,00	39,85	C
ATOM	19283	CE	LYS	D1097	35.351	44,771	30.467	1,00	46,22	C
ATOM	19284	NZ	LYS	D1097	36,639	44.036	30,186	1,00	63.44	N
ATOM	19285	O	THR	D1098	39.201	44,040	27,717	1,00	63.24	O
ATOM	19286	N	THR	D1098	38.032	46,005	25.971	1,00	46,31	N
ATOM	19287	CA	THR	D1098	39,101	45.083	25,579	1,00	52.94	C
ATOM	19288	C	THR	D1098	39.123	43.893	26;501	1,00	50.84	C
ATOM	19289	CB	THR	D1098	40.515	45,725	25.566	1,00	51,82	C
ATOM	19290	OG1	THR	D1098	40.834	46;251	26,856	1.00	46.35	0
ATOM	19291	CG2	THR	D1098	40,614	46.820	24,491	1,00	42.88	C
ATOM	19292	O	GLU	D1099	40.480	40,185	25;366	1,00	51,31	0
ATOM	19293	N	GLU	D1099	39.035	42,716	25.901	1.00	48.17	N
ATOM	19294	CA.	GLU	D1099	38,886	41.469	26,642	1,00	55.10	C
ATOM	19295	C	GLU	D1099	40.064	40,502	26;477	1.00	51,27	C
ATOM	19296	CB	GLU	D1099	37.596	40,773	26.213	1,00	54,81	C
ATOM	19297	CG	GLU	D1099	36,426	41.727	26,020	1,00	53.56	C
ATOM	19298	CD	GLU	D1099	35.438	41,738	27;188	1,00	51.76	C
ATOM	19299	OE1	GLU	D1099	35.831	41,484	28.347	1,00	54,02	0
ATOM	19300	OE2	GLU	D1099	34,250	41.994	26,924	1,00	50.59	0
ATOM	19301	O	VAL	D1100	40.160	37.304	28;488	1,00	48.11	0
ATOM	19302	N	VAL	D1100	40.573	40,054	27.617	1,00	47,74	N
ATOM	19303	CA	VAL	D11OO	41,601	39.054	27,723	1,00	45.54	C
ATOM	19304	C	VAL	D1100	40,970	37.657	27,638	1,00	49.05	C
ATOM	19305	CB	VAL	D1100	42.367	39,207	29.065	1,00	48,36	C
ATOM	19306	CG2	VAL	D1100	43.222	40;459	29,050	1.00	40.11	C
ATOM	19307	CGI	VAL	D1100	43,195	37.961	29,375	1,00	43.45	C
ATOM	19308	O	GLN	D1101	42..303	34,428	27,829	1.00	41,59	0
ATOM	19309	N	GLN	D1101	41.306	36;877	26,613	1,00	42.95	N
ATOM	19310	CA.	GLN	D11O1	40,676	35.562	26,438	1,00	44.91	C
ATOM	19311	C	GLN	D1101	41.117	34,549	27.521	1,00	44,56	C
ATOM	19312	CB	GLN	D1101	40.972	34,985	25.056	1,00	44,57	C
ATOM	19313	CG	GLN	D11Ol	40,474	35.791	23,859	1,00	45.69	C
ATOM	19314	CD	GLN	DU Ol	39;066	36;370	24,054	1,00	50.95	C
ATOM	19315	OE1	GLN	DU Ol	38.054	35,688	23.868	1,00	45,75	0
ATOM	19316	NE2	GLN	DU Ol	39,010	37;636	24,422	1,00	46.39	N
ATOM	19317	O	THR	DU 02	38,888	31.459	27,798	1,00	48.21	O
ATOM	19318	N	THR	D11O2	40.125	33,862	28.089	1,00	43,35	N
ATOM	19319	CA	THR	D1102	40.271	32;884	29,171	1.00	47.23	C
ATOM	1932 0	C	THR	DU 02	39,565	31.563	28,831	1,00	45.48	C
ATOM	1932 1	CB	THR	D11O2	39.669	33,393	30.484	1.00	50,46	C
ATOM	19322	OG1	THR	D1102	38.256	33;577	30.305	1.00	48.36	O
ATOM	19323	CG2	THR	D1102	40,315	34.679	30,909	1,00	41.38	C
ATOM	1932 4	O	GLY	DI 103	41.283	28,197	29;433	1.00	37,18	O
ATOM	1932 5	N	GLY	D1103	39.668	30,583	29.721	1,00	36,36	N
ATOM	19326	CA.	GLY	D11O3	39,107	29.259	29,459	1,00	41.21	C
ATOM	1932 7	C	GLY	DU 03	40;108	28;156	29,060	1,00	42.24	C
ATOM	1932 8	O	GLY	DU 04	41.800	27,374	26.359	1,00	46,01	O
ATOM	1932 9	N	GLY	DU 04	39,620	27.159	28,318	1,00	48.55	N
ATOM	19330	CA	GLY	DI 104	40;431	26.059	27;818	1,00	39.55	C
ATOM	19331	C	GLY	D11O4	41.743	26,430	27.144	1,00	44,69	C
ATOM	19332	O	PHE	DU 05	44,620	26.527	24,500	1,00	46.50	0
ATOM	19333	N	FHE	DI 105	42,804	25.690	27,458	1,00	42.65	N
ATOM	19334	CA	PHE	D11O5	44.087	25,843	26.747	1,00	47,18	C
ATOM	19335	C	PHE	D1105	43,940	25;793	25,219	1.00	44.61	C
ATOM	19336	CB	FHE	DI 105	45,092	24.769	27,207	1,00	34.85	C
ATOM	19337	CG	PHE	D11O5	45.554	24,960	28;620	1.00	44,12	C
ATOM	19338	CD1	PHE	D1105	45.372	26;200	29,272	1.00	42.13	C
ATOM	19339	CD2	PHE	D11O5	46,132	23.909	29,322	1,00	40.40	C

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ATOM  19340  CE1  PHE  D1105    45.783  26.382  30.597  1.00  36.92   c
ATOM  19341  CE2  PHE  D1105    46,555  24.073  30,635  1,00  41.83   C
ATOM  19342  CZ   PHE  D1105    46.386  25,332  31.276  1,00  47,56   C
ATOM  19343  O    SER  D1106    40.953  23:507  24.017  1.00  41.15   0
ATOM  19344  N    SER  DU O6    43,036  24.950  24,735  1,00  38.09   N
ATOM  19345  CA   SER  DU O6    42.793  24,825  23..308 1,00  38,83   C
ATOM  19346  C    SER  DU 06    41.569  23,986  23.073  1,00  40,13   c
ATOM  19347  CB   SER  D.1106   43,975  24.157  22,603  1,00  53.41   C
ATOM  19348  OG   SER  DU 06    44.006  22.757  22,877  1,00  41.48   0
ATOM  19349  O    LYS  DU 07    41.854  21,089  22.289  1,00  47,45   0
ATOM  19350  N    LYS  DU 07    41,245  23.785  21,801  I,00  46.51   N
ATOM  19351  CA   LYS  DU 07    40.313  22.727  21,393  1,00  53.34   C
ATOM  19352  C    LYS  D1107    40.678  21,359  22.008  1,00  47,23   C
ATOM  19353  CB   LYS  DU 07    40.271  22,628  19,871  1.00  54.15   c
ATOM  19354  CG   LYS  DU 07    39,357  23.662  19,191  1,00  58.25   C
ATOM  19355  CD   LYS  D1107    39.479  23,568  17.663  1,00  59,84   C
ATOM  19356  CE   LYS  D1107    38.160  23:877  16.955  1.00  65.90   c
ATOM  19357  NZ   LYS  D1107    38,240  23.664  15,472  1,00  77.54   N
ATOM  19358  O    GLU  D1108    40.519  17,075  23.076  1,00  50,88   O
ATOM  19359  N    GLU  D1108    39.672  20,514  22.218  1,00  47,82   N
ATOM  19360  CA.  GLU  D1108    39,806  19.373  23,125  1,00  49.28   C
ATOM  19361  C    GLU  D1108    40:066  18:023  22:442  1,00  53.05   C
ATOM  19362  CB   GLU  D1108    38.558  19,250  24.004  1,00  49,32   c
ATOM  19363  CG   GLU  D1108    38,744  19.823  25,413  I,00  48.97   C
ATOM  19364  CD   GLU  D1108    37:439  20.044  26:185  1,00  54.60   C
ATOM  19365  OE1  GLU  D1108    36.455  19,300  25.984  1,00  52,28   0
ATOM  19366  OE2  GLU  D1108    37,405  20.986  27,009  I,00  67,91   0
ATOM  19367  O    SER  D1109    42,116  17.151  19,693  1,00  54.41   0
ATOM  19368  N    SER  D1109    39.782  17,932  21.156  1,00  49,80   N
ATOM  19369  CA   SER  D1109    39:884  16:655  20.488  1.00  54.51   c
ATOM  19370  C    SER  D1109    41,353  16.332  20,213  1,00  54.03   C
ATOM  19371  CB   SER  D11O9    39.057  16,642  19.199  1,00  56,40   C
ATOM  19372  OG   SER  D1109    39.713  17:352  18.169  1.00  68.66   0
ATOM  19373  O    ILE  D1110    42,520  13.497  18,430  1,00  51.31   0
ATOM  19374  N    ILE  D1110    41.750  15,138  20.620  1,00  52,94   N
ATOM  19375  CA   ILE  D1110    43.112  14,700  20.423  1,00  52,70   c
ATOM  19376  C    ILE  D11 I 0   43,286  14.304  18,969  1,00  53.36   C
ATOM  19377  CB   ILE  D1110    43:447  13.576  21:362  1,00  51.82   C
ATOM  19378  CGI  ILE  D1110    43.208  14,069  22.788  1,00  50,07   C
ATOM  19379  CG2  ILE  D111O    44,895  13.124  21,162  I,00  56.66   C
ATOM  19380  CD1  ILE  D1110    43,156  12.978  23,835  1,00  54.69   C
ATOM  19381  O    LEU  D1111    46.497  13,566  17.726  1,00  55,45   0
ATOM  19382  N    LEU  Dim      44,247  14:951  18:322  1.00  51.61   N
ATOM  19383  CA   LEU  Dim      44,549  14.674  16,935  1,00  55,40   C
ATOM  19384  C    LEU  Dim      45.614  13,601  16.874  1,00  56,53   C
ATOM  19385  CB   LEU  Dim      45.019  15:935  16.228  1.00  59.25   c
ATOM  19386  CG   LEU  D1m      43,997  17.066  16,193  1,00  58.48   C
ATOM  19387  CD1  LEU  Dim      44.409  18,057  15.149  1,00  60,93   C
ATOM  19388  CD2  LEU  Dim      42.644  16,496  15.884  1,00  59,47   c
ATOM  19389  O    PRO  D1112    47,840  13.359  14,619  1,00  63.66   0
ATOM  19390  N    PRO  Dim      45:528  12.713  15:872  1,00  64.00   N
ATOM  19391  CA   PRO  Dim      46.541  11,663  15.674  1,00  61,98   c
ATOM  19392  C    PRO  D1m      47,849  12.252  15,166  I,00  62.74   C
ATOM  19393  CB   PRO  Dim      45:900  10.748  14:626  1,00  57.55   C
ATOM  19394  CG   PRO  D1m      44.996  11,643  13.861  1,00  60,16   C
ATOM  19395  CD   PRO  D1m      44,467  12.657  14,854  I,00  59.69   C
ATOM  19396  O    LYS  Dim      49,645  12.079  12,648  1,00  70.37   0
ATOM  19397  N    LYS  D1113    48.951  11,526  15.334  1,00  64,69   N
ATOM  19398  CA   LYS  Dim      50:270  12:048  14.986  1.00  62.19   c
ATOM  19399  C    LYS  Dim      50,377  12.534  13,537  1,00  69.22   C
ATOM  19400  CB   LYS  Di 113   51..324 10,993  15.256  1,00  65,39   C
ATOM  19401  CG   LYS  Dim      51.140   9:725  14.471  1.00  67.45   c
ATOM  19402  CD   LYS  D1m      52,110   8.687  14,966  1,00  70.41   C
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ATOM   19403   CE   LYS  D1113        52..322    7.575    13..957    1.00   71.10             C
ATOM   19404   NZ   LYS  D1113        53,,510    6..759   14,348     1,00   70..18            N
ATOM   19405   O    AP.G Di114        53..072   15.,807   11..373    1,00   84,,09            O
ATOM   19406   N    ARG  D1114        51..296   13..473   13..318    1.00   69..37            N
ATOM   19407   CA.  ARG  D1114        51 ,465   14.120    12.,023    1,00   64.50             C
ATOM   19408   C    ARG  Di114        52..871   14,718    11.922     1,00   73,.01            C
ATOM   19409   CE   ARG  D1114        50..386   15.,198   11.816     1,00   75,.37            C
ATOM   19410   O    ASP  D1117        53.,966   19. 730   14,547     1,00   89..70            0
ATOM   19411   N    ASP  D1117        52..536   19..099   11..678    1,00   82.70             N
ATOM   19412   CA   ASP  D1117        53..710   19.,815   12..163    1,00   88,.64            C
ATOM   19413   C    ASP  D1117        53.,484   20.323    13.,579    I,00   87.76             C
ATOM   19414   CB   ASP  D1117        54..057   20..988   11..240    1,00   88..87            C
ATOM   19415   O    LYS  D1118        50. 133   21.,986   15. 497    1,00   79,14             0
ATOM   19416   N    LYS  D1118        52..744   21..422   13..693    1.00   87.27             N
ATOM   19417   CA   LYS  D1118        52.,485   22.041    14,986     1,00   83..24            C
ATOM   19418   C    LYS  Di118        51..236   21.,479   15.678     1,00   81,I9             C
ATOM   19419   CB   LYS  D1118        52..349   23..552   14.825     1.00   82.08             C
ATOM   19420   O    LEU  D1119        52.,157   20. 438   18.,904    1,00   64.52             0
ATOM   19421   N    LEU  Di119        51..425   20.,414   16.453     1,00   71,83             N
ATOM   19422   CA   LEU  D1119        50..422   19.,931   17.388     1,00   65,.36            C
ATOM   19423   C    LEU  D1119        50.,970   20. 208   18.,769    1,00   64.42             C
ATOM   19424   CB   LEU  D1119        50..142   18..439   17.198     1,00   62.67             C
ATOM   19425   CG   LEU  D1119        49..232   18.,032   16..036    1,00   59,.34            C
ATOM   19426   CD2  LEU  D1119        47,835    18.595    16.,227    I,00   64.78             C
ATOM   19427   CD1  LEU  D1119        49..167   16..535   15..934    1,00   60..73            C
ATOM   19428   O    ILE  D1120        49. 522   18.,583   21 .922    1,00   65,42             0
ATOM   19429   N    ILE  D1120        50.,133   20.220    19.,802    I,00   66..69            N
ATOM   19430   CA   ILE  D1120        50.,657   20..533   21.,123    1,00   60..13            C
ATOM   19431   C    ILE  D1120        50. 516   19.,306   21 .995    1,00   64,06             C
ATOM   19432   CB   ILE  D1120        49..969   21..804   21..767    1.00   66..47            C
ATOM   19433   CGI  ILE  D1120        50.,367   21.973    23.,234    1,00   62.69             C
ATOM   19434   CG2  ILE  D1120        48..477   21.,744   21..687    1,00   69,.08            C
ATOM   19435   CD1  ILE  D1120        51..851   22..217   23..440    1.00   70..09            C
ATOM   19436   O    ALA  DU21         50.,460   18. 534   25,403     1,00   66..24            0
ATOM   19437   N    ALA  D1121        51..545   19.,069   22.798     1,00   64,20             N
ATOM   19438   CA   ALA  D1121        51..736   17,814    23..499    1,00   63,.15            C
ATOM   19439   C    ALA  DU21         50.,738   17.619    24.,630    1,00   63..32            C
ATOM   19440   CB   ALA  D1121        53..171   17.739    24..032    1,00   60..03            C
ATOM   19441   O    ARG  D1122        49. 546   16.,473   28. 135    1,00   60,97             0
ATOM   19442   N    ARG  D1122        50.,181   16.423    24.,717    I,00   55..99            N
ATOM   19443   CA   ARG  D1122        49.,266   16..132   25.,798    1,00   58..40            C
ATOM   19444   C    ARG  D1122        50. 041   16.,073   27.095     1,00   59,05             C
ATOM   19445   CB   ARG  D1122        48..525   14.822    25..561    1.00   53..47            C
ATOM   19446   CG   ARG  D1122        47,386    14.929    24.,587    1,00   56..10            C
ATOM   19447   CD   ARG  D1122        47.040    13.,563   23..984    1,00   59,.91            C
ATOM   19448   NE   ARG  D1122        46..831   12..529   24..993    1.00   58..90            N
ATOM   19449   CZ   ARG  D1122        46.,877   11.223    24.,744    1,00   57.97             C
ATOM   19450   NH1  ARG  D1122        47.121    10.,783   23..513    1,00   58,.78            N
ATOM   19451   NH2  ARG  D1122        46..683   10,351    25..726    1,00   55,.82            N
ATOM   19452   O    LYS  D1123        53.,747   16. 251   26.,606    1,00   60..30            O
ATOM   19453   N    LYS  D1123        51..261   15..557   27..040    1,00   58..73            N
ATOM   19454   CA   LYS  D1123        52..119   15.,566   28..212    1,00   56,.13            C
ATOM   19455   C    LYS  D1123        53.,452   16.160    27.,799    I,00   62.67             C
ATOM   19456   CB   LYS  D1123        52..282   14.171    28..801    1,00   58..70            C
ATOM   19457   CG   LYS  D1123        51. 008   13.,576   29. 416    1,00   56,22             C
ATOM   19458   CD   LYS  D1123        50.,693   14.155    .30.,787   I,00   48..14            C
ATOM   19459   CE   LYS  D1123        49.,527   13..418   31.,416    1,00   45..54            C
ATOM   19460   NZ   LYS  D1123        49. 357   13.,697   32. 865    1,00   42,02             N
ATOM   19461   O    LYS  D1124        57..135   16..768   26..839    1.00   63..34            0
ATOM   19462   N    LYS  D1124        54.,225   16..614   28..783    1,00   64.29             N
ATOM   19463   CA   LYS  D1124        55..491   17,289    28..515    1,00   66,.11            C
ATOM   19464   C    LYS  D1124        56..430   16..357   27..769    1.00   65..96            C
ATOM   19465   CB   LYS  D1124        56.,138   17.768    29.,821    1,00   65..71            C
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ATOM	19466	O	ASP	D1125	57.324	12.430	25.839	1.00	68.40	O
ATOM	19467	N	ASP	D1125	56,401	15.088	28,165	1,00	66.62	N
ATOM	19468	CA	ASP	D1125	57.286	14,080	27.582	1.00	75,11	C
ATOM	19469	C	ASP	D1125	56.709	13.382	26.336	1.00	72.26	C
ATOM	19470	CB	ASP	D1125	57,651	13.031	28,647	1,00	70.30	C
ATOM	19471	O	TP.P	D1126	54.111	14,798	23.057	1.00	6.3,15	0
ATOM	19472	N	TRP	D1126	55.561	13,853	25.823	1,00	67,06	N
ATOM	19473	CA.	TRP	DU 26	54,920	13.206	24,662	1,00	62.19	C
ATOM	19474	C	TRP	D1126	55.000	14.019	23.381	1,00	63.88	C
ATOM	19475	CB	TRP	D1126	53.446	12,871	24.937	1,00	58,95	C
ATOM	19476	CG	TRP	DU 26	53,245	11.891	26,072	1,00	63.67	C
ATOM	19477	CD1	TRP	D1126	54.217	11.266	26.793	1,00	57.12	C
ATOM	19478	CD2	TRP	D1126	51.992	11,451	26.629	1,00	62,20	C
ATOM	19479	NE1	TRP	D1126	53.655	10.473	27.760	1.00	56.75	N
ATOM	19480	CE2	TRP	D1126	52,293	10.562	27,678	1,00	56.60	C
ATOM	19481	CE.3	TRP	D1126	50.651	11,729	26.342	1.00	59,05	C
ATOM	19482	CZ2	TRP	D1126	51.303	9.946	28.443	1,00	52.59	C
ATOM	19483	CZ3	TRP	DU 26	49,669	11.113	27,106	1,00	54.70	C
ATOM	19484	CH2	TRP	D1126	50.002	10,236	28.145	1.00	48,38	C
ATOM	19485	O	ASP	D1127	54.524	12,933	20.295	1,00	67,15	0
ATOM	19486	N	ASP	D1127	56,080	13.805	22,648	1,00	66.71	N
ATOM	19487	CA	ASP	D1127	56.228	14.319	21.298	1,00	67.77	C
ATOM	19488	C	ASP	D1127	54.978	14,066	20.445	1,00	64,66	C
ATOM	19489	CB	ASP	D1127	57,456	13.671	20,662	1,00	68.30	C
ATOM	19490	CG	ASP	D1127	57.856	14.315	19.361	1,00	70.70	C
ATOM	19491	OD1	ASP	D1127	57.034	15,037	18.761	1,00	64,98	0
ATOM	19492	OD2	ASP	D1127	59,007	14.071	18,929	1,00	79.88	0
ATOM	19493	O	FRO	D1128	52,639	13.700	17,061	1,00	67.20	0
ATOM	19494	N	PRO	D1128	54.407	15,131	19.892	1,00	65,74	N
ATOM	19495	CA	PRO	D1128	53.243	14.974	19,008	1.00	66.88	C
ATOM	19496	C	FRO	D1128	53,551	14.214	17,712	1,00	63.98	C
ATOM	19497	CB	PRO	D1128	52.834	16,425	18.710	1.00	57,20	C
ATOM	19498	CG	PRO	D1128	53.320	17.187	19,878	1,00	60.75	C
ATOM	19499	CD	PRO	D1128	54,615	16.533	20,294	1,00	62.81	C
ATOM	19500	O	LYS	D1129	54.609	11,250	15.302	1.00	64,35	0
ATOM	19501	N	LYS	D1129	54.816	14,153	17.330	1,00	67,33	N
ATOM	19502	CA.	LYS	D1129	55,200	13.440	16,103	1,00	72.25	C
ATOM	19503	C	LYS	D1129	54.964	11.937	16.258	1,00	63.73	C
ATOM	19504	CB	LYS	D1129	56.666	13,717	15.750	1,00	72,22	C
ATOM	19505	O	LYS	D.I130	52,803	8.844	18,035	1,00	55.42	0
ATOM	19506	N	LYS	D1130	55,157	11.449	17,479	1,00	59.85	N
ATOM	19507	CA	LYS	D1130	54.876	10,069	17.846	1,00	59,43	C
ATOM	19508	C	LYS	D1130	53.441	9.853	18.351	1.00	62.36	C
ATOM	19509	CB	LYS	D1130	55,861	9.601	18,941	1,00	64.74	C
ATOM	19510	CG	LYS	D1130	57,.346	9,833	18.615	1.00	69,30	C
ATOM	19511	CD	LYS	D1130	58.293	9.414	19.750	1,00	64.97	C
ATOM	19512	CE	LYS	D1130	59,744	9.483	19,266	1,00	72.81	C
ATOM	19513	NZ	LYS	D1130	60.753	9,051	20.266	1.00	74,61	N
ATOM	19514	O	TYR	D1131	49.514	11,090	20.405	1,00	54,11	0
ATOM	19515	N	TYR	D1131	52,941	10.809	19,141	1,00	64.65	N
ATOM	19516	CA	TYR	D1131	51.811	10.543	20.030	1,00	53.84	C
ATOM	19517	C	TYR	D1131	50.510	11,287	19.727	1,00	55,75	C
ATOM	19518	CB	TYR	DU 31	52,239	10.842	21,456	1,00	54.32	C
ATOM	19519	CG	TYR	D1131	53.289	9.886	21.980	1,00	56.47	C
ATOM	1952 0	GDI	TYR	D1131	53.106	8,513	21.901	1,00	55,99	C
ATOM	1952 1	CD2	TYR	DU 31	54,460	10..356	22,549	1,00	58.25	C
ATOM	19522	CE1	TYR	D1131	54,074	7.623	22,386	1,00	60.07	C
ATOM	1952 3	CF.2	TYR	D1131	55.417	9,498	23.031	1,00	60,02	C
ATOM	1952 4	CZ	TYR	D1131	55.224	8.125	22.947	1.00	59.81	C
ATOM	1952 5	OH	TYR	D1131	56,176	7.261	23,440	1,00	59.71	0
ATOM	1952 6	O	GLY	D11.32	50.101	14,045	20.601	1.00	56,47	0
ATOM	1952 7	N	GLY	D1132	50.494	12.109	18.694	1.00	54.56	N
ATOM	19528	CA.	GLY	D1132	49,384	13.011	18,531	1,00	57.09	C

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ATOM   1952 9  C    GLY  D1132     49.311   14.048   19.646   1.00  56.10     C
ATOM   19530   0    GLY  D1133     46,408   16.869   19,001   1,00  57,50     O
ATOM   19531   N    GLY  D1133     48..337  14,940   19.521   1,00  55,05     N
ATOM   19532   CA   GLY  D1133     48.140   16.029   20.472   1.00  58.82     C
ATOM   19533   C    GLY  DU 33     47,081   17.050   20,034   1,00  59.17     C
ATOM   19534   O    PHE  D1134     47.323   20,460   19.220   1,00  63,74     0
ATOM   19535   N    PHE  D1134     46.946   18,134   20.800   1,00  55,12     N
ATOM   19536   CA.  PHE  D1134     45,872   19.124   20,563   1,00  55.17     C
ATOM   19537   C    PHE  D1134     46.177   20.132   19.490   1,00  55.05     C
ATOM   19538   CB   PHE  D1134     45.544   19,879   21.845   1,00  44,37     C
ATOM   19539   CG   PHE  DU 34     45,209   18.985   22,970   1,00  44.37     C
ATOM   19540   GDI  PHE  D1134     44.072   18.200   22,920   1,00  46.60     C
ATOM   19541   CD2  PHE  D1134     46.048   18,876   24.051   1,00  45,19     C
ATOM   19542   CE1  PHE  D1134     43.767   17.356   23.949   1.00  43.96     C
ATOM   19543   CE2  PHE  D1134     45,745   18.027   25,093   1,00  48.44     C
ATOM   19544   CZ   PHE  D1134     44.606   17,269   25.041   1,00  47,62     C
ATOM   19545   O    ASP  D1135     43.823   23.134   19.080   1.00  52.36     0
ATOM   19546   N    ASP  D1135     45,118   20.632   18,889   1,00  58.93     N
ATOM   19547   CA   ASP  D1135     45.221   21,621   17.831   1,00  62,14     C
ATOM   19548   C    ASP  D1135     44.743   23,011   18.275   1,00  59,36     C
ATOM   19549   CB   ASP  DU 35     44,396   21.164   16,642   1,00  60.29     C
ATOM   19550   CG   ASP  D1135     44.825   21.803   15.370   1,00  68.29     C
ATOM   19551   OD2  ASP  D1135     43.946   22,056   14.513   1,00  74,10     0
ATOM   19552   OD1  ASP  DU 35     46,042   22.048   15,231   1,00  72.24     0
ATOM   19553   O    SEP. D1136     43.337   25.989   19.539   1,00  52.70     0
ATOM   19554   N    SER  D1136     45..383  24,041   17.734   1,00  58,04     N
ATOM   19555   CA   SER  D1136     44,853   25.402   17,744   1,00  53.04     C
ATOM   19556   C    SER  D1136     44,513   25.954   19,132   1,00  56.23     C
ATOM   19557   CB   SER  D1136     43.620   25,457   16.849   1,00  54,06     C
ATOM   19558   OG   SER  D1136     42.599   24.650   17.383   1.00  53.17     0
ATOM   19559   O    FRO  D1137     44,815   29.034   20,232   1,00  51.82     0
ATOM   19560   N    PRO  D1137     45.547   26,409   19.857   1,00  54,01     N
ATOM   19561   CA   PRO  D1137     45.458   26.970   21.209   1.00  51.25     C
ATOM   19562   C    PRO  D1137     44,747   28..307  21,215   1,00  51.29     C
ATOM   19563   CB   PRO  D1137     46.916   27,170   21.598   1,00  56,21     C
ATOM   19564   CG   PRO  D1137     47.564   27,521   20.293   1,00  57,48     C
ATOM   19565   CD   PRO  D1137     46,891   26.608   19,284   1,00  57,26     C
ATOM   19566   O    THR  D1138     45.165   30.663   23.974   1,00  43.52     0
ATOM   19567   N    THR  D1138     44.090   28,634   22..314  1,00  51,10     N
ATOM   19568   CA   THR  D1138     43,486   29.942   22,452   1,00  43.40     C
ATOM   19569   C    THR  D1138     44,517   30.916   22,955   1,00  46.97     C
ATOM   19570   CB   THR  D1138     42..308  29,919   23.419   1,00  49,56     C
ATOM   19571   OG1  THR  D1138     41.350   28.967   22.960   1.00  51.44     0
ATOM   19572   CG2  THR  D1138     41,654   31.316   23,535   1,00  45.81     C
ATOM   19573   O    VAL  D1139     43.814   34,476   23.623   1,00  46,98     0
ATOM   19574   N    VAL  D1139     44.643   32.035   22.247   1.00  46.58     N
ATOM   19575   CA.  VAL  D1139     45,521   33.117   22,653   1,00  40.89     C
ATOM   19576   C    VAL  D1139     44.925   33.974   23.750   1,00  44,74     C
ATOM   19577   CB   VAL  D1139     45.852   34,046   21.485   1,00  40,44     C
ATOM   19578   CGI  VAL  D1139     46,978   34.961   21,873   1,00  43.07     C
ATOM   19579   CG2  VAL  D1139     46.199   33.249   20.251   1,00  45.69     C
ATOM   19580   O    ALA  D1140     44.195   37,179   25.545   1,00  49,84     0
ATOM   19581   N    ALA  D1140     45,680   34.165   24,818   1,00  42.14     N
ATOM   19582   CA   ALA  D1140     45.242   35.021   25.895   1,00  41.63     C
ATOM   19583   C    ALA  D1140     45.208   36,476   25.407   1,00  50,10     C
ATOM   19584   CB   ALA  D1140     46,141   34.861   27,088   1,00  40.05     C
ATOM   19585   O    TYR  D1141     48,510   37.300   23,306   1,00  44.04     0
ATOM   19586   N    TYR  D1141     46.330   36.910   24.853   1,00  47,09     N
ATOM   19587   CA   TYR  D1141     46.459   38.206   24.216   1.00  43.69     C
ATOM   19588   C    TYR  D1141     47,677   38.221   23,287   1,00  49.36     C
ATOM   19589   CB   TYR  D1141     46.576   39.334   25.258   1.00  41,63     C
ATOM   19590   CG   TYR  D1141     47.522   39.041   26.386   1.00  43.83     C
ATOM   19591   CD1  TYR  D1141     48,884   39.220   26,250   1,00  43.88     C
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ATOM	19592	CD2	TYR	D1141	47.043	38.600	27.602	1.00	48.32	C
ATOM	19593	CEl	TYR	D1141	49,746	38.951	27,296	1,00	46.15	C
ATOM	19594	CE2	TYR	D1141	47.887	38,331	28.648	1,00	42,72	C
ATOM	19595	CZ	TYR	D1141	49.229	38;503	28.498	1.00	48.94	C
ATOM	19596	OH	TYR	D1141	50,047	38.235	29,570	1,00	47,21	0
ATOM	19597	O	SEP.	D1142	49.467	41,133	23.242	1,00	45,30	0
ATOM	19598	N	SER	D1142	47.771	39,260	22.464	1,00	44,94	N
ATOM	19599	CA.	SER	D1142	48,945	39.456	21,638	1,00	43.34	C
ATOM	19600	C	SER	D1142	49.909	40;367	22;385	1,00	48.56	C
ATOM	19601	CB	SER	D1142	48.566	40,047	20.292	1,00	41,44	C
ATOM	19602	OG	SER	DU 42	47,892	39.107	19,496	1,00	51.81	0
ATOM	19603	O	VAL	D1143	53.217	41.196	20;486	1,00	50.79	0
ATOM	19604	N	VAL	D1143	51.212	40,276	22.091	1,00	43,52	N
ATOM	19605	CA	VAL	D1143	52.142	41;263	22,620	1.00	47.60	C
ATOM	19606	C	VAL	D1143	52,994	41.843	21,503	1,00	51.99	C
ATOM	19607	CB	VAL	D1143	53.072	40,698	23.719	1,00	44,58	C
ATOM	19608	CG2	VAL	D1143	53.759	39;449	23.254	1.00	51.20	C
ATOM	19609	CGI	VAL	D1143	52,298	40.440	24,984	1,00	49.01	C
ATOM	19610	O	LEU	D1144	56.277	43,522	22.217	1,00	53,05	0
ATOM	19611	N	LEU	D1144	53.434	43,087	21.702	1,00	51,92	N
ATOM	19612	CA.	LEU	D1144	54,346	43.764	20,797	1,00	48.34	C
ATOM	19613	C	LEU	D1144	55.800	43;384	21;085	1,00	54.36	C
ATOM	19614	CB	LEU	D1144	54.185	45,272	20.913	1,00	54,28	C
ATOM	19615	CG	LEU	D1144	55,192	46.069	20,086	1,00	57.77	C
ATOM	19616	CD1	LEU	D1144	54.831	46.007	18;636	1,00	53.19	C
ATOM	19617	CD2	LEU	D1144	55.229	47,493	20.567	1,00	63,96	C
ATOM	19618	O	VAL	D1145	58,736	43.254	18,145	1,00	52,81	0
ATOM	19619	N	VAL	D1145	56,505	42.899	20,069	1,00	51.59	N
ATOM	19620	CA	VAL	D1145	57.885	42,515	20.265	1,00	52,09	C
ATOM	19621	C	VAL	D1145	58;808	43;326	19;371	1.00	50.80	C
ATOM	19622	CB	VAL	D1145	58,086	41.006	20,011	1,00	54.44	C
ATOM	19623	CGI	VAL	D1145	59.525	40,588	20.333	1,00	47,24	C
ATOM	19624	CG2	VAL	D1145	57.086	40;211	20.835	1.00	49.07	C
ATOM	19625	O	VAL	D1146	62,511	44.264	20,749	1,00	53.96	0
ATOM	19626	N	VAL	D1146	59.662	44,121	20.001	1,00	49,27	N
ATOM	19627	CA	VAL	D1146	60.708	44,833	19.278	1,00	54,91	C
ATOM	19628	C	VAL	D1146	62,061	44.216	19,610	1,00	54.10	C
ATOM	19629	CB	VAL	D1146	60;727	46;322	19;625	1,00	58.71	C
ATOM	19630	CGI	VAL	D1146	61.831	47,016	18.856	1,00	58,95	C
ATOM	19631	CG2	VAL	D1146	59,370	46.955	19,313	1,00	58.49	C
ATOM	19632	O	ALA	D1147	64,469	43.207	16,592	1,00	60.01	0
ATOM	19633	N	ALA	D1147	62.701	43,633	18.610	1,00	54,04	N
ATOM	19634	CA	ALA	D1147	63;866	42;805	18;870	1.00	60.22	C
ATOM	19635	C	ALA	D1147	64,622	42.509	17,596	1,00	62.12	C
ATOM	19636	CB	ALA	D1147	63.451	41,507	19.534	1,00	55,60	C
ATOM	19637	O	LYS	D1148	65.527	38;837	17.358	1.00	62.12	0
ATOM	19638	N	LYS	D1148	65,447	41.469	17,656	1,00	61.97	N
ATOM	19639	CA	LYS	D1148	66.158	40,970	16.485	1,00	62,50	C
ATOM	19640	C	LYS	D1148	65.927	39,475	16.389	1,00	58,57	C
ATOM	19641	CB	LYS	D1148	67,657	41.289	16,557	1,00	64.42	C
ATOM	19642	CG	LYS	D1148	68;037	42,675	16;027	1,00	66.88	C
ATOM	19643	CD	LYS	D1148	69.449	42,712	15.392	1,00	72,11	C
ATOM	19644	CE	LYS	D1148	69,557	43.827	14,316	1,00	72.99	C
ATOM	19645	¥iZ	LYS	D1148	70;896	43.967	13;640	1,00	70.34	N
ATOM	19646	o	VAL	D1149	67.099	37,700	12.946	1,00	66,14	0
ATOM	19647	N	VAL	D1149	66,161	38.907	15,221	1,00	57.71	N
ATOM	19648	CA	VAL	D1149	65,998	37.466	15,068	1,00	65.10	C
ATOM	19649	C	VAL	D1149	66.870	36,970	13.900	1,00	61,02	C
ATOM	19650	CB	VAL	D1149	64,489	37;106	14,884	1.00	62.49	C
ATOM	19651	CGI	VAL	D1149	63,948	37.697	13,607	1,00	59.41	C
ATOM	19652	CG2	VAL	D1149	64.269	35,592	14.942	1,00	73,44	C
ATOM	19653	O	GLU	D1150	66.690	33;987	11.716	1.00	66.53	0
ATOM	19654	N	GLU	DU 50	67,393	35.752	13,995	1,00	68.90	N

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ATOM  19655  CA   GLU  DllSO    68.298  35.213  12.966  1.00  67.64      C
ATOM  19656  C    GLU  DllSO    67.559  34.852  11.695  1.00  64.62      C
ATOM  19657  CB   GLU  DllSO    69.025  33.976  13.475  1.00  64.81      C
ATOM  19658  CG   GLU  DllSO    69.896  34.201  14.679  1.00  71.36      C
ATOM  19659  CD   GLU  DllSO    70.410  32.898  15.265  1.00  80.66      C
ATOM  19660  OE1  GLU  DllSO    71.343  32.947  16.101  1.00  81.43      0
ATOM  19661  OE2  GLU  DllSO    69.873  31.829  14.888  1.00  80.95      0
ATOM  19662  O    LYS  D1151    69.356  34.650   8.342  1.00  74.65      0
ATOM  19663  N    LYS  D1151    67.908  35.499  10.589  1.00  68.76      N
ATOM  19664  CA   LYS  D1151    67.236  35.243   9.315  1.00  70.25      C
ATOM  19665  C    LYS  D1151    68.134  34.469   8.356  1.00  72.14      C
ATOM  19666  CB   LYS  D1151    66.785  36.557   8.664  1.00  64.85      C
ATOM  19667  O    GLY  D1152    69.475  31.680   8.217  1.00  77.95      0
ATOM  19668  N    GLY  D1152    67.529  33.597   7.561  1.00  65.16      N
ATOM  19669  CA   GLY  D1152    68.268  32.896   6.528  1.00  77.40      C
ATOM  19670  C    GLY  D1152    69.270  31.858   7.010  1.00  81.11      C
ATOM  19671  O    LYS  D1153    72.494  29.825   8.019  1.00  81.39      0
ATOM  19672  N    LYS  D1153    69.894  31.177   6.049  1.00  82.76      N
ATOM  19673  CA   LYS  D1153    70.804  30.070   6.328  1.00  82.57      C
ATOM  19674  C    LYS  D1153    71.992  30.547   7.152  1.00  81.18      C
ATOM  19675  CB   LYS  D1153    71.282  29.423   5.019  1.00  78.13      C
ATOM  19676  O    SEP. D1154    74.308  33.163   9.697  1.00  74.50      0
ATOM  19677  N    SER  D1154    72.421  31.779   6.885  1.00  80.67      N
ATOM  19678  CA   SER  D1154    73.584  32.377   7.549  1.00  81.75      C
ATOM  19679  C    SER  D1154    73.365  32.764   9.014  1.00  78.19      C
ATOM  19680  CB   SER  D1154    74.029  33.619   6.789  1.00  77.47      C
ATOM  19681  OG   SER  D1154    74.588  34.550   7.693  1.00  86.13      0
ATOM  19682  O    LYS  D1155    72.357  34.868  12.250  1.00  71.91      0
ATOM  19683  N    LYS  D1155    72.120  32.662   9.472  1.00  78.68      N
ATOM  19684  CA   LYS  D1155    71.739  33.016  10.833  1.00  74.85      C
ATOM  19685  C    LYS  D1155    72.027  34.500  11.124  1.00  72.81      C
ATOM  19686  CB   LYS  D1155    72.455  32.103  11.834  1.00  71.10      C
ATOM  19687  O    LYS  D1156    69.880  37.168  10.858  1.00  75.89      0
ATOM  19688  N    LYS  D1156    71.896  35.348  10.105  1.00  68.82      N
ATOM  19689  CA   LYS  D115 6   72.179  36.772  10.259  1.00  73.20      C
ATOM  19690  C    LYS  D1156    71.060  37.482  11.037  1.00  76.40      C
ATOM  19691  CB   LYS  D1156    72.374  37.430   8.891  1.00  72.13      C
ATOM  19692  O    LEU  D1157    70.383  41.156  11.382  1.00  71.86      0
ATOM  19693  N    LEU  D1157    71.430  38.430  11.899  1.00  67.00      N
ATOM  196 94 CA   LEU  D1157    70.449  39.157  12.711  1.00  73.83      C
ATOM  19695  C    LEU  D1157    69.739  40.273  11.942  1.00  71.56      C
ATOM  19696  CB   LEU  D1157    71.106  39.749  13.966  1.00  68.99      C
ATOM  19697  CG   LEU  D1157    71.502  38.773  15.076  1.00  70.73      C
ATOM  19698  CD1  LEU  D1157    71.693  39.491  16.401  1.00  71.01      C
ATOM  19699  CD2  LEU  D1157    70.475  37.671  15.221  1.00  73.32      C
ATOM  197 00 O    LYS  D1158    66.109  41.168  13.253  1.00  65.58      0
ATOM  19701  N    LYS  D1158    68.408  40.216  11.934  1.00  66.37      N
ATOM  19702  CA   LYS  D1158    67.573  41.271  11.368  1.00  67.66      C
ATOM  19703  C    LYS  D1158    66.725  41.889  12.472  1.00  68.34      C
ATOM  19704  CB   LYS  D1158    66.676  40.720  10.260  1.00  70.65      C
ATOM  19705  CG   LYS  D1158    66.709  41.516   8.956  1.00  77.17      C
ATOM  19706  CD   LYS  D1158    66.317  42.970   9.164  1.00  76.29      C
ATOM  197 07 CE   LYS  D1158    66.441  43.762   7.863  1.00  85.79      C
ATOM  19708  ¥iz  LYS  D1158    67.801  43.649   7.232  1.00  87.20      N
ATOM  19709  N    SER  D1159    66.701  43.218  12.553  1.00  67.23      N
ATOM  19710  CA   SER  D1159    65.852  43.878  13.532  1.00  62.62      C
ATOM  19711  C    SER  D1159    64.395  43.687  13.145  1.00  62.02      C
ATOM  19712  O    SER  D115 9   64.049  43.695  11.968  1.00  60.30      0
ATOM  19713  CB   SER  D1159    66.170  45.357  13.635  1.00  65.01      C
ATOM  19714  OG   SER  D1159    65.561  46.051  12.563  1.00  78.09      0
ATOM  19715  N    VAL  D1160    63.541  43.501  14.141  1.00  63.43      N
ATOM  19716  CA   VAL  D1160    62.142  43.200  13.870  1.00  58.55      C
ATOM  19717  C    VAL  D1160    61.190  43.893  14.853  1.00  55.74      C
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ATOM	19718	O	VAL	D1160	61.542	44.190	16.004	1.00	52.89	O
ATOM	19719	CB	VAL	D1160	61,869	41.661	13,899	1,00	56.56	C
ATOM	19720	CGI	VAL	D1160	62.464	40,968	12.677	1,00	52,94	C
ATOM	19721	CG2	VAL	D1160	62.400	41.044	15.183	1.00	59.05	C
ATOM	19722	O	LYS	D1161	57,316	43.620	13,611	1,00	57.45	0
ATOM	19723	N	LYS	D1161	59.980	44,129	14.354	1,00	53,44	N
ATOM	19724	CA	LYS	D1161	58.848	44,623	15.119	1,00	54,42	C
ATOM	19725	C	LYS	D1161	57,701	43.708	14,765	1,00	53.47	C
ATOM	19726	CB	LYS	D1161	58.528	46.084	14.770	1,00	55.27	C
ATOM	19727	CG	LYS	D1161	57.935	46,863	15.904	1,00	56,32	C
ATOM	19728	CD	LYS	D1161	57,879	48.358	15,597	I,00	67.77	C
ATOM	19729	CE	LYS	D1161	56.971	48.677	14.410	1,00	68.29	C
ATOM	19730	NZ	LYS	D1161	56.985	50,114	14.021	1,00	59,52	N
ATOM	19731	O	GLU	D1162	55.280	42.381	17.650	1.00	52.40	0
ATOM	19732	N	GLU	D1162	57,166	42.999	15,746	1,00	52.20	N
ATOM	19733	CA	GLU	D1162	56.185	41.959	15.458	1,00	50,54	C
ATOM	19734	C	GLU	D1162	55.096	41.886	16.525	1.00	53.97	C
ATOM	19735	CB	GLU	DU 62	56,870	40.583	15,355	1,00	55.91	C
ATOM	19736	CG	GLU	D1162	57.860	40,418	14.213	1,00	58,64	C
ATOM	19737	CE	GLU	D1162	58.312	38,961	14.028	1,00	62,41	C
ATOM	19738	OE1	GLU	DU 62	58,281	38.188	15,011	1,00	59.10	0
ATOM	19739	OE2	GLU	D1162	58.698	38.587	12.895	1,00	66.87	0
ATOM	19740	O	LEU	D1163	53.338	38,480	16.554	1,00	52,70	0
ATOM	19741	N	LEU	DU 63	53,981	41.250	16,159	I,00	53.70	N
ATOM	19742	CA	LEU	D1163	52.967	40.778	17.102	1,00	49.42	C
ATOM	19743	C	LEU	D1163	53.151	39,307	17.436	1,00	52,40	C
ATOM	19744	CB	LEU	DU 63	51,564	40.981	16,535	I,00	56.94	C
ATOM	19745	CG	LEU	D1163	51,070	42.426	16,539	1,00	58.22	C
ATOM	19746	GDI	LEU	D1163	49.581	42,473	16.229	1,00	56,61	C
ATOM	19747	CD2	LEU	D1163	51.402	43.096	17.869	1.00	45.81	C
ATOM	19748	O	LEU	D1164	51,554	37.724	20,819	1,00	51.82	0
ATOM	19749	N	LEU	D1164	53.091	38,967	18.714	1,00	52,98	N
ATOM	19750	CA	LEU	D1164	53.213	37.573	19.098	1.00	46.22	C
ATOM	19751	C	LEU	D1164	51,985	37.092	19,858	1,00	51.78	C
ATOM	19752	CB	LEU	D1164	54.467	37,368	19.946	1,00	47,64	C
ATOM	19753	CG	LEU	D1164	54.688	35,935	20.448	1,00	50,88	C
ATOM	19754	CD1	LEU	D1164	55,103	34.958	19,317	1,00	46.46	C
ATOM	19755	CD2	LEU	D1164	55.706	35.944	21.566	1,00	46.21	C
ATOM	19756	O	GLY	D1165	51.270	33,531	21.306	1,00	55,26	0
ATOM	19757	N	GLY	DU 65	51,426	35.964	19,441	I,00	52.96	N
ATOM	19758	CA	GLY	D1165	50,309	35.397	20,169	1,00	46.95	C
ATOM	19759	C	GLY	D1165	50.748	34,641	21.415	1,00	46,09	C
ATOM	19760	O	ILE	D1166	48.459	34.300	24.544	1.00	48.71	0
ATOM	19761	N	ILE	D1166	50,561	35.243	22,587	1,00	43.32	N
ATOM	19762	CA	ILE	D1166	50.740	34,560	23.866	1,00	45,81	C
ATOM	19763	C	ILE	D1166	49.515	33.728	24.237	1.00	48.86	C
ATOM	19764	CB	ILE	D1166	51,007	35.552	25,010	1,00	43.81	C
ATOM	19765	CGI	ILE	D1166	52.229	36,400	24.691	1,00	48,86	C
ATOM	19766	CG2	ILE	D1166	51.225	34,815	26.306	1,00	39,65	C
ATOM	19767	CD1	ILE	D1166	53,422	35.566	24,280	1,00	43.60	C
ATOM	19768	O	THR	D1167	48.977	31.724	26.792	1,00	41.07	0
ATOM	19769	N	THR	D1167	49.662	32,397	24.248	1,00	42,52	N
ATOM	19770	CA	THR	D1167	48,528	31.497	24,457	I,00	40.68	C
ATOM	19771	C	THR	D1167	48.168	31.386	25.932	1,00	43.69	C
ATOM	19772	CB	THR	D1167	48.813	30,076	23.910	1,00	43,21	C
ATOM	19773	OG1	THR	DU 67	49,450	29.294	24,928	I,00	53.98	0
ATOM	19774	CG2	THR	D1167	49,691	30.139	22,673	1,00	40.61	C
ATOM	19775	O	ILE	D1168	47.779	30,256	29.602	1,00	45,56	0
ATOM	19776	N	ILE	D1168	46,971	30.879	26.225	1.00	37.87	N
ATOM	19777	CA	ILE	D1168	46,523	30.773	27.608	1,00	36.34	C
ATOM	19778	C	ILE	D1168	47.435	29,900	28.468	1,00	42,05	C
ATOM	19779	CB	ILE	D1168	45.063	30.260	27.674	1.00	39.81	C
ATOM	19780	CGI	ILE	D1168	44.106	31.428	27.345	1,00	40.86	C

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ATOM   19781   CG2  ILE  D1168      44.730  29.740  29.064  1.00 35.61        C
ATOM   19782   GDI  ILE  D1168      42.717  31.022  26.902  1.00 37.91        C
ATOM   197 83  O    MET  D1169      50.608  28.248  30.011  1.00 41.62        0
ATOM   19784   N    MET  D1169      47.855  28.764  27.916  1.00 45.63        N
ATOM   197 85  CA.  MET  D1169      48.728  27.831  28.609  1.00 39.08        C
ATOM   19786   C    MET  D1169      50.065  28.470  28.934  1.00 41.41        C
ATOM   19787   CB   MET  D1169      48.929  26.567  27.748  1.00 40.51        C
ATOM   197 88  CG   MET  D1169      49.781  25.475  28.383  1.00 40.88        C
ATOM   19789   SD   MET  D1169      49.412  23.852  27.632  1.00 48.74        S
ATOM   19790   CE   MET  D1169      50.518  23.943  26.235  1.00 39.69        C
ATOM   197 91  O    GLU  D1170      52.878  31.834  29.249  1.00 52.26        0
ATOM   19792   N    GLU  D1170      50.601  29.265  28.010  1.00 39.65        N
ATOM   197 93  CA   GLU  D117 0     51.888  29.893  28.266  1.00 43.90        C
ATOM   197 94  C    GLU  D117 0     51.829  31.265  28.943  1.00 46.32        C
ATOM   19795   CB   GLU  D117 0     52.690  30.004  26.964  1.00 47.68        C
ATOM   197 96  CG   GLU  D117 0     51.967  30.627  25.806  1.00 51.89        C
ATOM   197 97  CD   GLU  D117 0     52.703  30.445  24.469  1.00 57.07        C
ATOM   197 98  OE1  GLU  D1170      52.591  31.370  23.613  1.00 56.11        0
ATOM   197 99  OE2  GLU  D117 0     53.389  29.397  24.275  1.00 50.53        0
ATOM   19800   O    ARG  D1171      51.963  34.241  31.326  1.00 52.25        0
ATOM   19801   N    ARG  D1171      50.629  31.781  29.216  1.00 48.94        N
ATOM   19802   CA   ARG  D1171      50.486  33.140  29.780  1.00 47.62        C
ATOM   19803   C    ARG  D1171      51.249  33.260  31.105  1.00 50.41        C
ATOM   19804   CB   ARG  D1171      48.988  33.506  29.969  1.00 44.03        C
ATOM   19805   CG   ARG  D1171      48.715  34.826  30.704  1.00 49.84        C
ATOM   19806   CD   ARG  D1171      47.207  35.088  30.880  1.00 50.48        C
ATOM   19807   NE   ARG  D1171      46.932  36.214  31.761  1.00 44.33        N
ATOM   19808   CZ   ARG  D1171      45.706  36.627  32.107  1.00 54.49        C
ATOM   19809   NH1  ARG  D1171      44.604  36.018  31.655  1.00 51.59        N
ATOM   19810   NH2  ARG  D1171      45.577  37.668  32.915  1.00 46.24        N
ATOM   19811   O    SEP. D1172      53.890  33.225  33.899  1.00 62.56        O
ATOM   19812   N    SEP. D1172      51.126  32.255  31.970  1.00 47.78        N
ATOM   19813   CA   SER  D1172      51.766  32.344  33.285  1.00 53.21        C
ATOM   19814   C    SER  DU72       53.278  32.415  33.193  1.00 58.39        C
ATOM   19815   CB   SER  D1172      51.378  31.169  34.180  1.00 53.59        C
ATOM   19816   OG   SER  D1172      50.023  31.267  34.568  1.00 69.79        0
ATOM   19817   O    SER  D1173      56.873  33.376  31.942  1.00 56.14        0
ATOM   19818   N    SER  D1173      53.887  31.583  32.341  1.00 53.56        N
ATOM   19819   CA   SER  D117 3     55.350  31.597  32.221  1.00 51.19        C
ATOM   19820   C    SER  D1173      55.832  32.873  31.575  1.00 48.64        C
ATOM   19821   CB   SER  D117 3     55.872  30.408  31.415  1.00 42.97        C
ATOM   19822   OG   SER  D117 3     54.818  29.560  31.042  1.00 55.66        0
ATOM   19823   O    PHE  D117 4     56.306  36.692  30.876  1.00 57.89        0
ATOM   19824   N    PHE  D117 4     55.081  33.392  30.605  1.00 51.56        N
ATOM   19825   CA   PHE  D117 4     55.442  34.668  29.966  1.00 49.98        C
ATOM   19826   C    PHE  D117 4     55.423  35.842  30.931  1.00 54.36        C
ATOM   19827   CB   PHE  D1174      54.520  34.989  28.788  1.00 49.69        C
ATOM   19828   CG   PHE  D117 4     54.638  36.418  28.302  1.00 52.96        C
ATOM   19829   CD2  PHE  D1174      53.666  37.368  28.632  1.00 47.89        C
ATOM   19830   CD1  PHE  D1174      55.719  36.819  27.524  1.00 48.34        C
ATOM   19831   CE2  PHE  D1174      53.786  38.678  28.197  1.00 47.70        C
ATOM   19832   CE1  PHE  D1174      55.830  38.134  27.085  1.00 45.96        C
ATOM   19833   CZ   PHE  D1174      54.859  39.059  27.423  1.00 48.11        C
ATOM   19834   O    GLU  D1175      55.773  38.014  34.304  1.00 60.90        0
ATOM   19835   N    GLU  D1175      54.417  35.902  31.803  1.00 53.21        N
ATOM   19836   CA   GLU  D1175      54.280  37.046  32.706  1.00 52.62        C
ATOM   19837   C    GLU  D117 5     55.282  36.985  33.853  1.00 56.31        C
ATOM   19838   CB   GLU  D1175      52.853  37.139  33.249  1.00 50.09        C
ATOM   19839   CG   GLU  D117 5     51.806  37.505  32.193  1.00 48.52        C
ATOM   19840   CD   GLU  D117 5     50.415  37.696  32.790  1.00 50.84        C
ATOM   19841   OE1  GLU  D117 5     50.326  37.833  34.031  1.00 55.61        0
ATOM   19842   OE2  GLU  D117 5     49.414  37.704  32.031  1.00 51.67        0
ATOM   19843   O    LYS  D117 6     58.867  36.546  35.488  1.00 68.67        0
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ATOM   19844   N    LYS  D117 6      55.605   35.784   34.318   1.00  57.32             N
ATOM   19845   CA   LYS  D117 6      56.657   35.636   35.327   1.00  56.81             C
ATOM   19846   C    LYS  D117 6      58.036   36.003   34.774   1.00  64.76             C
ATOM   19847   CB   LYS  D117 6      56.698   34.209   35.873   1.00  60.32             c
ATOM   19848   N    ASM  D1177      58.292   35.710   33.505   I.00  64.74             N
ATOM   19849   CA   ASN  D117 7      59.638   35.903   32.978   1.00  66.35             C
ATOM   19850   c    ASN  D1177      59.687   36.250   31.502   1.00  62.29             c
ATOM   19851   0    ASM  D1177      60.121   35.434   30.694   I.00  68.25             0
ATOM   19852   CB   ASN  D1177      60.478   34.637   33.218   1.00  69.04             c
ATOM   19853   CG   ASN  D1177      61.666   34.896   34.124   1.00  76.60             c
ATOM   19854   OD1  ASN  D1177      62.643   35.540   33.719   I.00  79.39             0
ATOM   19855   ND2  ASN  D1177      61.585   34.410   35.363   1.00  71.79             N
ATOM   19856   N    PRO  D1178      59.270   37.470   31.146   1.00  61.51             N
ATOM   19857   CA   PRO  D1178      59.122   37.876   29.739   1.00  58.12             c
ATOM   19858   C    FRO  D117 8      60.391   37.718   28.880   1.00  59.24             C
ATOM   19859   O    PRO  D117 8      60.293   37.162   27.783   1.00  59.94             O
ATOM   198 60  CB   PRO  D1178      58.719   39.354   29.843   1.00  59.05             c
ATOM   19861   CG   PRO  D1178      58.108   39.478   31.187   I.00  62.62             c
ATOM   19862   CD   PRO  D117 8      58.865   38.534   32.077   1.00  59.48             c
ATOM   19863   N    ILE  D117 9      61.538   38.198   29.353   1.00  60.66             N
ATOM   19864   CA.  ILE  D117 9      62.768   38.130   28.571   I.00  58.14             C
ATOM   19865   C    ILE  D1179      63.123   36.684   28.285   1.00  62.08             C
ATOM   19866   O    ILE  D117 9      63.374   36.307   27.138   1.00  64.38             O
ATOM   198 67  CB   ILE  D117 9      63.950   38.800   29.291   I.00  64.14             C
ATOM   19868   CGI  ILE  D1179      63.628   40.254   29.633   1.00  67.15             c
ATOM   19869   CG2  ILE  D1179      65.196   38.745   28.431   1.00  61.68             c
ATOM   19870   CD1  ILE  D117 9      64.706   40.906   30.516   I.00  74.10             c
ATOM   19871   N    ASP  D1180      63.129   35.871   29.334   1.00  64.66             N
ATOM   19872   CA   ASP  D1180      63.461   34.459   29.197   1.00  60.16             C
ATOM   19873   c    ASP  D1180      62.500   33.822   28.205   1.00  59.37             c
ATOM   19874   O    ASP  D1180      62.928   33.098   27.304   1.00  63.04             0
ATOM   19875   CB   ASP  D1180      63.412   33.757   30.568   1.00  69.41             c
ATOM   19876   CG   ASP  D1180      64.094   32.378   30.569   1.00  80.61             c
ATOM   19877   OD1  ASP  D1180      65.116   32.198   29.867   I.00  89.01             0
ATOM   19878   OD2  ASP  D1180      63.611   31.467   31.289   1.00  79.52             0
ATOM   19879   N    PHE  D1181      61.208   34.133   28.347   1.00  61.37             N
ATOM   19880   CA.  PHE  D1181      60.153   33.546   27.514   I.00  50.99             C
ATOM   19881   C    PHE  D1181      60.378   33.857   26.037   1.00  52.70             C
ATOM   19882   O    PHE  D1181      60.300   32.963   25.189   1.00  55.57             0
ATOM   19883   CB   PHE  D1181      58.764   34.035   27.965   I.00  52.06             c
ATOM   19884   CG   PHE  D1181      57.621   33.444   27.175   1.00  50.25             c
ATOM   19885   CD2  PHE  D1181      57.203   34.024   25.974   1.00  48.75             c
ATOM   19886   CD1  PHE  D1181      56.971   32.314   27.622   1.00  48.76             c
ATOM   19887   CE2  PHE  D1181      56.176   33.467   25.229   1.00  43.53             c
ATOM   19888   CE1  PHE  D1181      55.935   31.759   26.886   1.00  47.94             c
ATOM   19889   CZ   PHE  D1181      55.536   32.340   25.693   1.00  48.12             c
ATOM   198 90  N    LEU  D1182      60.678   35.112   25.730   I.00  50.02             N
ATOM   198 91  CA   LEU  D1182      60.866   35.513   24.340   1.00  57.08             C
ATOM   19892   c    LEU  D1182      62.239   35.113   23.797   1.00  58.40             c
ATOM   19893   0    LEU  D1182      62.408   34.958   22.587   I.00  55.96             0
ATOM   19894   CB   LEU  D1182      60.673   37.024   24.180   1.00  57.45             c
ATOM   19895   CG   LEU  D1182      59.279   37.557   24.526   1.00  56.51             c
ATOM   19896   CD1  LEU  D1182      59.298   39.074   24.694   I.00  55.18             c
ATOM   19897   CD2  LEU  D1182      58.307   37.162   23.468   1.00  50.81             c
ATOM   198 98  N    GLU  D1183      63.219   34.970   24.685   1.00  57.75             N
ATOM   19899   CA   GLU  D1183      64.532   34.490   24.275   I.00  57.58             C
ATOM   19900   C    GLU  D1183      64.366   33.086   23.707   1.00  55.42             C
ATOM   19901   O    GLU  D1183      64.945   32.741   22.680   1.00  58.96             O
ATOM   19902   CB   GLU  D1183      65.515   34.502   25.446   1.00  57.22             c
ATOM   19903   N    ALA  D1184      63.508   32.304   24.343   1.00  54.26             N
ATOM   19904   CA   ALA  D1184      63.295   30.925   23.934   1.00  49.84             C
ATOM   19905   c    ALA  D1184      62.568   30.783   22.598   1.00  58.19             c
ATOM   19906   O    ALA  D1184      62.711   29.760   21.937   I.00  65.71             0
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ATOM   19907  CB   ALA  D1184    62.536  30:184  25,011  1.00  51.80   C
ATOM   19908  N    LYS  D1185    61,777  31.780  22,199  1,00  57.59   N
ATOM   19909  CA   LYS  D1185    61.036  31,685  20:937  1,00  53,65   C
ATOM   19910  C    LYS  D1185    61.938  32,040  19,759  1.00  54.68   C
ATOM   19911  0    LYS  D1185    61,557  31.878  18,593  1,00  49,00   0
ATOM   19912  CB   LYS  D1185    59.798  .32,595  20:941  1,00  49,45   C
ATOM   19913  CG   LYS  D1185    58.730  32,210  21.966  1,00  51,90   C
ATOM   19914  CD   LYS  D1185    57,510  31.595  21,302  1,00  48.25   C
ATOM   19915  CE   LYS  D1185    56.747  30,708  22,271  1,00  51.85   C
ATOM   19916  NZ   LYS  D1185    55.685  29,901  21.565  1,00  61,29   N
ATOM   19917  O    GLY  D1186    65,177  34:842  18,142  1,00  59.59   O
ATOM   19918  N    GLY  D1186    63.131  32,537  20:071  1,00  56.19   N
ATOM   19919  CA   GLY  D1186    64.081  .32,925  19.045  1,00  57,70   C
ATOM   19920  C    GLY  D1186    64.378  34:413  18,976  1.00  59.74   C
ATOM   19921  O    TYR  D1187    65,470  36.488  21,670  1,00  61.77   0
ATOM   19922  N    TYR  D1187    63.742  35,204  19:838  1,00  53,91   N
ATOM   19923  CA   TYR  D1187    63.966  36:652  19,829  1.00  59.59   C
ATOM   19924  C    TYR  D1187    65,232  37.006  20,586  1,00  57.78   C
ATOM   19925  CB   TYR  D1187    62.777  37,416  20:434  1,00  54,80   C
ATOM   19926  CG   TYR  D1187    61.519  37,350  19,605  1,00  55,22   C
ATOM   19927  CD1  TYR  D1187    61,494  37.864  18,311  1,00  56.44   C
ATOM   19928  CD2  TYR  D1187    60:351  36,796  20:119  1,00  50.66   C
ATOM   19929  CE1  TYR  D1187    60.350  37,819  17.545  1,00  46,28   C
ATOM   19930  CE2  TYR  D1187    59,200  36:747  19,361  1,00  48.37   C
ATOM   19931  CZ   TYR  D1187    59:214  37,256  18:071  1,00  48.72   C
ATOM   19932  OH   TYR  D1187    58.091  37,186  17..304  1,00  46,19   0
ATOM   19933  O    LYS  D1188    66,736  40:618  20,054  1,00  58.89   0
ATOM   19934  N    LYS  D1188    66,033  37.898  20,014  1,00  54.81   N
ATOM   19935  CA   LYS  D1188    67.259  38,345  20.662  1,00  63,26   C
ATOM   19936  C    LYS  D1188    67,262  39:858  20,878  1.00  66.03   C
ATOM   19937  CB   LYS  D1188    68,489  37.938  19,837  1,00  64.01   C
ATOM   19938  CG   LYS  D1188    68:525  36,466  19:431  1,00  66,95   C
ATOM   19939  CD   LYS  D1188    69,967  35:942  19,360  1.00  75.60   C
ATOM   19940  CE   LYS  D1188    70,111  34.761  18,398  1,00  77,03   C
ATOM   19941  NZ   LYS  D1188    69:167  33,633  18:685  1,00  70,80   N
ATOM   19942  O    GLU  D1189    66,426  43,335  21.556  1,00  67,28   0
ATOM   19943  N    GLU  D1189    67,873  40.279  21,984  1,00  66.33   N
ATOM   19944  CA   GLU  D1189    68:024  41,691  22,284  1,00  65.18   C
ATOM   19945  C    GLU  D1189    66.663  42,369  22.269  1,00  65,95   C
ATOM   19946  CB   GLU  D1189    68,983  42:.340  21,291  1,00  69.79   C
ATOM   19947  CG   GLU  D1189    70,389  41.734  21,345  1,00  74.29   C
ATOM   19948  CD   GLU  D1189    71..321  42,258  20.261  1,00  73,75   C
ATOM   19949  OE1  GLU  D1189    71,884  43:361  20,432  1.00  80.72   0
ATOM   19950  OE2  GLU  D1189    71,502  41.563  19,241  1,00  74,50   0
ATOM   19951  N    VAL  D1190    65:757  41,814  23:049  1,00  66,38   N
ATOM   19952  CA   VAL  D1190    64,440  42,371  23,188  1.00  58.93   C
ATOM   19953  C    VAL  DU 90    64,519  43.649  23,998  1,00  68.43   C
ATOM   19954  O    VAL  D1190    65:236  43,711  24:998  1,00  72,38   0
ATOM   19955  CB   VAL  D1190    63,518  41,389  23.875  1,00  61,68   C
ATOM   19956  CGI  VAL  DU 90    62,137  42.001  24,068  1,00  61.21   C
ATOM   19957  CG2  VAL  D1190    63:473  40,078  23:081  1,00  60.68   C
ATOM   19958  N    LYS  D1191    63,798  44,674  23.558  1,00  65,21   N
ATOM   19959  CA   LYS  DU 91    63,688  45:903  24,323  1,00  66.14   C
ATOM   19960  C    LYS  D1191    62,558  45,771  25:334  1,00  64.49   C
ATOM   19961  O    LYS  D1191    61.404  46,058  25.021  1,00  61,14   0
ATOM   19962  CB   LYS  DU 91    63,449  47,098  23,399  1,00  63.50   C
ATOM   19963  N    LYS  D1192    62,902  45.333  26,541  1,00  63.54   N
ATOM   19964  CA   LYS  D1192    61.923  45,084  27.591  1,00  63,90   C
ATOM   19965  C    LYS  D1192    60,897  46:212  27,748  1.00  61.58   C
ATOM   19966  O    LYS  D1192    59,711  45.940  27,905  1,00  65.93   0
ATOM   19967  CB   LYS  D1192    62:639  44,833  28:926  1,00  66,80   C
ATOM   19968  N    ASP  D1193    61,329  47,469  27,665  1.00  64.49   N
ATOM   19969  CA.  ASP  DU 93    60,415  48.608  27,885  1,00  64.17   C
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ATOM   19970  c    ASP  D1193       59..396   48..806   26..753   1.00  66..47          c
ATOM   19971  0    ASP  D1193       58,,578   49..735   26.,794   1,00  68..71          0
ATOM   19972  CB   ASP  D1193       61..215   49.,907   28..080   1,00  60,.70          c
ATOM   19973  N    LEU  D1194       59..446   47.940    25..744   1.00  59..03          N
ATOM   19974  CA.  LEU  D1194       58.,576   48. 059   24.,573   1,00  59..61          C
ATOM   19975  C    LEU  D1194       57..597   46.,887   24..402   1,00  60,.65          C
ATOM   19976  O    LEU  D1194       56..836   46.,836   23..436   1,00  63,.17          O
ATOM   19977  CB   LEU  D1194       59.,424   48. 195   23.,303   1,00  56..75          c
ATOM   19978  CG   LEU  D1194       59..773   49..596   22.,803   1,00  63..60          c
ATOM   19979  CD1  LEU  D1194       60..491   50.,409   23..877   1,00  67,72           c
ATOM   19980  CD2  LEU  DU94        60.,587   49.539    21.,518   I,00  57.91           c
ATOM   19981  N    1LE  D1195       57..629   45..933   25.,320   1,00  60..05          N
ATOM   19982  CA   ILE  D1195       56. 726   44,803    25. 227   1,00  54,63           c
ATOM   19983  c    ILE  D1195       55..330   45..253   25.,628   1.00  55..58          c
ATOM   19984  O    ILE  D1195       55.,021   45..350   26.,810   1,00  58..04          0
ATOM   19985  CB   ILE  D1195       57..170   43.,647   26..126   1,00  51,40           c
ATOM   19986  CGI  ILE  D1195       58..562   43.145    25..714   1.00  57.23           c
ATOM   19987  CG2  ILE  DU95        56.,174   42.517    26.,041   1,00  48.,37          c
ATOM   19988  CD1  ILE  D1195       59.241    42.,268   26..750   1,00  51,13           c
ATOM   19989  N    ILE  D1196       54..479   45.,542   24.659    1,00  48,.81          N
ATOM   19990  CA.  ILE  D1196       53.,151   46. 012   25,018    1,00  52.90           c
ATOM   19991  C    ILE  D1196       52..115   44,907    24.,889   1,00  47.36           c
ATOM   19992  O    ILE  D1196       51..978   44,286    23..840   1,00  47,77           0
ATOM   19993  CB   ILE  D1196       52.,738   47.228    24.,165   I,00  53..74          c
ATOM   19994  CGI  ILE  D1196       53..689   48..396   24.,442   1,00  48..27          c
ATOM   19995  CG2  ILE  D1196       51. 289   47,616    24.443    1,00  43,90           c
ATOM   19996  CD1  ILE  D1196       53.,616   49.500    23.,450   I,00  50..62          c
ATOM   19997  N    LYS  D1197       51.,424   44.657    25.,996   1,00  44.21           N
ATOM   19998  CA   LYS  D1197       50. 223   43.,831   26. 023   1,00  48,08           c
ATOM   19999  c    LYS  D1197       49..140   44,374    25.,069   1.00  49..53          c
ATOM   20000  O    LYS  D1197       48.,899   45..569   25.,017   1,00  51.92           0
ATOM   20001  CB   LYS  D1197       49.663    43.,768   27.437    1,00  44,98           c
ATOM   20002  CG   LYS  D1197       49..274   42.,385   27..860   1.00  54.16           c
ATOM   20003  CD   LYS  DU97        48.,684   42..356   29.,268   1,00  63..57          c
ATOM   20004  CE   LYS  D1197       47.243    42.,867   29..299   1,00  57,92           c
ATOM   20005  NZ   LYS  D1197       46..514   42.,282   30..455   1,00  65,.08          N
ATOM   20006  O    LEU  D1198       46.,396   41.837    22.,691   1,00  43..88          O
ATOM   20007  N    LEU  D1198       48..503   43.,482   24.,328   1,00  40..52          N
ATOM   20008  CA   LEU  D1198       47.471    43.,835   23..394   1,00  43,10           c
ATOM   20009  C    LEU  D1198       46.,371   42.802    23.,442   I,00  45..34          c
ATOM   20010  CB   LEU  D1198       48.,019   43..941   21.,973   1,00  44.16           c
ATOM   20011  CG   LEU  D1198       49. 058   45,041    21.777    1,00  44,83           c
ATOM   20012  CD1  LEU  D1198       49..807   44,886    20.,465   1.00  41.12           c
ATOM   20013  CD2  LEU  D1198       48.,387   46.. 417  21.,855   1,00  51,40           c
ATOM   20014  O    PP.0 D1199       43..699   43.,246   22..250   1,00  48,.12          0
ATOM   20015  N    PRO  D1199       45..384   43,002    24..327   1.00  47.14           N
ATOM   20016  CA.  PRO  D1199       44,206    42.123    24.,298   1,00  43..00          C
ATOM   20017  C    PRO  D1199       43...368  42.,360   23..039   1,00  45,.26          c
ATOM   20018  CB   PRO  D1199       43..440   42.,520   25..548   1,00  45,.25          c
ATOM   20019  CG   PRO  D1199       44,417    43. 385   26.,374   1,00  43..92          c
ATOM   20020  CD   PRO  D1199       45..307   44,021    25.,389   1,00  44.46           c
ATOM   20021  O    LYS  D1200       40..145   42.,729   23..830   1,00  56,.51          0
ATOM   20022  N    LYS  D1200       42.,331   41.564    22..818   I,00  41.47           N
ATOM   20023  CA   LYS  D1200       41.315    41.999    21.,872   1,00  55..25          C
ATOM   20024  C    LYS  D1200       40. 404   42.,957   22.664    1,00  44,94           C
ATOM   20025  CB   LYS  D1200       40.,562   40..795   21.,281   I,00  55..55          C
ATOM   20026  CG   LYS  D1200       39.,529   40..150   22.,190   1,00  49..60          c
ATOM   20027  CD   LYS  D1200       38. 872   .38.,946  21.520    1,00  50,10           c
ATOM   20028  CE   LYS  D1200       38..523   39.,203   20.,080   1.00  48..90          c
ATOM   20029  NZ   LYS  D1200       37.,530   38..196   19.,625   1,00  53..14          N
ATOM   20030  N    TYR  D1201       39.917    44,041    22..112   1,00  59,.28          N
ATOM   20031  CA   TYR  D1201       39..937   44,436    20..742   1.00  57.66           c
ATOM   20032  C    TYR  D1201       40.,743   45. 730   20.,712   1,00  53..01          C
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ATOM	20033	O	TYR	D1201	40.171	46.785	20.555	1.00	55.87	O
ATOM	20034	CB	TYR	D1201	38.497	44.671	20.277	1.00	51.45	C
ATOM	20035	CG	TYR	D1201	37.550	43.494	20.528	1.00	51.32	C
ATOM	20036	GDI	TYR	D1201	37.197	43.098	21.815	1.00	47.10	C
ATOM	20037	CD2	TYR	D1201	36.984	42.803	19.460	1.00	48.72	C
ATOM	20038	CE1	TYR	D1201	36.341	42.021	22.025	1.00	47.60	C
ATOM	20039	CE2	TYR	D1201	36.120	41.747	19.658	1.00	49.57	C
ATOM	20040	CZ	TYR	D1201	35.803	41.352	20.935	1.00	52.96	C
ATOM	20041	OH	TYR	D1201	34.943	40.281	21.088	1.00	55.42	0
ATOM	20042	N	SER	D1202	42.056	45.636	20.912	1.00	54.90	N
ATOM	20043	CA	SER	D1202	42.901	46.809	21.030	1.00	49.55	C
ATOM	20044	C	SER	D1202	42.740	47.737	19.832	1.00	49.55	C
ATOM	20045	O	SER	D1202	42.639	47.286	18.682	1.00	50.24	O
ATOM	20046	CB	SER	D1202	44.365	46.397	21.195	1.00	44.93	C
ATOM	20047	OG	SER	D1202	44.604	45.976	22.521	1.00	42.23	0
ATOM	20048	N	LEU	D1203	42.724	49.036	20.116	1.00	47.79	N
ATOM	20049	CA	LEU	D1203	42.325	50.050	19.146	1.00	47.32	C
ATOM	20050	C	LEU	D1203	43.495	50.817	18.587	1.00	48.17	C
ATOM	20051	O	LEU	D1203	44.306	51.372	19.341	1.00	51.50	0
ATOM	20052	CB	LEU	D1203	41.337	51.039	19.787	1.00	49.86	C
ATOM	20053	CG	LEU	D1203	40.796	52.150	18.879	1.00	42.87	C
ATOM	20054	CD1	LEU	D1203	39.975	51.535	17.772	1.00	46.99	C
ATOM	20055	CD2	LEU	D1203	39.980	53.137	19.679	1.00	49.56	C
ATOM	20056	N	PHE	D1204	43.552	50.877	17.263	1.00	50.13	N
ATOM	20057	CA	FHE	D1204	44.575	51.638	16.558	1.00	54.21	C
ATOM	20058	C	PHE	D1204	43.975	52.667	15.591	1.00	57.33	C
ATOM	20059	O	PHE	D1204	43.000	52.376	14.875	1.00	56.45	0
ATOM	20060	CB	FHE	D1204	45.490	50.704	15.770	1.00	54.55	C
ATOM	20061	CG	PHE	D1204	46.118	49.608	16.593	1.00	60.62	C
ATOM	20062	CD1	PHE	D1204	47.387	49.779	17.136	1.00	56.35	C
ATOM	20063	CD2	FHE	D1204	45.453	48.393	16.800	1.00	55.10	C
ATOM	20064	CE1	PHE	D1204	47.977	48.781	17.874	1.00	53.88	C
ATOM	20065	CE2	PHE	D1204	46.048	47.378	17.542	1.00	52.41	C
ATOM	20066	CZ	PHE	D1204	47.308	47.571	18.077	1.00	53.77	C
ATOM	20067	0	GLU	D1205	46.514	54.817	13.747	1.00	62.65	0
ATOM	20068	N	GLU	D1205	44.565	53.858	15.545	1.00	52.05	N
ATOM	20069	CA.	GLU	D1205	44.224	54.802	14.484	1.00	54.32	C
ATOM	20070	C	GLU	D1205	45.324	54.842	13.426	1.00	59.76	C
ATOM	20071	CB	GLU	D1205	43.980	56.210	15.034	1.00	57.84	C
ATOM	20072	CG	GLU	D1205	43.531	57.173	13.944	1.00	57.59	C
ATOM	20073	CD	GLU	D1205	43.081	58.516	14.473	1.00	59.48	C
ATOM	20074	OE1	GLU	D1205	42.801	59.417	13.637	1.00	63.67	0
ATOM	20075	OE2	GLU	D1205	43.003	58.676	15.715	1.00	60.25	0
ATOM	20076	O	LEU	D1206	45.444	57.310	10.886	1.00	65.69	0
ATOM	20077	N	LEU	D1206	44.921	54.888	12.162	1.00	56.85	N
ATOM	20078	CA	LEU	D1206	45.870	54.958	11.070	1.00	57.16	C
ATOM	20079	C	LEU	D120 6	45.696	56.265	10.292	1.00	56.42	C
ATOM	20080	CB	LEU	D1206	45.710	53.735	10.168	1.00	61.72	C
ATOM	20081	CG	LEU	D1206	45.524	52.435	10.953	1.00	58.28	C
ATOM	20082	CD1	LEU	D120 6	44.076	51.969	10.917	1.00	57.22	C
ATOM	20083	CD2	LEU	D1206	46.449	51.353	10.459	1.00	67.36	C
ATOM	20084	O	GLU	D1207	43.383	56.912	7.746	1.00	62.93	0
ATOM	20085	N	GLU	D1207	45.834	56.227	8.975	1.00	57.61	N
ATOM	20086	CA	GLU	D1207	45.684	57.449	8.181	1.00	60.48	C
ATOM	20087	C	GLU	D1207	44.208	57.802	7.975	1.00	62.35	C
ATOM	20088	CB	GLU	D1207	46.402	57.294	6.827	1.00	61.60	C
ATOM	20089	CG	GLU	D1207	45.535	56.823	5.651	1.00	59.53	C
ATOM	20090	CD	GLU	D1207	45.054	55.387	5.790	1.00	66.54	C
ATOM	20091	OE1	GLU	D1207	44.330	54.902	4.893	1.00	66.98	0
ATOM	20092	OE2	GLU	D1207	45.411	54.738	6.793	1.00	67.25	0
ATOM	20093	O	ASN	D1208	40.362	59.088	8.522	1.00	67.37	0
ATOM	20094	N	ASN	D1208	43.894	59.098	8.080	1.00	67.22	N
ATOM	20095	CA.	ASM	D1208	42.549	59.652	7.835	1.00	62.47	C

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ATOM   20096   C    ASN  D1208        41.509   59.318    8.876   1.00  60.51              C
ATOM   20097   CB   ASM  D1208        41.985   59.193    6.480   1.00  65.09              C
ATOM   20098   CG   ASN  D1208        42.666   59.850    5.309   1.00  68.24              C
ATOM   20099   OD1  ASN  D1208        42.888   61.058    5.301   1.00  67.80              0
ATOM   20100   ND2  ASN  D1208        43.012   59.047    4.307   1.00  65.85              N
ATOM   20101   O    GLY  D1209        39.574   57.015   11.787   1.00  55.20              0
ATOM   20102   N    GLY  D1209        41.887   59.290   10.147   1.00  64.24              N
ATOM   20103   CA.  GLY  D1209        40.963   58.868   11.184   1.00  58.26              C
ATOM   20104   C    GLY  D1209        40.455   57.436   11.040   1.00  57.21              C
ATOM   20105   O    ARG  D1210        41.942   54.842   11.930   1.00  60.49              O
ATOM   20106   N    ARG  D1210        40.985   56.689   10.076   1.00  54.34              N
ATOM   20107   CA   ARG  D1210        40.629   55.279    9.952   1.00  59.77              C
ATOM   20108   C    ARG  D1210        40.969   54.526   11.243   1.00  58.27              C
ATOM   20109   CB   ARG  D1210        41.338   54.642    8.764   1.00  58.72              C
ATOM   20110   CG   ARG  D1210        40.779   53.304    8.364   1.00  60.33              C
ATOM   20111   CD   ARG  D1210        41.408   52.856    7.079   1.00  63.03              C
ATOM   20112   NE   ARG  D1210        42.864   52.908    7.175   1.00  65.36              N
ATOM   20113   CZ   ARG  D1210        43.656   51.838    7.171   1.00  65.66              C
ATOM   20114   NH1  ARG  D1210        44.967   51.993    7.265   1.00  66.52              N
ATOM   20115   NH2  ARG  D1210        43.142   50.616    7.067   1.00  57.99              N
ATOM   20116   N    LYS  D1211        40.139   53.554   11.594   1.00  57.29              N
ATOM   20117   CA   LYS  D1211        40.352   52.800   12.817   1.00  56.52              C
ATOM   20118   C    LYS  D1211        40.235   51.289   12.586   1.00  60.05              C
ATOM   20119   0    LYS  D1211        39.384   50.802   11.814   1.00  56.79              0
ATOM   20120   CB   LYS  D1211        39.383   53.286   13.900   1.00  52.87              C
ATOM   20121   CG   LYS  D1211        39.858   54.603   14.545   1.00  53.72              C
ATOM   20122   CD   LYS  D1211        38.835   55.263   15.477   1.00  57.64              C
ATOM   20123   CE   LYS  D1211        39.421   56.531   16.118   1.00  61.05              C
ATOM   20124   NZ   LYS  D1211        38.821   56.867   17.454   1.00  62.32              N
ATOM   20125   N    ARG  D1212        41.153   50.564   13.214   1.00  57.67              N
ATOM   20126   CA   ARG  D1212        41.102   49.113   13.255   1.00  50.87              C
ATOM   20127   C    ARG  D1212        41.179   48.658   14.696   1.00  50.83              C
ATOM   20128   O    ARG  D1212        41.919   49.218   15.500   1.00  50.88              0
ATOM   20129   CB   ARG  D1212        42.241   48.482   12.458   1.00  53.85              C
ATOM   20130   CG   ARG  D1212        42.248   48.785   10.993   1.00  54.78              C
ATOM   20131   CD   ARG  D1212        41.051   48.210   10.285   1.00  58.57              C
ATOM   20132   NE   ARG  D1212        40.417   49.233    9.448   1.00  65.76              N
ATOM   20133   CZ   ARG  D1212        40.163   49.067    8.161   1.00  62.80              C
ATOM   20134   NH1  ARG  D1212        40.480   47.934    7.575   1.00  71.69              N
ATOM   20135   NH2  ARG  D1212        39.612   50.023    7.458   1.00  61.94              N
ATOM   20136   N    MET  D1213        40.400   47.646   15.019   1.00  50.29              N
ATOM   20137   CA   MET  D1213        40.560   46.935   16.269   1.00  49.36              C
ATOM   20138   C    MET  D1213        41.244   45.572   16.055   1.00  47.52              C
ATOM   20139   O    MET  D1213        41.012   44.872   15.062   1.00  47.51              0
ATOM   20140   CB   MET  D1213        39.206   46.724   16.935   1.00  49.26              C
ATOM   20141   CG   MET  D1213        38.581   47.923   17.551   1.00  46.21              C
ATOM   20142   SD   MET  D1213        37.023   47.443   18.322   1.00  46.92              S
ATOM   20143   CE   MET  D1213        36.281   46.545   16.954   1.00  39.65              C
ATOM   20144   N    LEU  D1214        42.050   45.179   17.026   1.00  52.38              N
ATOM   20145   CA.  LEU  D1214        42.810   43.950   16.935   1.00  50.32              C
ATOM   20146   C    LEU  D1214        41.967   42.765   17.376   1.00  51.85              C
ATOM   20147   O    LEU  D1214        41.591   42.681   18.534   1.00  53.58              O
ATOM   20148   CB   LEU  D1214        44.074   44.064   17.781   1.00  51.92              C
ATOM   20149   CG   LEU  D1214        45.102   42.941   17.713   1.00  61.97              C
ATOM   20150   GDI  LEU  D1214        45.925   43.076   16.453   1.00  58.99              C
ATOM   20151   CD2  LEU  D1214        45.992   42.958   18.967   1.00  55.10              C
ATOM   20152   N    ALA  D1215        41.672   41.857   16.442   1.00  56.88              N
ATOM   20153   CA   ALA  D1215        40.899   40.645   16.728   1.00  57.45              C
ATOM   20154   C    ALA  D1215        41.793   39.460   17.096   1.00  56.70              C
ATOM   20155   O    ALA  D1215        41.387   38.560   17.831   1.00  53.84              0
ATOM   20156   CB   ALA  D1215        40.039   40.282   15.546   1.00  60.57              C
ATOM   20157   O    SER  D1216        45.336   40.119   15.716   1.00  67.35              0
ATOM   20158   N    SER  D1216        43.001   39.467   16.554   1.00  58.38              N
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ATOM   20159  CA   SER  D1216      44.043  38.493  16.888  1.00 65.53          C
ATOM   20160  C    SEP. D1216      45.347  39.050  16.340  1.00 67.56          C
ATOM   20161  CB   SER  D1216      43.757  37.102  16.300  1.00 61.29          C
ATOM   20162  OG   SER  D1216      44.270  36.996  14.988  1.00 64.20          0
ATOM   20163  O    ALA  D1217      48.776  39.037  13.865  1.00 68.99          0
ATOM   20164  N    ALA  D1217      46.460  38.342  16.556  1.00 66.54          N
ATOM   20165  CA   ALA  D1217      47.751  38.781  16.024  1.00 61.46          C
ATOM   20166  C    ALA  D1217      47.785  38.668  14.494  1.00 67.35          C
ATOM   20167  CB   ALA  D1217      48.887  37.986  16.644  1.00 61.22          C
ATOM   20168  O    GLY  D1218      44.776  37.710  10.904  1.00 78.12          0
ATOM   20169  N    GLY  D1218      46.694  38.162  13.908  1.00 66.19          N
ATOM   20170  CA   GLY  D1218      46.559  38.038  12.467  1.00 63.02          C
ATOM   20171  C    GLY  D1218      45.157  38.303  11.919  1.00 73.93          C
ATOM   20172  N    GLU  D1219      44.386  39.169  12.583  1.00 64.82          N
ATOM   20173  CA   GLU  D1219      43.091  39.613  12.061  1.00 64.63          C
ATOM   20174  C    GLU  D1219      42.648  40.985  12.608  1.00 62.13          C
ATOM   20175  O    GLU  D1219      42.719  41.242  13.811  1.00 59.69          0
ATOM   20176  CB   GLU  D1219      42.026  38.577  12.362  1.00 65.74          C
ATOM   20177  CG   GLU  D1219      40.883  38.605  11.390  1.00 71.02          C
ATOM   20178  CD   GLU  D1219      40.420  37.207  11.030  1.00 82.18          C
ATOM   20179  OE1  GLU  D1219      39.820  37.030   9.947  1.00 83.46          0
ATOM   20180  OE2  GLU  D1219      40.666  36.282  11.837  1.00 88.59          0
ATOM   20181  N    LEU  D1220      42.185  41.862  11.718  1.00 61.60          N
ATOM   20182  CA   LEU  D1220      41.712  43.191  12.116  1.00 53.41          C
ATOM   20183  C    LEU  D1220      40.208  43.328  12.011  1.00 52.79          C
ATOM   20184  O    LEU  D1220      39.585  42.706  11.159  1.00 54.75          O
ATOM   20185  CB   LEU  D1220      42.384  44.268  11.281  1.00 49.95          C
ATOM   20186  CG   LEU  D1220      43.856  44.481  11.651  1.00 60.40          C
ATOM   20187  GDI  LEU  D1220      44.450  45.619  10.847  1.00 58.18          C
ATOM   20188  CD2  LEU  D1220      44.036  44.717  13.153  1.00 53.99          C
ATOM   20189  N    GLN  D1221      39.642  44.131  12.910  1.00 52.30          N
ATOM   20190  CA   GLN  D1221      38.223  44.505  12.894  1.00 48.47          C
ATOM   20191  C    GLN  D1221      38.059  46.001  12.652  1.00 51.00          C
ATOM   20192  0    GLN  D1221      38.954  46.784  12.945  1.00 49.28          0
ATOM   20193  CB   GLN  D1221      37.533  44.114  14.205  1.00 47.17          C
ATOM   20194  CG   GLN  D1221      37.031  42.672  14.209  1.00 51.72          C
ATOM   20195  CD   GLN  D1221      36.281  42.287  15.480  1.00 54.81          C
ATOM   20196  OE1  GLN  D1221      35.867  43.145  16.267  1.00 49.81          0
ATOM   20197  NE2  GLN  D1221      36.096  40.984  15.680  1.00 52.94          N
ATOM   20198  N    LYS  D1222      36.908  46.383  12.104  1.00 54.57          N
ATOM   20199  CA   LYS  D1222      36.603  47.779  11.773  1.00 51.37          C
ATOM   20200  C    LYS  D1222      36.424  48.605  13.029  1.00 47.02          C
ATOM   20201  O    LYS  D1222      35.646  48.247  13.901  1.00 52.40          0
ATOM   20202  CB   LYS  D1222      35.341  47.862  10.912  1.00 47.19          C
ATOM   20203  CG   LYS  D1222      35.516  47.333   9.519  1.00 49.68          C
ATOM   20204  CD   LYS  D1222      34.236  47.461   8.714  1.00 61.03          C
ATOM   20205  CE   LYS  D1222      33.317  46.263   8.873  1.00 58.92          C
ATOM   20206  NZ   LYS  D1222      31.895  46.705   8.661  1.00 61.57          N
ATOM   20207  O    GLY  D1223      36.359  52.646  15.168  1.00 51.15          O
ATOM   20208  N    GLY  D1223      37.130  49.716  13.126  1.00 51.54          N
ATOM   20209  CA   GLY  D1223      37.040  50.525  14.330  1.00 53.51          C
ATOM   20210  C    GLY  D1223      36.332  51.865  14.214  1.00 52.48          C
ATOM   20211  0    ASM  D1224      32.917  52.325  12.415  1.00 54.27          0
ATOM   20212  N    ASN  D1224      35.711  52.147  13.066  1.00 56.32          N
ATOM   20213  CA   ASN  D1224      35.007  53.431  12.876  1.00 50.23          C
ATOM   20214  C    ASN  D1224      33.487  53.303  12.912  1.00 53.22          C
ATOM   20215  CB   ASN  D1224      35.385  54.081  11.558  1.00 48.77          C
ATOM   20216  CG   ASN  D1224      36.873  54.292  11.407  1.00 54.79          C
ATOM   20217  OD1  ASN  D1224      37.563  53.496  10.753  1.00 52.38          O
ATOM   20218  ND2  ASN  D1224      37.375  55.381  11.979  1.00 48.66          N
ATOM   20219  O    GLU  D1225      31.522  56.540  12.372  1.00 56.05          O
ATOM   20220  N    GLU  D1225      32.850  54.308  13.495  1.00 50.16          N
ATOM   20221  CA.  GLU  D1225      31.393  54.431  13.505  1.00 59.08          C
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ATOM  20222  C    GLU  D1225    30.893  55.508  12.513  1.00  50.77    C
ATOM  20223  CB   GLU  D1225    30.917  54.753  14.918  1.00  54.93    C
ATOM  20224  CG   GLU  D1225    29.556  54.202  15.195  1.00  58.49    C
ATOM  20225  CD   GLU  D1225    29.564  52.733  15.556  1.00  53.65    C
ATOM  20226  OE1  GLU  D1225    29.887  52.460  16.733  1.00  56.81    0
ATOM  20227  OE2  GLU  D1225    29.248  51.863  14.683  1.00  57.25    0
ATOM  20228  O    LEU  D1226    27.029  56.747  11.344  1.00  56.42    0
ATOM  20229  N    LEU  D1226    29.778  55.274  11.826  1.00  54.49    N
ATOM  20230  CA   LEU  D1226    29.315  56.218  10.780  1.00  57.08    C
ATOM  20231  C    LEU  D1226    28.188  57.152  11.240  1.00  53.45    C
ATOM  20232  CB   LEU  D1226    28.869  55.448   9.524  1.00  57.03    C
ATOM  20233  CG   LEU  D1226    28.125  56.141   8.371  1.00  61.38    C
ATOM  20234  GDI  LEU  D1226    28.746  57.480   8.008  1.00  63.08    C
ATOM  20235  CD2  LEU  D1226    28.078  55.246   7.137  1.00  56.82    C
ATOM  20236  O    ALA  D1227    27.157  60.588   9.835  1.00  62.08    0
ATOM  20237  N    ALA  D1227    28.538  58.407  11.517  1.00  54.65    N
ATOM  20238  CA   ALA  D1227    27.536  59.413  11.884  1.00  54.12    C
ATOM  20239  C    ALA  D1227    26.711  59.804  10.665  1.00  59.00    C
ATOM  20240  CB   ALA  D1227    28.194  60.635  12.486  1.00  50.48    C
ATOM  20241  O    LEU  D1228    23.181  60.697  11.043  1.00  64.16    0
ATOM  20242  N    LEU  D1228    25.523  59.224  10.542  1.00  63.61    N
ATOM  20243  CA   LEU  D1228    24.596  59.584   9.472  1.00  59.89    C
ATOM  20244  C    LEU  D1228    23.704  60.729   9.931  1.00  62.58    C
ATOM  20245  CB   LEU  D1228    23.744  58.389   9.078  1.00  57.41    C
ATOM  20246  CG   LEU  D1228    22.914  58.506   7.806  1.00  62.17    C
ATOM  20247  GDI  LEU  D1228    23.807  58.315   6.598  1.00  62.14    C
ATOM  20248  CD2  LEU  D1228    21.765  57.503   7.813  1.00  62.04    C
ATOM  20249  N    FRO  D1229    23.528  61.755   9.084  1.00  69.44    N
ATOM  20250  CA   PRO  D1229    22.629  62.863   9.436  1.00  62.95    C
ATOM  20251  C    PRO  D1229    21.239  62.383   9.870  1.00  60.84    C
ATOM  20252  O    FRO  D1229    20.705  61.443   9.282  1.00  60.82    0
ATOM  20253  CB   PRO  D1229    22.555  63.663   8.138  1.00  68.86    C
ATOM  20254  CG   PRO  D1229    23.869  63.371   7.449  1.00  66.63    C
ATOM  20255  CD   PRO  D1229    24.128  61.931   7.747  1.00  66.95    C
ATOM  20256  N    SEP. D1230    20.673  63.017  10.896  1.00  65.03    N
ATOM  20257  CA   SER  D1230    19.346  62.655  11.405  1.00  63.17    C
ATOM  20258  C    SER  D1230    18.265  62.683  10.329  1.00  68.98    C
ATOM  20259  O    SER  D1230    17.228  62.042  10.480  1.00  71.42    0
ATOM  20260  CB   SER  D1230    18.938  63.587  12.536  1.00  67.77    C
ATOM  20261  OG   SER  D1230    20.077  64.104  13.198  1.00  73.52    0
ATOM  20262  N    LYS  D1231    18.502  63.426   9.250  1.00  67.05    N
ATOM  20263  CA   LYS  D1231    17.558  63.471   8.143  1.00  67.07    C
ATOM  20264  C    LYS  D1231    17.354  62.089   7.588  1.00  69.08    C
ATOM  20265  O    LYS  D1231    16.231  61.597   7.432  1.00  64.63    0
ATOM  20266  CB   LYS  D1231    18.060  64.376   7.020  1.00  72.99    C
ATOM  20267  CG   LYS  D1231    18.686  65.690   7.455  1.00  75.34    C
ATOM  20268  CD   LYS  D1231    19.504  66.243   6.299  1.00  70.98    C
ATOM  20269  CE   LYS  D1231    20.647  67.109   6.780  1.00  71.90    C
ATOM  20270  NZ   LYS  D1231    21.649  67.259   5.691  1.00  67.81    N
ATOM  20271  N    TYR  D1232    18.479  61.465   7.282  1.00  71.06    N
ATOM  20272  CA   TYR  D1232    18.475  60.216   6.556  1.00  66.44    C
ATOM  20273  C    TYR  D1232    18.009  59.083   7.451  1.00  63.35    C
ATOM  20274  0    TYR  D1232    17.433  58.106   6.984  1.00  67.74    0
ATOM  20275  CB   TYR  D1232    19.865  59.947   5.995  1.00  71.39    C
ATOM  20276  CG   TYR  D1232    20.390  61.036   5.070  1.00  72.42    C
ATOM  20277  GDI  TYR  D1232    19.525  61.845   4.345  1.00  70.03    C
ATOM  20278  CD2  TYR  D1232    21.752  61.247   4.926  1.00  70.40    C
ATOM  20279  CE1  TYR  D1232    20.008  62.831   3.508  1.00  71.65    C
ATOM  20280  CE2  TYR  D1232    22.241  62.223   4.096  1.00  71.54    C
ATOM  20281  CZ   TYR  D1232    21.369  63.015   3.386  1.00  73.50    C
ATOM  20282  OH   TYR  D1232    21.873  63.987   2.549  1.00  71.78    0
ATOM  20283  N    VAL  D1233    18.239  59.228   8.747  1.00  65.59    N
ATOM  20284  CA.  VAL  D1233    17.857  58.194   9.694  1.00  63.93    C
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ATOM  20285  c    VAL  D1233   16.349  58.168   9.841  1.00  65.28   c
ATOM  20286  O    VAL  D1233   15.732  57.112   9.750  1.00  69.95   O
ATOM  20287  CB   VAL  D1233   18.533  58.413  11.068  1.00  64.55   c
ATOM  20288  CGI  VAL  D1233   17.873  57.565  12.164  1.00  50.25   c
ATOM  20289  CG2  VAL  D1233   20.022  58.123  10.957  1.00  63.97   c
ATOM  20290  N    ASN  D1234   15.759  59.336  10.072  1.00  69.30   N
ATOM  20291  CA   ASN  D1234   14.307  59.465  10.132  1.00  68.14   c
ATOM  20292  C    ASM  D1234   13.658  58.961   8.861  1.00  68.15   c
ATOM  20293  O    ASN  D1234   12.660  58.236   8.888  1.00  67.04   0
ATOM  20294  CB   ASN  D1234   13.925  60.911  10.374  1.00  61.11   c
ATOM  20295  CG   ASN  D1234   13.851  61.236  11.836  1.00  70.64   c
ATOM  20296  OD1  ASN  D1234   14.306  60.448  12.675  1.00  69.24   0
ATOM  20297  ND2  ASN  D1234   13.256  62.390  12.167  1.00  66.45   N
ATOM  20298  N    PHE  D1235   14.265  59.333   7.744  1.00  68.71   N
ATOM  20299  CA   PHE  D1235   13.760  58.948   6.446  1.00  67.08   C
ATOM  20300  C    PHE  D1235   13.706  57.440   6.292  1.00  71.95   C
ATOM  20301  O    PHE  D1235   12.704  56.903   5.825  1.00  74.91   O
ATOM  20302  CB   PHE  D1235   14.614  59.557   5.339  1.00  71.94   c
ATOM  20303  CG   PHE  D1235   14.417  58.897   4.012  1.00  77.52   c
ATOM  20304  CD1  PHE  D1235   13.208  59.010   3.347  1.00  77.80   c
ATOM  20305  CD2  PHE  D1235   15.432  58.145   3.440  1.00  76.59   c
ATOM  20306  CE1  PHE  D1235   13.008  58.390   2.139  1.00  79.65   c
ATOM  20307  CE2  PHE  D1235   15.244  57.520   2.221  1.00  80.38   c
ATOM  20308  CZ   PHE  D1235   14.027  57.647   1.566  1.00  84.11   c
ATOM  20309  N    LEU  D1236   14.773  56.755   6.698  1.00  69.70   N
ATOM  20310  CA   LEU  D1236   14.886  55.326   6.450  1.00  65.89   C
ATOM  20311  C    LEU  D1236   13.971  54.523   7.371  1.00  66.01   c
ATOM  20312  O    LEU  D1236   13.561  53.407   7.030  1.00  65.04   0
ATOM  20313  CB   LEU  D1236   16.346  54.873   6.596  1.00  72.26   c
ATOM  20314  CG   LEU  D1236   17.298  55.113   5.411  1.00  73.62   c
ATOM  20315  CD1  LEU  D1236   18.742  55.089   5.871  1.00  72.62   c
ATOM  20316  CD2  LEU  D1236   17.101  54.104   4.275  1.00  68.28   c
ATOM  20317  N    TYR  D1237   13.659  55.093   8.532  1.00  65.20   N
ATOM  20318  CA.  TYR  D1237   12.664  54.523   9.448  1.00  70.00   C
ATOM  20319  C    TYR  D1237   11.237  54.644   8.927  1.00  73.56   C
ATOM  20320  O    TYR  D1237   10.451  53.702   9.029  1.00  77.67   0
ATOM  20321  CB   TYR  D1237   12.728  55.201  10.811  1.00  71.48   c
ATOM  20322  CG   TYR  D1237   11.785  54.591  11.827  1.00  73.83   c
ATOM  20323  CD2  TYR  D1237   10.529  55.143  12.070  1.00  76.20   c
ATOM  20324  CD1  TYR  D1237   12.151  53.458  12.541  1.00  73.46   c
ATOM  20325  CE2  TYR  D1237    9.665  54.582  13.009  1.00  78.87   c
ATOM  20326  CE1  TYR  D1237   11.301  52.890  13.481  1.00  80.25   c
ATOM  20327  CZ   TYR  D1237   10.058  53.452  13.714  1.00  83.72   c
ATOM  20328  OH   TYR  D1237    9.217  52.877  14.651  1.00  79.87   0
ATOM  20329  N    LEU  D1238   10.891  55.815   8.403  1.00  69.83   N
ATOM  20330  CA   LEU  D1238    9.574  55.999   7.791  1.00  74.93   c
ATOM  20331  C    LEU  D1238    9.462  55.209   6.486  1.00  75.49   c
ATOM  20332  O    LEU  D1238    8.488  54.481   6.275  1.00  72.85   0
ATOM  20333  CB   LEU  D1238    9.291  57.485   7.556  1.00  69.55   c
ATOM  20334  CG   LEU  D1238    8.962  58.230   8.854  1.00  69.30   c
ATOM  20335  CD1  LEU  D1238    9.016  59.744   8.702  1.00  67.98   c
ATOM  20336  CD2  LEU  D1238    7.610  57.796   9.388  1.00  70.43   c
ATOM  20337  N    ALA  D1239   10.482  55.316   5.639  1.00  73.11   N
ATOM  20338  CA   ALA  D1239   10.464  54.665   4.334  1.00  70.70   C
ATOM  20339  C    ALA  D1239   10.498  53.150   4.406  1.00  74.17   c
ATOM  20340  O    ALA  D1239   10.252  52.483   3.407  1.00  78.82   0
ATOM  20341  CB   ALA  D1239   11.613  55.152   3.495  1.00  70.56   c
ATOM  20342  N    SER  D1240   10.805  52.593   5.570  1.00  74.28   N
ATOM  20343  CA   SER  D1240   10.857  51.137   5.687  1.00  83.79   c
ATOM  20344  C    SER  D1240    9.658  50.591   6.451  1.00  84.75   C
ATOM  20345  O    SER  D1240    9.432  49.381   6.485  1.00  90.92   O
ATOM  20346  CB   SER  D1240   12.162  50.687   6.364  1.00  84.46   c
ATOM  20347  OG   SER  D1240   12.411  51.406   7.563  1.00  83.40   0
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ATOM  20348  O    HIS  D1241    6.081  52.816   7.641  1.00 90.94   O
ATOM  20349  N    HIS  D1241    8,891  51.485   7,059  1,00 81.70   M
ATOM  20350  CA   HIS  D1241    7.747  51,081   7.861  1,00 87,08   C
ATOM  20351  c    HIS  D1241    6.415  51,660   7,357  1.00 93.15   c
ATOM  20352  CB   HIS  D1241    7,965  51.494   9,319  1,00 87.34   c
ATOM  20353  CG   HIS  D1241    8.939  50,629  10.060  1,00 85,75   c
ATOM  20354  ND1  HIS  D1241   10.251  50,995  10.273  1,00 83,08   M
ATOM  20355  CD2  HIS  D1241    8,786  49.422  10,654  1,00 82.95   C
ATOM  20356  CE1  HIS  D1241   10.865  50,050  10,961  1,00 81.99   C
ATOM  20357  NE2  HIS  D1241    9.997  49,084  11.205  1,00 87,40   M
ATOM  20358  O    TYR  D1242    2,453  49.948   7,212  I,00100.18   O
ATOM  20359  N    TYR  D1242    5.657  50.855   6,614  1,00 96.19   M
ATOM  20360  CA   TYR  D1242    4.280  51,211   6.276  1,00 95,47   C
ATOM  20361  c    TYR  D1242    3.365  50,758   7,411  1.00 99.65   c
ATOM  20362  CB   TYR  D1242    3,849  50.582   4,952  1,00 91.41   c
ATOM  20363  O    GLU  D1243    1.072  52,075  10.886  1,00 81,28   0
ATOM  20364  N    GLU  D1243    3.636  51,278   8,607  1.00 95.13   M
ATOM  20365  CA.  GLU  D1243    2,874  50.931   9,797  1,00 93.77   C
ATOM  20366  C    GLU  D1243    2.187  52,164  10..375  1,00 89,55   C
ATOM  20367  CB   GLU  D1243    3.783  50,287  10.846  1,00 92,04   c
ATOM  20368  N    GLU  D1250   -5,094  56.743   8,687  1,00 98.00   M
ATOM  20369  CA   GLU  D1250   -5.025  57,755   9,732  1,00 96,79   C
ATOM  20370  c    GLU  D1250  --4.374  59,036   9.209  1,00 98,56   c
ATOM  20371  0    GLU  D1250   -3,588  59.002   8,262  I,00 96,62   0
ATOM  20372  CB   GLU  D1250   -4.260  57.223  10,941  1,00 95.93   c
ATOM  20373  CG   GLU  D1250   -4.514  58,009  12.208  1,00100,92   c
ATOM  20374  CD   GLU  D1250   -3,239  58.497  12,846  I,00100.22   c
ATOM  2037 5 OE1  GLU  D1250   -2,273  57.707  12,900  1,00 98.68   0
ATOM  20376  OE2  GLU  D1250   -3.202  59,669  13.285  1,00103,15   0
ATOM  20377  N    ASP  D1251  --4,713  60,163   9,829  1.00 98.72   M
ATOM  20378  CA   ASP  D1251   -4,242  61.469   9,384  1,00 97.90   c
ATOM  20379  C    ASP  D1251   -2.729  61,595   9.478  1,00 97,52   c
ATOM  20380  O    ASP  D1251  --2.074  61,990   8,515  1.00 98.02   0
ATOM  20381  CB   ASP  D1251   -4,903  62.579  10,205  1,00105.56   c
ATOM  20382  CG   ASP  D1251   -6..351  62,262  10.559  1,00109,73   c
ATOM  20383  OD1  ASP  D1251  --6.678  61,066  10.741  1,00102,26   0
ATOM  20384  OD2  ASP  D1251   -7,159  63.213  10,659  1,00116.67   0
ATOM  20385  N    ASN  D1252   -2,181  61,264  10,645  1,00 98.72   M
ATOM  20386  CA   A.SM D1252   -0.743  61,359  10.877  1,00 94,46   C
ATOM  20387  C    ASM  D1252    0,049  60.418   9,970  I,00 91.03   c
ATOM  20388  O    ASM  D1252    1,057  60.814   9,380  1,00 86.93   0
ATOM  20389  CB   A.SM D1252   -0.425  61,067  12.347  1,00 97,92   c
ATOM  20390  N    GLU  D1253  --0,432  59,182   9.847  1.00 90.97   M
ATOM  20391  CA   GLU  D1253    0,239  58.151   9,059  1,00 89.45   C
ATOM  20392  C    GLU  D1253    0.224  58,434   7.548  1,00 91,56   c
ATOM  20393  O    GLU  D1253    0.887  57,748   6,775  1.00 88.21   0
ATOM  20394  CB   GLU  D1253   -0,394  56.782   9,340  1,00 86.80   c
ATOM  20395  N    GLN  D1254   -0.532  59,443   7.128  1,00 95,26   M
ATOM  20396  CA   GLM  D1254  --0.576  59,829   5.722  1,00 92,58   c
ATOM  20397  C    GLM  D1254    0,491  60.888   5,439  1,00 89.53   c
ATOM  20398  O    GLM  D1254    1,215  60,795   4,451  1,00 88.00   0
ATOM  20399  CB   GLM  D1254  --1.981  60,337   5.346  1,00 96,78   c
ATOM  20400  CG   GLM  D1254   -2,023  61.697   4,637  I,00 99.98   c
ATOM  20401  CD   GLM  D1254   -3,420  62,086   4,165  1,00104.29   c
ATOM  20402  OF.1 GLM  D1254   -4.163  61,260   3.630  1,00 97,43   0
ATOM  20403  NE2  GLM  D1254   -3,780  63.352   4,363  I,00106.41   M
ATOM  20404  N    LYS  D1255    0,596  61.871   6,332  1,00 91.31   M
ATOM  20405  CA   LYS  D1255    1.562  62,963   6.225  1,00 88,72   C
ATOM  20406  c    LYS  D1255    2,991  62,421   6,173  1.00 91.83   c
ATOM  20407  O    LYS  D1255    3,919  63.098   5,721  1,00 92.06   0
ATOM  20408  CB   LYS  D1255    1.396  63,908   7.415  1,00 85,52   c
ATOM  20409  CG   LYS  D1255    1.626  65,381   7,125  1.00 95.08   c
ATOM  20410  CD   LYS  D1255    1,548  66.189   8,424  1,00 96.83   c
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ATOM	20411	CE	LYS	D1255	1.255	67.668	8.182	1.00	95.46	c
ATOM	20412	NZ	LYS	D1255	1,251	68.441	9,462	1,00	84.43	N
ATOM	20413	N	GLN	D1256	3.143	61,186	6.648	1,00	89,87	N
ATOM	20414	CA	GLN	D1256	4.430	60.503	6.734	1.00	88.96	c
ATOM	20415	C	GLN	D1256	4,710	59.636	5.509	1,00	87.62	C
ATOM	20416	O	GLN	D1256	5.853	59,527	5.069	1,00	86,30	O
ATOM	20417	CE	GLN	D1256	4.491	59,652	8.010	1,00	86,61	c
ATOM	20418	CG	GLN	D1256	4,665	60.470	9,289	1,00	82.87	c
ATOM	20419	CD	GLN	D1256	4.555	59.630	10.545	1,00	81.03	c
ATOM	20420	OE1	GLN	D1256	4.222	58,449	10.485	1,00	79,22	0
ATOM	20421	NE2	GLN	D1256	4,833	60.240	11,694	I,00	85.78	N
ATOM	20422	N	LEU	D1257	3.681	59.014	4.951	1,00	86.37	N
ATOM	20423	CA	LEU	D1257	3.857	58,405	3.645	1,00	86,11	C
ATOM	20424	c	LEU	D1257	4.122	59.525	2.631	1.00	85.40	c
ATOM	20425	O	LEU	D1257	4,741	59.302	1,602	1,00	87.02	0
ATOM	20426	CB	LEU	D1257	2.643	57,560	3.254	1,00	86,75	c
ATOM	20427	CG	LEU	D1257	2.792	56.038	3.393	1.00	89.67	c
ATOM	20428	CD1	LEU	D1257	1,439	55.342	3,306	1,00	87.52	c
ATOM	20429	CD2	LEU	D1257	3.751	55,466	2.340	1,00	90,64	c
ATOM	20430	N	PHE	D1258	3.686	60,740	2.953	1,00	87,88	N
ATOM	20431	CA.	PHE	D1258	3,922	61.896	2,092	1,00	89.23	C
ATOM	20432	C	PHE	D1258	5.395	62.268	2.007	1,00	86.13	C
ATOM	20433	O	PHE	D1258	5.980	62,240	0.927	1,00	86,05	O
ATOM	20434	CB	PHE	D1258	3,122	63.104	2,583	I,00	92.62	c
ATOM	20435	N	VAL	D1259	5.990	62.618	3.146	1,00	89.73	N
ATOM	20436	CA	VAL	D1259	7.391	63,055	3.193	1,00	89,01	C
ATOM	20437	C	VAL	D1259	8,343	61.985	2,639	I,00	82.38	C
ATOM	20438	O	VAL	D1259	9,399	62.304	2,096	1,00	82.92	O
ATOM	20439	CB	VAL	D1259	7.798	63,439	4.632	1,00	86,74	c
ATOM	20440	CGI	VAL	D1259	7.547	62.286	5.571	1.00	86.92	c
ATOM	20441	CG2	VAL	D1259	9,249	63.907	4,700	1,00	88.62	c
ATOM	20442	N	GLU	D1260	7.949	60,722	2.734	1,00	78,04	N
ATOM	20443	CA	GLU	D1260	8.723	59.653	2.119	1.00	82.32	c
ATOM	20444	C	GLU	D1260	8,840	59.849	0,608	1,00	87.27	C
ATOM	20445	O	GLU	D1260	9.862	59,513	0.024	1,00	83,63	O
ATOM	20446	CB	GLU	D1260	8.108	58,285	2.421	1,00	81,84	c
ATOM	20447	N	GLN	D1261	7,802	60.392	-0,030	1,00	89.56	N
ATOM	20448	CA	GLN	D1261	7.874	60.656	-1.471	1,00	86.06	C
ATOM	20449	C	GLN	D1261	8.605	61,958	-1.744	1,00	84,43	C
ATOM	20450	O	GLN	D1261	9,217	62.128	-2,795	I,00	81.72	O
ATOM	20451	CB	GLN	D1261	6,487	60.688	-2,106	1,00	86.96	c
ATOM	20452	CG	GLN	D1261	5.915	59,309	-2.373	1,00	89,01	c
ATOM	20453	CD	GLN	D1261	5.268	58.711	-1.146	1.00	89.57	c
ATOM	20454	OE1	GLN	D1261	5,707	57.680	-0,633	1,00	91.68	0
ATOM	20455	NE2	GLN	D1261	4.214	59,362	-0.661	1,00	86,45	N
ATOM	20456	N	HIS	D1262	8.543	62.877	-0.790	1.00	84.99	N
ATOM	20457	CA.	HIS	D1262	9,413	64.043	-0,810	1,00	85.60	C
ATOM	20458	C	HIS	D1262	10.817	63,601	-0.343	1,00	91,36	C
ATOM	20459	O	HIS	D1262	11.317	64,047	0.705	1,00	90,40	O
ATOM	20460	CB	HIS	D1262	8,869	65.163	0,090	1,00	86.56	C
ATOM	20461	CG	HIS	D1262	7.440	65.544	-0.179	1,00	92.40	c
ATOM	20462	ND1	HIS	D1262	6.546	64,722	-0.834	1,00	89,81	N
ATOM	20463	CD2	HIS	D1262	6,752	66.671	0,131	I,00	90.10	C
ATOM	20464	CE1	HIS	D1262	5.373	65.326	-0.919	1,00	88.09	C
ATOM	20465	NE2	HIS	D1262	5.473	66,511	-0.345	1,00	86,20	N
ATOM	20466	O	LYS	D1263	13,238	60.611	-2,550	I,00	76.13	O
ATOM	20467	N	LYS	D1263	11,438	62.702	-1,107	1,00	85.78	N
ATOM	20468	CA	LYS	D1263	12.757	62,193	-0.748	1,00	85,90	C
ATOM	20469	c	LYS	D1263	13.585	61.608	-1.910	1.00	84.05	c
ATOM	20470	CB	LYS	D1263	12,617	61.147	0,350	1,00	91.55	c
ATOM	20471	O	HIS	D1264	18.046	61,399	-2.800	1,00	77,73	0
ATOM	20472	N	HIS	D1264	14.709	62.274	-2.122	1.00	83.08	N
ATOM	20473	CA.	HIS	D1264	15,718	61.986	-3,123	1,00	80.06	C

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ATOM  20474  C    HIS  D1264   16.897  61.429  -2.343  1.00  82.17   C
ATOM  20475  CB   HIS  D1264   16,090  63.272  -3,844  1,00  74.24   C
ATOM  20476  CG   HIS  D1264   16.149  64,452  -2.923  1,00  73,14   C
ATOM  20477  ND1  HIS  D1264   15.037  64;941  -2.268  1.00  75.08   N
ATOM  20478  CD2  HIS  D1264   17,191  65.210  -2,505  1,00  76.68   C
ATOM  20479  CE1  HIS  D1264   15.388  65,958  -1.500  1,00  74,10   C
ATOM  20480  NE2  HIS  D1264   16.690  66,143  -1.628  1,00  73,99   N
ATOM  20481  O    TYR  D1265   19,411  59.198   0,106  1,00  76.90   O
ATOM  20482  N    TYR  D1265   16.567  61.017  -1;127  1,00  83.30   N
ATOM  20483  CA   TYR  D1265   17.530  60,646  -0.105  1,00  80,64   C
ATOM  20484  C    TYR  D1265   18,318  59.376  -0,412  I,00  76.20   C
ATOM  20485  CB   TYR  D1265   16.797  60.504   1;227  1,00  77.44   C
ATOM  20486  CG   TYR  D1265   16.492  61,837   1.863  1,00  76,46   C
ATOM  20487  CD1  TYR  D1265   16.912  63;021   1,266  1.00  76.86   C
ATOM  20488  CD2  TYR  D1265   15,815  61.916   3,072  1,00  74.44   C
ATOM  20489  CE1  TYR  D1265   16.654  64,246   1.849  1,00  76,60   C
ATOM  20490  CE2  TYR  D1265   15.556  63;138   3.662  1.00  72.17   C
ATOM  20491  CZ   TYR  D1265   15,975  64.300   3,045  1,00  73.63   C
ATOM  20492  OH   TYR  D1265   15.722  65,520   3.633  1,00  77,62   0
ATOM  20493  N    LEU  D1266   17.756  58,511  -1.253  1,00  74,40   N
ATOM  20494  CA.  LEU  D1266   18,391  57.264  -1,669  1,00  71.72   C
ATOM  20495  C    LEU  D1266   19.774  57,530  -2;258  1,00  76.75   C
ATOM  20496  O    LEU  D1266   20.753  56,893  -1.882  1,00  75,17   0
ATOM  20497  CB   LEU  D1266   17,526  56.536  -2,700  I,00  70.11   C
ATOM  20498  CG   LEU  D1266   16.296  55.713  -2;312  1,00  71.98   C
ATOM  20499  GDI  LEU  D1266   16.668  54,261  -2.116  1,00  74,09   C
ATOM  20500  CD2  LEU  D1266   15,622  56.243  -1,072  I,00  73.57   C
ATOM  20501  N    ASP  D1267   19,837  58.466  -3,198  1,00  76.75   N
ATOM  20502  CA   ASP  D1267   21.100  58,946  -3.741  1,00  79,47   C
ATOM  20503  C    ASP  D1267   22.033  59;383  -2,623  1.00  78.58   C
ATOM  20504  O    ASP  D1267   23,212  59.043  -2,600  1,00  73.49   0
ATOM  20505  CB   ASP  D1267   20.875  60,137  -4.683  1,00  81,55   C
ATOM  20506  CG   ASP  D1267   20;360  59;729  -6.041  1.00  85.41   C
ATOM  20507  OD1  ASP  D1267   20,642  58.588  -6,475  1,00  82.29   0
ATOM  20508  OD2  ASP  D1267   19.683  60,570  -6.677  1,00  86,55   0
ATOM  20509  N    GLU  D1268   21.482  60,152  -1.696  1,00  76,50   N
ATOM  20510  CA.  GLU  D1268   22,288  60.820  -0,690  1,00  80.17   C
ATOM  20511  C    GLU  D1268   22;828  59;869   0;397  1,00  78.36   C
ATOM  20512  O    GLU  D1268   23.979  60,009   0.817  1,00  75,78   0
ATOM  20513  CB   GLU  D1268   21,475  61.966  -0,074  I,00  77.28   C
ATOM  20514  CG   GLU  D1268   20,895  62.890  -1,145  1,00  80.97   C
ATOM  20515  CD   GLU  D1268   20.448  64,239  -0.618  1,00  81,31   C
ATOM  20516  OE1  GLU  D1268   20;894  65;262  -1;178  1.00  85.48   0
ATOM  20517  OE2  GLU  D1268   19,642  64.281   0,337  1,00  83.08   0
ATOM  20518  N    ILE  D1269   22.025  58,901   0.839  1,00  73,89   N
ATOM  20519  CA   ILE  D1269   22.489  57;988   1.875  1.00  72.98   C
ATOM  20520  C    ILE  D1269   23,472  57.009   1,269  1,00  73.35   C
ATOM  20521  O    ILE  D1269   24.315  56,470   1.964  1,00  74,12   0
ATOM  20522  CB   ILE  D1269   21.342  57,221   2.557  1,00  72,33   C
ATOM  20523  CGI  ILE  D1269   20,695  56.245   1,578  1,00  77.21   C
ATOM  20524  CG2  ILE  D1269   20;323  58;184   3;125  1,00  69.31   C
ATOM  20525  CD1  ILE  D1269   19.261  55,896   1.928  1,00  81,99   C
ATOM  20526  N    ILE  D1270   23,363  56.785  -0,034  I,00  74.44   N
ATOM  20527  CA   ILE  D1270   24;341  55.982  -0;743  1,00  71.02   C
ATOM  20528  C    ILE  D1270   25.637  56,782  -0.834  1,00  71,77   C
ATOM  20529  O    ILE  D1270   26,731  56.240  -0,717  I,00  70.55   0
ATOM  20530  CB   ILE  D1270   23,839  55.587  -2,145  1,00  70.54   C
ATOM  20531  CGI  ILE  D1270   22.766  54,501  -2.050  1,00  71,18   C
ATOM  20532  CG2  ILE  D1270   24,974  55;107  -3;023  1.00  71.28   C
ATOM  20533  CD1  ILE  D1270   23,240  53.199  -1,490  1,00  75.55   C
ATOM  20534  N    GLU  D1271   25.503  58,086  -1.029  1,00  76,44   N
ATOM  20535  CA   GLU  D1271   26.663  58;962  -1.101  1.00  74.69   C
ATOM  20536  C    GLU  D1271   27,379  58.983   0,242  1,00  72.61   C
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ATOM   20537  O    GLU  D1271     28..608   58..992    0.295   1.00  74.74          O
ATOM   20538  CB   GLU  D1271     26,,256   60..384   -1,516   1,00  73..67         C
ATOM   20539  CG   GLU  D1271     25.823    60.,526   -2.977   1,00  83,,64         C
ATOM   20540  CD   GLU  D1271     26..887   60..058   --3..971 1.00  86..80         C
ATOM   20541  OE1  GLU  D1271     26.,510   59. 542   -5,049   1,00  93..45         0
ATOM   20542  OE2  GLU  D1271     28..094   60.,218   -3..681  1,00  79,,27         0
ATOM   20543  N    GLN  D1272     26..597   59.,000    1.319   1,00  68,.90         N
ATOM   20544  CA.  GLN  D127 2    27.,121   58. 926    2,678   1,00  69..60         C
ATOM   20545  C    GLN  D1272     27..920   57.. 641   2 ..911 1,00  68..05         C
ATOM   20546  O    GLN  D1272     29..053   57.,678    3 ..381 1,00  63,.68         O
ATOM   20547  CB   GLN  D1272     25.,982   58..994    3,682   I,00  67.85          C
ATOM   20548  CG   GLN  D1272     25..264   60..290    3 ..714 1,00  67.13          C
ATOM   20549  CD   GLN  D1272     25. 980   61.,333    4.534   1,00  68,21          C
ATOM   20550  OE1  GLN  D1272     26..487   61..052    5.617   1.00  68..66         0
ATOM   20551  NE2  GLN  D1272     26.,021   62..549    4,022   1,00  66..87         N
ATOM   20552  N    ILE  D127 3    27.297    56.,515    2.574   1,00  66,,57         N
ATOM   20553  CA   ILE  D1273     27..875   55..181    2.723   1.00  64.90          C
ATOM   20554  C    ILE  D127 3    29.,178   55. 038    1,948   1,00  69..74         C
ATOM   20555  O    ILE  D127 3    30..190   54.,581    2.482   1,00  66,,93         O
ATOM   20556  CB   ILE  D1273     26..872   54.,092    2.252   1,00  62,03          C
ATOM   20557  CGI  ILE  D127 3    25,764    53. 896    3,290   1,00  65..17         C
ATOM   20558  CG2  ILE  D1273     27..575   52.. 775   1..989  1,00  63..98         C
ATOM   20559  CD1  ILE  D1273     24.525    53.,221    2.752   1,00  62,92          C
ATOM   20560  N    SER  D1274     29.,144   55..448    0,688   I,00  70..16         N
ATOM   20561  CA   SER. D1274     30..275   55..297   -0..215  1,00  70..88         C
ATOM   20562  C    SER  D1274     31. 489   56.,133    0.191   1,00  69,01          C
ATOM   20563  O    SER  D1274     32.,626   55..667    0,117   I,00  68..26         0
ATOM   20564  CB   SER  D1274     29.,845   55..660   -1,638   1,00  72.68          C
ATOM   20565  OG   SER  D1274     30. 974   55.,871   -2.467   1,00  78,82          0
ATOM   20566  N    GLU  D1275     31..230   57..370    0.602   1.00  72.70          N
ATOM   20567  CA   GLU  D1275     32.,261   58..323    1,014   1,00  67.35          C
ATOM   20568  C    GLU  D127 5    33..012   57.,803    2.231   1,00  70,,09         C
ATOM   20569  O    GLU  D1275     34..239   57..770    2.258   1.00  73..53         0
ATOM   20570  CB   GLU  D127 5    31.,615   59. 673    1,301   1,00  68..96         C
ATOM   20571  CG   GLU  D127 5    32..488   60.,703    1.980   1,00  82,59          C
ATOM   20572  CD   GLU  D1275     31.. 742  62.,022    2.231   1,00  89,.14         C
ATOM   20573  OE1  GLU  D127 5    30.,719   62. 283    1,550   1,00  86..53         0
ATOM   20574  OE2  GLU  D1275     32..182   62.. 794   3 ..115 1,00  93..83         0
ATOM   20575  N    PHE  D1276     32. 245   57,380     3.224   1,00  69,57          N
ATOM   20576  CA   PHE  D1276     32.,756   56..782    4,445   I,00  64.38          C
ATOM   20577  C    PHE  D127 6    33.,571   55..552    4,125   1,00  67.37          C
ATOM   20578  O    PHE  D1276     34. 654   55.,338    4.662   1,00  64,93          0
ATOM   20579  CB   PHE  D1276     31.. 584  56..416    5.351   1.00  62.94          C
ATOM   20580  CG   PHE  D127 6    31.,978   55..814    6,660   1,00  61.45          C
ATOM   20581  CD2  PHE  D1276     31..892   54.,449    6 ..860 1,00  54,43          C
ATOM   20582  CD1  PHE  D1276     32..388   56..616    7.712   1.00  60..62         C
ATOM   20583  CE2  PHE  D127 6    32.,228   53. 887    8,077   1,00  52.20          C
ATOM   20584  CE1  PHE  D1276     32..731   56.,057    8 ..930 1,00  57,88          C
ATOM   20585  CZ   PHE  D1276     32..647   54.,681    9 ..106 1,00  53,.57         C
ATOM   20586  N    SER  D127 7    33.,017   54. 755    3,225   1,00  68..09         N
ATOM   20587  CA   SER  D1277     33..546   53.. 450   2.896   1,00  63..85         C
ATOM   20588  C    SER  D1277     34..936   53.,599    2.303   1,00  71,05          C
ATOM   20589  0    SER  D1277     35..858   52..840    2,628   I,00  70..74         0
ATOM   20590  CB   SER  D1277     32..601   52..738    1.923   1,00  64.19          C
ATOM   20591  OG   SER  D1277     32. 871   51,360     1.823   1,00  68,14          0
ATOM   20592  N    LYS  D1278     35.,087   54..602    1,445   I,00  74.31          N
ATOM   20593  CA   LYS  D127 8    36.,344   54..819    0,744   1,00  72.10          C
ATOM   20594  C    LYS  D127 8    37. 373   55.,411    1.702   1,00  69,22          C
ATOM   20595  O    LYS  D1278     38.. 576  55..312    1..478  1.00  69..93         0
ATOM   20596  CB   LYS  D127 8    36.,139   55..734   -0.,470  1,00  66..73         C
ATOM   20597  N    AP.G D1279     36..905   56.,021    2.781   1,00  66,.35         N
ATOM   20598  CA   ARG  D1279     37..830   56..606    3 ..740 1.00  66..14         C
ATOM   20599  C    ARG  D127 9    38.,413   55. 546    4,668   1,00  66..19         C
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ATOM   20600   O    ARG  D1279       39..618   55.,511   4 ,898   1 .00  66..85        O
ATOM   20601   CB   ARG  D127 9      37.,148   57..690   4 ,572   1 ,00  60..08        C
ATOM   20602   CG   ARG  D1279       38..113   58.,637   5 ..293  1 ,00  67 ,47        C
ATOM   20603   CD   ARG  D1279       37..340   59.,697   6 ,086   1 .00  67 .43        C
ATOM   20604   NE   ARG  D127 9      .38.,175  60. 790   6 ,596   1 ,00  82 ,20        N
ATOM   20605   CZ   ARG  D1279       37..996   62.,085   6 ..311  1 ,00  86,.95        C
ATOM   20606   NH1  ARG  D1279       37 .003   62.,470   5 ..511  1 ,00  85,.81        N
ATOM   20607   NH2  ARG  D127 9      .38.,811  63. 002   6 ,829   1 ,00  82 ,87        N
ATOM   20608   N    VAL  D1280       37..559   54.,686   5 ,207   1 ,00  65..21        N
ATOM   20609   CA   VAL  D1280       37 .969   53.,880   6 ..341  1 ,00  62 ,08        C
ATOM   20610   C    VAL  D1280       .37.,713  52...389  6 ,213   I ,00  62 .83        C
ATOM   20611   O    VAL  D1280       38..312   51.,617   6 ,934   1 ,00  64 .98        O
ATOM   20612   CB   VAL  D1280       37. 284   54 ,353   7 .633   1 ,00  57 ,01        C
ATOM   20613   CG2  VAL  D1280       35..780   54.,112   7 ;568   1 .00  53..99        C
ATOM   20614   CGI  VAL  D1280       37.,589   55..800   7 ,877   1 ,00  59..09        C
ATOM   20615   N    ILE  D1281       36..825   51.,972   5 ...325 1 ,00  62 ,86        N
ATOM   20616   CA   ILE  D1281       36..507   50.,559   5 ,247   1 .00  60..50        C
ATOM   20617   C    ILE  D1281       .37.,440  49. 874   4 ,244   1 ,00  66.,26        C
ATOM   20618   O    ILE  D1281       37..963   48.,782   4 .497   1 ,00  65,.01        O
ATOM   20619   CB   ILE  D1281       35..040   50.,334   4 .874   1 ,00  57 ,56        C
ATOM   20620   CGI  ILE  D1281       .34.,223  50. 017   6 ,127   1 ,00  63.,88        C
ATOM   20621   CG2  ILE  D1281       34..899   49.,140   3 ,971   1 ,00  58..36        C
ATOM   20622   CD1  ILE  D1281       34..281   51.,049   7 .220   1 ,00  60,.62        C
ATOM   20623   O    LEU  D1282       3 9 ,201  47 .843   1 ,546   I ,00  73..66        0
ATOM   20624   N    LEU  D1282       37.,642   50.,532   3 ,110   1 ,00  68..17        N
ATOM   20625   CA   LEU  D1282       38. 623   50.,110   2 .114   1 ,00  67 ,07        C
ATOM   20626   C    LEU  D1282       .38.,331  48..718   1 ,543   I ,00  73..4.3       C
ATOM   20627   CB   LEU  D1282       40.,032   50..148   2 ,715   1 ,00  59..44        C
ATOM   20628   CG   LEU  D1282       40. 738   51 ,506   2.878    1 ,00  66 ,99        C
ATOM   20629   CD2  LEU  D1282       41 ,959   51.,406   3 ,803   1 .00  60..94        C
ATOM   20630   CD1  LEU  D1282       39.,815   52..609   3 ,365   1 ,00  60..01        C
ATOM   20631   O    ALA  D1283       35..176   47 ,825   -1 ..363 1 ,00  77 ,98        0
ATOM   2 0632  N    ALA  D1283       37.,111   48.,518   1 ,047   1 .00  66..26        N
ATOM   20633   CA.  ALA  D1283       3 6 ,780  47.292    0 ,330   1 ,00  62 ,31        C
ATOM   20634   C    ALA  D1283       36...361  47 ,641   -1 .083  1 ,00  76,.18        C
ATOM   20635   CB   ALA  D1283       35..684   46.,529   1 .039   1 ,00  64 ,17        C
ATOM   20636   O    ASP  D1284       .35.,188  48. 046   -4 ,691  1 ,00  77 ,57        0
ATOM   20637   N    ASP  D1284       37.,338   47 ,735   -1 ,974  1 ,00  77 .12        N
ATOM   20638   CA   ASP  D1284       37. 107   48.,294   -3 .298  1 ,00  75 ,89        C
ATOM   20639   C    ASP  D1284       3 6 ,139  47 .483   -4 ,159  I ,00  77 .97        C
ATOM   20640   CB   ASP  D1284       38.,447   48..467   -4 ,007  1 ,00  78..60        C
ATOM   20641   CG   ASP  D1284       39. .369   49.,430   -3 .266  1 ,00  85 ,99        C
ATOM   20642   OD1  ASP  D1284       38.,865   50.,140   -2 ,363  1 .00  84 .55        0
ATOM   20643   OD2  ASP  D1284       40.,581   49..487   -3.,587  1 ,00  85..47        0
ATOM   20644   O    ALA  D1285       33..092   45.,420   -5.. 260 1 ,00  79,.18        0
ATOM   20645   N    ALA  D1285       36.,360   46.,175   --4 ,285 1 .00  75..06        N
ATOM   20646   CA.  ALA  D1285       .35.,480  45. .328   -5 ,099  1 ,00  75.,11        C
ATOM   20647   C    ALA  D1285       34..063   45.,257   -4 .528  1 ,00  75,.94        C
ATOM   20648   CB   ALA  D1285       36..059   43.,926   --5.. 234 1 ,00  75,.79        C
ATOM   20649   N    ASM  D128 6      .33.,957  45. 004   -3.,226  1 ,00  74 ,71        N
ATOM   20650   CA   ASN  D1286       32.,676   44 ,997   -2.,527  1 ,00  75..24        C
ATOM   20651   C    ASN  D1286       31..939   46.,333   -2 .653  1 ,00  77 ,89        C
ATOM   2 0652  0    ASM  D1286       .30.,714  46...368  -2.,703  I ,00  78..78        0
ATOM   20653   CB   ASN  D1286       32.,872   44 ,672   -1 ,045  1 ,00  76..38        C
ATOM   20654   CG   ASN  D1286       32. 909   43.,182   -0. 762  1 ,00  77 ,89        C
ATOM   20655   OD1  ASN  D1286       .32.,839  42 ..354   -1 ,674  I ,00  73..75        0
ATOM   20656   ND2  ASN  D1286       33.,020   42..834   0 ,520   1 ,00  77 .50        N
ATOM   20657   N    LEU  D1287       32. 686   47 ,429   -2 .703  1 ,00  75 ,40        N
ATOM   20658   CA   LEU  D1287       32.,087   48.,754   -2 ,832  1 .00  76..73        C
ATOM   20659   C    LEU  D1287       31.,393   48..965   -4 ,179  1 ,00  81 .76        C
ATOM   20660   O    LEU  D1287       30..260   49.,452   -4 .228  1 ,00  80,.69        O
ATOM   20661   CB   LEU  D1287       33.,139   49.,845   -2 ,631  1 .00  72 .16        C
ATOM   20662   CG   LEU  D1287       .32.,637  51. 278   -2.,834  1 ,00  79.,52        C
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ATOM  20663  GDI  LEU   D1287   31.407   51.571   --1.980   1.00  75.85   C
ATOM  20664  CD2  LEU   D1287   33,738   52.285   -2,551    1,00  74.39   C
ATOM  20665  K    ASP   D1288   32.081   48,615   -5.263    1,00  81,81   K
ATOM  20666  CA   ASP   D1288   31.541   48,783   --6.608   1.00  79.52   C
ATOM  20667  C    ASP   D1288   30,329   47.890   -6,831    1,00  83.92   C
ATOM  20668  O    ASP   D1288   29.366   48,296   -7.493    1,00  83,95   0
ATOM  20669  CB   ASP   D1288   32.604   48,483   --7.667   1,00  80,41   C
ATOM  20670  CG   ASP   D1288   33,605   49.606   -7,822    1,00  85.33   C
ATOM  20671  OD1  ASP   D1288   33.260   50,763   -7,504    1,00  86.54   0
ATOM  20672  OD2  ASP   D1288   34.740   49,332   --8.266   1,00  91,19   0
ATOM  20673  N    LYS   D1289   30,381   46.671   -6,299    1,00  81.27   N
ATOM  20674  CA   LYS   D1289   29.242   45.771   -6,417    1,00  84.65   C
ATOM  20675  C    LYS   D1289   28.015   46,433   -5.761    1,00  82,50   C
ATOM  20676  O    LYS   D1289   26.910   46,390   --6,301   1.00  82.37   0
ATOM  20677  CB   LYS   D1289   29,551   44.404   -5.,789    1,00  80.28   C
ATOM  20678  K    VAL   D1290   28.230   47,077   -4.620    1.00  77,40   K
ATOM  20679  CA   VAL   D1290   27.159   47,765   --3.917   1,00  76.61   C
ATOM  20680  C    VAL   D1290   26,643   48.938   -4,740    1,00  80.98   C
ATOM  20681  O    VAL   D1290   25.436   49,091   -4.923    1,00  83,43   0
ATOM  20682  CB   VAL   D1290   27.620   48,272   --2.538   1,00  72,95   C
ATOM  20683  CGI  VAL   D1290   26,576   49.165   -1,940    1,00  76.43   C
ATOM  20684  CG2  VAL   D1290   27.876   47.113   -1,611    1,00  75.07   C
ATOM  20685  N    LEU   D1291   27.562   49,761   --5.237   1,00  82,53   N
ATOM  20686  CA   LEU   D1291   27,212   50.901   -6,080    1,00  79.66   C
ATOM  20687  C    LEU   D1291   26.420   50.469   -7,309    1,00  81.37   C
ATOM  20688  O    LEU   D1291   25.405   51,075   -7.655    1,00  81,65   0
ATOM  20689  CB   LEU   D1291   28,472   51.646   -6,519    1,00  81.58   C
ATOM  20690  CG   LEU   D1291   29,235   52.437   -5.,457    1,00  79,62   C
ATOM  20691  GDI  LEU   D1291   30.549   52,966   -6.025    1,00  80,46   C
ATOM  20692  CD2  LEU   D1291   28,368   53,569   --4,940   1.00  80.57   C
ATOM  20693  N    SEP.  D1292   26,887   49.410   -7,960    1,00  82.36   M
ATOM  20694  CA   SEP.  D1292   26.271   48,944   -9.193    1,00  83,33   C
ATOM  20695  C    SER   D1292   24.914   48,302   --8.941   1.00  83.35   C
ATOM  20696  0    SER   D1292   23,983   48.506   -9,711    1,00  87.27   0
ATOM  20697  CB   SER   D1292   27.195   47,961   -9.9.10   1,00  86,48   C
ATOM  20698  OG   SER   D1292   28.404   48,597   --10.290  1,00  89,86   0
ATOM  20699  O    ALA   D1293   21,318   47.840   -7,597    1,00  81.91   0
ATOM  20700  K    ALA   D1293   24,802   47,528   -7,868    1,00  83.71   K
ATOM  20701  CA   ALA   D1293   23.527   46,914   ~7.513    1,00  82,77   C
ATOM  20702  C    ALA   D1293   22,484   47.980   -7,214    1,00  79.72   C
ATOM  20703  CB   ALA   D1293   23,684   45.979   --g,319   1,00  77.60   C
ATOM  20704  O    TYR   D1294   20.155   50.,973   ~7.468    1,00  79,47   0
ATOM  20705  N    TYR   D1294   22.907   49,040   --6,531   1.00  77.13   N
ATOM  20706  CA   TYR   D1294   22,002   50.128   --g,179   1,00  80.97   C
ATOM  20707  C    TYR   D1294   21.378   50,777   -7.404    1.00  80,14   C
ATOM  20708  CB   TYR   D1294   22.718   51,203   --5.368   1.00  76.85   C
ATOM  20709  CG   TYR   D1294   21,903   52.468   ~5,287    1,00  75.51   C
ATOM  20710  CD2  TYR   D1294   22.296   53,609   -5.967    1,00  74,78   C
ATOM  20711  CD1  TYR   D1294   20.723   52,512   --4.553   1,00  73,65   C
ATOM  20712  CE2  TYR   D1294   21,550   54.766   ~5,908    1,00  77.62   C
ATOM  20713  CE1  TYR   D1294   19,971   53,662   -4,488    1,00  75.28   C
ATOM  20714  CZ   TYR   D1294   20.388   54,790   --5.172   1,00  76,43   C
ATOM  20715  OH   TYR   D1294   19,650   55.948   -5,126    1,00  77.84   0
ATOM  20716  O    ASN   D1295   19,672   51.425   --10,676  1,00  82.86   0
ATOM  20717  N    A.SK  D1295   22.232   51,129   -8.360    1,00  78,64   N
ATOM  20718  CA   ASM   D1295   21,783   51:754   -9,591    1,00  82.87   C
ATOM  20719  C    ASM   D1295   20,728   50.916   --10,293  1,00  84.31   C
ATOM  20720  CB   ASN   D1295   22.955   51,992   -10.541   1,00  80,45   C
ATOM  20721  CG   ASN   D1295   22,512   52,606   -11,854   1.00  93.18   C
ATOM  20722  OD1  ASM   D1295   21,585   53.429   --11,888  1,00  98.30   0
ATOM  20723  KD2  ASN   D1295   23.154   52,200   -12.947   1.00  84,99   K
ATOM  20724  O    LYS   D1296   17.825   48,340   -11.418   1.00  80.27   0
ATOM  20725  N    LYS   D1296   21,013   49.625   -10,430   1,00  76.52   N
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ATOM  20726  CA   LYS  D1296   20.177  48.742  -11.219  1.00  77.99   C
ATOM  20727  C    LYS  D1296   18.763  48.620  -10.669  1.00  79.50   C
ATOM  20728  CB   LYS  D1296   20.828  47.360  -11.328  1.00  78.86   C
ATOM  20729  CG   LYS  D1296   20.318  46.292  -10.378  1.00  78.04   C
ATOM  20730  CD   LYS  D1296   20.673  44.913  -10.947  1.00  84.52   C
ATOM  20731  CE   LYS  D1296   20.271  43.767  -10.029  1.00  88.93   C
ATOM  20732  NZ   LYS  D1296   20.468  42.428  -10.673  1.00  87.88   N
ATOM  20733  O    HIS  D1297   15.717  50.199   -7.693  1.00  75.92   O
ATOM  20734  N    HIS  D1297   18.607  48.851   -9.370  1.00  79.71   N
ATOM  20735  CA   HIS  D1297   17.302  48.740   -8.733  1.00  78.19   C
ATOM  20736  C    HIS  D1297   16.661  50.103   -8.472  1.00  77.50   C
ATOM  20737  CB   HIS  D1297   17.417  47.965   -7.422  1.00  75.72   C
ATOM  20738  CG   HIS  D1297   17.540  46.485   -7.604  1.00  83.50   C
ATOM  20739  ND1  HIS  D1297   16.477  45.692   -7.980  1.00  83.51   N
ATOM  20740  CD2  HIS  D1297   18.596  45.650   -7.451  1.00  84.63   C
ATOM  20741  CE1  HIS  D1297   16.873  44.433   -8.051  1.00  82.92   C
ATOM  20742  NE2  HIS  D1297   18.154  44.380   -7.732  1.00  83.44   N
ATOM  20743  O    ARG  D1298   14.462  53.470   -8.772  1.00  74.67   O
ATOM  20744  N    ARG  D1298   17.162  51.145   -9.131  1.00  76.23   N
ATOM  20745  CA   ARG  D1298   16.647  52.499   -8.922  1.00  78.67   C
ATOM  20746  C    ARG  D1298   15.167  52.613   -9.296  1.00  78.65   C
ATOM  20747  CB   ARG  D1298   17.470  53.524   -9.712  1.00  75.16   C
ATOM  20748  O    ASP  D1299   11.156  51.283   -9.629  1.00  81.76   0
ATOM  20749  N    ASP  D1299   14.700  51.732  -10.180  1.00  82.35   N
ATOM  20750  CA   ASP  D1299   13.293  51.720  -10.602  1.00  82.29   C
ATOM  20751  C    ASP  D1299   12.359  51.056   -9.592  1.00  80.20   C
ATOM  20752  CB   ASP  D1299   13.142  51.017  -11.954  1.00  83.25   C
ATOM  20753  O    LYS  D1300   12.023  51.798   -9.697  1.00  80.19   0
ATOM  20754  N    LYS  D1300   12.905  50.225   -8.707  1.00  81.99   N
ATOM  20755  CA   LYS  D1300   12.107  49.588   -7.662  1.00  76.96   C
ATOM  20756  C    LYS  D1300   11.520  50.667   -9.738  1.00  79.01   C
ATOM  20757  CB   LYS  D1300   12.955  48.574   -6.883  1.00  71.52   C
ATOM  20758  O    PRO  D1301   11.495  51.064   -3.580  1.00  84.47   0
ATOM  20759  N    PRO  D1301   10.441  50.340   -6.007  1.00  77.92   N
ATOM  20760  CA   PRO  D1301    9.784  51.381   -5.202  1.00  76.38   C
ATOM  20761  C    PRO  D1301   10.602  51.797   -3.983  1.00  81.47   C
ATOM  20762  CB   PRO  D1301    8.482  50.711   -4.772  1.00  74.37   C
ATOM  20763  CG   PRO  D1301    8.809  49.249   -4.765  1.00  74.49   C
ATOM  20764  CD   PRO  D1301    9.738  49.048   -5.918  1.00  71.29   C
ATOM  20765  O    ILE  D1302   12.226  52.333   -0.513  1.00  81.63   0
ATOM  20766  N    ILE  D1302   10.282  52.943   -3.392  1.00  83.79   N
ATOM  20767  CA   ILE  D1302   11.044  53.468   -2.257  1.00  85.84   C
ATOM  20768  C    ILE  D1302   11.150  52.505   -1.074  1.00  81.91   C
ATOM  20769  CB   ILE  D1302   10.439  54.786   -1.732  1.00  81.37   C
ATOM  20770  CGI  ILE  D1302   10.362  55.823   -2.848  1.00  83.20   C
ATOM  20771  CG2  ILE  D1302   11.254  55.319   -0.570  1.00  79.69   C
ATOM  20772  CD1  ILE  D1302    8.975  55.960   -3.458  1.00  97.70   C
ATOM  20773  N    ARG  D1303   10.035  51.892   -0.691  1.00  79.40   N
ATOM  20774  CA   ARG  D1303   10.008  51.023    0.485  1.00  83.40   C
ATOM  20775  C    ARG  D1303   10.940  49.830    0.324  1.00  82.38   C
ATOM  20776  O    ARG  D1303   11.674  49.483    1.246  1.00  80.31   0
ATOM  20777  CB   ARG  D1303    8.586  50.522    0.768  1.00  82.96   C
ATOM  20778  N    GLU  D1304   10.891  49.203   -0.848  1.00  82.54   N
ATOM  20779  CA   GLU  D1304   11.727  48.047   -1.141  1.00  86.26   C
ATOM  20780  C    GLU  D1304   13.201  48.450   -1.092  1.00  83.00   C
ATOM  20781  O    GLU  D1304   14.018  47.775   -0.472  1.00  82.91   0
ATOM  20782  CB   GLU  D1304   11.367  47.443   -2.509  1.00  81.51   C
ATOM  20783  N    GLN  D1305   13.525  49.572   -1.724  1.00  80.52   N
ATOM  20784  CA   GLN  D1305   14.896  50.054   -1.766  1.00  83.11   C
ATOM  20785  C    GLN  D1305   15.408  50.467   -0.379  1.00  82.75   C
ATOM  20786  O    GLN  D1305   16.523  50.115   -0.001  1.00  80.85   0
ATOM  20787  CB   GLN  D1305   15.016  51.226   -2.748  1.00  82.35   C
ATOM  20788  CG   GLN  D1305   15.010  50.812   -4.223  1.00  81.37   C
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ATOM	20789	CD	GLN	D1305	15.063	52.001	-5.176	1.00	83.50	C
ATOM	20790	OE1	GLN	D1305	15.609	53.058	-4.848	1.00	86.73	O
ATOM	20791	NE2	GLN	D1305	14.487	51.834	-6.361	1.00	82.91	N
ATOM	20792	N	ALA	D1306	14.593	51.197	0.378	1.00	82.21	N
ATOM	20793	CA.	ALA	D1306	15.000	51.711	1.691	I.00	79.35	C
ATOM	20794	C	ALA	D1306	15.487	50.625	2.650	1.00	80.20	C
ATOM	20795	O	ALA	D1306	16.449	50.830	3.384	1.00	81.16	O
ATOM	20796	CB	ALA	D1306	13.859	52.477	2.328	I.00	79.25	C
ATOM	20797	O	GLU	D1307	17.208	47.227	3.995	1.00	81.55	O
ATOM	20798	N	GLU	D1307	14.826	49.474	2.634	1.00	81.25	N
ATOM	20799	CA	GLU	D1307	15.154	48.380	3.536	I.00	80.57	C
ATOM	20800	C	GLU	D1307	16.445	47.680	3.137	1.00	80.84	C
ATOM	20801	CB	GLU	D1307	14.000	47.383	3.585	1.00	83.44	C
ATOM	20802	CG	GLU	D1307	12.741	48.003	4.151	1.00	91.47	C
ATOM	20803	CD	GLU	D1307	11.551	47.072	4.141	1.00	100.88	C
ATOM	20804	OE1	GLU	D1307	11.664	45.963	3.565	1.00	105.06	0
ATOM	20805	OE2	GLU	D1307	10.504	47.463	4.710	1.00	95.69	0
ATOM	20806	N	ASM	D1308	16.688	47.597	1.833	I.00	80.51	N
ATOM	20807	CA	ASN	D1308	17.928	47.027	1.315	1.00	77.81	C
ATOM	20808	C	ASN	D1308	19.120	47.945	1.543	1.00	77.48	C
ATOM	20809	0	ASM	D1308	20.257	47.487	1.633	I.00	77.65	0
ATOM	20810	CB	ASN	D1308	17.799	46.722	-0.177	1.00	79.15	C
ATOM	20811	CG	ASN	D1308	17.036	45.447	-0.445	1.00	81.42	C
ATOM	20812	OD1	ASN	D1308	17.593	44.349	-0.363	I.00	81.35	0
ATOM	20813	ND2	ASN	D1308	15.754	45.581	-0.768	1.00	76.10	N
ATOM	20814	N	ILE	D1309	18.858	49.245	1.615	1.00	76.12	N
ATOM	20815	CA	ILE	D1309	19.903	50.199	1.922	I.00	73.28	C
ATOM	20816	C	ILE	D1309	20.381	49.911	3.326	1.00	71.29	C
ATOM	20817	O	ILE	D1309	21.569	49.964	3.603	1.00	70.31	O
ATOM	20818	CB	ILE	D1309	19.409	51.653	1.813	1.00	69.94	C
ATOM	20819	CGI	ILE	D1309	18.988	51.958	0.383	1.00	75.78	C
ATOM	20820	CG2	ILE	D1309	20.495	52.613	2.192	1.00	65.28	C
ATOM	20821	CD1	ILE	D1309	20.063	51.659	-0.628	1.00	76.65	C
ATOM	20822	N	ILE	D13I0	19.429	49.604	4.203	I.00	74.75	N
ATOM	20823	CA	ILE	D1310	19.698	49.333	5.609	1.00	71.66	C
ATOM	20824	C	ILE	D1310	20.622	48.143	5.741	1.00	66.82	C
ATOM	20825	0	ILE	D13I0	21.505	48.116	6.593	I.00	61.90	0
ATOM	20826	CB	ILE	D1310	18.400	49.069	6.379	1.00	67.55	C
ATOM	20827	CGI	ILE	D131.0	17.648	50.384	6.573	1.00	69.47	C
ATOM	20828	CG2	ILE	D1310	18.687	48.429	7.722	I.00	62.19	C
ATOM	20829	CD1	ILE	D1310	16.216	50.207	7.007	1.00	68.73	C
ATOM	20830	N	HIS	D1311	20.409	47.165	4.874	1.00	68.10	N
ATOM	20831	CA	HIS	D1311	21.256	45.984	4.822	1.00	71.86	C
ATOM	20832	C	HIS	D1311	22.714	46.400	4.588	1.00	71.33	C
ATOM	20833	O	HIS	D1311	23.641	45.863	5.205	1.00	66.93	0
ATOM	20834	CB	HIS	D1311	20.772	45.041	3.717	1.00	72.13	C
ATOM	20835	CG	HIS	Dl311	19.604	44.183	4.107	I.00	73.59	C
ATOM	20836	ND1	HIS	D1311	18.572	43.893	3.241	1.00	72.40	N
ATOM	20837	CD2	HIS	D1311	19.331	43.508	5.250	1.00	78.18	C
ATOM	20838	CE1	HIS	Dl311	17.706	43.095	3.839	I.00	70.43	C
ATOM	20839	ME2	HIS	D1311	18.144	42.842	5.058	1.00	70.22	N
ATOM	20840	N	LEU	D1312	22.897	47.399	3.728	1.00	69.39	N
ATOM	20841	CA	LEU	D1312	24.225	47.841	3.299	I.00	68.01	C
ATOM	20842	C	LEU	D1312	25.102	48.412	4.409	1.00	65.69	C
ATOM	20843	O	LEU	D1312	26.329	48.453	4.274	1.00	61.12	O
ATOM	20844	CB	LEU	D1312	24.099	48.890	2.197	I.00	67.86	C
ATOM	20845	CG	LEU	D1312	23.402	48.533	0.891	1.00	69.13	C
ATOM	20846	GD1	LEU	D1312	23.337	49.788	0.038	1.00	73.71	C
ATOM	20847	CD2	LEU	D1312	24.129	47.430	0.156	1.00	69.86	C
ATOM	20848	N	PHE	D1313	24.489	48.870	5.496	1.00	62.14	N
ATOM	20849	CA	PHE	D1313	25.269	49.401	6.610	1.00	61.10	C
ATOM	20850	C	PHE	D1313	26.109	48.314	7.260	1.00	63.08	C
ATOM	20851	0	PHE	D1313	27.004	48.607	8.058	I.00	60.95	0

ATOM	20852	CB	PHE	D1313	24.366	50.055	7.644	1.00	58.44	C
ATOM	20853	CG	PHE	D1313	23.795	51.329	7.181	1.00	59.03	C
ATOM	20854	CD1	PHE	D1313	24.566	52.473	7.169	1.00	59.92	C
ATOM	20855	CD2	PHE	D1313	22.508	51.385	6.701	1.00	59.62	C
ATOM	20856	CE1	PHE	D1313	24.050	53.657	6.715	1.00	61.81	C
ATOM	20857	CE2	PHE	D1313	21.986	52.566	6.247	1.00	61.90	C
ATOM	20858	CZ	PHE	D1313	22.753	53.704	6.254	1.00	60.04	C
ATOM	20859	N	THR	D1314	25.812	47.063	6.920	1.00	61.09	N
ATOM	20860	CA	THP,	D1314	26.598	45.952	7.408	1.00	60.64	C
ATOM	20861	C	THR	D1314	28.042	46.178	6.988	1.00	61.04	C
ATOM	20862	0	THR	D1314	28.961	46.097	7.796	1.00	60.63	0
ATOM	20863	CB	THR	D1314	26.070	44.634	6.868	1.00	69.83	C
ATOM	20864	OG1	THR	D1314	24.763	44.395	7.417	1.00	73.41	0
ATOM	20865	CG2	THR	D1314	27.006	43.494	7.223	1.00	60.40	C
ATOM	20866	N	LEU	D1315	28.215	46.520	5.718	1.00	63.65	N
ATOM	20867	CA	LEU	D1315	29.502	46.934	5.179	1.00	58.98	C
ATOM	20868	C	LEU	D1315	30.262	47.922	6.072	1.00	62.50	C
ATOM	20869	0	LEU	D1315	31.457	47.748	6.310	1.00	59.58	0
ATOM	20870	CB	LEU	D1315	29.292	47.565	3.813	1.00	63.18	C
ATOM	20871	CG	LEU	D1315	30.538	48.113	3.138	1.00	66.17	C
ATOM	20872	CD1	LEU	D1315	31.334	46.971	2.560	1.00	57.68	C
ATOM	20873	CD2	LEU	D1315	30.137	49.117	2.067	1.00	69.09	C
ATOM	20874	N	THR	D1316	29.560	48.946	6.568	1.00	57.39	N
ATOM	20875	CA	THR	D1316	30.185	50.033	7.315	1.00	51.26	C
ATOM	20876	C	THR	D1316	30.202	49.835	8.836	1.00	52.11	C
ATOM	20877	O	THR	D1316	30.840	50.605	9.544	1.00	49.95	O
ATOM	20878	CB	THR	D1316	29.478	51.403	7.024	1.00	59.43	C
ATOM	20879	OG1	THR	D1316	28.181	51.450	7.655	1.00	57.77	0
ATOM	20880	CG2	THR	D1316	29.338	51.633	5.541	1.00	53.49	C
ATOM	20881	N	ASN	D1317	29.499	48.826	9.340	1.00	55.33	N
ATOM	20882	CA	ASM	D1317	29.387	48.631	10.786	1.00	50.55	C
ATOM	20883	C	ASN	D1317	30.711	48.367	11.490	1.00	56.71	C
ATOM	20884	O	ASN	D1317	31.588	47.665	10.957	1.00	52.17	0
ATOM	20885	CB	ASN	D1317	28.451	47.472	11.094	1.00	51.20	C
ATOM	20886	CG	ASN	D1317	27.005	47.867	11.055	1.00	57.42	C
ATOM	20887	OD1	ASN	D1317	26.668	49.050	10.980	1.00	59.88	0
ATOM	20888	ND2	ASN	D1317	26.128	46.872	11.110	1.00	60.68	N
ATOM	20889	O	LEU	D1318	31.075	46.307	13.598	1.00	53.89	0
ATOM	20890	N	LEU	D1318	30.836	48.917	12.697	1.00	52.79	N
ATOM	20891	CA	LEU	D1318	31.934	48.576	13.606	1.00	53.03	C
ATOM	20892	C	LEU	D1318	32.059	47.040	13.771	1.00	54.66	C
ATOM	20893	CB	LEU	D1318	31.708	49.255	14.962	1.00	49.76	C
ATOM	20894	CG	LEU	D1318	32.734	48.975	16.059	1.00	56.14	C
ATOM	20895	CD2	LEU	D1318	32.156	49.131	17.461	1.00	46.80	C
ATOM	20896	CD1	LEU	D1318	33.954	49.842	15.881	1.00	52.08	C
ATOM	20897	O	GLY	D1319	34.150	44.786	12.092	1.00	52.57	0
ATOM	20898	N	GLY	D1319	33.259	46.545	14.069	1.00	53.75	N
ATOM	20899	CA	GLY	D1319	33.437	45.120	14.337	1.00	46.12	C
ATOM	20900	C	GLY	D1319	33.741	44.272	13.113	1.00	46.05	C
ATOM	20901	0	ALA	D1320	31.877	42.200	10.958	1.00	64.07	0
ATOM	20902	N	ALA	D1320	33.530	42.970	13.205	1.00	48.28	N
ATOM	20903	CA	ALA	D1320	33.961	42.050	12.146	1.00	49.48	C
ATOM	20904	C	ALA	D1320	33.104	42.136	10.878	1.00	55.46	C
ATOM	20905	CB	ALA	D1320	33.965	40.628	12.670	1.00	40.69	C
ATOM	20906	O	PRO	D1321	32.432	39.924	8.759	1.00	65.81	0
ATOM	20907	N	PRO	D1321	33.756	42.154	9.705	1.00	49.06	N
ATOM	20908	CA	FRO	D1321	33.109	42.170	8.390	1.00	58.21	C
ATOM	20909	C	PRO	D1321	32.194	40.980	8.191	1.00	63.69	C
ATOM	20910	CB	PRO	D1321	34.286	42.110	7.413	1.00	65.30	C
ATOM	20911	CG	FRO	D1321	35.412	42.696	8.158	1.00	62.64	C
ATOM	20912	CD	PRO	D1321	35.217	42.283	9.588	1.00	59.57	C
ATOM	20913	O	ALA	D1322	29.250	41.433	5.403	1.00	75.79	0
ATOM	20914	N	ALA	D1322	31.159	41.156	7.379	1.00	72.71	N

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ATOM   20915   CA   ALA  D1322       30..130   40 .138    7 ..217   1 .00  72 .26          C
ATOM   20916   C    ALA  D1322       29,,390   40..317    5 ,907    1 ,00  73..22          C
ATOM   20917   CB   ALA  D1322       29..147   40.,179    8 ...381   1 .00  68,,04          C
ATOM   20918   O    ALA  D132 3      26..247   39.,820    5 ..494   1 .00  79..57          0
ATOM   20919   N    ALA  D132 3      28.,921   39. 203    5 ,359    1 ,00  79..53          N
ATOM   20920   CA   ALA  D1323       28..144   3 9 ,222   4 .134    1 .00  80,,23          C
ATOM   20921   C    ALA  D1323       26..781   39.,866    4 .383    1 ,00  78,.25          C
ATOM   20922   CB   ALA  D132 3      27.,988   37. 809    3 ,581    1 ,00  79..70          C
ATOM   20923   O    PHE  D1324       25..105   41 ,265    1 ,024    1 ,00  77 .26          0
ATOM   20924   N    PHE  D1324       26..237   40.,475    3 ..340   1 ,00  76 ,40          N
ATOM   20925   CA   PHE  D132 4      24.,940   41 .124    3 ,399    1 ,00  74 .83          C
ATOM   20926   C    PHE  D1324       24..361   41 .143    1 ,994    1 ,00  76..23          C
ATOM   20927   CB   PHE  D132 4      25. 063   42.,548    3 .963    1 ,00  75 ,62          C
ATOM   20928   CG   PHE  D132 4      26..129   43 ,373    3 ,299    1 .00  72 .30          C
ATOM   20929   CD2  PHE  D1324       25.,833   44 .157    2 ,196    1 ,00  73..71          C
ATOM   20930   CD1  PHE  D132 4      27 .432   43.,359    3 .773    1 .00  73,.02          C
ATOM   20931   CE2  PHE  D132 4      26..820   44 ,904    1 ,579    1 .00  71 .43          C
ATOM   20932   CE1  PHE  D132 4      28.,420   44 .111    3 ,160    1 ,00  70..65          C
ATOM   20933   CZ   PHE  D132 4      28..114   44 ,878    2 .064    1 .00  67 ,44          C
ATOM   20934   O    LYS  D1325       21 .254   43.,039    1 .081    1 ,00  72 ,97          0
ATOM   20935   N    LYS  D132 5      23.,042   41 .024    1 ,872    1 ,00  83.,39          N
ATOM   20936   CA   LYS  D1325       22..408   41 ,017    0 ,552    1 ,00  79..77          C
ATOM   20937   C    LYS  D1325       21 .778   42.,360    0 ..210   1 ,00  72 ,20          C
ATOM   20938   CB   LYS  D132 5      21.,352   39 .911    0 ,475    1 ,00  79 .34          C
ATOM   20939   O    TYR  D1326       20..671   42..976   -3.,784    1 ,00  85..57          0
ATOM   20940   N    TYR  D132 6      21 .863   42.,744   -1 .060    1 ,00  79 ,90          N
ATOM   20941   CA   TYR  D132 6      21.,1ll   43..878   -1 ,596    1 ,00  78..68          C
ATOM   20942   C    TYR  D1326       20.,198   43..373   -2.,714    1 ,00  84 .25          C
ATOM   20943   CB   TYR  D132 6      22 .045   44 ,971   -2 .112    1 ,00  77 ,67          C
ATOM   20944   CG   TYR  D132 6      21..345   46.,248   --2 .545   1 .00  76..75          C
ATOM   20945   CD1  TYR  D1326       20.,943   47 .198   -1 ,613    1 ,00  75..90          C
ATOM   20946   CD2  TYR  D1326       21..110   46.,510   -3..884    1 .00  77 ,17          C
ATOM   20947   CE1  TYR  D132 6      20..309   48.,373   --2 .007   1 .00  79..40          C
ATOM   20948   CE2  TYR  D132 6      20.,486   47 .673   -4 ,287    1 ,00  79..22          C
ATOM   20949   CZ   TYR  D1326       20 .083   48.,604   -3...349   1 .00  80,.69          C
ATOM   20950   OH   TYR  D1326       19..457   49.,759   --3..762   1 ,00  77 ,67          0
ATOM   20951   O    PHE  D132 7      18.,171   40. 416   -2.,634    1 ,00  88..03          0
ATOM   20952   N    PHE  D132 7      18..891   43.,398   -2.,449    1 ,00  84 .63          N
ATOM   20953   CA   PHE  D132 7      17 .889   42.,702   -3 .258    1 ,00  84 ,57          C
ATOM   20954   C    PHE  D132 7      18.,276   41 .258   -3.,523    1 ,00  84 .79          C
ATOM   20955   CB   PHE  D132 7      17 ,652   43..434   -4 ,568    1 ,00  84 .46          C
ATOM   20956   CG   PHE  D132 7      16. 855   44 ,689   -4 .406    1 ,00  85 ,64          C
ATOM   20957   CD2  PHE  D132 7      15.,471   44 ,660   -4 ,490    1 .00  84 .74          C
ATOM   20958   CD1  PHE  D132 7      17 ,485   45..896   -4 ,144    1 ,00  82 .79          C
ATOM   20959   CE2  PHE  D132 7      14 .726   45.,818   -4 ..335   1 .00  80,.58          C
ATOM   20960   CE1  PHE  D132 7      16..754   47 ,053   --3..991   1 .00  83..56          C
ATOM   20961   CZ   PHE  D132 7      15.,365   47 .015   -4 ,084    1 ,00  83..92          C
ATOM   20962   0    ASP  D132 8      20 .968   .38.,245  -4 .547    1 .00  89,.77          0
ATOM   20963   N    ASP  D1328       18..722   40.,969   -4 .740    1 ,00  89,.84          N
ATOM   20964   CA.  ASP  D132 8      19.,079   39. 600   -5 ,109    1 ,00  89..46          C
ATOM   20965   C    ASP  D1328       20.,574   39.,328   -4 ,972    1 ,00  89..69          C
ATOM   20966   CB   ASP  D1328       18..623   39.,301   --6..537   1 ,00  87 ,83          C
ATOM   20967   CG   ASP  D132 8      18.,935   40..432   -7 ,491    1 ,00  90..81          C
ATOM   20968   OD1  ASP  D1328       18.,318   40..488   -8.,576    1 ,00  93..38          0
ATOM   20969   OD2  ASP  D132 8      19. 789   41 ,278   -7 .148    1 ,00  92 ,83          0
ATOM   20970   O    THR  D132 9      22.,852   40..617   -2.,972    1 ,00  87 .27          0
ATOM   20971   N    THR  D1329       21.,401   40..310   -5.,330    1 ,00  89..27          N
ATOM   20972   CA   THR  D132 9      22 .849   40.,121   -5. 326    1 ,00  84 ,59          C
ATOM   20973   C    THR  D132 9      23.,390   40 ,015   --3..904   1 .00  86..26          C
ATOM   20974   CB   THR  D1329       23.,590   41 .264   --g,072    1 ,00  85..09          C
ATOM   20975   OG1  THR  D132 9      23..279   42.,525   -5..477    1 .00  79,.51          0
ATOM   20976   CG2  THR  D132 9      23..205   41 ,297   --7 .551   1 .00  85..68          C
ATOM   20977   N    THR  D1330       24.,454   39. 233   -3.,751    1 ,00  82 .60          N
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ATOM	20978	CA	THR	D1330	25..068	38..986	-2.456	1.00	78..63	C
ATOM	20979	C	THR	D1330	26,,481	39..541	-2.,366	1,00	80..15	C
ATOM	20980	O	THR	D1330	27.340	39,196	-3..178	1,00	78,,58	0
ATOM	20981	CB	THR	D1330	25..120	37.,492	-2.156	1.00	81.06	C
ATOM	20982	OG1	THR	D1330	23.,786	37. 017	-1,961	1,00	89..99	0
ATOM	20983	CG2	THR	D1330	25.943	37.,220	-0..904	1,00	72,68	C
ATOM	20984	N	ILE	D1331	26..714	40.,390	-1.369	1,00	78,.24	N
ATOM	20985	CA.	ILE	D1331	28.,042	40. 925	-1,104	1,00	78..56	C
ATOM	20986	C	ILE	D1331	28..788	40.,097	-0.,051	1,00	82.56	C
ATOM	20987	O	ILE	D1331	28..389	40.,059	1.117	1,00	77,26	0
ATOM	20988	CB	ILE	D1331	27.,980	42.383	-0.,631	I,00	78..43	C
ATOM	20989	CGI	ILE	D1331	26..984	43..173	-1,481	1,00	76..20	C
ATOM	20990	CG2	ILE	D1331	29. 366	43.,021	-0. 688	1,00	74,36	C
ATOM	20991	CD1	ILE	D1331	27..374	43,265	-2,939	1.00	82.43	C
ATOM	20992	N	ASP	D1332	29.,877	39..456	-0.,480	1,00	81.82	N
ATOM	20993	CA	ASP	D1332	30..716	38.,637	0..393	1,00	84,58	C
ATOM	20994	C	ASP	D1332	31..513	39.,437	1.419	1.00	84.24	C
ATOM	20995	O	ASP	D1332	31.,488	40. 673	1.,442	1,00	81.01	0
ATOM	20996	CB	ASP	D1332	31..697	37.,803	-0..435	1,00	79,.65	C
ATOM	20997	CG	ASP	D1332	31..010	36.,734	-1.241	1,00	87,39	C
ATOM	20998	OD1	ASP	D1332	30.,198	35. 978	-0.,661	1,00	89..22	0
ATOM	20999	OD2	ASP	D1332	31..277	36.,654	-2.,460	1,00	89..10	0
ATOM	21000	N	ARG	D1333	32..249	38.,694	2.239	1,00	82,03	N
ATOM	21001	CA	ARG	D1333	32.,985	39.239	3,366	I,00	81.47	C
ATOM	21002	C	ARG	D1333	34..355	39..752	2,952	1,00	79..67	C
ATOM	21003	O	ARG	D1333	35. 034	39.,132	2.139	1,00	83,23	O
ATOM	21004	CB	ARG	D1333	33.,124	38..163	4,434	I,00	78..73	C
ATOM	21005	CG	ARG	D1333	33.,643	38..626	5,770	1,00	75..16	C
ATOM	21006	CD	ARG	D1333	33. 583	37.,463	6.740	1,00	75,73	C
ATOM	21007	NE	ARG	D1333	33..760	36,199	6,028	1.00	79..05	N
ATOM	21008	CZ	ARG	D1333	34.,235	35..089	6,579	1,00	85..76	C
ATOM	21009	NH1	ARG	D1333	34..586	35.,090	7.856	1,00	86,.45	N
ATOM	21010	NH2	ARG	D1333	34..366	33.,981	5,854	1.00	88..51	N
ATOM	21011	N	LYS	D1334	34.,753	40. 887	3,518	1,00	74.96	N
ATOM	21012	CA	LYS	D1334	36..061	41,471	3.239	1,00	73,.92	C
ATOM	21013	C	LYS	D1334	36..965	41,430	4.467	1,00	71,89	C
ATOM	21014	0	LYS	D1334	37.,193	42.456	5,109	1,00	73..30	0
ATOM	21015	CB	LYS	D1334	35.,910	42.,916	2,758	1,00	80..46	C
ATOM	21016	N	ARG	D1335	37. 481	40.,245	4.789	1,00	73,95	N
ATOM	21017	CA	ARG	D1335	38.,298	40..061	5,985	I,00	66..62	C
ATOM	21018	C	ARG	D1335	39.,564	40..890	5,900	1,00	62.64	C
ATOM	21019	O	ARG	D1335	40. 082	41.,131	4.818	1,00	60,94	0
ATOM	21020	CB	ARG	D1335	38.,651	38.,591	6,186	1.00	65..50	C
ATOM	21021	CG	ARG	D1335	37.,463	37.654	6,168	1,00	76..39	C
ATOM	21022	CD	ARG	D1335	37...356	36,833	7.454	1,00	84,.65	C
ATOM	21023	NE	ARG	D1335	38..419	35.,834	7.615	1.00	87.67	N
ATOM	21024	CZ	ARG	D1335	38.,325	34. 562	7,228	1,00	86..78	C
ATOM	21025	NH1	ARG	D1335	39.342	33.,730	7.423	1,00	96,.54	N
ATOM	21026	NH2	ARG	D1335	37.219	34.,120	6..644	1,00	82,71	N
ATOM	21027	N	TYR	D1336	40.,041	41.352	7,047	1,00	64.80	N
ATOM	21028	CA	TYR	D1336	41,297	42.,083	7,111	1,00	63..55	C
ATOM	21029	C	TYR	D1336	42..348	41,154	7.656	1,00	62,06	C
ATOM	21030	0	TYR	D133 6	42.,605	41.153	8,864	I,00	62.28	0
ATOM	21031	CB	TYR	D1336	41,180	43..329	7,996	1,00	60..48	C
ATOM	21032	CG	TYR	D133 6	40. 190	44,339	7.491	1,00	63,34	C
ATOM	21033	CD1	TYR	D133 6	40.,228	44.788	6,168	I,00	64.16	C
ATOM	21034	CD2	TYR	D1336	39.,202	44.845	8,330	1,00	63..59	C
ATOM	21035	CE1	TYR	D133 6	39. 305	45,719	5.701	1,00	62,90	C
ATOM	21036	CE2	TYR	D133 6	38.,273	45.,775	7,869	1.00	62.42	C
ATOM	21037	CZ	TYR	D1336	38..327	46..205	6,557	1,00	61.57	C
ATOM	21038	OH	TYR	D1336	37..409	47,131	6.123	1,00	62,66	0
ATOM	21039	O	THR	D1337	45..478	39.,351	8,901	1.00	69..99	0
ATOM	21040	N	THR	D1337	42.,949	40. 364	6,765	1,00	66..93	N

ATOM	21041	CA	THR	D1337	43.855	39.274	7.152	1.00	58.38	C
ATOM	21042	C	THR	D1337	45.124	39.784	7.813	1.00	61.94	C
ATOM	21043	CB	THR	D1337	44.240	38.421	5.947	1.00	60.83	C
ATOM	21044	OG1	THR	D1337	45.144	39.152	5.105	1.00	72.31	0
ATOM	21045	CG2	THR	D1337	43.003	38.060	5.161	1.00	58.23	C
ATOM	21046	O	SEP.	D1338	45.813	42.916	9.039	1.00	61.27	0
ATOM	21047	N	SER	D1338	45.799	40.720	7.168	1.00	53.74	N
ATOM	21048	CA.	SER	D1338	47.015	41.273	7.732	1.00	59.69	C
ATOM	21049	C	SER	D1338	46.783	42.167	8.965	1.00	65.65	C
ATOM	21050	CB	SER	D1338	47.760	42.061	6.662	1.00	55.46	C
ATOM	21051	OG	SER	D1338	48.851	42.744	7.248	1.00	68.18	0
ATOM	21052	N	THR	D1339	47.693	42.081	9.931	1.00	63.61	N
ATOM	21053	CA	THR	D1339	47.701	42.979	11.081	1.00	61.97	C
ATOM	21054	C	THR	D1339	48.938	43.855	11.015	1.00	62.67	C
ATOM	21055	O	THR	D1339	49.177	44.700	11.886	1.00	64.31	0
ATOM	21056	CB	THR	D1339	47.704	42.210	12.416	1.00	68.63	C
ATOM	21057	OG1	THR	D1339	48.690	41.168	12.367	1.00	71.84	0
ATOM	21058	CG2	THR	D1339	46.352	41.592	12.686	1.00	63.79	C
ATOM	21059	N	LYS	D1340	49.716	43.630	9.962	1.00	64.04	N
ATOM	21060	CA	LYS	D1340	51.003	44.280	9.771	1.00	65.67	C
ATOM	21061	C	LYS	D1340	50.903	45.798	9.912	1.00	65.37	C
ATOM	21062	O	LYS	D1340	51.697	46.403	10.627	1.00	65.13	0
ATOM	21063	CB	LYS	D1340	51.577	43.891	8.400	1.00	66.14	C
ATOM	21064	CG	LYS	D1340	53.010	44.352	8.147	1.00	78.10	C
ATOM	21065	CD	LYS	D1340	53.677	43.570	7.002	1.00	83.62	C
ATOM	21066	CE	LYS	D1340	54.024	42.124	7.413	1.00	97.08	C
ATOM	21067	NZ	LYS	D1340	54.738	41.317	6.359	1.00	93.37	N
ATOM	21068	N	GLU	D1341	49.898	46.394	9.265	1.00	65.33	N
ATOM	21069	CA	GUI	D1341	49.737	47.852	9.207	1.00	66.56	C
ATOM	21070	C	GLU	D1341	49.587	48.524	10.574	1.00	64.01	C
ATOM	21071	O	GLU	D1341	49.747	49.740	10.717	1.00	68.52	0
ATOM	21072	CB	GLU	D1341	48.522	48.215	8.347	1.00	66.90	C
ATOM	21073	CG	GLU	D1341	47.174	47.870	8.988	1.00	62.56	C
ATOM	21074	CD	GLU	D1341	46.015	48.640	8.370	1.00	67.65	C
ATOM	21075	OE1	GLU	D1341	46.286	49.667	7.725	1.00	71.70	0
ATOM	21076	OE2	GLU	D1341	44.840	48.230	8.530	1.00	69.35	0
ATOM	21077	N	VAL	D1342	49.265	47.732	11.577	1.00	59.89	N
ATOM	21078	CA	VAL	D1342	48.931	48.289	12.859	1.00	65.04	C
ATOM	21079	C	VAL	D1342	50.187	48.604	13.690	1.00	65.27	C
ATOM	21080	O	VAL	D1342	50.148	49.450	14.590	1.00	66.22	0
ATOM	21081	CB	VAL	D1342	47.946	47.326	13.586	1.00	67.96	C
ATOM	21082	CGI	VAL	D1342	48.471	46.850	14.927	1.00	61.91	C
ATOM	21083	CG2	VAL	D1342	46.560	47.987	13.692	1.00	61.15	C
ATOM	21084	N	LEU	D1343	51.311	47.974	13.351	1.00	65.10	N
ATOM	21085	CA	LEU	D1343	52.551	48.164	14.111	1.00	66.77	C
ATOM	21086	C	LEU	D1343	53.176	49.555	13.934	1.00	70.89	C
ATOM	21087	0	LEU	D1343	54.097	49.904	14.664	1.00	70.76	0
ATOM	21088	CB	LEU	D1343	53.589	47.094	13.733	1.00	66.09	C
ATOM	21089	CG	LEU	D1343	53.339	45.609	14.021	1.00	62.90	C
ATOM	21090	CD1	LEU	D1343	54.129	44.785	13.034	1.00	60.29	C
ATOM	21091	CD2	LEU	D1343	53.732	45.221	15.440	1.00	56.77	C
ATOM	21092	N	ASP	D1344	52.685	50.341	12.972	1.00	76.30	N
ATOM	21093	CA	ASP	D1344	53.125	51.736	12.794	1.00	73.60	C
ATOM	21094	C	ASP	D1344	51.978	52.730	13.051	1.00	73.33	C
ATOM	21095	O	ASP	D1344	52.138	53.947	12.890	1.00	73.09	0
ATOM	21096	CB	ASP	D1344	53.688	51.958	11.383	1.00	75.24	C
ATOM	21097	CG	ASP	D1344	54.886	51.061	11.069	1.00	81.07	C
ATOM	21098	OD1	ASP	D1344	55.906	51.114	11.802	1.00	74.73	0
ATOM	21099	OD2	ASP	D1344	54.805	50.301	10.077	1.00	86.28	0
ATOM	21100	N	ALA	D1345	50.822	52.210	13.453	1.00	71.52	N
ATOM	21101	CA	ALA	D1345	49.662	53.059	13.724	1.00	63.84	C
ATOM	21102	C	ALA	D1345	49.799	53.727	15.073	1.00	60.65	C
ATOM	21103	O	ALA	D1345	50.890	53.825	15.609	1.00	65.32	0

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ATOM   21104   CB   ALA  D134 5      48..371   52.,249   13..662   1 .00  61 .62           C
ATOM   21105   N    THR  D1346       48,,686   54..195   15.,620   1 ,00  56..80           N
ATOM   21106   CA   THR  D1346       48..693   54.,794   16 .935   1 ,00  48,.52           C
ATOM   21107   C    THR  D134 6      47 .784   53.,997   17 .827   1 .00  56..54           C
ATOM   21108   0    THR  D1346       46.,586   53. 913   17 ,560   1 ,00  57 .63           0
ATOM   21109   CB   THR  D1346       48..234   56.,246   16 .893   1 ,00  56,.55           C
ATOM   21110   OG1  THR  D1346       49..118   56.,974   16..041   1 ,00  59,.84           0
ATOM   21111   CG2  THR  D1346       48.,195   56. 891   18.,315   1 ,00  47 .01           C
ATOM   21112   N    LEU  D134 7      48..357   53.,406   18.,875   1 ,00  53..65           N
ATOM   21113   CA   LEU  D1347       47 .604   52.,598   19..828   1 ,00  53,.02           C
ATOM   21114   C    LEU  D134 7      46.,873   53..515   20.,794   I ,00  53..37           C
ATOM   21115   O    LEU  D134 7      47 .444   54.,489   21.,269   1 ,00  54 .34           O
ATOM   211 1 6  CB   LEU  D134 7      48. 539   51 ,629   20. 581   1 ,00  52 ,43           C
ATOM   21117   CG   LEU  D134 7      48..053   50.,808   21.,786   1 .00  48..92           c
ATOM   21118   CD2  LEU  D1347       49.,205   50..053   22.,475   1 ,00  49..38           C
ATOM   21119   CD1  LEU  D134 7      46..949   49.,833   21..411   1 ,00  50,.83           C
ATOM   21120   N    ILE  D134 8      45.,609   53.,218   21..079   1 .00  50..35           N
ATOM   21121   CA.  ILE  D1348       44 ,836   54. 110   21.,932   1 ,00  52 .14           C
ATOM   21122   C    ILE  D1348       44 .321   53.,411   23..170   1 ,00  49,.79           C
ATOM   21123   O    ILE  D1348       43..332   52.,718   23..114   1 ,00  50,.81           O
ATOM   21124   CB   ILE  D1348       43.,639   54. 724   21.,167   1 ,00  53..92           C
ATOM   21125   CGI  ILE  D1348       44 ,128   55.,406   19.,885   1 ,00  54 .02           C
ATOM   21126   CG2  ILE  D1348       42..862   55.,695   22 ..049   1 ,00  45,.33           c
ATOM   21127   CDI  ILE  D134 8      43.,038   56.. 039   19.,080   I ,00  45..77           C
ATOM   21128   N    HIS  D1349       44 ,977   53.,607   24.,301   1 ,00  50..73           N
ATOM   21129   CA   HIS  D134 9      44 .471   53.,041   25. 538   1 ,00  48 ,15           C
ATOM   21130   C    HIS  D134 9      43.,308   53.. 855   26.,056   I ,00  47 .38           C
ATOM   21131   O    HIS  D1349       43.,428   55..062   26.,224   1 ,00  52..01           0
ATOM   21132   CB   HIS  D134 9      45. 572   52.,980   26. 585   1 ,00  50 ,16           C
ATOM   21133   CG   HIS  D134 9      46.,656   52.,008   26.. 257   1 .00  56..48           C
ATOM   21134   ND1  HIS  D1349       46.,417   50..660   26..088   1 ,00  54 .95           N
ATOM   21135   CD2  HIS  D1349       47 .986   52.,184   26..073   1 ,00  53,.69           C
ATOM   21136   CE1  HIS  D134 9      47 ,556   50.,047   25..820   1 .00  55..78           C
ATOM   21137   NE2  HIS  D1349       48.,521   50. 949   25 ,806   1 ,00  55..54           N
ATOM   21138   N    GLN  D1350       42 .188   53.,195   26...318  1 ,00  47 ,31           N
ATOM   21139   CA   GLN  D1350       40..949   53.,882   26..719   1 ,00  49,.90           C
ATOM   21140   C    GLN  D1350       40.,434   53. 535   28.,110   1 ,00  46..43           C
ATOM   21141   O    GLN  D1350       40 ,377   52.,355   28.,477   1 ,00  50..56           O
ATOM   21142   CB   GLN  D1350       39. 825   53.,569   25. 735   1 ,00  47 ,74           C
ATOM   21143   CG   GLN  D1350       40.,092   53..885   24.,298   I ,00  47 .88           C
ATOM   21144   CD   GLN  D1350       38.,824   53.. 744   23.,480   1 ,00  57 .52           C
ATOM   21145   OE1  GLN  D1350       38. 352   52.,629   23 .231   1 ,00  62 ,55           0
ATOM   21146   NE2  GLN  D1350       38.,238   54.,876   23.,090   1 .00  52 .39           N
ATOM   21147   N    SEP. D1351       40.,004   54..551   28.,857   1 ,00  43..97           N
ATOM   21148   CA   SEP. D1351       39 .277   54.,334   30..102   1 ,00  40,.98           C
ATOM   21149   C    SER  D1351       37.,870   53.,892   29..782   1 .00  36..21           C
ATOM   21150   O    SER  D1351       37.,472   53. 862   28.,632   1 ,00  35..56           0
ATOM   21151   CB   SER  D1351       39 .247   55.,604   30..961   1 ,00  49,.66           C
ATOM   21152   OG   SER  D1351       38..521   56.,635   30..313   1 ,00  49,.94           0
ATOM   21153   O    ILE  D1352       34.,113   53. 198   28.,942   1 ,00  46..00           0
ATOM   21154   N    ILE  D1352       37.,115   53.,532   30.,801   1 ,00  33..71           N
ATOM   21155   CA   ILE  D1352       35..857   52.,869   30..555   1 ,00  35,.35           C
ATOM   21156   C    ILE  D1352       34..907   53..736   29.,716   I ,00  47 .21           C
ATOM   21157   CB   ILE  D1352       35.,171   52.,451   31.,890   1 ,00  43..00           C
ATOM   21158   CGI  ILE  D1352       34. 095   51 ,392   31. 629   1 ,00  44 ,53           C
ATOM   21159   CG2  ILE  D1352       34.,603   53..679   .32.,655  I ,00  40..77           C
ATOM   21160   CD1  ILE  D1352       33.,333   50..947   32.,866   1 ,00  39..42           C
ATOM   21161   O    THR  D1353       34. 133   57 ,278   27 .124   1 ,00  50 ,51           0
ATOM   21162   N    THR  D1353       35.,001   55.,069   29..843   1 .00  48..80           N
ATOM   21163   CA   THR  D1353       34.,113   55..976   29.,106   1 ,00  45..94           C
ATOM   21164   C    THR  D1353       34..734   56.,467   27 .823   1 ,00  48,.70           C
ATOM   21165   CB   THR  D1353       33.,732   57.,252   29..891   1 .00  43..81           C
ATOM   21166   OG1  THR  D1353       34.,908   58. 042   30.,075   1 ,00  53..01           0
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ATOM   21167   CG2  THR  D1353    33..100   56..946   31..229   1 .00   43..68        C
ATOM   21168   O    GLY  D1354    37.,805   58..509   25.,612   1 ,00   57 .73        O
ATOM   21169   N    GLY  D1354    35..945   56.,025   27.524    1 ,00   46,.74        N
ATOM   21170   CA   GLY  D1354    36..672   56.,553   26.,374   1 .00   44 .62        C
ATOM   21171   C    GLY  D1354    37.,130   58. 002   26.,511   1 ,00   49.,68        C
ATOM   21172   O    LEU  D1355    39 .218   61.,127   27.298    1 ,00   60,.80        0
ATOM   21173   N    LEU  D1355    36..762   58.,675   27.609    1 ,00   47 ,77        N
ATOM   21174   CA.  LEU  D1355    37.,090   60. 093   27.,790   1 ,00   51 ,53        C
ATOM   21175   C    LEU  D1355    38..592   60.,303   27.,987   1 ,00   63..30        C
ATOM   21176   CB   LEU  D1355    36..326   60.,685   28.. 975   1 ,00   49,.57        C
ATOM   21177   CG   LEU  D1355    34.,803   60..757   28.,809   I ,00   52 .50        C
ATOM   21178   CD2  LEU  D1355    34..439   61..618   27.,631   1 ,00   49..88        C
ATOM   21179   GDI  LEU  D1355    34. 097   61.,191   30. 076   1 ,00   38 ,15        C
ATOM   21180   O    TYR  D135 6   41 .115   57.,456   28.,44 9  1 .00   59..80        0
ATOM   21181   N    TYR  D1356    39.,175   59..560   28.,928   1 ,00   58..75        N
ATOM   21182   CA   TYR  D1356    40..601   59.,665   29.. 157   1 ,00   52 ,92        C
ATOM   21183   C    TYR  D135 6   41 .311   58.,665   28.,292   1 .00   52 .66        C
ATOM   21184   CB   TYR  D1356    40.,946   59. 410   .30.,605  1 ,00   52 .76        C
ATOM   21185   CG   TYR  D1356    40..194   60.,237   31.. 610   1 ,00   56,.22        C
ATOM   21186   CD1  TYR  D1356    40..582   61.,542   31.. 891   1 ,00   57 ,50        C
ATOM   21187   CD2  TYR  D1356    39.,132   59. 694   .32.,322  1 ,00   54 .15        C
ATOM   21188   CE1  TYR  D1356    39..923   62.,291   32.,834   1 ,00   61 .20        C
ATOM   21189   CE2  TYR  D1356    38..463   60.,431   33.. 274   1 ,00   59,.74        C
ATOM   21190   CZ   TYR  D135 6   38.,858   61..738   .33.,522  I ,00   66..59        C
ATOM   21191   OH   TYR  D1356    38..192   62..484   34.,465   1 ,00   66..34        0
ATOM   21192   N    GLU  D1357    42 .152   59.,130   27 .387   1 ,00   52 ,48        N
ATOM   21193   CA   GLU  D1357    42.,914   58..159   26.,636   I ,00   54 .43        C
ATOM   21194   C    GLU  D1357    44 ,440   58..390   26.,691   1 ,00   58..23        C
ATOM   21195   O    GLU  D1357    44 .912   59.,495   26. 961   1 ,00   59 ,23        0
ATOM   21196   CB   GLU  D1357    42..385   58.,094   25.,192   1 .00   52 .92        C
ATOM   21197   CG   GLU  D1357    42.,573   59..300   24.,302   1 ,00   58..49        C
ATOM   21198   CD   GLU  D1357    41 .829   59.,137   22. 963   1 ,00   64 ,87        C
ATOM   21199   OE1  GLU  D1357    42..397   59.,496   21.,905   1 .00   59..31        0
ATOM   21200   OE2  GLU  D1357    40.,670   58. 643   22.,967   1 ,00   64 .50        0
ATOM   21201   N    THR  D1358    45..194   57.,304   26.. 496   1 ,00   58,.32        N
ATOM   21202   CA   THR  D1358    46..645   57.,341   26.. 313   1 ,00   48,.68        C
ATOM   21203   C    THR  D1358    46.,955   56. 896   24.,903   1 ,00   52 .73        C
ATOM   21204   O    THR  D1358    46..613   55.,772   24.,522   1 ,00   60..60        0
ATOM   21205   CB   THR  D1358    47 .377   56.,421   27 .295   1 ,00   50 ,23        C
ATOM   21206   OG1  THR  D1358    47 ,107   56..828   28.,635   I ,00   54 .59        0
ATOM   212 07   CG2  THR  D1358    48.,886   56..456   27.,053   1 ,00   49..18        C
ATOM   21208   N    A.P.G D135 9  47 .596   57 ,753   24 .119   1 ,00   54 ,31        N
ATOM   21209   CA   ARG  D135 9   47 .857   57.,446   22.,709   1 .00   54 .33        C
ATOM   21210   C    ARG  D1359    49.,332   57..163   22.,497   1 ,00   62 .73        C
ATOM   21211   O    ARG  D1359    50..183   57.,869   23.. 040   1 ,00   64 ,94        0
ATOM   21212   CB   ARG  D135 9   47 .401   58.,595   21.,797   1 .00   59..89        C
ATOM   21213   CG   ARG  D1359    45 ,891   58. 892   21.,862   1 ,00   57 .69        C
ATOM   21214   CD   ARG  D1359    45..463   59.,935   20 .830   1 ,00   58,.97        C
ATOM   21215   NE   ARG  D1359    44 .058   59.,788   20.. 452   1 ,00   56,.23        N
ATOM   21216   CZ   ARG  D1359    43.,629   59. 640   19.,203   1 ,00   53..40        C
ATOM   21217   NH1  ARG  D1359    44 .490   59.,636   18.,199   1 ,00   50..30        N
ATOM   21218   NH2  ARG  D1359    42..336   59.,503   18.. 958   1 ,00   50,.94        N
ATOM   21219   N    ILE  D1360    49.,634   56..124   21.,715   I ,00   60..73        N
ATOM   21220   CA   ILE  D1360    51..004   55..647   21.,560   1 ,00   56..66        C
ATOM   21221   C    ILE  D1360    51. 411   55.,422   20. 112   1 ,00   62 ,47        C
ATOM   21222   O    ILE  D1360    51.,027   54..417   19.,499   I ,00   61 .61        0
ATOM   21223   CB   ILE  D1360    51.,223   54..330   22.,295   1 ,00   58..57        C
ATOM   21224   CGI  ILE  D1360    50. 657   54 ,398   23 .713   1 ,00   59 ,05        C
ATOM   21225   CG2  ILE  D1360    52.,701   53.,989   22.,292   1 .00   58..59        C
ATOM   21226   CD1  ILE  D1360    51.,403   55..319   24.,610   1 ,00   56..92        C
ATOM   21227   N    ASP  D1361    52..212   56.,334   19 .571   1 ,00   60,.48        N
ATOM   21228   CA   ASP  D1361    52..618   56.,222   18.,181   1 .00   63..36        C
ATOM   21229   C    ASP  D1361    53.,672   55. 130   18 ,010   1 ,00   68..56        C
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ATOM   21230   O    ASP  D1361        54.791   55.248   18.493   1.00  71.56              O
ATOM   21231   CB   ASP  D1361        53.142   57.552   17.667   1.00  67.27              C
ATOM   21232   CG   ASP  D1361        53.301   57.570   16.165   1.00  71.14              C
ATOM   21233   OD1  ASP  D1361        52.795   56.647   15.500   1.00  69.36              O
ATOM   21234   OD2  ASP  D1361        53.930   58.516   15.646   1.00  76.69              O
ATOM   21235   O    LEU  D1362        55.983   52.119   15.888   1.00  70.72              O
ATOM   21236   N    LEU  D1362        53.303   54.065   17.313   1.00  68.22              N
ATOM   21237   CA.  LEU  D1362        54.160   52.897   17.222   1.00  69.25              C
ATOM   21238   C    LEU  D1362        55.137   52.987   16.056   1.00  72.60              C
ATOM   21239   CB   LEU  D1362        53.313   51.625   17.101   1.00  69.48              c
ATOM   21240   CG   LEU  D1352        52.273   51.410   18.210   1.00  69.34              c
ATOM   21241   CD1  LEU  D1362        51.650   50.013   18.137   1.00  59.51              c
ATOM   21242   CD2  LEU  D1362        52.873   51.692   19.583   1.00  60.27              c
ATOM   21243   O    SER  D1363        58.387   54.631   14.134   1.00  75.38              0
ATOM   21244   N    SEP. D1363        55.035   54.033   15.248   1.00  72.97              N
ATOM   21245   CA   SER  D1363        56.016   54.224   14.185   1.00  74.58              c
ATOM   21246   c    SER  D1363        57.348   54.668   14.792   1.00  75.81              c
ATOM   21247   CB   SER  D1363        55.522   55.241   13.154   1.00  73.59              c
ATOM   21248   OG   SER  D1363        55.085   56.437   13.780   1.00  75.61              0
ATOM   21249   O    GLN  D1364        60.525   54.529   17.596   1.00  79.90              0
ATOM   21250   N    GLN  D1364        57.299   55.078   16.058   1.00  73.18              N
ATOM   21251   CA   GLN  D1364        58.480   55.521   16.804   1.00  77.88              C
ATOM   21252   c    GLN  D1364        59.331   54.368   17.338   1.00  79.70              c
ATOM   21253   CB   GLN  D1364        58.041   56.414   17.969   1.00  68.70              c
ATOM   21254   CG   GLN  D1364        57.803   57.857   17.597   1.00  78.87              c
ATOM   21255   CD   GLN  D1364        56.963   58.026   16.341   1.00  84.46              c
ATOM   21256   OE1  GLN  D1364        56.213   57.126   15.947   1.00  83.71              0
ATOM   212 57  NE2  GLN  D1364        57.085   59.186   15.703   1.00  85.92              N
ATOM   21258   O    LEU  D1365        61.188   50.654   17.481   1.00  83.27              O
ATOM   21259   N    LEU  D1365        58.711   53.206   17.504   1.00  76.00              N
ATOM   21260   CA   LEU  D1365        59.375   52.088   18.147   1.00  70.76              C
ATOM   21261   C    LEU  D1365        60.184   51.276   17.134   1.00  76.91              C
ATOM   21262   CB   LEU  D1365        58.344   51.230   18.870   1.00  66.09              c
ATOM   21263   CG   LEU  D1365        57.376   52.073   19.718   1.00  75.55              c
ATOM   212 64  CD1  LEU  D1365        56.340   51.217   20.422   1.00  67.07              c
ATOM   21265   CD2  LEU  D1365        58.108   52.965   20.726   1.00  72.34              c
ATOM   21266   O    GLY  D136 6       62.883   50.631   15.139   1.00  93.43              0
ATOM   21267   N    GLY  D1366        59.758   51.300   15.879   1.00  77.33              N
ATOM   21268   CA   GLY  D1366        60.505   50.655   14.814   1.00  79.49              C
ATOM   21269   C    GLY  D1366        61.909   51.216   14.658   1.00  89.40              C
TER
ATOM   21270   P       G E    1        6.565   47.540   40.092   1.00  95.23              P
ATOM   21271   OP1     G E    1        6.252   48.948   39.738   1.00  79.66              O
ATOM   21272   OP2     G E    1        5.488   46.664   40.636   1.00  83.74              O
ATOM   21273   OP3     G E    1        7.127   46.891   38.878   1.00  93.40              0
ATOM   21274   05'     G E    1        7.703   47.551   41.207   1.00  75.87              0
ATOM   21275   C5'     G E    1        8.781   48.466   41.144   1.00  65.48              c
ATOM   212 76  C4'     G E    1        9.330   48.754   42.519   1.00  72.78              c
ATOM   21277   04'     G E    1        8.539   49.798   43.157   1.00  72.57              0
ATOM   21278   C3'     G E    1        9.309   47.606   43.528   1.00  68.57              c
ATOM   212 79  03'     G E    1       10.364   46.664   43.368   1.00  77.57              0
ATOM   21280   C2'     G E    1        9.361   48.353   44.850   1.00  66.29              c
ATOM   21281   02'     G E    1       10.663   48.853   45.103   1.00  64.03              0
ATOM   21282   CI'     G E    1        8.439   49.536   44.544   1.00  74.43              c
ATOM   21283   N9      G E    1        7.047   49.161   44.852   1.00  73.36              N
ATOM   21284   C8      G E    1        6.017   48.877   43.982   1.00  69.51              c
ATOM   21285   N7      G E    1        4.930   48.520   44.608   1.00  72.56              N
ATOM   21286   C5      G E    1        5.267   48.556   45.962   1.00  68.71              C
ATOM   21287   C4      G E    1        6.575   48.940   46.126   1.00  66.81              c
ATOM   21288   Nl      G E    1        5.259   48.439   48.291   1.00  62.46              N
ATOM   21289   C2      G E    1        6.575   48.823   48.347   1.00  64.05              C
ATOM   21290   N3      G E    1        7.287   49.094   47.267   1.00  66.14              N
ATOM   212 91  C6      G E    1        4.509   48.279   47.129   1.00  65.32              C
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ATOM	21292	06	G	E	1	3.333	47.921	47.217	1.00	65.23	O
ATOM	21293	N2	G	E	1	7.134	48.915	49.570	1.00	58.94	N
ATOM	21294	05'	G	E	2	10.014	45.088	45.365	1.00	69.47	O
ATOM	21295	C4'	G	E	2	10.593	45.454	47.680	1.00	65.88	C
ATOM	21296	C3'	G	E	2	10.004	44.152	48.210	1.00	64.56	C
ATOM	21297	C2'	G	E	2	9.193	44.641	49.400	1.00	64.14	C
ATOM	21298	P	G	E	2	10.186	45.107	43.778	1.00	72.23	P
ATOM	21299	OP1	G	E	2	11.476	44.434	43.459	1.00	85.77	0
ATOM	21300	OP2	G	E	2	8.928	44.570	43.213	1.00	62.78	0
ATOM	21301	C5'	G	E	2	11.066	45.458	46.246	1.00	58.21	C
ATOM	21302	04'	G	E	2	9.512	46.418	47.867	1.00	71.37	0
ATOM	21303	03'	G	E	2	10.994	43.206	48.569	1.00	66.96	0
ATOM	21304	02'	G	E	2	10.061	44.980	50.472	1.00	70.22	0
ATOM	21305	CI '	G	E	2	8.608	45.934	48.842	1.00	61.39	C
ATOM	21306	N9	G	E	2	7.298	45.681	48.207	1.00	66.02	N
ATOM	21307	C8	G	E	2	6.964	45.704	46.867	1.00	65.79	C
ATOM	21308	N7	G	E	2	5.710	45.417	46.639	1.00	63.16	N
ATOM	21309	C5	G	E	2	5.178	45.179	47.904	1.00	63.68	C
ATOM	21310	C4	G	E	2	6.146	45.338	48.882	1.00	64.29	C
ATOM	21311	N1	G	E	2	3.777	44.687	49.699	1.00	61.01	N
ATOM	21312	C2	G	E	2	4.809	44.873	50.588	1.00	60.27	C
ATOM	21313	N3	G	E	2	6.035	45.206	50.227	1.00	61.90	N
ATOM	21314	C6	G	E	2	3.855	44.829	48.306	1.00	65.74	C
ATOM	21315	06	G	E	2	2.850	44.643	47.586	1.00	59.83	0
ATOM	21316	N2	G	E	2	4.537	44.698	51.890	1.00	62.01	N
ATOM	21317	05'	A	E	3	9.769	41.648	50.143	1.00	65.70	0
ATOM	21318	C4'	A	E	3	9.436	41.448	52.515	1.00	59.04	C
ATOM	21319	C3'	A	E	3	8.876	40.040	52.440	1.00	57.59	C
ATOM	21320	C2'	A	E	3	7.567	40.161	53.202	1.00	61.10	C
ATOM	21321	P	A	E	3	10.633	41.663	48.814	1.00	63.16	P
ATOM	21322	OP1	A	E	3	11.939	41.060	49.187	1.00	71.16	0
ATOM	21323	OP2	A	E	3	9.778	41.118	47.740	1.00	53.61	0
ATOM	21324	C5'	A	E	3	10.387	41.817	51.410	1.00	62.83	C
ATOM	21325	04'	A	E	3	8.256	42.303	52.449	1.00	64.37	0
ATOM	21326	03'	A	E	3	9.753	39.070	52.986	1.00	62.69	0
ATOM	21327	02'	A	E	3	7.814	40.152	54.606	1.00	60.71	0
ATOM	21328	C1'	A	E	3	7.109	41.563	52.795	1.00	59.30	C
ATOM	21329	N9	A	E	3	6.175	41.563	51.646	1.00	62.07	N
ATOM	21330	C8	A	E	3	6.395	41.900	50.332	1.00	55.43	C
ATOM	21331	N7	A	E	3	5.318	41.808	49.578	1.00	56.87	N
ATOM	21332	C5	A	E	3	4.312	41.399	50.459	1.00	62.54	C
ATOM	21333	C4	A	E	3	4.837	41.252	51.731	1.00	58.49	C
ATOM	21334	N1	A	E	3	2.257	40.728	51.421	1.00	61.17	N
ATOM	21335	C2	A	E	3	2.914	40.624	52.576	1.00	59.27	C
ATOM	21336	N3	A	E	3	4.187	40.866	52.837	1.00	56.35	N
ATOM	21337	C6	A	E	3	2.924	41.120	50.318	1.00	64.02	C
ATOM	21338	N6	A	E	3	2.211	41.198	49.187	1.00	58.83	N
ATOM	21339	05'	A	E	4	8.438	36.905	53.151	1.00	57.84	O
ATOM	21340	C4'	A	E	4	7.070	36.148	54.994	1.00	60.90	C
ATOM	21341	C3'	A	E	4	6.480	34.963	54.238	1.00	61.42	C
ATOM	21342	C2'	A	E	4	4.987	35.133	54.497	1.00	59.57	C
ATOM	21343	P	A	E	4	9.717	37.550	52.459	1.00	59.04	P
ATOM	21344	OP1	A	E	4	10.912	36.919	53.059	1.00	59.47	0
ATOM	21345	OP2	A	E	4	9.436	37.524	50.997	1.00	52.22	0
ATOM	21346	C5'	A	E	4	8.430	36.617	54.541	1.00	63.07	C
ATOM	21347	04'	A	E	4	6.095	37.208	54.787	1.00	52.03	0
ATOM	21348	03'	A	E	4	6.999	33.697	54.642	1.00	56.29	0
ATOM	21349	02'	A	E	4	4.651	34.706	55.804	1.00	61.21	0
ATOM	21350	CI '	A	E	4	4.844	36.648	54.448	1.00	53.37	C
ATOM	21351	N9	A	E	4	4.441	37.095	53.103	1.00	55.97	N
ATOM	21352	C8	A	E	4	5.222	37.586	52.100	1.00	56.04	C
ATOM	21353	N7	A	E	4	4.557	37.891	51.019	1.00	58.86	N
ATOM	21354	C5	A	E	4	3.242	37.576	51.327	1.00	60.96	C

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ATOM  21355  C4    A E  4      3.154  37.082  52.615  1.00 61.17      c
ATOM  21356  Nl    A E  4      0.899  37.294  51.192  1.00 65.84      N
ATOM  21357  C2    A E  4      0.969  36.827  52.452  1.00 66.32      C
ATOM  21358  N3    A E  4      2.031  36.689  53.293  1.00 55.75      N
ATOM  21359  C6    A E  4      2.047  37.679  50.589  1.00 62.27      C
ATOM  21360  N6    A E  4      1.992  38.138  49.336  1.00 64.58      N
ATOM  21361  05'   A E  5      5.354  32.120  53.516  1.00 62.30      O
ATOM  21362  C4'   A E  5      3.090  31.755  54.217  1.00 62.87      C
ATOM  21363  C3'   A E  5      2.827  30.868  53.020  1.00 61.44      C
ATOM  21364  C2'   A E  5      1.497  31.397  52.508  1.00 63.89      c
ATOM  21365  P     A E  5      6.906  32.413  53.665  1.00 63.51      P
ATOM  21366  OP1   A E  5      7.535  31.253  54.353  1.00 59.76      0
ATOM  21367  OP2   A E  5      7.361  32.788  52.307  1.00 56.76      0
ATOM  21368  C5'   A E  5      4.533  31.831  54.635  1.00 61.74      c
ATOM  21369  04'   A E  5      2.616  33.057  53.783  1.00 58.03      0
ATOM  21370  03'   A E  5      2.805  29.499  53.360  1.00 66.75      0
ATOM  21371  02'   A E  5      0.440  30.921  53.321  1.00 66.00      0
ATOM  21372  C1'   A E  5      1.661  32.894  52.751  1.00 61.74      c
ATOM  21373  N9    A E  5      2.123  33.594  51.539  1.00 63.17      N
ATOM  21374  C8    A E  5      3.370  34.074  51.244  1.00 62.66      c
ATOM  21375  N7    A E  5      3.445  34.653  50.068  1.00 63.95      N
ATOM  21376  C5    A E  5      2.164  34.555  49.556  1.00 62.57      c
ATOM  21377  C4    A E  5      1.344  33.904  50.455  1.00 63.48      c
ATOM  21378  Nl    A E  5      0.270  34.714  48.158  1.00 66.27      N
ATOM  21379  C2    A E  5     -0.395  34.070  49.119  1.00 63.78      c
ATOM  21380  N3    A E  5      0.043  33.628  50.293  1.00 62.99      N
ATOM  21381  C6    A E  5      1.581  34.980  48.346  1.00 67.39      C
ATOM  21382  N6    A E  5      2.239  35.625  47.375  1.00 67.66      N
ATOM  21383  05'   U E  6      2.201  28.236  51.278  1.00 59.43      O
ATOM  21384  C4'   U E  6     -0.098  28.176  50.552  1.00 66.25      c
ATOM  21385  C3'   u E  6      0.304  27.500  49.258  1.00 69.39      c
ATOM  21386  C2'   υ E  6     -0.479  28.281  48.216  1.00 70.79      c
ATOM  21387  P     u E  6      3.373  28.407  52.335  1.00 59.85      P
ATOM  21388  OP1   u E  6      3.599  27.175  53.135  1.00 57.76      0
ATOM  21389  OP2   υ E  6      4.489  29.033  51.593  1.00 68.72      0
ATOM  21390  C5'   u E  6      0.867  28.004  51.698  1.00 65.74      c
ATOM  21391  04'   u E  6     -0.204  29.577  50.193  1.00 69.01      0
ATOM  21392  03'   u E  6      0.039  26.109  49.263  1.00 79.41      0
ATOM  21393  02'   u E  6     -1.827  27.846  48.185  1.00 74.86      0
ATOM  21394  CI '  u E  6     -0.436  29.697  48.805  1.00 67.99      c
ATOM  21395  Nl    u E  6      0.633  30.530  48.204  1.00 67.27      N
ATOM  21396  C2    u E  6      0.326  31.148  47.022  1.00 65.76      c
ATOM  21397  N3    u E  6      1.326  31.906  46.471  1.00 64.69      N
ATOM  21398  C4    u E  6      2.587  32.113  46.979  1.00 63.10      C
ATOM  21399  C5    υ E  6      2.843  31.436  48.211  1.00 61.78      C
ATOM  21400  C6    u E  6      1.884  30.684  48.767  1.00 67.94      c
ATOM  21401  02    u E  6     -0.761  31.023  46.507  1.00 70.09      0
ATOM  21402  04    υ E  6      3.370  32.838  46.360  1.00 64.21      0
ATOM  21403  05'   u E  7     -0.115  24.785  47.162  1.00 78.58      0
ATOM  21404  C4'   u E  7     -0.441  25.485  44.883  1.00 79.10      c
ATOM  21405  C3'   u E  7      0.102  25.477  43.475  1.00 81.36      c
ATOM  21406  C2'   u E  7     -0.402  26.789  42.895  1.00 82.73      c
ATOM  21407  P     u E  7      0.897  25.118  48.330  1.00 78.92      P
ATOM  21408  OP1   u E  7      1.171  23.858  49.062  1.00 71.09      0
ATOM  21409  OP2   u E  7      2.003  25.896  47.718  1.00 76.15      0
ATOM  21410  C5'   u E  7      0.359  24.653  45.843  1.00 82.44      c
ATOM  21411  04'   u E  7     -0.416  26.881  45.271  1.00 82.64      0
ATOM  21412  03'   u E  7     -0.315  24.326  42.779  1.00 86.89      0
ATOM  21413  02'   u E  7     -1.746  26.672  42.455  1.00 89.24      0
ATOM  21414  CI '  u E  7     -0.357  27.703  44.123  1.00 79.04      c
ATOM  21415  Nl    υ E  7      0.894  28.490  44.196  1.00 74.52      N
ATOM  21416  C2    u E  7      1.195  29.399  43.197  1.00 72.02      c
ATOM  21417  N3    u E  7      2.381  30.061  43.378  1.00 67.88      N
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ATOM   21418   C4    U E   7     3 ..266   29..925   44.428   1,00  67.51    C
ATOM   21419   C5    U E   7     2 ,885    28..976   45.,424  1,00  67.55    C
ATOM   21420   C6    υ E   7     1 .737    28.,313   45..272  1 .00  72,02    C
ATOM   21421   02    u E   7     0..494    29.,609   42.,222  1,00  73..56    0
ATOM   21422   04    u E   7     4„284     30. 612   44,439   1,00  66..68    0
ATOM   21423   P     G E   8     0 ..755   23.,174   42.484   1 .00  9.3,.49   P
ATOM   21424   OF1   G E   8     0 ..019   21.,892   42..330  1,00  97,31    0
ATOM   21425   OP2   G E   8     1„838     23.266    4.3.,505 1,00  89..80    0
ATOM   21426   05'   G E   8     1 .310    23.,624   41,063   1,00  91.05    0
ATOM   21427   C5'   G E   8     0 ..392   24.,100   40..088  1,00  90,.17    C
ATOM   21428   C4'   G E   8     0„938     25.252    3 9,282  1,00  89..46    C
ATOM   21429   04'   G E   8     1 .043    26.,461   40,086   1,00  85..77    0
ATOM   21430   C3'   G E   8     2.331     25,082    38. 715  1,00  84,90    C
ATOM   21431   03'   G E   8     2 .368    24.,222   37.,597  1,00  90..92    0
ATOM   21432   C2'   G E   8     2 ,719    26.. 517  38.,403  1,00  85..39    C
ATOM   21433   02'   G E   8     2 .058    26.,962   37..228  1.00  89,.75    0
ATOM   21434   CI'   G E   8     2 .117    27.,252   39.,607  1,00  83..83    C
ATOM   21435   N9    G E   8     3„111     27.432    40.,691  1,00  73..99    N
ATOM   21436   C8    G E   8     3 ..213   26.,707   41.855   1.00  78,.47    C
ATOM   21437   N7    G E   8     4 .207    27.,082   42..617  1,00  75,.23    N
ATOM   21438   C5    G E   8     4„802     28. 117   4.1. ,907 1,00  68..17    C
ATOM   21439   C4    G E   8     4 .145    28..340   40,721   1,00  66..93    C
ATOM   21440   Nl    G E   8     6 ..200   29.,854   41.246   1,00  65,.41    N
ATOM   21441   C2    G E   8     5„482     29.. 992  40.,094  1,00  66..46    C
ATOM   21442   N3    G E   8     4 .427    29.,255   39.,776  1,00  68..32    N
ATOM   21443   C6    G E   8     5 . 924   28.,920   42.233   1,00  68,36    C
ATOM   21444   06    G E   8     6„635     28..875   4.3.,246 1,00  74.28    O
ATOM   21445   N2    G E   8     5„912     30.. 950  39.,265  1,00  62.57    N
ATOM   21446   05'   G E   9     4.439     2.3.,269  36. 531  1,00  86,74    0
ATOM   21447   C4'   G E   9     5 ..808   25.,232   36.,136  1,00  83..47    C
ATOM   21448   C3'   G E   9     7,241     25.. 506  35.,706  1,00  78..39    C
ATOM   21449   C2'   G E   9     7 ..311   27.,024   35.. 662 1.00  77,27    C
ATOM   21450   P     G E   9     3 ..323   22.,923   37.,612  1,00  97.72    P
ATOM   21451   OP1   G E   9     2„538     21 .770   37.,095  1,00  94.26    0
ATOM   21452   OP2   G E   9     3 ..966   22.,806   38.. 949 1.00  86,.40    0
ATOM   21453   C5'   G E   9     5 ..624   23.,948   36.. 904 1,00  84,88    C
ATOM   21454   04'   G E   9     5„458     26. 359   36.,986  1,00  84.01    0
ATOM   21455   03'   G E   9     7,553     24..894   34.,474  1,00  89..81    0
ATOM   21456   02'   G E   9     6 . 753   27.,515   34. 453  1,00  81,62    0
ATOM   21457   CI'   G E   9     6„392     27.404    3 6,823  1,00  77.34    C
ATOM   21458   N9    G E   9     7,126     27.555    38.,098  1,00  68..62    N
ATOM   21459   C8    G E   9     7.036     26.,728   39. 195  1,00  69,29    C
ATOM   21460   N7    G E   9     7,796     27.,091   40.,190  1,00  66..82    N
ATOM   21461   C5    G E   9     8„427     28..233   39.,717  1,00  63..62    C
ATOM   21462   C4    G E   9     8 ..032   28.,536   38.. 433 1.00  66,.94    C
ATOM   21463   Nl    G E   9     9 ..754   30.,133   39.,546  1,00  57.76    N
ATOM   214 64  C2    G E   9     9„308     30. 353   38.,259  1,00  64.91    C
ATOM   21465   N3    G E   9     8 ..426   29.,571   37.. 651 1.00  68,.25    N
ATOM   21466   C6    G E   9     9 ..357   29.,074   40.. 359 1,00  59,.67    C
ATOM   214 67  06    G E   9     9„808     28. 939   41,500   1,00  62.84    0
ATOM   21468   N2    G E   9     9,799     31.,419   37.,604  1,00  61.31    N
ATOM   21469   05'   G E  10     9 . 984   25.,229   35.. 004 1,00  77,12    0
ATOM   21470   C4'   G E  10    11„406     27.016    .34.,168 1,00  79.9.3    C
ATOM   21471   C3'   G E  10    12.,822    27.,534   34.,369  1,00  72.95    C
ATOM   21472   C2'   G E  10    12 .600    28.,996   34. 740  1,00  74,09    C
ATOM   21473   P     G E  10     8„999     24..238   .34.,247 1,00  87.44    P
ATOM   214 74  OP1   G E  10     9„295     24.358    32.,793  1,00100.20    0
ATOM   21475   OP2   G E  10     9 .037    22.,911   34. 911  1,00  80,35    0
ATOM   21476   C5'   G E  10    11,249     25.,542   34.,454  1,00  77.39    C
ATOM   214 77  04'   G E  10    10,,587    27.815    35.,080  1,00  82.07    0
ATOM   21478   03'   G E  10    13.. 630   27.,330   33..225  1.00  78,.76    0
ATOM   21479   02'   G E  10    12.,270    29.,753   33.,582  1,00  74.99    0
ATOM   21480   C1'   G E  10    11 ,350    28. 876   35,615   1,00  72.31    C
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ATOM  21481  N9    G E  10   11.680  28.471  37.004  1.00  67.65   N
ATOM  21482  C8    G E  10   11,145  27.350  37,608  1,00  65.47   C
ATOM  21483  N1    G E  10   11.568  27,149  38.824  1,00  62,38   N
ATOM  21484  C5    G E  10   12.447  28.195  39,047  1.00  56.68   C
ATOM  21485  C4    G E  10   12,535  29.023  37,944  1,00  59,65   C
ATOM  21486  Nl.   G E  10   13.973  29,627  40.030  1,00  50,54   N
ATOM  21487  C2    G E  10   14.003  30,383  38.898  1,00  54,45   C
ATOM  21488  N3    G E  10   13,291  30.129  37,805  1,00  60.32   N
ATOM  21489  C6    G E  10   13.207  28.484  40.203  1,00  56.31   C
ATOM  21490  06    G E  10   13.248  27,855  41.271  1,00  54,73   O
ATOM  21491  N2    G E  10   14,824  31.445  38,942  1,00  53.36   N
ATOM  21492  05'   U E  11   15.989  27,150  34.012  1,00  65.80   O
ATOM  21493  C4'   U E  11   16.992  29,258  34.605  1,00  60,35   C
ATOM  21494  C3'   U E  11   18.274  28,694  35,170  1.00  56.82   C
ATOM  21495  C2'   U E  11   18,397  29.461  36,467  1,00  56.76   C
ATOM  21496  P     υ E  11   14.869  26,306  33,278  1,00  73,66   P
ATOM  21497  OP1   U E  11   15.275  26.143  31,864  1.00  75.39   0
ATOM  21498  OP2   U E  11   14,601  25.126  34,151  1,00  67,37   0
ATOM  21499  C5'   υ E  11   16.316  28,442  33,540  1,00  66,74   C
ATOM  21500  04'   u E  11   16.141  29,357  35,770  1,00  56,79   0
ATOM  21501  03'   u E  11   19,390  28.852  34,328  1,00  58.90   0
ATOM  21502  02'   u E  11   18.793  30,794  36,181  1,00  52.71   0
ATOM  21503  CI '  u E  11   16.942  29,486  36,922  1,00  50,50   C
ATOM  21504  Nl    u E  11   16,592  28.403  37,876  1,00  52.41   N
ATOM  21505  C2    u E  11   17.081  28.505  39,173  1,00  49.69   C
ATOM  21506  N3    u E  11   16.694  27,510  40.033  1,00  47,05   N
ATOM  21507  C4    u E  11   15,873  26.436  39,743  1,00  55.42   C
ATOM  21508  C5    u E  11   15,391  26.411  38,390  1,00  52.28   C
ATOM  21509  C6    u E  11   15.755  27,368  37.524  1,00  54,05   C
ATOM  21510  02    u E  11   17.818  29.411  39,538  1.00  53.18   0
ATOM  21511  04    u E  11   15,619  25.616  40,635  1,00  55.15   0
ATOM  21512  05'   G E  12   21.437  28,284  35,701  I,00  48,01   0
ATOM  21513  C4'   G E  12   22.214  30,020  37,219  1.00  50.52   C
ATOM  21514  C3'   G E  12   23,333  29.200  37,829  1,00  46.18   C
ATOM  21515  C2'   G E  12   23.079  29,342  39,.324 I,00  46,37   C
ATOM  21516  P     G E  12   20.588  27,789  34.441  1,00  58,38   P
ATOM  21517  OP1   G E  12   21,384  27.956  33,202  1,00  57.21   0
ATOM  21518  OP2   G E  12   19.992  26,472  34,780  1,00  51.92   0
ATOM  21519  C5'   G E  12   21.850  29,639  35.804  1,00  52,03   C
ATOM  21520  04'   G E  12   21,091  29.822  38,122  1,00  49.28   0
ATOM  21521  03'   G E  12   24,598  29.690  37,427  1,00  49.16   0
ATOM  21522  02'   G E  12   23.549  30,595  39.789  1,00  51.,75   0
ATOM  21523  CI '  G E  12   21.557  29.384  39,380  1.00  48.94   C
ATOM  21524  N9    G E  12   20,930  28.080  39,714  1,00  42.18   N
ATOM  21525  C8    G E  12   20.245  27,247  38,880  I,00  44,97   C
ATOM  21526  N7    G E  12   19.750  26,202  39,476  1.00  42.87   N
ATOM  21527  C5    G E  12   20,122  26.362  40,794  1,00  39.40   C
ATOM  21528  C4    G E  12   20.841  27,512  40,961  I,00  39,99   C
ATOM  21529  Nl    G E  12   20.416  26,091  43.063  1,00  39,70   N
ATOM  21530  C2    G E  12   21,129  27.248  43,136  1,00  39.58   C
ATOM  21531  N3    G E  12   21.372  28,018  42,099  1,00  41.79   N
ATOM  21532  C6    G E  12   19.868  25,546  41.914  1,00  40,17   C
ATOM  21533  06    G E  12   19,253  24.466  41,963  1,00  47.37   0
ATOM  21534  N2    G E  12   21.569  27.604  44,345  1,00  38.16   N
ATOM  21535  05'   C E  13   26.222  28,504  38.957  1,00  41,23   0
ATOM  21536  C4'   C E  13   26,870  29.052  41,187  1,00  39.52   C
ATOM  21537  C3'   C E  13   27,580  27.739  41,458  1,00  38.00   C
ATOM  21538  C2'   C E  13   27.026  27,351  42.817  1,00  38,23   C
ATOM  21539  P     C E  13   25,894  28.747  37,426  1.00  48.63   P
ATOM  21540  OP1   C E  13   26,964  29.559  36,808  1,00  45.15   0
ATOM  21541  OP2   C E  13   25.485  27,377  36,961  I,00  44,35   0
ATOM  21542  C5'   C E  13   26.845  29.488  39,749  1.00  38.26   C
ATOM  21543  04'   C E  13   25,524  28.791  41,659  1,00  41.30   0
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ATOM	21544	03'	C	E	13	28..980	27..844	41.393	1,00	42.96	O
ATOM	21545	02'	C	E	13	27.,644	28..121	43.,839	1,00	41.78	O
ATOM	21546	CI'	C	E	13	25.565	27.,795	42.668	1.00	42,17	C
ATOM	21547	Nl	C	E	13	24..709	26.,664	42.,260	1,00	40..78	N
ATOM	21548	C2	C	E	13	24.,305	25. 797	43.,251	1,00	39..86	C
ATOM	21549	N3	C	E	13	23..539	24.,736	42.936	1.00	4.3,.15	N
ATOM	21550	C4	C	E	13	23..184	24.,515	41.670	1,00	43,.15	C
ATOM	21551	C5	C	E	13	23.,585	25. .391	40.,643	1,00	40..09	C
ATOM	21552	C6	C	E	13	24..349	26..447	40,970	1,00	43..00	C
ATOM	21553	02	C	E	13	24.669	26.,035	44.403	1,00	46,.51	0
ATOM	21554	N4	C	E	13	22.,425	23..441	41,392	1,00	41.84	N
ATOM	21555	05'	G	E	14	29..690	25..579	42.,119	1,00	39..26	O
ATOM	21556	C4'	G	E	14	29. 707	24.,900	44..396	1,00	34,75	C
ATOM	21557	C3'	G	E	14	30..046	23.,453	44.053	1,00	35..08	C
ATOM	21558	C2'	G	E	14	29.,103	22.701	44,976	1,00	38..00	C
ATOM	21559	P	G	E	14	29..840	26.,577	40.. 905	1.00	40,.70	P
ATOM	21560	OP1	G	E	14	31..245	27.,026	40.,815	1,00	42.74	0
ATOM	21561	OP2	G	E	14	29.,175	25. 932	39.,737	1,00	36..94	0
ATOM	21562	C5'	G	E	14	30..142	25.,930	43.. 402	1.00	32,14	C
ATOM	21563	04'	G	E	14	28..259	24.,888	44.532	1,00	36,.07	0
ATOM	21564	03'	G	E	14	31.,424	23.127	44,199	1,00	41.24	0
ATOM	21565	02'	G	E	14	29..586	22..733	46.,310	1,00	35..49	0
ATOM	21566	CI'	G	E	14	27.840	23.,583	44.884	1,00	43,.72	C
ATOM	21567	N9	G	E	14	26.,927	23..057	4.3.,849	1,00	40..81	N
ATOM	21568	C8	G	E	14	26..794	23..450	42.,542	1,00	39..28	C
ATOM	21569	N7	G	E	14	25. 929	22.,722	41.885	1,00	39,13	N
ATOM	21570	C5	G	E	14	25.,485	21..785	42.,814	1,00	37.26	C
ATOM	21571	C4	G	E	14	26.,093	21.964	44,030	1,00	38..92	C
ATOM	21572	Nl	G	E	14	24..398	20.,039	43. 888	1,00	40,51	N
ATOM	21573	C2	G	E	14	25..060	20.,297	45.,059	1,00	39..62	C
ATOM	21574	N3	G	E	14	25.,945	21.260	45.,185	1,00	37.39	N
ATOM	21575	C6	G	E	14	24..553	20.,731	42.693	1.00	4.1 ,47	C
ATOM	21576	06	G	E	14	23..898	20.,384	41,708	1,00	39..51	O
ATOM	21577	N2	G	E	14	24.,757	19. 493	46.,099	1,00	39.,39	N
ATOM	21578	05'	C	E	15	31..465	20.,610	44.249	1.00	30,.78	O
ATOM	21579	C4'	C	E	15	30..994	19.,286	46.. 183	1,00	42,18	C
ATOM	21580	C3'	C	E	15	31.,208	17.937	45,483	1,00	33..15	C
ATOM	21581	C2'	C	E	15	29..970	17,179	45.,912	1,00	37.81	C
ATOM	21582	P	C	E	15	32. 059	21.,823	43. 451	1,00	37,51	P
ATOM	21583	OP1	C	E	15	33.,508	21..855	4.3.,654	1,00	36..06	0
ATOM	21584	OP2	C	E	15	31.,488	21.745	42.,088	1,00	39..53	0
ATOM	21585	C5'	C	E	15	31. 761	20.,454	45. 621	1,00	39,97	C
ATOM	21586	04'	C	E	15	29..567	19.,527	46.,043	1,00	35..28	0
ATOM	21587	03'	C	E	15	32.,430	17.332	45.,851	1,00	44.46	0
ATOM	21588	02'	C	E	15	30..119	16.,793	47.271	1.00	36,.53	0
ATOM	21589	CI'	C	E	15	28.,902	18.,294	45.,829	1,00	40..32	C
ATOM	21590	N1	C	E	15	28.,256	18. .338	44,489	1,00	38..61	N
ATOM	215 91	C2	C	E	15	27.158	17,512	44.194	1.00	4.1 ,77	C
ATOM	21592	N3	C	E	15	26..577	17,535	42..963	1,00	39,.17	N
ATOM	21593	C4	C	E	15	27.,057	18. 370	42.,042	1,00	40...35	C
ATOM	21594	C5	C	E	15	28.,156	19.,236	42.,302	1,00	37.08	C
ATOM	21595	C6	C	E	15	28..725	19.,181	43.. 522	1,00	38,.37	C
ATOM	21596	02	C	E	15	26.,737	16.. 754	45.,080	1,00	47.27	0
ATOM	21597	N4	C	E	15	26.,479	18..379	40,839	1,00	37.84	N
ATOM	21598	05'	u	E	16	32. 012	14,951	45. 111	1,00	41,41	O
ATOM	21599	C4'	u	E	16	30.,788	13.. 120	46.,025	1,00	43..66	C
ATOM	21600	C3'	u	E	16	31.,087	12..200	44,838	1,00	42,40	C
ATOM	21601	C2'	u	E	16	29. 711	11,662	44.496	1,00	43,91	C
ATOM	21602	P	u	E	16	33.,106	16.,102	45.,030	1,00	39..27	P
ATOM	21603	OP1	u	E	16	34.,307	15..856	45.,825	1,00	40..83	0
ATOM	21604	OP2	υ	E	16	33...318	16.,345	43.. 578	1.00	38,.96	0
ATOM	21605	C5'	u	E	16	31..779	14,222	46.,296	1,00	37.80	C
ATOM	21606	04'	u	E	16	29.,515	13. 716	45,683	1,00	43..82	0

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ATOM  21607  03'   U E  16    32.016  11:186  45.131  1,00  49.59   O
ATOM  21608  02'   U E  16    29,329  10.645  45,406  1,00  43.03   O
ATOM  21609  CI '  ʋ E  16    28.838  12,898  44:755  1,00  44,57   C
ATOM  21610  Nl    u E  16    28.648  13:668  43.517  1,00  39.74   N
ATOM  21611  C2    u E  16    27,596  13.224  42,780  1,00  37,91   C
ATOM  21612  N3    ʋ E  16    27.387  13,917  41:617  1,00  40,25   N
ATOM  21613  C4    u E  16    28.143  14,967  41.130  1,00  37,46   C
ATOM  21614  C5    u E  16    29,257  15.355  41,951  1,00  35,66   C
ATOM  21615  C6    u E  16    29.471  14.700  43.114  1,00  37.44   C
ATOM  21616  02    u E  16    26.895  12,318  43.179  1,00  38,39   0
ATOM  21617  04    u E  16    27,815  15:454  40,046  1,00  40.65   0
ATOM  21618  05'   u E  17    31.955   9:892  42:934  1,00  40.01   0
ATOM  21619  C4'   u E  17    30.231   8,349  42.254  1,00  50,17   C
ATOM  21620  C3'   u E  17    30.648   8:044  40:828  1,00  43.60   C
ATOM  21621  C2'   u E  17    29,284   7.946  40,184  1,00  47.72   C
ATOM  21622  P     ʋ E  17    32:950  10,564  43:974  1,00  50,35   P
ATOM  21623  OP1   u E  17    33:730   9:530  44.692  1,00  51.52   0
ATOM  21624  OP2   u E  17    33,602  11.630  43,179  1,00  46.96   0
ATOM  21625  C5'   ʋ E  17    31:271   8,720  43:278  1,00  44,59   C
ATOM  21626  04'   u E  17    29.234   9,400  42.063  1,00  49,58   0
ATOM  21627  03'   u E  17    31,428   6.868  40,675  1,00  53.45   0
ATOM  21628  02'   u E  17    28:630   6:772  40:637  1,00  45.65   0
ATOM  21629  CI '  u E  17    28.571   9,150  40.835  1,00  45,05   C
ATOM  21630  Nl    u E  17    28,659  10:326  39,965  1,00  41.69   N
ATOM  21631  C2    u E  17    27:964  10:226  38:783  1,00  45.05   C
ATOM  21632  N.3   u E  17    28.084  11,312  37.954  1,00  42,37   N
ATOM  21633  C4    u E  17    28,825  12:452  38,214  1,00  42.35   C
ATOM  21634  C5    u E  17    29,528  12.450  39,451  1,00  39.67   C
ATOM  21635  C6    u E  17    29.431  11,406  40.266  1,00  41,55   C
ATOM  21636  02    u E  17    27.268   9:260  38.511  1,00  45.84   0
ATOM  21637  04    u E  17    28,851  13.360  37,385  1,00  43.50   0
ATOM  21638  05'   G E  18    31:361   5,973  38:279  1,00  41,46   0
ATOM  21639  C4'   G E  18    29.487   4:638  37.617  1,00  42.24   C
ATOM  21640  C3'   G E  18    29,845   4.493  36,152  1,00  42.98   C
ATOM  21641  C2'   G E  18    28:554   4,938  35:469  1,00  41,78   C
ATOM  21642  P     G E  18    32.349   6,584  39.357  1,00  50,12   P
ATOM  21643  OP1   G E  18    33,232   5.501  39,824  1,00  44.84   0
ATOM  21644  OP2   G E  18    32.920   7.779  38:720  1,00  44.06   0
ATOM  21645  C5'   G E  18    30.641   4,797  38.561  1,00  44,08   C
ATOM  21646  04'   G E  18    28,663   5:837  37,656  1,00  46.80   0
ATOM  21647  03'   G E  18    30,265   3.172  35,809  1,00  46.35   0
ATOM  21648  02'   G E  18    27.546   3,952  35.564  1,00  45,79   0
ATOM  21649  CI '  G E  18    28.131   6:095  36.374  1,00  45.09   C
ATOM  21650  N9    G E  18    28,705   7.353  35,877  1,00  40.09   N
ATOM  21651  C8    G E  18    29:681   8,108  36:469  1,00  38,16   C
ATOM  21652  N7    G E  18    30:016   9:116  35:732  1,00  40.43   N
ATOM  21653  C5    G E  18    29,222   8.988  34,586  1,00  41.21   C
ATOM  21654  C4    G E  18    28:416   7,894  34:662  1,00  34,08   C
ATOM  21655  Nl    G E  18    28.216   9,322  32.520  1,00  37,27   N
ATOM  21656  C2    G E  18    27,481   8.193  32,696  1,00  36.96   C
ATOM  21657  N3    G E  18    27:517   7.430  33:773  1,00  34.92   N
ATOM  21658  C6    G E  18    29.119   9,815  33.433  1,00  40.61   C
ATOM  21659  06    G E  18    29,738  10:847  33,168  1,00  42.18   0
ATOM  21660  N2    G E  18    26:665   7.936  31:690  1,00  36.99   N
ATOM  21661  05'   G E  19    30.923   3,074  33.362  1,00  38,95   0
ATOM  21662  C4'   G E  19    29,158   2:984  31,745  1,00  39.47   C
ATOM  21663  C3'   G E  19    30,058   3.115  30,544  1,00  38.92   C
ATOM  21664  C2'   G E  19    29.348   4,203  29.736  1,00  39,21   C
ATOM  21665  P     G E  19    31.520   2:894  34.820  1,00  42.79   P
ATOM  21666  OP1   G E  19    31,795   1.445  35,033  1,00  48.56   0
ATOM  21667  OP2   G E  19    32:632   3,854  34:869  1,00  36,41   0
ATOM  21668  C5'   G E  19    29.773   2:356  32.957  1,00  36.72   C
ATOM  21669  04'   G E  19    28,774   4.367  32,039  1,00  43,01   0
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ATOM   21670   03 '   G E   19        30..274     1.881    29..853    1.00   38..16          O
ATOM   21671   02 '   G E   19        28,,236     3 ..670  29..038    1,00   35..67          O
ATOM   21672   CI '   G E   19        28..829     5 ,127   30.. 857   1,00   40,.90          C
ATOM   21673   Nl     G E   19        30..442     9 ..631  29.. 098   1.00   36..09          N
ATOM   21674   N9     G E   19        29.,717     6 .280   .3.1.,079  1,00   37 ,40          N
ATOM   21675   C8     G E   19        30..614     6 ,452   32.. 094   1,00   40,.40          C
ATOM   21676   N7     G E   19        31..297     7,564    32.. 004   1,00   39,.04          N
ATOM   21677   C5     G E   19        30.,802     8 .163   .30.,858   1,00   37 .04          C
ATOM   21678   C6     G E   19        31..152     9 .405   30.. 271   1,00   39..73          C
ATOM   21679   06     G E   19        31..994     10.,217  30.. 695   1,00   41 ,71          O
ATOM   21680   C2     G E   19        29.,467     8 .794   28.,582    1,00   40..14          C
ATOM   21681   N2     G E   19        28..856     9 .172   27.. 449   1,00   43..29          N
ATOM   21682   N.3    G E   19        29. 107     7,655    29. 141    1,00   4.1 ,27         N
ATOM   21683   C4     G E   19        29..833     7..390   30..267    1.00   38..96          C
ATOM   21684   05 '   C E   20        31.,184     2 .530   27.,581    1,00   39..62          O
ATOM   21685   C4 '   C E   20        31..373     4,318    26.. 017   1,00   42 ,43          C
ATOM   21686   C3 '   C E   20        32..181     4..976   24.. 926   1.00   44 .32          C
ATOM   21687   C2 '   C E   20        3.1.,358     6 .229   24.,643    1,00   40..14          C
ATOM   21688   P      C E   20        31..553     1,717    28.. 885   1,00   38,.29          P
ATOM   21689   OF1    C E   20        31..608     0 ,320   28.. 369   1,00   41 ,52          0
ATOM   21690   OP2    C E   20        32.,692     2 .384   29.,540    1,00   37 ..3.3        0
ATOM   21691   C5 '   C E   20        32.. 112    3 .375   26.. 933   1,00   40..70          C
ATOM   21692   04 '   C E   20        30..821     5 ,438   26.. 783   1,00   44,44           0
ATOM   21693   03 '   C E   20        32.,321     4..120   2.3.,794   1,00   41 .16          0
ATOM   21694   02 '   C E   20        30.. 195    5 ..870  23.. 933   1,00   48..28          0
ATOM   21695   C1 '   C E   20        30. 913     6 ,621   26. 041    1,00   39 ,83          C
ATOM   21696   Nl     C E   20        31.,913     7.482    26.,699    1,00   42 .7.3         N
ATOM   21697   C2     C E   20        32.,195     8 .772   26.,219    1,00   40..91          C
ATOM   21698   N.3    C E   20        33. 155     9 ,485   26. 859    1,00   44 ,89          N
ATOM   21699   C4     C E   20        33..799     8 .976   27.. 932   1.00   42 .56          C
ATOM   21700   C5     C E   20        33.,508     7.683    28.,443    1,00   37 .43          C
ATOM   21701   C6     C E   20        32..570     6 ,985   27..799    1,00   40,.76          C
ATOM   21702   02     C E   20        31..601     9..241   25.. 240   1.00   38..22          O
ATOM   21703   N4     C E   20        34.,724     9 .725   28.,543    1,00   43..29          N
ATOM   21704   05 '   G E   21        33..944     5 ,545   22. 521    1,00   4.3,.46         O
ATOM   21705   C4 '   G E   21        33..473     7,656    21..547    1,00   43,.17          C
ATOM   21706   C3 '   G E   21        34.,895     7.851    2.1.,093   1,00   43..94          C
ATOM   21707   C2 '   G E   21        35.. 254    9 .216   21.. 658   1,00   44 .74          C
ATOM   21708   P      G E   21        33. 687     4,051    22.942     1,00   46,60           P
ATOM   21709   OP1    G E   21        3.3.,500    3 ..288  21.,694    1,00   39..36          0
ATOM   21710   OP2    G E   21        34.,758     3 ..625  23.,883    1,00   51 .37          0
ATOM   21711   C5 '   G E   21        33.066      6 ,219   21 .641    1,00   44 ,31          C
ATOM   21712   04 '   G E   21        33.. 445    8 .269   22.. 863   1.00   39..35          0
ATOM   21713   03 '   G E   21        35.,021     7.755    19.,703    1,00   47 .18          0
ATOM   21714   02 '   G E   21        34.. 727    10.,255  20..849    1,00   51 ,38          0
ATOM   21715   CI '   G E   21        34.. 503    9 ..195  22.. 981   1.00   39..41          C
ATOM   21716   N9     G E   21        35.,350     8 .775   24.,098    1,00   41 .54          N
ATOM   21717   C8     G E   21        35.. 319    7,557    24.. 741   1,00   42 ,27          C
ATOM   21718   N7     G E   21        36.. 143    7,493    25.. 731   1,00   35,.02          N
ATOM   21719   C5     G E   21        36.,785     8 .711   25,727     1,00   37 .88          C
ATOM   21720   C4     G E   21        36..301     9 .524   24.. 729   1,00   42 .22          C
ATOM   21721   Nl     G E   21        38.. 130    10.,509  26.. 216   1,00   48,.23          N
ATOM   21722   C2     G E   21        .37.,585    11.246   25.,208    1,00   42 .46          C
ATOM   21723   N3     G E   21        36..650     10.. 781 24.. 412   1,00   42 .45          N
ATOM   21724   C6     G E   21        37. 789     9 ,220   26. 563    1,00   39 ,32          C
ATOM   21725   06     G E   21        .38.,362    8 .717   27.,522    1,00   43..50          O
ATOM   21726   N2     G E   21        38.,081     12.. 482 25.,074    1,00   46..97          N
ATOM   21727   05 '   U E   22        37. 453     8 ,159   19. 509    1,00   45 ,99          O
ATOM   21728   C4 '   U E   22        38.. 670    10.. 207 19.. 380   1.00   42 .54          C
ATOM   21729   C3 '   U E   22        40.,078     9 .647   19.,324    1,00   42 .49          C
ATOM   21730   C2 '   υ E   22        40.. 754    10.,359  20..484    1,00   52 ,22          C
ATOM   21731   P      U E   22        36.. 342    7..109   19.. 097   1.00   48..30          P
ATOM   21732   OP1    U E   22        3 6 ,193    7.107    17,628     1,00   49..69          0
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ATOM	21733	OP2	U	E	22	36..655	5 ..849	19..806	1 .00	50..25	O
ATOM	217 34	C5 '	U	E	22	37.,612	9 ..345	18.,766	1 ,00	48..05	C
ATOM	21735	04 '	υ	E	22	38..402	10.,349	20 .801	I .00	37 ,.69	O
ATOM	21736	03 '	U	E	22	40..708	9 ,876	18..079	1 .00	48..39	O
ATOM	21737	02 '	U	E	22	41 ,043	11 .701	20.,104	1 ,00	53..00	O
ATOM	21738	CI '	υ	E	22	39 .617	10.,407	21..512	I .00	44 ,66	C
ATOM	21739	Nl	U	E	22	39..617	9 ,303	22 .507	1 ,00	42 ,02	N
ATOM	21740	C2	U	E	22	40.,434	9 . .394	23.,600	1 ,00	40. .35	C
ATOM	21741	N3	U	E	22	40 .336	8 ..373	24.,490	1 ,00	41 .28	N
ATOM	21742	C4	U	E	22	39..508	7 ,278	24 .439	1 ,00	38,.94	C
ATOM	21743	C5	U	E	22	38.,671	7 .232	23.,297	1 ,00	35..83	C
ATOM	21744	C6	U	E	22	38..754	8 ..227	22.,402	1 ,00	43..00	C
ATOM	21745	02	U	E	22	41 .211	10.,295	23 .779	1 ,00	48 ,21	O
ATOM	21746	04	U	E	22	39..545	6 ,487	25.,383	1 .00	41 .67	O
ATOM	217 47	05 '	U	E	23	43.,001	8 ..837	18.,054	1 ,00	48..92	O
ATOM	21748	C4 '	υ	E	23	44 .706	10.,110	19 .155	I .00	49,.93	C
ATOM	21749	C3 '	U	E	23	45..737	8 ,997	19..188	1 .00	47 .46	C
ATOM	21750	C2 '	U	E	23	46.,157	8 .961	20.,650	1 ,00	51 .49	C
ATOM	217 51	P	υ	E	23	41 .573	8 ,713	17 .378	I .00	52 ,76	P
ATOM	21752	OF1	U	E	23	41 .707	9 ,041	15..946	1 ,00	58,.09	0
ATOM	21753	OP2	U	E	23	41 ,007	7 .413	17 ,778	1 ,00	48..57	0
ATOM	21754	C5 '	U	E	23	43 .720	10.,054	18.,018	1 ,00	48..12	C
ATOM	21755	04 '	U	E	23	44 .020	9 ,991	20..424	1 ,00	44 ,11	0
ATOM	21756	03 '	U	E	23	46.,808	9 .270	18.,316	1 ,00	59..20	0
ATOM	21757	02 '	U	E	23	47 .108	9 ..984	20.,896	1 ,00	45..50	0
ATOM	21758	C1 '	U	E	23	44 .855	9 ,346	21 .362	1 ,00	46 ,21	C
ATOM	21759	Nl	U	E	23	44 ,092	8 ..22 4	21.,965	1 ,00	43..42	N
ATOM	217 60	C2	U	E	23	44 ,384	7 .877	23.,260	1 ,00	44 .81	C
ATOM	21761	N3	U	E	23	43. 596	6 ,893	23 .813	1 ,00	41. ,19	N
ATOM	21762	C4	U	E	23	42..541	6 ,231	23.,217	1 .00	38..17	C
ATOM	217 63	C5	U	E	23	42.,305	6 ..642	21.,888	1 ,00	37 .11	C
ATOM	21764	C6	υ	E	23	43..047	7 ,609	21...32 4	I .00	43,.03	C
ATOM	21765	02	U	E	23	45..283	8 ,413	23..866	1 .00	49..36	0
ATOM	217 66	04	U	E	23	41 ,929	5 . .351	23.,836	1 ,00	37 .29	0
ATOM	21767	05 '	υ	E	24	48..248	7 ,244	18..333	I .00	49,.29	0
ATOM	21768	C4 '	U	E	24	50..202	6 ,850	19..715	1 ,00	53,.25	C
ATOM	217 69	C3 '	U	E	24	50.,337	5 . .35 9	19.,427	1 ,00	50..46	C
ATOM	21770	C2 '	U	E	24	50..460	4 .779	20.,823	1 ,00	49..92	C
ATOM	21771	P	U	E	24	47 .373	8 ,125	17 . .34 5	1 ,00	49 ,87	P
ATOM	21772	OP1	U	E	24	48.,322	8 ..790	16.,426	1 ,00	51 .51	0
ATOM	217 73	OP2	U	E	24	46.,241	7 .352	16.,788	1 ,00	48..36	0
ATOM	21774	C5 '	U	E	24	49. 550	7 ,697	18. 658	1 ,00	5.1 ,44	C
ATOM	21775	04 '	U	E	24	49.,419	6 ,906	20.,927	1 .00	45..42	0
ATOM	217 76	03 '	U	E	24	51.,455	5 ..069	18.,602	1 ,00	60..55	0
ATOM	21777	02 '	υ	E	24	51..766	5 ,030	21..319	I .00	47 ,23	0
ATOM	21778	CI '	U	E	24	49..502	5 ,673	21..605	1 .00	48..58	C
ATOM	21779	Nl	U	E	24	48.,130	5 .131	21.,763	1 ,00	45..89	N
ATOM	21780	C2	υ	E	24	47 .940	4 ,313	22..846	I .00	45,.39	C
ATOM	21781	N3	U	E	24	46..649	3 ,842	23..044	1 ,00	45,.41	N
ATOM	21782	C4	U	E	24	45 ,525	4 .146	22.,257	1 ,00	45..74	C
ATOM	21783	C5	U	E	24	45.,832	5 ..007	21.,161	1 ,00	42 .61	C
ATOM	217 84	C6	U	E	24	47 .073	5 ,479	20..957	1 ,00	41 ,09	C
ATOM	21785	02	U	E	24	48.,886	4 .044	23.,548	1 ,00	47 .88	0
ATOM	21786	04	U	E	24	44 ,390	3 ..687	22.,516	1 ,00	37 .96	0
ATOM	21787	05 '	U	E	25	51. 772	2 ,568	19. 023	1 ,00	42 ,07	0
ATOM	21788	C4 '	U	E	25	52.,660	1 .576	21.,008	1 ,00	49 .70	C
ATOM	21789	C3 '	U	E	25	52.,27 5	0 ..156	20.,619	1 ,00	51 .46	C
ATOM	21790	C2 '	U	E	25	51. 556	-0.,335	21 .859	1 ,00	50 ,34	C
ATOM	21791	P	U	E	25	51.,641	3 ,638	17 ,857	1 .00	60..88	P
ATOM	21792	0P1	U	E	25	52.. 927	3 ..715	17 ,132	1 ,00	61 .11	0
ATOM	21793	0P2	υ	E	25	50..442	3 ,304	17 .069	I .00	61 ,35	0
ATOM	21794	C5 '	U	E	25	52..901	2 ,529	19..867	1 .00	49..70	C
ATOM	217 95	04 '	U	E	25	51 ,538	2 .037	21.,791	1 ,00	51 .00	0

ATOM	21796	03'	U	E	25	53.397	-0.638	20.285	1.00	57.57	O
ATOM	21797	02'	U	E	25	52,504	-0.685	22,853	1,00	45.43	O
ATOM	21798	CI '	U	E	25	50.818	0,934	22.300	1.00	49,27	C
ATOM	21799	Nl	U	E	25	49.415	0.990	21.787	1.00	44.33	N
ATOM	21800	C2	U	E	25	48,441	0.379	22,542	1,00	46.26	C
ATOM	21801	N3	U	E	25	47.167	0,432	22.028	1.00	41,84	N
ATOM	21802	C4	U	E	25	46.751	1,055	20.871	1,00	45,35	C
ATOM	21803	C5	U	E	25	47,808	1.662	20,122	1,00	40.08	C
ATOM	21804	C6	U	E	25	49.056	1,607	20.605	1,00	48.22	C
ATOM	21805	02	U	E	25	48.702	-0,176	23.602	1,00	51,98	0
ATOM	21806	04	U	E	25	45,545	1.041	20,575	1,00	46.15	0
ATOM	21807	05'	A	E	26	52.472	-3.004	20.305	1,00	44.36	0
ATOM	21808	C4'	A	E	26	52.164	-4,488	22.167	1,00	52,34	C
ATOM	21809	C3'	A	E	26	51.343	-5.451	21.313	1.00	53.87	C
ATOM	21810	C2'	A	E	26	50,217	-5.825	22,277	1,00	52.95	C
ATOM	21811	P	A	E	26	53.255	-1,978	19.389	1.00	55,88	P
ATOM	21812	OP1	A	E	26	54.646	-2,476	19.319	1,00	60.65	0
ATOM	21813	OP2	A	E	26	52,521	-1.692	18,130	1,00	44.78	0
ATOM	21814	C5'	A	E	26	53.082	-3,529	21.458	1.00	45,65	C
ATOM	21815	04'	A	E	26	51.168	-3,749	22.903	1,00	52,49	0
ATOM	21816	03'	A	E	26	52,097	-6.563	20,833	1,00	54.60	0
ATOM	21817	02'	A	E	26	50.642	-6,731	23.285	1,00	55.65	0
ATOM	21818	CI '	A	E	26	49.965	-4,485	22.959	1,00	50,68	C
ATOM	21819	N9	A	E	26	48,935	-3.790	22,197	1,00	47,05	N
ATOM	21820	C8	A	E	26	49.082	-2.977	21.105	1,00	44.81	C
ATOM	21821	N7	A	E	26	47.936	-2,619	20.605	1,00	47,75	N
ATOM	21822	C5	A	E	26	46,995	-3.255	21,420	1,00	43.25	C
ATOM	21823	C4	A	E	26	47,608	-3.999	22,396	1,00	42.80	C
ATOM	21824	in.	A	E	26	44.974	-3,984	22.339	1,00	41,65	N
ATOM	21825	C2	A	E	26	45.721	-4,674	23.223	1.00	49.26	C
ATOM	21826	N3	A	E	26	47,052	-4.750	23,354	1,00	42.69	N
ATOM	21827	C6	A	E	26	45.598	-3,252	21.396	1.00	43,79	C
ATOM	21828	N6	A	E	26	44.897	-2.551	20.474	1.00	48.65	N
ATOM	21829	05'	G	E	27	50,562	-7.907	19,373	1,00	50.89	O
ATOM	21830	C4'	G	E	27	48.900	-9,275	20.403	1.00	55,32	C
ATOM	21831	C3'	G	E	27	48.297	-9,550	19.035	1,00	59,46	C
ATOM	21832	C2'	G	E	27	46,809	-9.426	19,334	1,00	52.05	C
ATOM	21833	P	G	E	27	51.939	-7.136	19.327	1,00	54.23	P
ATOM	21834	OP1	G	E	27	52.966	-8,219	19.245	1,00	63,86	0
ATOM	21835	OP2	G	E	27	51,918	-6.174	18,207	1,00	44.82	0
ATOM	21836	C5'	G	E	27	50,333	-8.851	20,400	1,00	48.46	C
ATOM	21837	04'	G	E	27	48.068	-8,203	20.935	1,00	57,87	0
ATOM	21838	03'	G	E	27	48.690	-10.820	18.526	1.00	59.15	0
ATOM	21839	02'	G	E	27	46,345	-10.583	20,013	1,00	51.72	0
ATOM	21840	CI '	G	E	27	46.800	-8,249	20.329	1.00	52,25	C
ATOM	21841	N9	G	E	27	46.511	-7.004	19.602	1.00	51,27	N
ATOM	21842	C8	G	E	27	47,325	-6.153	18,890	1,00	51,16	C
ATOM	21843	N1	G	E	27	46.665	-5,201	18.279	1.00	47,24	N
ATOM	21844	C5	G	E	27	45.348	-5,487	18.585	1,00	45,04	C
ATOM	21845	C4	G	E	27	45,229	-6.593	19,379	1,00	45.99	C
ATOM	21846	Ml	G	E	27	43.000	-5.407	18.711	1,00	40.24	N
ATOM	21847	C2	G	E	27	42.995	-8,521	19.521	1,00	47,70	C
ATOM	21848	N3	G	E	27	44,110	-7.158	19,891	1,00	47.69	N
ATOM	21849	C6	G	E	27	44.170	-4.826	18.210	1,00	44.33	C
ATOM	21850	06	G	E	27	44.148	-3,850	17.485	1,00	53,13	O
ATOM	21851	N2	G	E	27	41,806	-6.980	19,949	1,00	43.74	N
ATOM	21852	P	A	E	28	48,578	-11.231	16,967	1,00	57.96	P
ATOM	21853	OP1	A	E	28	47.828	-10,334	16.075	1,00	56,24	O
ATOM	21854	OP2	A	E	28	48.146	-12.646	17.063	1.00	61.16	O
ATOM	21855	05'	A	E	28	50,082	-11.220	16,446	1,00	61.41	O
ATOM	21856	C5'	A	E	28	50.921	-10,080	16.592	1.00	62,41	C
ATOM	21857	C4'	A	E	28	52.142	-10.174	15.710	1.00	63.43	C
ATOM	21858	04'	A	E	28	53,088	-11.127	16,263	1,00	65.42	0

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ATOM  21859  C3'   A E  28     51.887 --10.623  14.283  1.00 65.05    C
ATOM  21860  03'   A E  28     52.827  -9.971   13.442  1.00 63.84    O
ATOM  21861  C2'   A E  28     52.226 -12.108   14.331  1.00 62.36    C
ATOM  21862  02'   A E  28     52.581 --12.638  13.081  1.00 65.69    0
ATOM  21863  C1'   A E  28     53.401 -12.106   15.295  1.00 64.34    C
ATOM  21864  N9    A E  28     53.629 -13.355   16.026  1.00 67.64    N
ATOM  21865  C8    A E  28     52.713 -14.160   16.653  1.00 66.36    C
ATOM  21866  N7    A E  28     53.253 -15.189   17.279  1.00 68.23    N
ATOM  21867  C5    A E  28     54.616 -15.045   17.063  1.00 65.56    C
ATOM  21868  C4    A E  28     54.861 -13.912   16.308  1.00 64.39    C
ATOM  21869  N1    A E  28     56.958 -15.405   17.091  1.00 62.90    N
ATOM  21870  C2    A E  28     57.039 -14.282   16.362  1.00 70.68    C
ATOM  21871  N3    A E  28     56.067 -13.469   15.920  1.00 63.98    N
ATOM  21872  C6    A E  28     55.726 -15.815   17.460  1.00 64.91    C
ATOM  21873  N6    A E  28     55.620 -16.918   18.189  1.00 65.70    N
ATOM  21874  P     G E  29     52.414  -8.604   12.735  1.00 66.72    P
ATOM  21875  OP1   G E  29     53.490  -8.054   11.879  1.00 74.17    O
ATOM  21876  OP2   G E  29     51.932  -7.772   13.855  1.00 67.80    O
ATOM  21877  05'   G E  29     51.183  -9.021   11.806  1.00 68.58    O
ATOM  21878  C5'   G E  29     51.334  -9.309   10.423  1.00 63.66    C
ATOM  21879  C4'   G E  29     50.697 -10.632   10.094  1.00 72.88    C
ATOM  21880  04'   G E  29     49.271 -10.482    9.856  1.00 74.06    0
ATOM  21881  C3'   G E  29     51.175 -11.350    8.846  1.00 69.98    C
ATOM  21882  03'   G E  29     52.458 -11.933    8.973  1.00 71.61    0
ATOM  21883  C2'   G E  29     50.066 -12.369    8.641  1.00 73.72    C
ATOM  21884  02'   G E  29     50.208 -13.435    9.567  1.00 77.65    0
ATOM  21885  CI'   G E  29     48.831 -11.550    9.030  1.00 78.42    C
ATOM  21886  N9    G E  29     48.105 -11.046    7.838  1.00 74.99    N
ATOM  21887  C8    G E  29     47.370 -11.826    6.967  1.00 73.86    C
ATOM  21888  N7    G E  29     46.833 -11.166    5.977  1.00 71.41    N
ATOM  21889  C5    G E  29     47.251  -9.862    6.202  1.00 71.59    C
ATOM  21890  C4    G E  29     48.041  -9.773    7.337  1.00 71.06    C
ATOM  21891  N1    G E  29     47.602  -7.586    6.040  1.00 76.52    N
ATOM  21892  C2    G E  29     48.370  -7.597    7.176  1.00 79.95    C
ATOM  21893  N3    G E  29     48.628  -8.691    7.884  1.00 71.81    N
ATOM  21894  C6    G E  29     46.983  -8.676    5.462  1.00 72.14    C
ATOM  21895  06    G E  29     46.318  -8.494    4.437  1.00 67.61    0
ATOM  21896  N2    G E  29     48.856  -6.392    7.536  1.00 88.01    N
ATOM  21897  P     C E  30     53.442 -11.984    7.700  1.00 73.49    P
ATOM  21898  OP1   C E  30     54.623 -12.769    8.141  1.00 75.25    0
ATOM  21899  OP2   C E  30     53.633 -10.635    7.127  1.00 73.01    0
ATOM  21900  05'   C E  30     52.618 -12.787    6.597  1.00 66.74    0
ATOM  21901  C5'   C E  30     52.260 -14.140    6.807  1.00 70.25    C
ATOM  21902  C4'   C E  30     51.355 -14.644    5.720  1.00 75.11    C
ATOM  21903  04'   C E  30     50.143 -13.853    5.673  1.00 77.87    0
ATOM  21904  C3'   C E  30     51.896 -14.550    4.306  1.00 80.50    C
ATOM  21905  03'   C E  30     52.839 -15.568    4.003  1.00 80.79    0
ATOM  21906  C2'   C E  30     50.623 -14.604    3.466  1.00 79.43    C
ATOM  21907  02'   C E  30     50.149 -15.938    3.351  1.00 84.06    0
ATOM  21908  C1'   C E  30     49.642 -13.828    4.349  1.00 76.89    C
ATOM  21909  N1    C E  30     49.473 -12.421    3.911  1.00 74.78    N
ATOM  21910  C2    C E  30     48.654 -12.142    2.804  1.00 77.05    C
ATOM  21911  N3    C E  30     48.495 -10.860    2.409  1.00 75.23    N
ATOM  21912  C4    C E  30     49.110  -9.884    3.061  1.00 73.74    C
ATOM  21913  C5    C E  30     49.944 -10.135    4.187  1.00 75.41    C
ATOM  21914  C6    C E  30     50.095 -11.405    4.576  1.00 73.81    C
ATOM  21915  02    C E  30     48.084 -13.068    2.203  1.00 71.78    0
ATOM  21916  N4    C E  30     48.924  -8.642    2.628  1.00 70.04    N
ATOM  21917  P     u E  31     54.066 -15.261    3.010  1.00 79.33    P
ATOM  21918  OP1   u E  31     54.979 -16.423    3.161  1.00 85.47    0
ATOM  21919  OP2   υ E  31     54.603 -13.892    3.237  1.00 80.53    0
ATOM  21920  05'   u E  31     53.386 -15.241    1.565  1.00 75.03    0
ATOM  21921  C5'   u E  31     52.713 -16.391    1.073  1.00 80.15    C
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ATOM  21922  C4'   u E  31      51.905 --16.112  -0.173  1.00 85.66           c
ATOM  21923  04'   u E  31      50,787 --15.234   0.127  1,00 88.76           O
ATOM  21924  C3'   ʋ E  31      52.605 -15,403  -1..321 1,00 89,15           c
ATOM  21925  03'   u E  31      53.486 --16:224  -2.062  1.00 90.58           0
ATOM  21926  C2'   u E  31      51,427 -14.887  -2,131  1,00 87.95           c
ATOM  21927  02'   ʋ E  31      50.811 -15,954  -2:839  1,00 80,37           0
ATOM  21928  CI '  u E  31      50.482 -14,450  -1.013  1,00 86,06           c
ATOM  21929  N1    u E  31      50,661 -13.020  -0,679  1,00 83.02           N
ATOM  21930  C2    u E  31      49.975 -12,123  -1:460  1,00 87.44           C
ATOM  21931  N3    u E  31      50.160 -10,803  -1.135  1,00 89,45           N
ATOM  21932  C4    u E  31      50,958 -10..305  -0,125  1,00 89.06           C
ATOM  21933  C5    u E  31      51.648 -11.302   0:636  1,00 85.19           C
ATOM  21934  C6    u E  31      51.478 -12,593   0.338  1,00 82,18           c
ATOM  21935  02    u E  31      49.251 -12:481  -2.369  1.00 90.78           0
ATOM  21936  04    u E  31      51,027  -9.088   0,051  1,00 89.98           0
ATOM  21937  P     A E  32      54.754 -15,563  -2:795  1,00 92,11           P
ATOM  21938  OP1   A E  32      55.606 -16:709  -3:167  1.00100.71           0
ATOM  21939  OP2   A E  32      55,315 -14.460  -1,980  1,00 91.52           0
ATOM  21940  05'   A E  32      54.167 -14,916  -4:126  1,00 97,47           0
ATOM  21941  C5'   A E  32      54.035 -15,682  -5.317  1,00103,40           c
ATOM  21942  C4'   A E  32      53,311 -14.906  -6,384  1,00103.70           c
ATOM  21943  04'   A E  32      52.150 -14,278  -5:783  1,00103.83           0
ATOM  21944  CI '  A E  32      51.963 -12,987  -6.320  1,00109,36           c
ATOM  21945  C2'   A E  32      52,970 -12.806  -7,450  1,00112.54           c
ATOM  21946  02'   A E  32      52.380 -13.258  -8:662  1,00113.41           0
ATOM  21947  C3'   A E  32      54.083 -13,746  -7.008  1,00113,66           c
ATOM  21948  03'   A E  32      54,951 -14.142  -8,065  1,00114.39           0
ATOM  21949  N9    A E  32      52,160 -11.999  -5,242  1,00104.59           N
ATOM  21950  C8    A E  32      52.792 -12,162  -4.035  1,00101,60           c
ATOM  21951  N7    A E  32      52.793 -11.083  -3,291  1.00103.79           N
ATOM  21952  C5    A E  32      52,114 -10.145  -4,060  1,00107.85           C
ATOM  21953  C4    A E  32      51.721 -10,700  -5:264  1,00108,52           C
ATOM  21954  Nl    A E  32      51.093  -8:155  -4,822  1.00110.68           N
ATOM  21955  C2    A E  32      50,784  -8.826  -5,937  1,00111.03           C
ATOM  21956  N3    A E  32      51.047 -10,091  -6:255  1,00110,84           N
ATOM  21957  C6    A E  32      51.770  -8,797  -3.847  1,00109,33           c
ATOM  21958  N6    A E  32      52,074  -8.114  -2,742  1,00111.86           N
ATOM  21959  P     G E  33      56.233 -13.243  -8:457  1,00115.95           P
ATOM  21960  OP1   G E  33      56.631 -13,607  -9.841  1,00113,16           O
ATOM  21961  OP2   G E  33      57,213 -13:298  -7,341  1,00103.78           O
ATOM  21962  05'   G E  33      55,683 -11.749  -8,531  1,00119.71           O
ATOM  21963  C5'   G E  33      55.057 -11,258  -9.706  1,00123,34           C
ATOM  21964  C4'   G E  33      54.810  -9:774  -9:621  1.00129.17           c
ATOM  21965  04'   G E  33      53,941  -9.469  -8,497  1,00126.53           0
ATOM  21966  CI '  G E  33      54.276  -8,196  -7.968  1,00128,15           c
ATOM  21967  N9    G E  33      54.682  -8:337  -6:554  1.00123.84           N
ATOM  21968  C8    G E  33      55,261  -9.416  -5,920  1,00119.95           c
ATOM  21969  N1    G E  33      55.494  -9,197  -4.652  1,00118,04           N
ATOM  21970  C5    G E  33      55.049  -7,896  -4.438  1,00120,91           c
ATOM  21971  C4    G E  33      54,552  -7.351  -5,604  1,00123.81           c
ATOM  21972  N3    G E  33      54.026  -6.121  -5:812  1,00126.77           N
ATOM  21973  C2    G E  33      54.015  -5,387  -4.711  1,00126,44           c
ATOM  21974  N2    G E  33      53,527  -4:135  -4,743  1,00127.95           N
ATOM  21975  Nl    G E  33      54.488  -5.833  -3:502  1,00124.48           N
ATOM  21976  C6    G E  33      55.033  -7,097  -3.262  1,00125,50           C
ATOM  21977  06    G E  33      55,429  -7.393  -2,124  1,00127.27           O
ATOM  21978  C2'   G E  33      55,406  -7.627  -8,823  1,00134.54           C
ATOM  21979  02'   G E  33      54.828  -6,863  -9.873  1,00138,27           O
ATOM  21980  C3'   G E  33      56.029  -8:909  -9.362  1.00133.47           c
ATOM  21981  03'   G E  33      56,851  -8.723 -10,496  1,00137.66           0
ATOM  21982  P     A E  34      58.427  -8,505 -10:286  1,00141,07           P
ATOM  21983  0P1   A E  34      58.996  -8:245 -11:634  1.00140.99           0
ATOM  21984  0P2   A E  34      58,947  -9.642  -9,482  1,00139.98           0
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ATOM	21985	05'	A	E	34	58.518	-7.172	-9.405	1.00139.94	O
ATOM	21986	C5'	A	E	34	59,002	-7.183	-8,064	1,00137.58	C
ATOM	21987	C4'	A	E	34	59.936	-6,021	-7.821	1,00139,71	C
ATOM	21988	04'	A	E	34	60.388	-5:526	-9:108	1.00142.05	O
ATOM	21989	C1'	A	E	34	60,465	-4.118	-9,094	1,00139,17	C
ATOM	21990	N9	A	E	34	59.459	-3,589	-10:035	1,00140,95	N
ATOM	21991	C8	A	E	34	58.733	-2,436	-9.891	1,00142,55	C
ATOM	21992	N7	A	E	34	57,917	-2.199	-10,888	1,00144,80	N
ATOM	21993	C5	A	E	34	58.116	-3.265	-11:752	1,00145.72	C
ATOM	21994	C4	A	E	34	59.071	-4,130	-11:246	1,00144,84	C
ATOM	21995	N3	A	E	34	59,505	-5:265	-11,830	1,00145.01	N
ATOM	21996	C2	A	E	34	58.894	-5.470	-12.998	1,00142.38	C
ATOM	21997	N1.	A	E	34	57.962	-4,726	-13.606	1,00144,86	N
ATOM	21998	C6	A	E	34	57.543	-3:593	-12.997	1.00146.85	C
ATOM	21999	N6	A	E	34	56,615	-2.845	-13,600	1,00146.62	N
ATOM	22000	C2'	A	E	34	60.201	-3,654	-7.665	1,00137,04	C
ATOM	22001	02'	A	E	34	61.441	-3:587	-6.974	1.00125.78	O
ATOM	22002	C3'	A	E	34	59,341	-4.794	-7,131	1,00141,53	C
ATOM	22003	03'	A	E	34	59..353	-4,885	-5:713	1,00144,18	O
ATOM	22004	P	A	E	35	58.278	-4,075	-4.823	1,00143,61	P
ATOM	22005	OP1	A	E	35	56,942	-4.678	-5,076	1,00136,24	0
ATOM	22006	OP2	A	E	35	58.795	-3.948	-3:432	1,00131.76	0
ATOM	22007	05'	A	E	35	58.270	-2,606	-5.435	1,00143,93	0
ATOM	22008	C5'	A	E	35	57,448	-1:596	-4,872	1,00141.77	C
ATOM	22009	C4'	A	E	35	56.970	-0:621	-5:917	1,00143.86	C
ATOM	22010	04'	A	E	35	57.316	-1,097	-7.242	1,00145,47	0
ATOM	22011	CI'	A	E	35	56,331	-0:689	-8,169	1,00144.09	C
ATOM	22012	C2'	A	E	35	55,273	0:103	-7,410	1,00143.32	C
ATOM	22013	02'	A	E	35	55.602	1,479	-7.495	1,00143,98	0
ATOM	22014	C3'	A	E	35	55:469	-0:409	-5,990	1.00144.09	C
ATOM	22015	03'	A	E	35	54,992	0.478	-4,998	1,00148.39	0
ATOM	22016	N9	A	E	35	55.765	-1,878	-8:827	1,00143,46	N
ATOM	22017	C8	A	E	35	55.820	-3:189	-8,426	1.00143.15	C
ATOM	22018	N7	A	E	35	55,218	-4.012	-9,251	1,00144,08	N
ATOM	22019	C5	A	E	35	54.738	-3,184	-10:260	1,00145,35	C
ATOM	22020	C4	A	E	35	55.067	-1,866	-10,007	1,00144,10	C
ATOM	22021	N1	A	E	35	53,693	-2.380	-12,222	1,00146,83	N
ATOM	22022	C2	A	E	35	54:088	-1.157	-11:844	1,00146.43	C
ATOM	22023	N3	A	E	35	54.775	-0,795	-10.764	1,00145,75	N
ATOM	22024	C6	A	E	35	54,008	-3:437	-11,437	1,00145.96	C
ATOM	22025	N6	A	E	35	53,611	-4:657	-11,817	1,00144.94	N
ATOM	22026	P	A	E	36	53.505	0,305	-4.417	1,00154,02	P
ATOM	22027	OP1	A	E	36	53:271	-1:147	-4,197	1.00148.18	O
ATOM	22028	OP2	A	E	36	53,334	1.274	-3,301	1,00149.73	O
ATOM	22029	05'	A	E	36	52:566	0,749	-5:623	1,00148,79	O
ATOM	22030	C5'	A	E	36	52:691	2:034	-6:217	1.00150.95	C
ATOM	22031	C4'	A	E	36	51,775	2.163	-7,404	1,00151,52	C
ATOM	22032	04'	A	E	36	52:282	1,356	-8:498	1,00149,40	0
ATOM	22033	CI'	A	E	36	51.211	0,767	-9.205	1,00148,97	C
ATOM	22034	N9	A	E	36	51,331	-0.699	-9,089	1,00147,70	N
ATOM	22035	C8	A	E	36	51:831	-1.422	-8:030	1,00144.54	C
ATOM	22036	N7	A	E	36	51.808	-2,720	-8,224	1,00143,52	N
ATOM	22037	C5	A	E	36	51,257	-2:864	-9,495	1,00145.75	C
ATOM	22038	C4	A	E	36	50:958	-1.624	-10:039	1,00147.32	C
ATOM	22039	N3	A	E	36	50.417	-1,383	-11.249	1,00145,95	N
ATOM	22040	C2	A	E	36	50,186	-2:522	-11,900	1,00143.76	C
ATOM	22041	Nl	A	E	36	50,418	-3.782	-11,509	1,00143.90	N
ATOM	22042	C6	A	E	36	50.962	-3,994	-10.288	1,00144,99	C
ATOM	22043	N6	A	E	36	51:192	-5:255	-9,906	1.00141.62	N
ATOM	22044	C2'	A	E	36	49,909	1.289	-8,596	1,00150.42	C
ATOM	22045	02'	A	E	36	49:507	2,448	-9:312	1,00151,73	O
ATOM	22046	C3'	A	E	36	50:360	1:649	-7.185	1.00151.84	C
ATOM	22047	03'	A	E	36	49,524	2.592	-6,534	1,00156,60	0

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ATOM  22048  P    U E  37    49.346   2;565  -4,932  1,00159.49   P
ATOM  22049  OP1  U E  37    48,055   3.234  -4,628  1,00160.38   O
ATOM  22050  OP2  U E  37    50.587   3,048  -4;273  1,00155,77   O
ATOM  22051  05'  u E  37    49.174   1;022  -4,578  1,00150.11   O
ATOM  22052  C5'  u E  37    47,895   0.412  -4,620  1,00144,76   C
ATOM  22053  C4'  u E  37    47.735  -0,413  -5;866  1,00140,43   C
ATOM  22054  04'  u E  37    48.988  -1,082  -6.159  1,00143,52   O
ATOM  22055  C1'  u E  37    48,744  -2.383  -6,638  1,00137,66   C
ATOM  22056  C2'  u E  37    47.231  -2.538  -6;803  1,00133.79   C
ATOM  22057  02'  u E  37    46.883  -2,135  -8.120  1,00135,00   O
ATOM  22058  C3'  u E  37    46,714  -1;532  -5,782  1,00136.73   C
ATOM  22059  03'  u E  37    45.398  -1,069  -6;035  1,00141.57   O
ATOM  22060  N1.  u E  37    49.324  -3,338  -5.663  1,00134,38   N
ATOM  22061  C2   u E  37    49.500  -4;660  -6;040  1,00129.88   C
ATOM  22062  N3   u E  37    50,056  -5.464  -5,068  1;00125.09   N
ATOM  22063  C4   u E  37    50.457  -5,095  -3;793  1,00124,38   C
ATOM  22064  C5   u E  37    50.251  -3;711  -3,486  1,00127.25   C
ATOM  22065  C6   u E  37    49,713  -2.906  -4,410  1,00132,04   C
ATOM  22066  02   u E  37    49.177  -5,089  -7,140  1,00128,75   0
ATOM  22067  04   u E  37    50.943  -5,941  -3,034  1,00118,09   0
ATOM  22068  P    A E  38    44,133  -2.046  -5,872  1,00139,49   P
ATOM  22069  OP1  A E  38    42.925  -1,189  -5;745  1,00135.96   0
ATOM  22070  OF2  A E  38    44,427  -3,063  -4,824  1,00132,57   0
ATOM  22071  05'  A E  38    44,053  -2;795  -7,273  1,00132.36   0
ATOM  22072  C5'  A E  38    43.116  -3,836  -7;475  1,00129.31   C
ATOM  22073  C4'  A E  38    43.784  -5,120  -7.895  1,00125,39   C
ATOM  22074  04'  A E  38    45,184  -5;131  -7,519  1,00126.60   0
ATOM  22075  CI'  A E  38    45,607  -6,461  -7,299  1,00119.15   C
ATOM  22076  C2'  A E  38    44.380  -7,374  -7.402  1,00118,27   C
ATOM  22077  02'  A E  38    44.379  -7;986  -8,683  1,00118.77   0
ATOM  22078  C3'  A E  38    43,225  -6.377  -7,263  1,00121.03   C
ATOM  22079  03'  A E  38    42;010  -6,770  -7,883  1,00120,80   0
ATOM  22080  N9   A E  38    46;307  -6;554  -6,003  1,00114.42   N
ATOM  22081  C8   A E  38    46,555  -5.521  -5,139  1,00118,88   C
ATOM  22082  N1   A E  38    47,223  -5,875  -4;068  1,00117,42   N
ATOM  22083  C5   A E  38    47.442  -7,234  -4.234  1,00109,86   C
ATOM  22084  C4   A E  38    46,892  -7.670  -5,428  1,00111,43   C
ATOM  22085  M1   A E  38    48;147  -9;465  -3;873  1,00100.53   N
ATOM  22086  C2   A E  38    47.569  -9,747  -5.050  1,00104,40   C
ATOM  22087  N3   A E  38    46,925  -8;936  -5,893  1,00108.76   N
ATOM  22088  C6   A E  38    48,100  -8,186  -3,430  1,00103.62   C
ATOM  22089  N6   A E  38    48.671  -7,887  -2.256  1,00102,77   N
ATOM  22090  P    G E  39    41,331  -8;214  -7,650  1,00126.07   P
ATOM  22091  OP1  G E  39    42,233  -9.297  -8,132  1,00123.51   0
ATOM  22092  OP2  G E  39    40;001  -8,122  -8;.307  1,00125,48   0
ATOM  22093  05'  G E  39    41,033  -8;303  -6;081  1,00116,97   0
ATOM  22094  C5'  G E  39    42,025  -8.679  -5,136  1,00108,81   C
ATOM  22095  C4'  G E  39    42;492 -10,103  -5;312  1,00101,07   C
ATOM  22096  04'  G E  39    43,942 --10,117  -5.290  1,00 99,73   0
ATOM  22097  C3'  G E  39    42,060 -11.058  -4,205  1,00 97,59   C
ATOM  22098  03'  G E  39    40;832 -11,709  -4,506  1,00104.13   0
ATOM  22099  C2'  G E  39    43,246 -12,004  -4.047  1,00 91,72   C
ATOM  22100  02'  G E  39    43,192 -13;061  -4,990  1,00 76.79   0
ATOM  22101  CI'  G E  39    44;415 -11;094  -4;401  1,00 95.77   C
ATOM  22102  N9   G E  39    44.949 -10,373  -3.233  1,00 90,21   N
ATOM  22103  C8   G E  39    44,899  -9;010  -3,058  1,00 90.53   C
ATOM  22104  N7   G E  39    45,449  -8,606  -1,951  1,00 88.46   N
ATOM  22105  C5   G E  39    45.895  -9,782  -1.361  1,00 88,41   C
ATOM  22106  C4   G E  39    45,598 -10;881  -2,142  1,00 87.24   C
ATOM  22107  N1   G E  39    46,845 -11.330   0,083  1,00 82,80   N
ATOM  22108  C2   G E  39    46;497 -12,350  -0;764  1,00 82,05   C
ATOM  22109  N3   G E  39    45,862 -12;179  -1,910  1,00 84.96   N
ATOM  22110  C6   G E  39    46,575  -9.984  -0,136  1,00 82,27   C
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ATOM   22111  06    G E  39      46.930  -y.137    0.688  1.00 78.34           O
ATOM   22112  N2    G E  39      46.842 --13.581  -0.373  1.00 84.82           N
ATOM   22113  P     C E  40      39.677 -11.796  -3..394  1.00 97.38           P
ATOM   22114  OP1   C E  40      39.120 --13.174  -3.397  1.00 89.56           O
ATOM   22115  OP2   C E  40      38.775 -10.622  -3.545  1.00 87.22           O
ATOM   22116  05'   C E  40      40.496 -11.598  -2.047  1.00 94.09           0
ATOM   22117  C5'   C E  40      40.047 -12.158  -0.831  1.00 86.92           C
ATOM   22118  C4'   C E  40      41.094 -13.041  -0.207  1.00 85.7.3           C
ATOM   22119  04'   C E  40      42.428 -12.518  -0.445  1.00 82.26           0
ATOM   22120  C3'   C E  40      41.008 -13.162   1.299  1.00 79.31           C
ATOM   22121  03'   C E  40      40.010 -14.079   1.692  1.00 80.24           0
ATOM   22122  C2'   C E  40      42.422 -13.578   1.675  1.00 76.89           C
ATOM   22123  02'   C E  40      42.633 -14.952   1.392  1.00 77.98           0
ATOM   22124  CI'   C E  40      43.242 -12.754   0.684  1.00 79.74           C
ATOM   22125  Nl    C E  40      43.634 -11.438   1.235  1.00 76.87           N
ATOM   22126  C2    C E  40      44.491 -11.329   2..335  1.00 75.74           C
ATOM   22127  N3    C E  40      44.818 -10.101   2.792  1.00 75.76           N
ATOM   22128  C4    C E  40      44.342  -9.003   2.204  1.00 74.3.3           C
ATOM   22129  C5    C E  40      43.479  -9.084   1.077  1.00 77.18           C
ATOM   22130  C6    C E  40      43.161 -10.306   0.633  1.00 77.32           C
ATOM   22131  02    C E  40      44.932 -12.336   2.900  1.00 76.26           0
ATOM   22132  N4    C E  40      44.712  -7.820   2.700  1.00 70.13           N
ATOM   22133  P     A E  41      38.948 -13.677   2.817  1.00 74.74           P
ATOM   22134  OP1   A E  41      37.869 -14.693   2.786  1.00 73.0.3           0
ATOM   22135  OP2   A E  41      38.639 -12.229   2.694  1.00 75.38           0
ATOM   22136  05'   A E  41      39.757 -13.872   4.170  1.00 74.72           0
ATOM   22137  C5'   A E  41      40.450 -15.079   4.429  1.00 70.99           C
ATOM   22138  C4'   A E  41      41.503 -14.856   5.472  1.00 69.57           C
ATOM   22139  04'   A E  41      42.518 -13.966   4.951  1.00 7.1.14           0
ATOM   22140  C3'   A E  41      41.024 -14.158   6.725  1.00 65.43           C
ATOM   22141  03'   A E  41      40.379 -15.041   7.616  1.00 69.16           0
ATOM   22142  C2'   A E  41      42.309 -13.556   7.273  1.00 66.74           C
ATOM   22143  02'   A E  41      43.096 -14.542   7.917  1.00 62.95           0
ATOM   22144  Cl'   A E  41      43.019 -13.153   5.987  1.00 68.22           C
ATOM   22145  N9    A E  41      42.784 -11.737   5.632  1.00 7.1.61           N
ATOM   22146  C8    A E  41      42.049 -11.238   4.579  1.00 70.18           C
ATOM   22147  N7    A E  41      42.045  -9.927   4.506  1.00 67.35           N
ATOM   22148  C5    A E  41      42.825  -9.538   5.586  1.00 65.02           C
ATOM   22149  C4    A E  41      43.292 -10.640   6.287  1.00 65.94           C
ATOM   22150  Nl    A E  41      43.988  -8.221   7.149  1.00 62.65           N
ATOM   22151  C2    A E  41      44.357  -9.377   7.731  1.00 65.22           C
ATOM   22152  N3    A E  41      44.072 -10.636   7.383  1.00 60.50           N
ATOM   22153  C6    A E  41      43.205  -8.272   6.056  1.00 58.73           C
ATOM   22154  N6    A E  41      42.834  -7.140   5.479  1.00 62.78           N
ATOM   22155  P     A E  42      39.114 -14.558   8.473  1.00 65.29           P
ATOM   22156  OP1   A E  42      38.897 -15.644   9.462  1.00 62.48           O
ATOM   22157  OP2   A E  42      38.031 -14.060   7.580  1.00 62.9.3           O
ATOM   22158  05'   A E  42      39.662 -13.320   9.299  1.00 64.65           O
ATOM   22159  C5'   A E  42      40.475 -13.532  10.443  1.00 61.32           C
ATOM   22160  C4'   A E  42      41.117 -12.249  10.900  1.00 59.42           C
ATOM   22161  04'   A E  42      41.552 -11.490   9.750  1.00 58.05           0
ATOM   22162  C3'   A E  42      40.231 -11.279  11.661  1.00 50.76           C
ATOM   22163  03'   A E  42      40.120 -11.629  13.034  1.00 57.26           0
ATOM   22164  C2'   A E  42      40.949  -9.958  11.458  1.00 54.37           C
ATOM   22165  02'   A E  42      42.026  -9.871  12.374  1.00 5.3.77           0
ATOM   22166  CI'   A E  42      41.533 -10.120  10.052  1.00 55.76           C
ATOM   22167  N9    A E  42      40.811  -9.393   8.982  1.00 55.93           N
ATOM   22168  C8    A E  42      40.012  -9.925   7.999  1.00 58.11           C
ATOM   22169  N7    A E  42      39.539  -y.033   7.153  1.00 58.15           N
ATOM   22170  C5    A E  42      40.071  -7.823   7.593  1.00 55.28           C
ATOM   22171  C4    A E  42      40.864  -8.038   8.7.11  1.00 56.77           C
ATOM   22172  Nl    A E  42      40.611  -5.512   7.795  1.00 58.99           N
ATOM   22173  C2    A E  42      41.338  -5.873   8.859  1.00 56.39           C
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ATOM  22174  N3    A E  42    41.526   -7.086    9.395  1.00 56.51   N
ATOM  22175  C6    A E  42    39.957   -6.486    7.129  1.00 58.53   C
ATOM  22176  N6    A E  42    39.235   -6.105    6.072  1.00 60.64   N
ATOM  22177  P     G E  43    38.732  --11.479   13.840  1.00 52.97   P
ATOM  22178  OP1   G E  43    37.604  -11.800   12.935  1.00 48.29   0
ATOM  221 79 OP2   G E  43    38.838  -12.222   15.098  1.00 54.63   0
ATOM  22180  05'   G E  43    38.706   -9.937   14.243  1.00 54.05   0
ATOM  22181  C5'   G E  43    39.839   -9.313   14.844  1.00 53.45   c
ATOM  22182  C4'   G E  43    39.770   -7.800   14.772  1.00 49.52   c
ATOM  22183  04'   G E  43    39.736   -7.396   13.377  1.00 49.93   0
ATOM  22184  C3'   G E  43    38.541   -7.168   15.420  1.00 49.78   c
ATOM  22185  03'   G E  43    38.875   -5.863   15.888  1.00 50.76   0
ATOM  22186  C2'   G E  43    37.580   -7.036   14.244  1.00 49.19   c
ATOM  22187  02'   G E  43    36.574   -6.057   14.394  1.00 51.47   0
ATOM  22188  CI'   G E  43    38.536   -6.685   13.111  1.00 51.47   c
ATOM  22189  N9    G E  43    38.025   -7.095   11.804  1.00 5.3.48  N
ATOM  22190  C8    G E  43    37.518   -8.333   11.465  1.00 48.94   c
ATOM  22191  N7    G E  43    37.129   -8.379   10.224  1.00 48.01   N
ATOM  22192  C5    G E  43    37.385   -7.106    9.725  1.00 52.18   c
ATOM  22193  C4    G E  43    37.939   -6.302   10.698  1.00 52.14   c
ATOM  22194  N1    G E  43    37.564   -5.215    8.374  1.00 55.78   N
ATOM  22195  C2    G E  43    38.109   -4.511    9.420  1.00 55.87   c
ATOM  22196  N3    G E  43    38.326   -5.016   10.629  1.00 52.45   N
ATOM  22197  C6    G E  43    37.159   -6.546    8.438  1.00 56.80   c
ATOM  22198  06    G E  43    36.678   -7.088    7.435  1.00 56.79   O
ATOM  22199  N2    G E  43    38.438   -3.234    9.159  1.00 62.46   N
ATOM  22200  P     U E  44    39.184   -5.622   17.435  1.00 46.52   P
ATOM  22201  OP1   U E  44    39.755   -6.822   18.054  1.00 51.63   O
ATOM  22202  OP2   U E  44    39.896   -4.327   17.535  1.00 54.04   O
ATOM  22203  05'   U E  44    37.745   -5.585   18.102  1.00 53.25   O
ATOM  22204  C5'   U E  44    36.753   -4.635   17.724  1.00 44.60   C
ATOM  22205  C4'   ʋ E  44    35.537   -4.787   18.601  1.00 42.89   C
ATOM  22206  04'   U E  44    34.657   -5.791   18.026  1.00 39.90   O
ATOM  22207  C3'   U E  44    35.843   -5.256   20.024  1.00 44.60   C
ATOM  22208  03'   ʋ E  44    34.860   -4.733   20.925  1.00 41.76   O
ATOM  22209  C2'   u E  44    35.684   -6.763   19.899  1.00 42.63   c
ATOM  22210  02'   u E  44    35.471   -7.448   21.109  1.00 42.52   0
ATOM  22211  CI'   u E  44    34.482   -6.849   18.951  1.00 45.56   c
ATOM  22212  Nl    u E  44    34.413   -8.115   18.213  1.00 43.61   N
ATOM  22213  C2    u E  44    33.499   -9.078   18.603  1.00 45.58   c
ATOM  22214  N3    u E  44    33.530  -10.272   17.888  1.00 43.58   N
ATOM  22215  C4    u E  44    34.381  -10.546   16.833  1.00 41.27   C
ATOM  22216  C5    u E  44    35.296   -9.513   16.483  1.00 43.74   c
ATOM  22217  C6    u E  44    35.289   -8.361   17.178  1.00 47.88   c
ATOM  22218  02    ʋ E  44    32.743   -8.904   19.526  1.00 44.94   0
ATOM  22219  04    u E  44    34.294  -11.622   16.259  1.00 47.54   0
ATOM  22220  05'   u E  45    36.445   -4.644   22.897  1.00 43.40   0
ATOM  22221  C4'   ʋ E  45    37.427   -6.182   24.493  1.00 41.83   c
ATOM  22222  C3'   u E  45    38.286   -5.184   25.242  1.00 39.42   c
ATOM  22223  C2'   u E  45    39.658   -5.863   25.213  1.00 41.61   c
ATOM  22224  P     u E  45    35.298   -3.804   22.164  1.00 44.21   P
ATOM  22225  OF1   u E  45    34.148   -3.664   23.112  1.00 41.59   0
ATOM  22226  OP2   u E  45    35.969   -2.627   21.608  1.00 38.40   0
ATOM  22227  C5'   u E  45    36.154   -5.634   23.878  1.00 39.84   c
ATOM  22228  04'   u E  45    38.329   -6.690   23.447  1.00 39.32   0
ATOM  22229  03'   u E  45    37.803   -4.894   26.550  1.00 41.19   0
ATOM  22230  02'   u E  45    39.707   -6.948   26.135  1.00 49.65   0
ATOM  22231  C1'   u E  45    39.670   -6.450   23.803  1.00 38.94   c
ATOM  22232  Nl    u E  45    40.257   -5.504   22.825  1.00 43.39   N
ATOM  22233  C2    u E  45    41.598   -5.185   22.903  1.00 44.03   c
ATOM  22234  N3    ʋ E  45    42.052   -4.263   21.986  1.00 42.63   N
ATOM  22235  C4    u E  45    41.330   -3.624   21.004  1.00 42.60   c
ATOM  22236  C5    u E  45    39.955   -3.994   20.986  1.00 46.36   c
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ATOM   22237  C6    U E   45      39.480  -4.888  21.870  1.00 49.02          c
ATOM   22238  02    U E   45      42.337  -5.672  23.735  1.00 45.43          O
ATOM   22239  04    U E   45      41.873  -2.827  20.239  1.00 45.78          0
ATOM   22240  05'   A E   46      39.597  -3.508  27.753  1.00 39.66          0
ATOM   22241  C4'   A E   46      41.550  -4.608  28.694  1.00 38.34          c
ATOM   22242  C3'   A E   46      42.228  -3.365  29.212  1.00 39.13          c
ATOM   22243  C2'   A E   46      43.594  -3.420  28.549  1.00 39.94          c
ATOM   22244  P     A E   46      38.091  -3.454  27.226  1.00 38.63          P
ATOM   22245  OP1   A E   46      37.257  -3.454  28.448  1.00 38.55          0
ATOM   22246  OF2   A E   46      38.107  -2.412  26.130  1.00 32.83          0
ATOM   22247  C5'   A E   46      40.042  -4.531  28.654  1.00 45.14          c
ATOM   22248  04'   A E   46      42.051  -4.737  27.338  1.00 40.61          0
ATOM   22249  03'   A E   46      42.264  -3.327  30.618  1.00 41.16          0
ATOM   22250  02'   A E   46      44.379  -4.400  29.219  1.00 49.57          0
ATOM   22251  CI '  A E   46      43.232  -3.987  27.180  1.00 38.24          c
ATOM   22252  N9    A E   46      43.040  -3.017  26.062  1.00 45.40          N
ATOM   22253  C8    A E   46      41.861  -2.730  25.404  1.00 36.88          c
ATOM   22254  N7    A E   46      41.992  -1.920  24.364  1.00 37.67          N
ATOM   22255  C5    A E   46      43.348  -1.626  24.312  1.00 40.16          c
ATOM   22256  C4    A E   46      44.003  -2.316  25.325  1.00 44.88          c
ATOM   22257  N1    A E   46      45.489  -0.752  23.700  1.00 47.57          N
ATOM   22258  C2    A E   46      45.975  -1.462  24.715  1.00 40.94          c
ATOM   22259  N3    A E   46      45.327  -2.254  25.556  1.00 44.34          N
ATOM   22260  C6    A E   46      44.153  -0.807  23.470  1.00 44.16          C
ATOM   22261  N6    A E   46      43.734  -0.081  22.431  1.00 43.67          N
ATOM   22262  05'   A E   47      43.683  -1.399  31.433  1.00 46.41          O
ATOM   22263  C4'   A E   47      46.073  -1.758  31.358  1.00 39.06          C
ATOM   22264  C3'   A E   47      46.280  -0.290  31.672  1.00 44.64          C
ATOM   22265  C2'   A E   47      47.223   0.190  30.570  1.00 46.59          C
ATOM   22266  P     A E   47      42.176  -1.899  31.355  1.00 45.56          P
ATOM   22267  OP1   A E   47      41.637  -2.123  32.715  1.00 40.95          0
ATOM   22268  OP2   A E   47      41.507  -1.027  30.378  1.00 41.39          0
ATOM   22269  C5'   A E   47      44.737  -2.294  31.807  1.00 46.05          c
ATOM   22270  04'   A E   47      46.150  -1.830  29.922  1.00 37.81          0
ATOM   22271  03'   A E   47      46.718  -0.056  32.999  1.00 55.42          0
ATOM   22272  02'   A E   47      48.577  -0.068  30.886  1.00 45.58          0
ATOM   22273  C1'   A E   47      46.814  -0.699  29.403  1.00 36.79          c
ATOM   22274  N9    A E   47      45.922  -0.034  28.435  1.00 40.00          N
ATOM   22275  C8    A E   47      44.554  -0.095  28.379  1.00 40.29          c
ATOM   22276  N7    A E   47      44.035   0.533  27.342  1.00 37.27          N
ATOM   22277  C5    A E   47      45.109   1.086  26.696  1.00 36.27          c
ATOM   22278  C4    A E   47      46.288   0.725  27.348  1.00 42.41          c
ATOM   22279  Nl    A E   47      46.458   2.242  25.158  1.00 43.47          N
ATOM   22280  C2    A E   47      47.508   1.814  25.886  1.00 41.80          C
ATOM   22281  N3    A E   47      47.537   1.055  26.987  1.00 41.65          N
ATOM   22282  C6    A E   47      45.201   1.881  25.548  1.00 40.69          c
ATOM   22283  N6    A E   47      44.147   2.298  24.821  1.00 39.06          N
ATOM   22284  05'   A E   48      46.627   2.403  32.978  1.00 41.23          O
ATOM   22285  C4'   A E   48      48.276   3.844  32.018  1.00 40.86          c
ATOM   22286  C3'   A E   48      47.443   5.121  32.165  1.00 36.21          c
ATOM   22287  C2'   A E   48      47.565   5.734  30.781  1.00 39.69          c
ATOM   22288  P     A E   48      46.076   1.183  33.807  1.00 41.34          P
ATOM   22289  OP1   A E   48      46.553   1.264  35.192  1.00 39.27          0
ATOM   22290  OP2   A E   48      44.618   1.041  33.604  1.00 41.93          0
ATOM   22291  C5'   A E   48      47.996   2.731  32.992  1.00 38.68          c
ATOM   22292  04'   A E   48      47.987   3.396  30.674  1.00 39.60          0
ATOM   22293  03'   A E   48      47.909   5.971  33.200  1.00 43.19          0
ATOM   22294  02'   A E   48      48.843   6.315  30.622  1.00 41.16          0
ATOM   22295  CI '  A E   48      47.524   4.489  29.895  1.00 43.07          c
ATOM   22296  N9    A E   48      46.166   4.211  29.359  1.00 39.62          N
ATOM   22297  C8    A E   48      45.187   3.368  29.831  1.00 36.45          c
ATOM   22298  N7    A E   48      44.099   3.343  29.065  1.00 40.87          N
ATOM   22299  C5    A E   48      44.358   4.240  28.034  1.00 32.61          c
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ATOM 22300 C4   A E 48  45.631  4.773  28.210 1,00 39.11 C
ATOM 22301 N1   A E 48  44,202  5.592  26,120 1,00 44.21 N
ATOM 22302 C2   A E 48  45.449  6,007  26.413 1.00 43,68 C
ATOM 22303 N3   A E 48  46.237  5.674  27.429 1,00 41.65 N
ATOM 22304 C6   A E 48  43,612  4.689  26,933 1,00 38.70 C
ATOM 22305 N6   A E 48  42.376  4,303  26.605 1,00 38,20 N
ATOM 22306 05'  A E 49  46.802  8,212  32.805 1,00 36,95 O
ATOM 22307 C4'  A E 49  47,607  9.851  31,257 1,00 41.27 C
ATOM 22308 C3'  A E 49  46.396 10.778  31.455 1,00 38.05 C
ATOM 22309 C2'  A E 49  45.974 11,069  30.027 1,00 35,19 C
ATOM 22310 P    A E 49  46,965  7.090  33,909 1,00 44.19 P
ATOM 22311 OP1  A E 49  47.765  7.714  34.978 1,00 45.28 0
ATOM 22312 OP2  A E 49  45.678  6,440  34.257 1,00 40,36 0
ATOM 22313 C5'  A E 49  47.936  8.934  32.395 1,00 37.31 C
ATOM 22314 04'  A E 49  47,270  9.058  30,102 1,00 34.23 0
ATOM 22315 03'  A E 49  46.694 11,930  32.214 1.00 43,85 0
ATOM 22316 02'  A E 49  46.834 12.044  29.479 1,00 35.89 0
ATOM 22317 C1'  A E 49  46,265  9.707  29,346 1,00 41.48 C
ATOM 22318 N9   A E 49  45.081  8,822  29.345 1,00 35,92 N
ATOM 22319 C8   A E 49  44.713  7,930  30.337 1,00 35,25 C
ATOM 22320 N7   A E 49  43,587  7.285  30,056 1,00 40.19 N
ATOM 22321 C5   A E 49  43.203  7.804  28.811 1,00 37.27 C
ATOM 22322 C4   A E 49  44.115  8,743  28.371 1,00 36,19 C
ATOM 22323 Nl   A E 49  42,015  8.222  26,804 1,00 31.83 N
ATOM 22324 C2   A E 49  42.975  9.097  26.528 1,00 35.24 C
ATOM 22325 N3   A E 49  44.047  9,429  27.227 1,00 39,57 N
ATOM 22326 C6   A E 49  42,ill  7.563  27,965 1,00 37.37 C
ATOM 22327 N6   A E 49  41,154  6.681  28,241 1,00 45.42 N
ATOM 22328 05'  U E 50  44.509 13,099  32.719 1,00 36,83 O
ATOM 22329 C4'  U E 50  43.605 14.175  30,756 1,00 38.55 C
ATOM 22330 C3'  U E 50  42,229 14.401  31,395 1,00 40.44 C
ATOM 22331 C2'  U E 50  41.274 13,938  30.305 1.00 36,40 C
ATOM 22332 P    U E 50  45.731 12.383  33.444 1,00 47.45 P
ATOM 22333 OP1  U E 50  46,434 13.424  34,211 1,00 42.35 0
ATOM 22334 OP2  U E 50  45.312 11,147  34.149 1,00 48,12 0
ATOM 22335 C5'  U E 50  44.775 14,023  31.682 1,00 35,40 C
ATOM 22336 04'  U E 50  43,449 12.983  29,975 1,00 38.18 0
ATOM 22337 03'  U E 50  42.013 15.758  31.729 1,00 51.65 0
ATOM 22338 02'  U E 50  41.028 14,996  29.399 1,00 38,56 0
ATOM 22339 CI ' U E 50  42,095 12.839  29,590 1,00 38.02 C
ATOM 22340 Nl   U E 50  41,602 11.479  29,933 1,00 35.86 N
ATOM 22341 C2   U E 50  40.672 10,958  29.074 1,00 40,78 C
ATOM 22342 N3   U E 50  40.172  9.720  29.422 1,00 36.55 N
ATOM 22343 C4   U E 50  40,496  8.979  30,545 1,00 43.01 C
ATOM 22344 C5   U E 50  41.462  9,612  31.402 1.00 38,18 C
ATOM 22345 C6   U E 50  41.966 10.803  31.072 1,00 37.40 C
ATOM 22346 02   U E 50  40,359 11.566  28,061 1,00 38.63 0
ATOM 22347 04   U E 50  39.961  7,868  30.757 1,00 42,69 0
ATOM 22348 P    A E 51  41.581 16,220  33.209 1,00 47,64 P
ATOM 22349 OP1  A E 51  40,129 16.275  33,210 1,00 40.12 0
ATOM 22350 OP2  A E 51  42.237 15.309  34.199 1,00 43.84 0
ATOM 22351 05'  A E 51  42.444 17,544  33.477 1,00 40,14 0
ATOM 22352 C5'  A E 51  42,437 18.687 .32,667 1,00 38.23 C
ATOM 22353 C4'  A E 51  43.239 18.626  31.394 1,00 39.49 C
ATOM 22354 04'  A E 51  42.603 19,581  30.540 1,00 41,15 0
ATOM 22355 C3'  A E 51  44,744 18.992  31,417 1,00 48.16 C
ATOM 22356 03'  A E 51  45,584 17.833  31,264 1,00 43.16 0
ATOM 22357 C2'  A E 51  44.942 19,913  30.213 1,00 47,24 C
ATOM 22358 02'  A E 51  45.434 19.198  29.098 1,00 49.47 0
ATOM 22359 CI ' A E 51  43,531 20.378  29,878 1,00 48.28 C
ATOM 22360 N9   A E 51  43.275 21,794  30.196 1.00 43,77 N
ATOM 22361 C8   A E 51  42.729 22.660  29.289 1,00 42.31 C
ATOM 22362 N7   A E 51  42,598 23.865  29,731 1,00 46.41 N
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ATOM	22363	C5	A	E	51	43.094	23.784	31.017	1.00	43.77	C
ATOM	22364	C4	A	E	51	43,523	22.507	31,326	1,00	41.40	C
ATOM	22365	N1	A	E	51	43.760	24,400	33.212	1.00	48,01	N
ATOM	22366	C2	A	E	51	44.144	23.102	33,360	1.00	41.58	C
ATOM	22367	N3	A	E	51	44,048	22.106	32,488	1,00	44,19	N
ATOM	22368	C6	A	E	51	43.221	24,766	32.014	1.00	44,37	C
ATOM	22369	N6	A	E	51	42.835	26,008	31.801	1,00	42,69	N
ATOM	22370	P	A	E	52	46.997	17.631	32,011	1,00	46,70	P
ATOM	22371	OP1	A	E	52	47.404	16.257	31.592	1,00	55.60	O
ATOM	22372	OF2	A	E	52	46.921	17.927	33.460	1,00	36,44	O
ATOM	22373	05'	A	E	52	48,023	18.641	31,339	1,00	39.30	O
ATOM	22374	C5'	A	E	52	48.407	18.550	29.975	1,00	44.26	C
ATOM	22375	C4'	A	E	52	49.645	19,373	29.694	1,00	45,81	C
ATOM	22376	04'	A	E	52	49.284	20.765	29.524	1.00	52.63	0
ATOM	22377	C3'	A	E	52	50,687	19.374	30,802	1,00	50.21	C
ATOM	22378	03'	A	E	52	51.603	18.307	30.657	1.00	51,85	0
ATOM	22379	C2'	A	E	52	51.363	20.726	30.660	1,00	48.70	C
ATOM	22380	02'	A	E	52	52,377	20.672	29,672	1,00	51,70	0
ATOM	22381	CI'	A	E	52	50.221	21,602	30.165	1.00	48,09	C
ATOM	22382	N9	A	E	52	49.540	22,249	31.300	1,00	51,94	N
ATOM	22383	C8	A	E	52	48,501	21.688	31,998	1,00	47,51	C
ATOM	22384	N7	A	E	52	48.071	22.405	32.987	1,00	45.29	N
ATOM	22385	C5	A	E	52	48.868	23,540	32.942	1,00	48,31	C
ATOM	22386	C4	A	E	52	49,795	23.463	31,917	1,00	51.15	C
ATOM	22387	Ml	A	E	52	49.787	25.658	33.459	1,00	52.87	N
ATOM	22388	C2	A	E	52	50.645	25.448	32.439	1,00	49,52	C
ATOM	22389	N3	A	E	52	50.727	24.400	31,608	1,00	53.72	N
ATOM	22390	C6	A	E	52	48,868	24.705	33,746	1,00	54.27	C
ATOM	22391	N6	A	E	52	48.019	24,875	34.778	1,00	44,75	N
ATOM	22392	05'	G	E	53	53.263	19.132	32.363	1.00	51.75	O
ATOM	22393	C4'	G	E	53	52,917	20.730	34,172	1,00	51.45	C
ATOM	22394	C3'	G	E	53	53.073	21,043	35.656	1.00	49,45	C
ATOM	22395	C2'	G	E	53	51.895	21.972	35.933	1.00	50.33	C
ATOM	22396	P	G	E	53	52,492	17.823	31,893	1,00	53,21	P
ATOM	22397	OP1	G	E	53	53.504	16,884	31..321	1,00	63,21	0
ATOM	22398	OF2	G	E	53	51.608	17,332	32.980	1,00	46,52	0
ATOM	22399	C5'	G	E	53	53,479	19.390	33,744	1,00	49,48	C
ATOM	22400	04'	G	E	53	51.478	20.760	33.945	1,00	48.30	0
ATOM	22401	03'	G	E	53	54.350	21,588	35.964	1,00	50,58	0
ATOM	22402	02'	G	E	53	52,155	23.280	35,450	1,00	52.32	0
ATOM	22403	CI'	G	E	53	50,825	21.354	35,044	1,00	48.54	C
ATOM	22404	N9	G	E	53	50.044	20,314	35.739	1,00	44,38	N
ATOM	22405	C8	G	E	53	49.988	18.992	35.426	1.00	42.49	C
ATOM	22406	N7	G	E	53	49,203	18.300	36,220	1,00	46.90	N
ATOM	22407	C5	G	E	53	48.680	19,217	37.123	1.00	43,03	C
ATOM	22408	C4	G	E	53	49.192	20.476	36.829	1.00	49.11	C
ATOM	22409	N1	G	E	53	47,519	20.290	38,840	1,00	46,90	N
ATOM	22410	C2	G	E	53	48.079	21,478	38.483	1.00	45,04	C
ATOM	22411	N3	G	E	53	48.933	21,633	37.480	1,00	45,06	N
ATOM	22412	C6	G	E	53	47,751	19.079	38,202	1,00	42,49	C
ATOM	22413	06	G	E	53	47.155	18.107	38.663	1,00	40.84	O
ATOM	22414	N2	G	E	53	41.696	22,510	39.246	1,00	47,08	N
ATOM	22415	05'	G	E	54	54,077	22.263	38,391	1,00	50.86	O
ATOM	22416	C4'	G	E	54	53.098	24.229	39.363	1,00	55.89	C
ATOM	22417	C3'	G	E	54	53.540	23,913	40.783	1,00	52,35	C
ATOM	22418	C2'	G	E	54	52,234	24.002	41,562	1,00	57.64	C
ATOM	22419	P	G	E	54	55,014	21.417	37,422	1,00	55.29	P
ATOM	22420	OP1	G	E	54	56.322	22,129	37.350	1,00	58,97	O
ATOM	22421	OP2	G	E	54	54.930	20.023	37.901	1.00	47.03	O
ATOM	22422	C5'	G	E	54	53,969	23.671	38,266	1,00	53.42	C
ATOM	22423	04'	G	E	54	51.776	23,648	39.264	1.00	53,52	0
ATOM	22424	03'	G	E	54	54,527	24.826	41,236	1.00	63.52	0
ATOM	22425	02'	G	E	54	51,888	25.365	41,798	1,00	57,57	0

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ATOM   22426   CI '   G E   54      51..234   23..456   40..550   1 .00  52 .04          C
ATOM   22427   Nl     G E   54      48,,380   20..037   43.,021   1 ,00  48..77          N
ATOM   22428   N9     G E   54      50..896   22.,025   40..719   1 .00  52 ,.30         N
ATOM   22429   C8     G E   54      51..378   20..957   39.,984   1 .00  50..17          C
ATOM   22430   N7     G E   54      50.,860   19. 804   40.,335   1 ,00  46..09          N
ATOM   22431   C5     G E   54      49 .975   20.,113   41 ..339  1 .00  42 ,.55         C
ATOM   22432   C6     G E   54      49..118   19.,290   42..097   1 ,00  46,.55          C
ATOM   22433   06     G E   54      48.,934   18. 085   42.,060   1 ,00  40..94          0
ATOM   22434   C2     G E   54      48..459   21.,382   43 .189   1 ,00  44 .18          C
ATOM   22435   N2     G E   54      47 .658   21.,882   44 .131   1 ,00  52 ,.06         N
ATOM   22436   N3     G E   54      49.,244   22..162   42.,483   1 ,00  47 .65          N
ATOM   22437   C4     G E   54      49..973   21..480   41 .584   1 ,00  49..94          C
ATOM   22438   05 '   C E   55      55. 073    24.,185   43. 643   1 ,00  70 ,81          O
ATOM   22439   C4 '   C E   55      54..208   25..046   45.,716   1 .00  66..91          C
ATOM   22440   C3 '   C E   55      54.,332   24 .016   46.,837   1 ,00  70..99          C
ATOM   22441   C2 '   C E   55      52..880   23.,722   47 .174   1 .00  73,.43          C
ATOM   22442   P      C E   55      55..733   24..385   42..202   1 .00  63..73          P
ATOM   22443   OP1    C E   55      56.,593   25. 582   42.,305   1 ,00  75..51          0
ATOM   22444   OP2    C E   55      56..297   23.,092   41 .752   1 .00  67 ,.13         0
ATOM   22445   C5 '   C E   55      55..332   25.,089   44 .717   1 ,00  70,.84          C
ATOM   22446   04 '   C E   55      53.,032   24 .610   44 ,989   1 ,00  63..47          0
ATOM   22447   03 '   C E   55      55..158   24.,374   47 .949   1 ,00  86..67          0
ATOM   22448   02 '   C E   55      52..283   24.,780   41 .905   1 ,00  82 ,.63         0
ATOM   22449   CI '   C E   55      52.,257   23..741   45.,790   1 ,00  65..91          C
ATOM   224 50  Ml     C E   55      52..211   22..381   45.,203   1 ,00  59..51          N
ATOM   22451   C2     C E   55      51. 278   21.,517   45. 790   1 ,00  59 ,08          C
ATOM   224 52  N3     C E   55      51.,161   20 .249   45.,333   1 ,00  56..11          N
ATOM   22453   C4     C E   55      51.,936   19..809   44 ,337   1 ,00  56..01          C
ATOM   22454   C5     C E   55      52. 903   20.,663   43. 712   1 ,00  55 ,69          C
ATOM   22455   C6     C E   55      53.,007   21..931   44 ,178   1 .00  59..69          C
ATOM   22456   02     C E   55      50.,564   21 .923   46.,727   1 ,00  59..47          0
ATOM   22457   N4     C E   55      51..747   18.,543   43..948   1 .00  48,.08          N
ATOM   22458   05 '   u E   56      54..443   24..729   50..408   1 .00  84 .49          0
ATOM   22459   C4 '   u E   56      52.,249   23 .978   51 ,129    1 ,00  84 .59          C
ATOM   22460   C3 '   υ E   56      51..194   22.,883   51..278   1 .00  83,.42          C
ATOM   22461   C2 '   u E   56      49..887   23.,669   51..370   1 ,00  89,.00          C
ATOM   22462   P      u E   56      54 ,763   25. 510   49.,039   1 ,00  88..97          P
ATOM   224 63  OP1    u E   56      53..596   26.,331   48..637   1 ,00  88..44          0
ATOM   22464   OP2    u E   56      56. 040   26.,229   49. 241   1 ,00  93 ,51          0
ATOM   22465   C5 '   u E   56      53.,562   23..606   50.,481   1 ,00  85..81          C
ATOM   22466   04 '   u E   56      51.,592   24 .986   50.,333   1 ,00  88..01          0
ATOM   22467   03 '   u E   56      51. 388   22.,095   52. 437   1 ,00  85 ,83          0
ATOM   22468   02 '   u E   56      49..605   24..012   52.,720   1 .00  92 .23          0
ATOM   22469   CI '   u E   56      50.,203   24 .950   50.,578   1 ,00  87 .09          C
ATOM   22470   Nl     υ E   56      49 .432   25.,046   49 .312   1 .00  80,.36          N
ATOM   22471   C2     u E   56      49.,119   26..302   48..798   1 .00  89..59          C
ATOM   22472   N3     u E   56      48.,357   26. 298   47 ,639   1 ,00  88..55          N
ATOM   22473   C4     υ E   56      47 .852   25.,194   46..971   1 .00  81 ,82          C
ATOM   22474   C5     u E   56      48..192   23.,971   47 .601   1 ,00  74 ,.71         C
ATOM   22475   C6     u E   56      48.,926   23 .929   48.,715   1 ,00  76..57          C
ATOM   22476   02     u E   56      49..517   27.,344   49..312   1 ,00  91 .95          0
ATOM   22477   04     u E   56      47 .169   25.,292   45..938   1 ,00  87 ,.78         0
ATOM   22478   P      A E   57      51.,653   20 .516   52.,339   1 ,00  93..72          P
ATOM   22479   OP1    A E   57      53..085   20..381   51..944   1 ,00  80..38          0
ATOM   22480   OP2    A E   57      51. 113   19.,876   53. 577   1 ,00  79 ,22          0
ATOM   22481   05 '   A E   57      50.,741   20 .025   51.,123   1 ,00  78..62          0
ATOM   22482   C5 '   A E   57      49.,729   19..043   51.,328   1 ,00  67 .84          C
ATOM   22483   C4 '   A E   57      49. 865   17 ,875   50. .380   1 ,00  62 ,.91         C
ATOM   22484   04 '   A E   57      50.,428   18..331   49..116   1 .00  64 .21          0
ATOM   22485   C3 '   A E   57      50.,767   16..736   50.,857   1 ,00  62 .55          C
ATOM   22486   03 '   A E   57      50..248   15.,504   50...370  1 .00  57 ,.21         0
ATOM   22487   C2 '   A E   57      52..081   17 .039   50..146   1 .00  65..80          C
ATOM   22488   02 '   A E   57      52.,940   15. 937   49.,972   1 ,00  69..67          0
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ATOM   22489   CI '   A  E   57      51..584   17.571   48..813   1.00  59..45          c
ATOM   224 90  N9     A  E   57      52.,554   18..439   48.,160   1,00  57 .90         N
ATOM   224 91  C8     A  E   57      52..877   19.,720   48..526   1.00  57 ,78         C
ATOM   22492   N7     A  E   57      53..793   20..255   47 .763   1.00  60..41         N
ATOM   22493   C5     A  E   57      54 ,093   19. 250   46.,850   1,00  50..72         C
ATOM   22494   C4     A  E   57      53..335   18.,122   47 .079   1.00  53,.33         C
ATOM   22495   Nl     A  E   57      55..044   18.,048   45..057   1,00  55,.30         N
ATOM   22496   C2     A  E   57      54 ,250   17.021   45 ,395   1,00  51 .04         C
ATOM   22497   N3     A  E   57      53..368   16.. 962  46..392   1,00  58..40         N
ATOM   22498   C6     A  E   57      54..987   19.,197   45..783   1,00  51 ,01         c
ATOM   22499   N6     A  E   57      55.,777   20.220   45.,461   1,00  51 .28         N
ATOM   22500   P      G  E   58      49..465   14 .516   51.. 356  1,00  65..53         P
ATOM   22501   OP1    G  E   58      50. 029   14 ,622   52. 726   1,00  65 ,55         O
ATOM   22502   OP2    G  E   58      49..329   13..218   50.. 636  1.00  60..24         O
ATOM   22503   05 '   G  E   58      47 ,997   15..114   51.,443   1,00  61 .70         O
ATOM   22504   C5 '   G  E   58      47 .577   15.,961   52..503   1.00  60,.67         C
ATOM   22505   C4 '   G  E   58      46..250   16..565   52..137   1.00  61 .26         c
ATOM   22506   04 '   G  E   58      46.,467   17.592   51 ,138   1,00  53..52         0
ATOM   22507   C3 '   G  E   58      45..298   15.,576   51..476   1.00  54 ,33         C
ATOM   22508   03 '   G  E   58      44 .496   14 ,885   52..413   1,00  50,.05         0
ATOM   22509   C2 '   G  E   58      44 ,512   16. 438   50.,506   1,00  52 .43         C
ATOM   22510   02 '   G  E   58      43 .495   17..149   51..196   1,00  52 .69         0
ATOM   22511   CI '   G  E   58      45..570   17 ,436   50..069   1,00  51 ,05         c
ATOM   22512   N9     G  E   58      46.,368   16..985   48.,917   1,00  47 ,23         N
ATOM   22513   C8     G  E   58      46..558   15..752   48..350   1,00  52 .57         C
ATOM   22514   N7     G  E   58      47 .403   15.,786   47 .346   1,00  51 ,76         N
ATOM   22515   C5     G  E   58      47 ,807   17 .103   47 ,262   1,00  43..92         C
ATOM   22516   C4     G  E   58      47 ,172   17 .843   48.,226   1,00  50..24         C
ATOM   22517   Nl     G  E   58      48. 781   19.,115   46. 652   1,00  51 ,80         N
ATOM   22518   C2     G  E   58      48.. 097  19..754   47 .653   1.00  55..48         c
ATOM   22519   N3     G  E   58      47 ,258   19..162   48.,483   1,00  53..34         N
ATOM   22520   C6     G  E   58      48..690   17 ,764   46...37 6  1.00  48,.43        C
ATOM   22521   06     G  E   58      49..362   17 .335   45..436   1.00  54 .57         O
ATOM   22522   N2     G  E   58      48.,327   21 .061   47 ,748   1,00  53..77         N
ATOM   22523   P      υ  E   59      44 .476   13.,291   52..419   1.00  52 ,75         P
ATOM   22524   OF1    U  E   59      43..322   12.,787   53..212   1,00  48,.76         O
ATOM   22525   OP2    U  E   59      45 ,869   12 .887   52.,737   1,00  64 .75         O
ATOM   22526   05 '   U  E   59      44 .201   12.. 895  50..903   1,00  51 .99         0
ATOM   22527   C5 '   U  E   59      42 .872   12.,856   50. 413   1,00  51 ,73         C
ATOM   22528   C4 '   U  E   59      42.,837   12 .520   48.,945   1,00  52 .68         C
ATOM   22529   04 '   U  E   59      42.,913   11 .086   48.,776   1,00  53..34         0
ATOM   22530   C3 '   U  E   59      41 .584   12.,911   48. 172   1,00  52 ,93         C
ATOM   22531   03 '   U  E   59      41 .579   14 .297   47 .850   1.00  54 .45         0
ATOM   22532   C2 '   U  E   59      41 ,666   11 .987   46.,963   1,00  50..06         C
ATOM   22533   02 '   υ  E   59      42 .587   12.,510   46..019   1.00  49,.98         0
ATOM   22534   CI '   u  E   59      42..281   10..717   47 .581   1.00  48..90         c
ATOM   22535   N1     u  E   59      41 ,270    9 . 689  47 ,898   1,00  50..86         N
ATOM   22536   C2     υ  E   59      40..870    8 ,919   46..835   1.00  49,.48         C
ATOM   22537   N3     u  E   59      39..925    7 ,979   47 .125   1,00  50,.03         N
ATOM   22538   C4     u  E   59      39.,354    7 .730   48.,337   1,00  50..23         C
ATOM   22539   C5     u  E   59      39..819    8 .563   49..406   1,00  46..94         C
ATOM   22540   C6     u  E   59      40..750    9 ,497   49..159   1,00  50,.39         c
ATOM   22541   02     u  E   59      41 ,325    9 .067   45.,715   1,00  45..79         0
ATOM   22542   04     u  E   59      38..504    6 .837   48..392   1,00  57 .71         0
ATOM   22543   05 '   C  E   60      40. 926   16.,500   46. 831   1,00  48 ,01         0
ATOM   22544   C4 '   c  E   60      41 ,846   18..512   47 ,871   1,00  49 .97         C
ATOM   22545   C3 '   C  E   60      41 ,653   19..319   46.,606   1,00  48..81         C
ATOM   22546   C2 '   C  E   60      42 .943   20.,131   46. 526   1,00  47 ,83         C
ATOM   22547   P      c  E   60      40.. 479  14 .971   46.. 882  1.00  48..27         P
ATOM   22548   OP1    C  E   60      40.,596   14 .383   45.,521   1,00  46..47         0
ATOM   22549   OP2    C  E   60      39 .170   14 ,898   47 .557   1.00  45,.39         0
ATOM   22550   C5 '   c  E   60      40..985   17 .275   48..022   1.00  47 .37         c
ATOM   22551   04 '   c  E   60      43.,258   18. 189   47 ,856   1,00  49..15         0
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ATOM   22552   03'    C E   60      40..489    20..113    46..651    1,00  50..18          O
ATOM   22553   02'    C E   60      42.,915    21.251     47,402     1,00  47.99           O
ATOM   22554   CI'    C E   60      43..958    19.,136    47.072     1,00  44,48           C
ATOM   22555   Nl     C E   60      44.680     18..432    45..996    1,00  46..49          N
ATOM   22556   C2     C E   60      45,649     19.128     45,285     1,00  44.76           C
ATOM   22557   N3     C E   60      46..338    18.,511    44.297     1,00  47,10           N
ATOM   22558   C4     C E   60      46..Ill    17,223     44.033     1,00  48,.65          C
ATOM   22559   C5     C E   60      45,134     16.475     44,742     1,00  45.,37          C
ATOM   22560   C6     C E   60      44.437     17.113     45..701    1,00  48..57          C
ATOM   22561   02     C E   60      45..860    20.,300    45..560    1,00  44,97           0
ATOM   22562   N4     C E   60      46.,819    16..652    43.,054    1,00  43..79          N
ATOM   22563   05'    C E   61      40.778     21..455    44.551     1,00  42.10           0
ATOM   22564   C4'    C E   61      42.113     23.,463    44.320     1,00  39,44           C
ATOM   22565   C3'    C E   61      41.925     23..616    42..829    1,00  44.24           C
ATOM   22566   C2'    C E   61      43.,347    23..857    42.,340    1,00  44.36           C
ATOM   22567   P      C E   61      39.753     20.,499    45..288    1,00  4.3,.90         P
ATOM   22568   OP1    C E   61      38..599    21..377    45..643    1,00  49..28          0
ATOM   22569   OP2    C E   61      39.,466    19.300     44,514     1,00  39..12          0
ATOM   22570   C5'    C E   61      41.008     22.,757    45..059    1,00  40,.57          C
ATOM   22571   04'    C E   61      43..345    22.,718    44.430     1,00  44,58           0
ATOM   22572   03'    C E   61      41,015     24.638     42.,488    1,00  41.48           0
ATOM   22573   02'    C E   61      43.767     25..194    42..577    1,00  43..23          0
ATOM   22574   CI'    C E   61      44.134     22.,932    43..273    1,00  45,.59          C
ATOM   22575   Nl     C E   61      44,417     21..633    42.,638    1,00  40..4.3         N
ATOM   22576   C2     C E   61      45..428    21..544    41.692     1,00  42.46           C
ATOM   22577   N.3    C E   61      45.690     20.,353    41.109     1,00  46,50           N
ATOM   22578   C4     C E   61      44,981     19.269     41,420     1,00  47.75           C
ATOM   22579   C5     C E   61      43.,918    19..334    42.,369    1,00  44.61           C
ATOM   22580   C6     C E   61      43.681     20.,524    42.953     1,00  47,31           C
ATOM   22581   02     C E   61      46..100    22..540    41.410     1,00  43..32          0
ATOM   22582   N4     C E   61      45.,293    18..123    40.,794    1,00  43..77          N
ATOM   22583   05'    G E   62      41.069     24.,519    40..013    1,00  42,18           0
ATOM   22584   C4'    G E   62      42..597    25..546    38..476    1,00  38..60          C
ATOM   22585   C3'    G E   62      41,989     24.957     37.,223    1,00  39..79          C
ATOM   22586   C2'    G E   62      43..207    24.,329    36..536    1,00  39,.17          C
ATOM   22587   P      G E   62      40..062    24.,456    41.225     1,00  37,32           P
ATOM   22588   OP1    G E   62      39.,170    25.663     41,108     1,00  46..04          0
ATOM   22589   OP2    G E   62      39..386    23..157    41.224     1,00  36..49          0
ATOM   22590   C5'    G E   62      41.643     25,751     39.616     1,00  42,92           C
ATOM   22591   04'    G E   62      43.,602    24..564    .38.,866   1,00  42.86           0
ATOM   22592   03'    G E   62      41,345     25..923    36.,401    1,00  42.58           0
ATOM   22593   02'    G E   62      43.942     25,280     35.789     1,00  43,61           0
ATOM   22594   CI'    G E   62      44.066     23..889    37..728    1,00  40..14          C
ATOM   22595   Nl     G E   62      45.,382    19..288    36.,089    1,00  39..73          N
ATOM   22596   N9     G E   62      43..923    22.,449    37..932    1,00  4.3,.47         N
ATOM   22597   C8     G E   62      43..079    21..848    38..804    1,00  42.71           C
ATOM   22598   N7     G E   62      43.,136    20.566     38.,691    1,00  47.85           N
ATOM   22599   C5     G E   62      44.036     20.,331    37..672    1,00  4.1,03          C
ATOM   22600   C6     G E   62      44.463     19.,096    37.119     1,00  43,.88          C
ATOM   22601   06     G E   62      44,095     17.969     37.,466    1,00  44.09           0
ATOM   22602   C2     G E   62      45..827    20..523    35..658    1,00  47.22           C
ATOM   22603   N2     G E   62      46..714    20.,505    34..645    1,00  44,45           N
ATOM   22604   N3     G E   62      45.,416    21..691    3 6,185    1,00  43..77          N
ATOM   22605   C4     G E   62      44.526     21..495    37..177    1,00  37.59           C
ATOM   22606   P      U E   63      39.810     26.,371    36.579     1,00  42,94           P
ATOM   22607   OP1    U E   63      39.,836    27.582     .37,393    1,00  40..37          0
ATOM   22608   OP2    U E   63      38.,889    25..260    36.,857    1,00  39..89          0
ATOM   22609   05'    U E   63      39.395     26.,861    35.139     1,00  42,56           0
ATOM   22610   C5'    U E   63      39..921    28..045    34..563    1,00  38..43          C
ATOM   22611   C4'    U E   63      39.,242    28..338    33.,250    1,00  39..69          C
ATOM   22612   04'    υ E   63      39.655     27.,367    32..257    1,00  4.3,.89         0
ATOM   22613   C3'    U E   63      37..714    28..269    33..285    1,00  43..16          C
ATOM   22614   03'    U E   63      37.,186    29.168     32.,289    1,00  43..94          0
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ATOM  22615  C2'  U E  63     37.460  26.811  32.891  1,00  36.83      C
ATOM  22616  02'  U E  63     36,155  26.492  32,437  1,00  45,10      O
ATOM  22617  CI ' ʋ E  63     38.520  26,626  31:808  1,00  44,35      C
ATOM  22618  Nl   U E  63     38.935  25:224  31:592  1,00  44.59      N
ATOM  22619  C2   U E  63     38,540  24.580  30,438  1,00  42.79      C
ATOM  22620  N3   ʋ E  63     38.997  23,271  30:298  1,00  45,85      N
ATOM  22621  C4   u E  63     39.785  22,579  31:184  1,00  44,03      C
ATOM  22622  C5   u E  63     40,133  23.332  32,360  1,00  50.25      C
ATOM  22623  C6   u E  63     39:724  24,586  32,522  1,00  40.34      C
ATOM  22624  02   u E  63     37.862  25,133  29:585  1,00  33.95      0
ATOM  22625  04   u E  63     40,114  21:411  30,975  1,00  47.47      0
ATOM  22626  05'  u E  64     35:803  30:953  33:424  1,00  41.91      0
ATOM  22627  C4'  u E  64     33.440  31,165  33.821  1,00  42,09      C
ATOM  22628  C3'  u E  64     33:404  32:588  34,378  1,00  41.97      C
ATOM  22629  C2'  u E  64     32,705  32.391  35,712  1,00  38.70      C
ATOM  22630  P    ʋ E  64     37:132  30,768  32:552  1,00  39,73      P
ATOM  22631  OP1  u E  64     36:938  31:397  31:228  1,00  39.87      0
ATOM  22632  OP2  u E  64     38,264  31.219  33,414  1,00  38.08      0
ATOM  22633  C5'  ʋ E  64     34:520  30,872  32:826  1,00  39,65      C
ATOM  22634  04'  u E  64     33.652  30,343  34,986  1,00  37,95      0
ATOM  22635  03'  u E  64     32,753  33.502  33,518  1,00  44,31      0
ATOM  22636  02'  u E  64     31:311  32,204  35:525  1,00  42.20      0
ATOM  22637  CI ' u E  64     33:289  31,057  36.151  1,00  42,27      C
ATOM  22638  Nl   u E  64     34,491  31:249  36,979  1,00  49.29      N
ATOM  22639  C2   u E  64     34:269  31:710  38:260  1,00  48.00      C
ATOM  22640  N.3  u E  64     35.421  31,865  38.987  1,00  46,72      N
ATOM  22641  C4   u E  64     36,720  31:642  38,548  1,00  47.34      C
ATOM  22642  C5   u E  64     36,850  31:180  37,198  1,00  44.25      C
ATOM  22643  C6   u E  64     35.750  30,996  36.473  1,00  44,31      C
ATOM  22644  02   u E  64     33:147  31:916  38,707  1,00  46.78      0
ATOM  22645  04   u E  64     37,658  31:844  39,320  1,00  49.11      0
ATOM  22646  05'  A E  65     33:.349  35,792  34:404  1,00  48,59      0
ATOM  22647  C4'  A E  65     32:367  36:374  36:565  1,00  46.16      C
ATOM  22648  C3'  A E  65     33,331  37.547  36,723  1,00  51.97      C
ATOM  22649  C2'  A E  65     33.749  37,426  38:178  1,00  50,42      C
ATOM  22650  P    A E  65     33:459  34,882  33.087  1,00  42,17      P
ATOM  22651  OP1  A E  65     32,675  35.386  31,947  1,00  48.18      0
ATOM  22652  OP2  A E  65     34:882  34.637  32:769  1,00  50.95      0
ATOM  22653  C5'  A E  65     32.143  35,845  35.169  1,00  43,34      C
ATOM  22654  04'  A E  65     32,901  35:.345  37,435  1,00  47.21      0
ATOM  22655  03'  A E  65     32,714  38.793  36,442  1,00  52.22      0
ATOM  22656  02'  A E  65     32.683  37,880  38.998  1,00  52,26      0
ATOM  22657  CI ' A E  65     33:848  35:908  38:330  1,00  47.13      C
ATOM  22658  N9   A E  65     35,184  35.428  37,926  1,00  49.05      N
ATOM  22659  C8   A E  65     35:432  34,755  36:754  1,00  47,67      C
ATOM  22660  N7   A E  65     36:681  34:464  36:549  1,00  49.55      N
ATOM  22661  C5   A E  65     37,324  34.970  37,658  1,00  52.33      C
ATOM  22662  C4   A E  65     36:427  35,582  38:514  1,00  50,10      C
ATOM  22663  Nl   A E  65     39.024  35,561  39.166  1,00  57,37      N
ATOM  22664  C2   A E  65     38,056  36.122  39,897  1,00  48.65      C
ATOM  22665  N3   A E  65     36:750  36.184  39:669  1,00  52.15      N
ATOM  22666  C6   A E  65     38.685  34,960  38.016  1,00  58,93      C
ATOM  22667  N6   A E  65     39,637  34:395  37,269  1,00  55.86      N
ATOM  22668  P    U E  66     33:517  39.961  35:683  1,00  58.08      P
ATOM  22669  OP1  U E  66     32.731  41,201  35.932  1,00  60,45      O
ATOM  22670  OP2  U E  66     33,894  39.528  34,324  1,00  52.28      O
ATOM  22671  05'  U E  66     34,875  40.143  36,485  1,00  59.94      O
ATOM  22672  C5'  U E  66     34.938  40,996  37.614  1,00  56,45      C
ATOM  22673  C4'  U E  66     36:354  41:165  38:090  1,00  57.89      C
ATOM  22674  04'  U E  66     36,934  39.862  38:327  1,00  61.77      0
ATOM  22675  C3'  ʋ E  66     37:316  41,819  37:113  1,00  58,07      C
ATOM  22676  03'  u E  66     37:231  43:229  37.112  1,00  60.04      0
ATOM  22677  C2'  u E  66     38,669  41.304  37,580  1,00  61.69      C
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ATOM   22678   02 '   U E   66       39..133   42..047   38..696   1 .00   62 .25          O
ATOM   22679   CI '   U E   66       38,,317   39..896   38.,051   1 ,00   60..83          C
ATOM   22680   Nl     υ E   66       38..630   .38.,862  37..042   1 .00   59,.18          N
ATOM   22681   C2     u E   66       39..935   38.,410   36..993   1 .00   61 .88          C
ATOM   22682   N3     u E   66       40.,166   37. 442   36.,046   1 ,00   64 .10          N
ATOM   22683   C4     υ E   66       39 .259   3 6 ,889  35..166   1 .00   65,.93          C
ATOM   22684   C5     u E   66       37 .924   37.,416   35..284   1 ,00   59,.68          C
ATOM   22685   C6     u E   66       37.,662   38. 355   36.,206   1 ,00   58..78          C
ATOM   22686   02     u E   66       40 .820   38.,835   37.,726   1 ,00   59..07          0
ATOM   22687   04     u E   66       39..641   36.,012   34..377   1 ,00   63,.52          0
ATOM   22688   05 '   c E   67       39.,004   43..604   .35.,398  1 ,00   60..10          0
ATOM   22689   C4 '   c E   67       41 .277   44 .124   35.,072   1 ,00   69..04          C
ATOM   22690   C3 '   c E   67       40. 953   44 ,815   33. 761   1 ,00   7.3 ,57         C
ATOM   22691   C2 '   c E   67       41 .819   44 ,068   32.,742   1 .00   75..96          C
ATOM   22692   P      c E   67       37.,531   44 .035   35.,767   1 ,00   64 .03          P
ATOM   22693   OP1    c E   67       37..534   45.,482   36..070   I .00   78,.96          0
ATOM   22694   OP2    c E   67       36..646   43 ,532   34..675   1 .00   60..49          0
ATOM   22695   C5 '   c E   67       40.,135   44 .146   36.,040   1 ,00   61 .41          C
ATOM   22696   04 '   c E   67       41 .564   42.,745   34..705   I .00   75,.39          0
ATOM   22697   03 '   c E   67       41 .186   46.,214   33..862   1 ,00   76 ,35          0
ATOM   22698   02 '   c E   67       43.,152   44 .551   32.,738   1 ,00   76..25          0
ATOM   22699   CI '   c E   67       41 .828   42.,646   33.,322   1 ,00   77 .35          C
ATOM   22700   Nl     c E   67       40..812   41 ,759   32..680   1 ,00   75,.79          N
ATOM   227 01  C2     c E   67       40.,203   40..696   .3.3.,377 1 ,00   71 .8.3         C
ATOM   22702   N3     c E   67       39.,295   39..911   32.,731   1 ,00   72 .98          N
ATOM   22703   C4     c E   67       38. 987   40.,130   31. 441   1 ,00   70 ,41          C
ATOM   22704   C5     c E   67       39.,600   41 .182   .30.,698  1 ,00   66..11          C
ATOM   22705   C6     c E   67       40.,493   41 .947   31.,351   1 ,00   73..17          C
ATOM   22706   02     c E   67       40. 481   40.,4 92  34. 571   1 ,00   76 ,14          0
ATOM   22707   N4     c E   67       38.,088   39.,337   30.,839   1 .00   70..41          N
ATOM   22708   05 '   A E   68       41 ,140   47 .125   31.,578   1 ,00   69..20          0
ATOM   22709   C4 '   A E   68       42 .861   48.,024   30..214   I .00   48,.30          C
ATOM   22710   C3 '   A E   68       44 .190   48.,737   30..196   1 .00   49..02          C
ATOM   22711   C2 '   A E   68       43.,960   49. 880   29.,219   1 ,00   49..72          C
ATOM   22712   P      A E   68       40...387  47 ,276   32..962   I .00   75,.60          P
ATOM   22713   OF1    A E   68       40..645   48.,649   33..492   1 ,00   68,.69          0
ATOM   22714   OP2    A E   68       38.,957   46. 890   32.,802   1 ,00   74 .53          0
ATOM   22715   C5 '   A E   68       42..538   47 ,324   31.,494   1 ,00   49..13          C
ATOM   22716   04 '   A E   68       41 .879   49.,061   29. 997   1 ,00   47 ,56          0
ATOM   22717   03 '   A E   68       45.,241   47 .874   29.,828   1 ,00   55..31          0
ATOM   22718   02 '   A E   68       44 ,114   49..481   27.,873   1 ,00   48..93          0
ATOM   22719   CI '   A E   68       42 .489   50.,204   29. 464   1 ,00   51 ,10          C
ATOM   22720   Nl     A E   68       43.,687   55.,033   30.,448   1 .00   52 .72          N
ATOM   22721   N9     A E   68       42.,320   51..305   30.,422   1 ,00   42 .90          N
ATOM   22722   C8     A E   68       41 .623   51.,337   31..602   I .00   50,.76          C
ATOM   22723   N7     A E   68       41 .667   52.,499   32..218   1 .00   46..35          N
ATOM   22724   C5     A E   68       42.,465   53. 266   31.,382   1 ,00   46..8.3         C
ATOM   22725   C6     A E   68       42 .906   54.,591   31..450   I .00   52 ,26          C
ATOM   22726   N6     A E   68       42..614   55.,443   32..437   1 ,00   47 ,28          N
ATOM   22727   C2     A E   68       44 ,002   54. 227   29.,433   1 ,00   47 .73          C
ATOM   22728   N3     A E   68       43 .633   52.,967   29.,250   1 ,00   50..10          N
ATOM   22729   C4     A E   68       42..868   52.,548   30.. 277  1 ,00   48,.25          C
ATOM   22730   P      A E   69       46.,576   47 .789   .30.,703  1 ,00   50..9.3         P
ATOM   22731   OP1    A E   69       47 .482   46..838   29.,984   1 ,00   51 .78          O
ATOM   22732   OP2    A E   69       46. 225   47 ,545   32. 118   1 ,00   45 ,63          O
ATOM   22733   05 '   A E   69       47 ,195   49 .247   .30.,556  1 ,00   49 .02          O
ATOM   227 34  C5 '   A E   69       47 ,657   49.. 717  29.,305   1 ,00   49..69          C
ATOM   22735   C4 '   A E   69       48. 086   51 ,151   29. 412   1 ,00   58 ,03          C
ATOM   22736   04 '   A E   69       46.,926   52.,004   29.,617   1 .00   49..94          0
ATOM   227 37  C3 '   A E   69       48.,984   51.. 471  30.,588   1 ,00   54 .96          C
ATOM   22738   03 '   A E   69       50...337  51.,112   30...34 3 I .00   6.3,.92         0
ATOM   22739   C2 '   A E   69       48..756   52.,966   30..759   1 .00   55..06          C
ATOM   22740   02 '   A E   69       49.,456   53. 676   29.,753   1 ,00   56..85          0
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ATOM  22741  CI '  A E  69    47.261  53.075  30.459  1,00 49.96      c
ATOM  22742  N9    A E  69    46,435  52.965  31,671  1,00 47.16      N
ATOM  22743  C8    A E  69    45.748  51,866  32.108  1.00 49,60      c
ATOM  22744  N7    A E  69    45.089  52.064  33.234  1,00 52.85      N
ATOM  22745  C5    A E  69    45,360  53.384  33,547  1,00 51.55      c
ATOM  22746  C4    A E  69    46.186  53,951  32.591  1.00 52,32      c
ATOM  22747  Nl    A E  69    45.440  55,461  34.648  1,00 58,37      N
ATOM  22748  C2    A E  69    46,225  55.882  33,645  1,00 53.96      c
ATOM  22749  N3    A E  69    46.650  55.219  32.579  1,00 57.38      N
ATOM  22750  C6    A E  69    44.974  54,200  34.622  1,00 53,50      c
ATOM  22751  N6    A E  69    44,195  53.799  35,621  1,00 54.57      N
ATOM  22752  P     C E  70    51.274  50.553  31.526  1,00 61.77      P
ATOM  22753  OP1   C E  70    52.592  50,256  30.930  1,00 62,18      O
ATOM  22754  OP2   c E  70    50.536  49.486  32.245  1,00 60.20      O
ATOM  22755  05'   C E  70    51,492  51.815  32,472  1,00 56.07      O
ATOM  22756  C5'   C E  70    52.035  53,013  31.939  1.00 60,49      c
ATOM  22757  C4'   c E  70    51.894  54.157  32.905  1,00 67.36      c
ATOM  22758  04'   C E  70    50,497  54.531  33,048  1,00 65.76      0
ATOM  22759  C3'   C E  70    52.335  53,867  34.328  1.00 71,13      c
ATOM  22760  03'   c E  70    53.740  53,911  34.476  1,00 76,95      0
ATOM  22761  C2'   c E  70    51,582  54.928  35,123  1,00 68.52      c
ATOM  22762  02'   c E  70    52.206  56.196  35.002  1,00 67.97      0
ATOM  22763  CI '  c E  70    50.254  54,970  34.369  1,00 61,09      c
ATOM  22764  Nl    c E  70    49,277  54.062  34,995  1,00 60.57      N
ATOM  22765  C2    c E  70    48.576  54.562  36.088  1,00 63.54      c
ATOM  22766  N3    c E  70    47.678  53,760  36.712  1,00 65,52      N
ATOM  22767  C4    c E  70    47,478  52.510  36,288  1,00 59.37      c
ATOM  22768  C5    c E  70    48,190  51.978  35,176  1,00 56.98      c
ATOM  22769  C6    c E  70    49.075  52,779  34.563  1,00 57,98      c
ATOM  22770  02    c E  70    48.797  55.732  36.445  1,00 65.86      0
ATOM  22771  N4    c E  70    46,578  51.774  36,939  1,00 56.26      N
ATOM  22772  P     u E  71    54.450  53,323  35.790  1.00 79,61      P
ATOM  22773  OP1   u E  71    53.877  52.027  36.227  1,00 79.04      0
ATOM  22774  OP2   u E  71    55,896  53.426  35,482  1,00 84.40      0
ATOM  22775  05'   u E  71    54.085  54,367  36.924  1.00 78,11      0
ATOM  22776  C5'   u E  71    54.441  54,093  38.260  1,00 84,55      c
ATOM  22777  C4'   u E  71    53,916  55.134  39,204  1,00 86.44      c
ATOM  22778  04'   u E  71    52.543  55.457  38.874  1,00 83.64      0
ATOM  22779  C1'   u E  71    51.776  55,567  40.049  1,00 83,88      c
ATOM  22780  C2'   u E  71    52,728  55.486  41,236  1,00 92.33      c
ATOM  22781  02'   u E  71    53,154  56.801  41,562  1,00 95.07      0
ATOM  22782  C3'   u E  71    53.869  54,675  40.647  1,00 93,33      c
ATOM  22783  03'   u E  71    55.103  54.874  41.292  1,00 97.95      0
ATOM  22784  Nl    u E  71    50,787  54.473  40,028  1,00 80.54      N
ATOM  22785  C2    u E  71    49.891  54,323  41.066  1.00 85,00      c
ATOM  22786  N3    u E  71    49.010  53.285  40.896  1,00 82.05      N
ATOM  22787  C4    u E  71    48,922  52.416  39,833  1,00 79.35      c
ATOM  22788  C5    u E  71    49.882  52,646  38.802  1.00 77,11      c
ATOM  22789  C6    u E  71    50.753  53,646  38.931  1,00 76,67      c
ATOM  22790  02    u E  71    49,867  55.033  42,059  1,00 88.38      0
ATOM  22791  04    u E  71    48.061  51.534  39.844  1,00 80.16      0
ATOM  22792  P     u E  72    56.036  53,621  41.606  1,00 97,20      P
ATOM  22793  OP1   u E  72    57,433  54.102  41,487  1,00105.98      0
ATOM  22794  OP2   u E  72    55.604  52.468  40.779  1,00102.31      0
ATOM  22795  05'   u E  72    55.690  53,300  43.126  1,00106,19      0
ATOM  22796  C5'   u E  72    55,572  54.357  44,065  1,00108.78      c
ATOM  22797  C4'   u E  72    54,595  54.023  45,161  1,00111,50      c
ATOM  22798  04'   u E  72    53.235  54,157  44.680  1,00110,53      0
ATOM  22799  CI '  u E  72    52.404  53.225  45.351  1,00115.27      c
ATOM  22800  C2'   u E  72    53,278  52.472  46,352  1,00118.31      c
ATOM  22801  02'   u E  72    53.256  53,168  47.590  1.00116,24      0
ATOM  22802  C3'   u E  72    54.635  52.601  45.691  1,00118.77      c
ATOM  22803  03'   u E  72    55,709  52.335  46,560  1,00123.53      0
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ATOM    22804    Nl     U  E   72         51..809    52..292    44.368     1.00107..06            N
ATOM    22805    C2     U  E   72         50,,747    51..539    44,823     1,00109..81            C
ATOM    22806    N3     U  E   72         50..209    50.,668    43.920     1.00109,.98            N
ATOM    22807    C4     u  E   72         50..622    50.,475    42.,628    1.00105..50            C
ATOM    22808    C5     u  E   72         51,734     51. 282    42.,224    1,00102..56            C
ATOM    22809    C6     U  E   72         52..283    52.,142    43.089     1.00103,.01            C
ATOM    22810    02     u  E   72         50..298    51.,635    45..947    1,00112,.39            0
ATOM    22811    04     u  E   72         50.,020    49. 650    41,946     1,00107..02            0
ATOM    22812    P      G  E   73         56..398    50.,890    46.,500    1,00132..81            P
ATOM    22813    OF1    G  E   73         57..399    50.,818    47.593     1,00139,.58            0
ATOM    22814    OP2    G  E   73         56.,824    50..679    45.,091    1,00126..38            0
ATOM    22815    05'    G  E   73         55..217    49..869    46.,847    1,00136..77            0
ATOM    22816    C5'    G  E   73         54. 891    49.,561    48. 198    1,00137 ,96            C
ATOM    22817    C4'    G  E   73         53..806    48.,512    48..319    1.00140..59            C
ATOM    22818    04'    G  E   73         52.,691    48..842    47,450     1,00136..93            0
ATOM    22819    CI'    G  E   73         52..079    47,656     46..982    1,00137,.75            C
ATOM    22820    N9     G  E   73         52..216    47,595     45..518    1.00133..10            N
ATOM    22821    C8     G  E   73         53.,250    48. 065    44,743     1,00130..05            C
ATOM    22822    N1     G  E   73         53..084    47,823     43..472    1.00128,.73            N
ATOM    22823    C5     G  E   73         51..875    47,141     43.417     1,00130,.10            C
ATOM    22824    C4     G  E   73         51,329     46. 985    44,672     1,00131.,37            C
ATOM    22825    N3     G  E   73         50..174    46.,386    45.,038    1,00131..49            N
ATOM    22826    C2     G  E   73         49..524    45.,900    43..993    1,00132,.77            C
ATOM    22827    N2     G  E   73         48.,354    45..269    44,172     1,00135..54            N
ATOM    22828    Ml     G  E   73         49..982    45..998    42.,698    1,00132..17            N
ATOM    22829    C6     G  E   73         51.172     46.,616    42.307     1,00129,.90            C
ATOM    22830    06     G  E   73         51.,504    46..659    41,115     1,00130..88            0
ATOM    22831    C2'    G  E   73         52.,798    46..475    47,635     1,00141 .41            C
ATOM    22832    02'    G  E   73         52. 122    46.,140    48. 839    1,00142 ,46            0
ATOM    22833    C3'    G  E   73         54..165    47,085     47,921     1.00144..01            C
ATOM    22834    03'    G  E   73         54.,901    46..384    48.,912    1,00150..12            0
ATOM    22835    P      A  E   74         56..159    45.,467    48..496    1.00155,.47            P
ATOM    22836    OP1    A  E   74         56..596    44,713     49..701    1.00157..01            0
ATOM    22837    OP2    A  E   74         57,137     46. 318    47,771     1.00149..45            0
ATOM    22838    05'    A  E   74         55..558    44,429     47.446     1.00154,.48            0
ATOM    22839    C5'    A  E   74         56..352    43.,378    46..910    1,00154,.39            C
ATOM    22840    C4'    A  E   74         55.,616    42.064     46.,960    1,00154..54            C
ATOM    22841    04'    A  E   74         55..647    41,544     48.,318    1,00156..22            0
ATOM    22842    CI'    A  E   74         54. 397    40.,975    48. 648    1,00155,.90            C
ATOM    22843    N9     A  E   74         53.,782    41.808     49.,704    1,00156..84            N
ATOM    22844    C8     A  E   74         54.,410    42..802    50.,419    1,00155..62            C
ATOM    22845    N7     A  E   74         53. 648    43.,395    51. 303    1,00155,.47            N
ATOM    22846    C5     A  E   74         52..429    42.,747    51..167    1.00154..82            C
ATOM    22847    C4     A  E   74         52.,491    41.765     50.,190    1,00154..92            C
ATOM    22848    N.3    A  E   74         51..486    40.,954    49.810     1,00152,.44            N
ATOM    22849    C2     A  E   74         50..385    41,207     50..512    1.00151..27            C
ATOM    22850    N1     A  E   74         50.,177    42.117     51,472     1,00150..50            N
ATOM    22851    C6     A  E   74         51..203    42.,918    51..832    1.00151,.05            C
ATOM    22852    N6     A  E   74         51..012    43.,825    52..792    1,00149,.08            N
ATOM    22853    C2'    A  E   74         53.,557    40. 948    47,372     1,00154..80            C
ATOM    22854    02'    A  E   74         53..836    39.,740    46.,681    1,00154..06            O
ATOM    22855    C3'    A  E   74         54..133    42.,135    46..618    1,00153,.53            C
ATOM    22856    03'    A  E   74         53.,874    42.103     45.,224    1,00152..10            0
ATOM    22857    P      G  E   75         52..544    42..788    44,639     1,00146..90            P
ATOM    22858    OP1    G  E   75         52. 334    44,038     45. 411    1,00145 ,25            0
ATOM    22859    OP2    G  E   75         52.,643    42.840     43.,156    1,00143..46            0
ATOM    22860    05'    G  E   75         51.,374    41.772     45.,019    1,00148..33            0
ATOM    22861    C5'    G  E   75         50. 022    42.,066    44.693     1,00147 ,11            C
ATOM    22862    C4'    G  E   75         49..053    41,271     45.,535    1.00148..16            C
ATOM    22863    04'    G  E   75         49.,452    41.325     46.,929    1,00150..26            0
ATOM    22864    CI'    G  E   75         48...310   41,355     47.760     1.00148,.94            C
ATOM    22865    N9     G  E   75         48..328    42.,611    48..534    1.00148..88            N
ATOM    22866    C8     G  E   75         48.,941    43. 791    48.,186    1,00147..01            C
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ATOM	22867	N7	G	E	75	48..785	44.729	49..080	1.00148..07	N
ATOM	22868	C5	G	E	75	48,,027	44.131	50,,081	1,00148..04	C
ATOM	22869	C4	G	E	75	47.731	42.,824	49.753	1.00148,.42	C
ATOM	22870	N3	G	E	75	47.027	41.914	50.,460	1.00147 .96	N
ATOM	22871	C2	G	E	75	46,,581	42.415	51,600	1,00147.,9.3	C
ATOM	22872	N2	G	E	75	45..857	41,643	52..422	1.00147,.61	N
ATOM	22873	Nl	G	E	75	46..809	43,,706	52..015	1,00146,.03	N
ATOM	22874	C6	G	E	75	47,538	44.659	51,308	1,00144.,57	C
ATOM	22875	06	G	E	75	47.685	45.,797	51.,772	1,00139..39	O
ATOM	22876	C2'	G	E	75	47.076	41,245	46..865	1,00147,13	C
ATOM	22877	02'	G	E	75	46.,718	39.875	46.,765	1,00148..14	0
ATOM	22878	C3'	G	E	75	47.613	41.768	45.,537	1,00148..27	C
ATOM	22879	03'	G	E	75	46.878	41,323	44.408	1,00150,.53	0
ATOM	22880	P	A	E	76	45..722	42..237	43.,759	1.00150..69	P
ATOM	22881	OP1	A	E	76	46,,335	43..489	43,,238	1,00144 .97	0
ATOM	22882	OP2	A	E	76	44.913	41,381	42.855	1.00146,.82	0
ATOM	22883	05'	A	E	76	44.791	42..603	44,994	1.00147 .34	0
ATOM	22884	C5'	A	E	76	43,,386	42.719	44,849	1,00143.,76	C
ATOM	22885	C4'	A	E	76	42.683	42.,270	46..101	1.0014.3,.72	C
ATOM	22886	04'	A	E	76	43..653	42,,083	47.168	1,00146,.91	0
ATOM	22887	C1'	A	E	76	43,,084	42.460	48,,405	1,00143.,60	C
ATOM	22888	N9	A	E	76	43.835	43.,606	48..957	1,00142..79	N
ATOM	22889	C8	A	E	76	43..715	44,107	50..227	1,00143,.64	C
ATOM	22890	N7	A	E	76	44,481	45..142	50.,470	1,00143..76	N
ATOM	22891	C5	A	E	76	45..150	45..352	49..273	1,00143..13	C
ATOM	22892	C4	A	E	76	44.757	44,418	48..329	1,0014.3,.50	C
ATOM	228 93	N3	A	E	76	45.,215	44..336	47,069	1,00143..20	N
ATOM	22894	C2	A	E	76	46,,120	45..276	46,,812	1,00140..20	C
ATOM	22895	Nl	A	E	76	46.585	46,,240	47.616	1,00140,09	N
ATOM	22896	C6	A	E	76	46..113	46.,305	48.,881	1.00141..86	C
ATOM	22897	N6	A	E	76	46,,583	47.264	49,,684	1,00140..53	N
ATOM	22898	C2'	A	E	76	41.622	42.,814	48..145	1.00144,.26	C
ATOM	22899	02'	A	E	76	40..851	41.628	48..278	1.00145..52	O
ATOM	22900	C3'	A	E	76	41,683	43.249	46,,689	1,00141.,88	C
ATOM	22901	03'	A	E	76	40..426	43.,236	46..032	1.0014.3,.83	O
ATOM	22902	P	A	E	77	39..703	44,617	45..624	1,00142,.34	P
ATOM	22903	OP1	A	E	77	38,,372	44.667	46,,290	1,00130.,82	0
ATOM	22904	OP2	A	E	77	39..796	44,757	44,144	1,00130..87	0
ATOM	22905	05'	A	E	77	40.623	45,752	46.266	1,00140,99	0
ATOM	22906	C5'	A	E	77	40.,351	46..295	47,553	1,00136..60	C
ATOM	22907	C4'	A	E	77	41,461	47.217	47,984	1,00134..19	C
ATOM	22908	04'	A	E	77	42.732	46,,638	47.595	1,00136,.93	0
ATOM	22909	CI'	A	E	77	43..616	47.647	47,162	1.00132..46	C
ATOM	22910	C2'	A	E	77	42,,924	48..991	47,358	1,00126..45	C
ATOM	22911	02'	A	E	77	43..288	49.,501	48..630	1.00125,.36	0
ATOM	22912	C3'	A	E	77	41.457	48..589	47,330	1.00127..61	C
ATOM	22913	03'	A	E	77	40,,607	49.502	47,996	1,00126.,90	0
ATOM	22914	N9	A	E	77	43..963	47,389	45..752	1.00131,.87	N
ATOM	22915	C8	A	E	77	43..218	46,,700	44.827	1,00132,.34	C
ATOM	22916	N7	A	E	77	43,,783	46.625	43,,649	1,00132.,11	N
ATOM	22917	C5	A	E	77	44.983	47,303	43.815	1,00126..49	C
ATOM	22918	C4	A	E	77	45..Ill	47,782	45..103	1,00128,.16	C
ATOM	22919	Nl	A	E	77	47,093	48..276	43.,399	1,00117..84	N
ATOM	22920	C2	A	E	77	47.079	48..674	44.675	1,00119..44	C
ATOM	22921	N3	A	E	77	46.147	48,,479	45.605	1,00125,.13	N
ATOM	22922	C6	A	E	77	46.,037	47.575	42.,932	1,00123..18	C
ATOM	22923	N6	A	E	77	46,,037	47.173	41,660	1,00127..93	N
ATOM	22924	P	A	E	78	40.120	50.,835	47.249	1,00129,.66	P
ATOM	22925	OP1	A	E	78	39..021	51..444	48.,048	1.00125..09	O
ATOM	22926	OP2	A	E	78	39,,897	50..494	45,,819	1.00126..79	O
ATOM	22927	05'	A	E	78	41..390	51.,795	47..324	1.00122,.42	O
ATOM	22928	C5'	A	E	78	41.894	52.,239	48..574	1.00119..29	C
ATOM	22929	C4'	A	E	78	43,,244	52.890	48,,423	1,00113.,82	C

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ATOM  22930  04'   A E  78      44.220  51.919  47.956  1,00115.44          O
ATOM  22931  CI '  A E  78      45,161  52.557  47,114  1,00110.69          C
ATOM  22932  C2 '  A E  78      44.819  54,048  47.092  1.00108,89          C
ATOM  22933  02'   A E  78      45.531  54.704  48.132  1,00109.77          O
ATOM  22934  C3'   A E  78      43,330  54.003  47,395  1,00108.87          C
ATOM  22935  03'   A E  78      42.789  55,229  47.843  1.00107,83          O
ATOM  22936  N9    A E  78      45.044  51,987  45.761  1,00109,60          N
ATOM  22937  C8    A E  78      44,088  51.150  45,247  1,00112.25          C
ATOM  22938  N7    A E  78      44.264  50.849  43.984  1,00110.08          N
ATOM  22939  C5    A E  78      45.408  51,554  43.640  1,00103,40          c
ATOM  22940  C4    A E  78      45,891  52.260  44,724  1,00102.89          c
ATOM  22941  Ml    A E  78      47.216  52.455  42.451  1,00 94.64          N
ATOM  22942  C2    A E  78      47.557  53,077  43.587  1,00 96,85          c
ATOM  22943  N3    A E  78      46.970  53.048  44.773  1,00 98.93          N
ATOM  22944  C6    A E  78      46,124  51.666  42,439  1,00 97.88          C
ATOM  22945  N6    A E  78      45.788  51,047  41.303  1.00 93,79          N
ATOM  22946  P     G E  79      41.401  55.755  47.226  1,00106.15          P
ATOM  22947  OP1   G E  79      40,420  55.816  48,337  1,00108.98          O
ATOM  22948  OP2   G E  79      41.069  54,962  46.018  1.00112,58          O
ATOM  22949  05'   G E  79      41.737  57,229  46.728  1,00104,51          0
ATOM  22950  C5'   G E  79      42,082  57.483  45,374  1,00 97.15          c
ATOM  22951  C4'   G E  79      43.576  57.547  45.190  1,00 93.68          c
ATOM  22952  04'   G E  79      44.102  56,208  44.991  1,00 99,70          0
ATOM  22953  CI '  G E  79      45,188  56.246  44,089  1,00 94.81          c
ATOM  22954  C2'   G E  79      45.425  57.708  43.710  1,00 88.21          c
ATOM  22955  02'   G E  79      46.378  58,249  44.604  1,00 86,30          0
ATOM  22956  C3'   G E  79      44,058  58.314  43,972  1,00 87.44          c
ATOM  22957  03'   G E  79      44,106  59.705  44,187  1,00 80.97          0
ATOM  22958  N9    G E  79      44.870  55,395  42.920  1,00 91,88          N
ATOM  22959  C8    G E  79      43.851  54.468  42.837  1,00 93.87          c
ATOM  22960  N7    G E  79      43,810  53.846  41,687  1,00 90.19          N
ATOM  22961  C5    G E  79      44.868  54,391  40.968  1.00 84,77          c
ATOM  22962  C4    G E  79      45.538  55.342  41.707  1,00 85.83          c
ATOM  22963  N1    G E  79      46,425  54.889  39,299  1,00 72.60          N
ATOM  22964  C2    G E  79      47.025  55,817  40.109  1.00 75,16          C
ATOM  22965  N3    G E  79      46.613  56,077  41.336  1,00 80,54          N
ATOM  22966  C6    G E  79      45,323  54.117  39,655  1,00 76.38          C
ATOM  22967  06    G E  79      44.860  53.307  38.854  1,00 73.53          O
ATOM  22968  N2    G E  79      48.081  56,478  39.607  1,00 68,84          N
ATOM  22969  P     U E  80      43,570  60.695  43,049  1,00 85.80          P
ATOM  22970  OP1   U E  80      42,267  60.152  42,589  1,00 87.64          0
ATOM  22971  OP2   U E  80      43.615  62,093  43.558  1,00 85,76          0
ATOM  22972  05'   U E  80      44.613  60.519  41.865  1,00 78.27          0
ATOM  22973  C5'   U E  80      45,778  61.319  41,782  1,00 76.54          c
ATOM  22974  C4'   U E  80      46.353  61,306  40.385  1.00 77,78          c
ATOM  22975  04'   U E  80      46.677  59.946  39.994  1,00 79.03          0
ATOM  22976  C3'   U E  80      45,435  61.806  39,281  1,00 73.41          c
ATOM  22977  03'   U E  80      45.442  63,220  39.185  1.00 74,12          0
ATOM  22978  C2'   u E  80      45.994  61,122  38.038  1,00 74,87          c
ATOM  22979  02'   u E  80      47,110  61.840  37,535  1,00 75.23          0
ATOM  22980  CI '  u E  80      46.486  59.785  38.605  1,00 73.13          c
ATOM  22981  Nl    u E  80      45.533  58,667  38.375  1,00 73,83          N
ATOM  22982  C2    u E  80      45,561  58.039  37,141  1,00 70.98          c
ATOM  22983  N3    u E  80      44.666  57.008  36.985  1,00 69.58          N
ATOM  22984  C4    u E  80      43.764  56,546  37.919  1,00 67,78          c
ATOM  22985  C5    u E  80      43,795  57.236  39,168  1,00 70.70          C
ATOM  22986  C6    u E  80      44.658  58.243  39,350  1,00 74.59          c
ATOM  22987  02    u E  80      46.325  58,377  36.253  1,00 67,69          0
ATOM  22988  04    u E  80      43.021  55.608  37.633  1,00 67.57          0
ATOM  22989  P     G E  81      44,080  64.046  38,981  1,00 74.66          P
ATOM  22990  OP1   G E  81      42.905  63,195  39.313  1.00 71,50          0
ATOM  22991  OP2   G E  81      44.257  65.323  39.707  1,00 79.69          0
ATOM  22992  05'   G E  81      44,096  64.409  37,432  1,00 62.93          0
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ATOM	22993	C5'	G	E	81	45.204	65.093	36.872	1.00	64.16	C
ATOM	22994	C4'	G	E	81	44,968	65.456	35.431	1,00	70.45	C
ATOM	22995	04'	G	E	81	45.108	64,280	34.597	1.00	70,65	0
ATOM	22996	C3'	G	E	81	43.596	66:038	35.127	1.00	73.88	C
ATOM	22997	03'	G	E	81	43,728	66.990	34,075	1,00	74.32	0
ATOM	22998	C2'	G	E	81	42.793	64,831	34.645	1.00	69,39	C
ATOM	22999	02'	G	E	81	41.745	65,182	33.756	1,00	65,92	0
ATOM	23000	C1'	G	E	81	43,871	63.968	33,965	1,00	71.56	C
ATOM	23001	N9	G	E	81	43.703	62.514	34.131	1,00	64.49	N
ATOM	23002	C8	G	E	81	43.434	61,821	35.291	1,00	64,81	C
ATOM	23003	N7	G	E	81	43,394	60.529	35,130	1,00	62.62	N
ATOM	23004	C5	G	E	81	43.682	60.357	33:788	1,00	58.82	C
ATOM	23005	C4	G	E	81	43.890	61,559	33.166	1,00	56,91	C
ATOM	23006	Nl	G	E	81	44.101	59.445	31.683	1.00	56.16	N
ATOM	23007	C2	G	E	81	44,283	60.702	31,158	1,00	51.15	C
ATOM	23008	N3	G	E	81	44.192	61,799	31.874	1.00	60,03	N
ATOM	23009	C6	G	E	81	43.797	59:176	33.018	1,00	59.18	C
ATOM	23010	06	G	E	81	43,653	58.016	33,411	1,00	59,39	O
ATOM	23011	N2	G	E	81	44.578	60,806	29.858	1.00	52,72	N
ATOM	23012	P	G	E	82	43.963	68,527	34.457	1,00	82,15	P
ATOM	23013	OP1	G	E	82	43,925	69.361	33,219	1,00	71.57	0
ATOM	23014	OP2	G	E	82	45.128	68.560	35:376	1,00	74.97	0
ATOM	23015	05'	G	E	82	42.673	68,872	35.319	1,00	73,79	0
ATOM	23016	C5'	G	E	82	41,456	69.229	34,681	1,00	77.47	C
ATOM	23017	C4'	G	E	82	40.886	70.482	35:292	1,00	79.35	C
ATOM	23018	04'	G	E	82	41.915	71,511	35..327	1,00	81,71	0
ATOM	23019	C3'	G	E	82	39,736	71.135	34,540	1,00	79.68	C
ATOM	2302 0	03'	G	E	82	38,482	70.532	34,806	1,00	70,00	0
ATOM	2302 1	C2'	G	E	82	39.840	72,578	35.004	1,00	85,49	C
ATOM	23022	02'	G	E	82	39.381	72.689	36.345	1.00	84.54	0
ATOM	2302 3	CI'	G	E	82	41,353	72.763	35,004	1,00	83,80	C
ATOM	2302 4	N9	G	E	82	41.847	73,138	33.665	1.00	82,91	N
ATOM	2302 5	C8	G	E	82	42.567	72:343	32.809	1,00	86.07	C
ATOM	23026	N7	G	E	82	42,867	72.921	31,677	1,00	89.35	N
ATOM	2302 7	C5	G	E	82	42.312	74,182	31.790	1.00	88,41	C
ATOM	2302 8	C4	G	E	82	41.678	74,334	33.007	1,00	89,48	C
ATOM	23029	Nl	G	E	82	41,636	76.356	31,385	1,00	90.53	N
ATOM	23030	C2	G	E	82	41.036	76.407	32:618	1,00	89.94	C
ATOM	23031	N.3	G	E	82	41.027	75,412	33.484	1,00	90,73	N
ATOM	23032	C6	G	E	82	42,317	75.259	30,875	1,00	88.93	C
ATOM	23033	06	G	E	82	42,829	75.309	29,753	1,00	92.09	0
ATOM	23034	N2	G	E	82	40.428	77,553	32.937	1,00	97,09	N
ATOM	23035	05'	C	E	83	36.962	72:296	33:808	1.00	86.87	0
ATOM	23036	C4'	C	E	83	36,165	74.410	34,606	1,00	86.66	C
ATOM	23037	C3'	C	E	83	35.232	74,665	33.430	1.00	87,37	C
ATOM	23038	C2'	C	E	83	35:650	76:055	32.973	1.00	86.65	C
ATOM	23039	P	C	E	83	37,234	70.730	33,807	1,00	80.03	P
ATOM	23040	OP1	C	E	83	36.080	70,071	34.469	1.00	73,58	0
ATOM	23041	OF2	C	E	83	37.598	70,448	32.398	1,00	72,70	0
ATOM	23042	C5'	C	E	83	36,409	72.961	34,933	1,00	82.60	C
ATOM	23043	04'	C	E	83	37:415	75:029	34:193	1,00	86.80	0
ATOM	23044	03'	C	E	83	33.856	74,562	33.760	1,00	85,70	0
ATOM	23045	02'	C	E	83	35,107	77.042	33,831	1,00	88.86	0
ATOM	23046	CI'	C	E	83	37:161	76.008	33:201	1,00	87.59	C
ATOM	23047	Nl	C	E	83	37.892	75,663	31.960	1,00	88,73	N
ATOM	23048	C2	C	E	83	37,951	76.615	30,934	1,00	88.02	C
ATOM	23049	N3	C	E	83	38,604	76.329	29,786	1,00	89.51	N
ATOM	23050	C4	C	E	83	39.188	75,141	29.635	1,00	89,38	C
ATOM	23051	C5	C	E	83	39.143	74:148	30:657	1.00	85.01	C
ATOM	23052	C6	C	E	83	38,489	74.442	31,790	1,00	87.31	C
ATOM	23053	02	C	E	83	37.407	77,712	31:088	1.00	90,33	0
ATOM	23054	N4	C	E	83	39:822	74:910	28:483	1.00	90.43	N
ATOM	23055	05'	A	E	84	32,739	75.731	31,812	1,00	89.23	0

ATOM	23056	C4'	A	E	84	32.329	78.080	31.450	1.00	78.97	c
ATOM	23057	C3'	A	E	84	31,630	77.878	30,116	1,00	80,40	C
ATOM	23058	C2'	A	E	84	32.389	78,818	29.191	1,00	84,99	c
ATOM	23059	P	A	E	84	32.768	74,343	32.596	1.00	87.12	P
ATOM	23060	OP1	A	E	84	31,448	74.110	33,235	1,00	75.76	0
ATOM	23061	OP2	A	E	84	33.330	73,360	31.637	1,00	89,35	0
ATOM	23062	C5'	A	E	84	32.233	76,921	32.408	1,00	82,29	c
ATOM	23063	04'	A	E	84	33,719	78.292	31,086	1,00	82.34	0
ATOM	23064	03'	A	E	84	30.242	78,129	30,174	1,00	83.71	0
ATOM	23065	02'	A	E	84	31.947	80,160	29.350	1,00	86,59	0
ATOM	23066	CI '	A	E	84	33,812	78.697	29,735	1,00	83.95	c
ATOM	23067	N9	A	E	84	34.600	77.697	28,989	1,00	86.25	N
ATOM	23068	C8	A	E	84	34.822	76,389	29.339	1,00	86,44	c
ATOM	23069	N7	A	E	84	35.557	75,731	28.472	1.00	90.07	N
ATOM	23070	C5	A	E	84	35,841	76.659	27,474	1,00	89.27	c
ATOM	23071	C4	A	E	84	35.254	77,876	27.786	1,00	86,08	c
ATOM	23072	Nl	A	E	84	36.671	77,702	25.501	1.00	90.23	N
ATOM	23073	C2	A	E	84	36,040	78.805	25,933	1,00	88.50	c
ATOM	23074	N3	A	E	84	35.323	78,989	27.041	1,00	87,18	N
ATOM	23075	C6	A	E	84	36.587	76,586	26.267	1,00	89,66	c
ATOM	23076	N6	A	E	84	37,217	75.490	25,833	1,00	86.28	N
ATOM	23077	05'	C	E	85	29.391	78,364	27,791	1,00	83.30	O
ATOM	23078	C4'	c	E	85	29.878	80,401	26.624	1,00	81,53	c
ATOM	23079	C3'	C	E	85	29,368	79.875	25,299	1,00	82.67	c
ATOM	23080	C2'	c	E	85	30.502	80.213	24,340	1,00	82.04	c
ATOM	23081	P	c	E	85	29.250	77,463	29.097	1,00	91,54	P
ATOM	23082	OP1	C	E	85	27,877	77.554	29,654	1,00	79.77	0
ATOM	23083	OP2	c	E	85	29,793	76.138	28,711	1,00	95.81	0
ATOM	23084	C5'	c	E	85	29.264	79,775	27.846	1,00	80,24	c
ATOM	23085	04'	c	E	85	31,296	80,114	26,582	1.00	82.80	0
ATOM	23086	03'	c	E	85	28,125	80.439	24,933	1,00	81.87	0
ATOM	23087	02'	c	E	85	30.421	81,565	23.915	1,00	80,38	0
ATOM	23088	CI '	c	E	85	31.730	80,044	25.238	1.00	82.77	c
ATOM	23089	N1	C	E	85	32,425	78.753	25,026	1,00	86.62	N
ATOM	23090	C2	c	E	85	33.265	78,558	23.910	1,00	86,72	c
ATOM	23091	N3	c	E	85	33.879	77,355	23.767	1,00	85,46	N
ATOM	23092	C4	C	E	85	33,695	76.388	24,667	1,00	83.59	c
ATOM	23093	C5	c	E	85	32,860	76.567	25,808	1,00	81.70	C
ATOM	23094	C6	c	E	85	32.257	77,749	25.942	1,00	83,50	c
ATOM	23095	02	C	E	85	33,432	79.456	23,063	1,00	78.61	O
ATOM	23096	N4	c	E	85	34,326	75.229	24,472	1,00	78.02	N
ATOM	23097	05'	c	E	86	27.750	79,634	22.579	1,00	74,06	O
ATOM	23098	C4'	c	E	86	28,823	80,802	20,730	1.00	78.89	c
ATOM	23099	C3'	c	E	86	28,520	79.744	19,691	1,00	79.59	c
ATOM	23100	C2'	c	E	86	29.857	79,558	19.004	1,00	82,30	c
ATOM	23101	P	c	E	86	27.107	79,583	24.042	1.00	80.52	P
ATOM	23102	OP1	C	E	86	25,798	80.276	24,067	1,00	92.22	0
ATOM	23103	OP2	c	E	86	27.141	78,186	24.526	1,00	88,25	0
ATOM	23104	C5'	c	E	86	27.881	80,872	21.902	1,00	80,79	c
ATOM	23105	04'	C	E	86	30,159	80.470	21,177	1,00	81.16	0
ATOM	23106	03'	c	E	86	27,489	80,104	18,810	1,00	83.19	0
ATOM	23107	02'	c	E	86	30.107	80,606	18.083	1,00	85,76	0
ATOM	23108	CI '	C	E	86	30,812	79.689	20,188	1,00	85.81	c
ATOM	23109	*N l*	c	E	86	31,120	78.357	20,758	1,00	81.72	N
ATOM	23110	C2	c	E	86	31.938	77,469	20.057	1,00	80,86	c
ATOM	23111	N3	C	E	86	32,187	76.255	20,606	1,00	83.20	N
ATOM	23112	C4	c	E	86	31,653	75.913	21,784	1,00	82.25	c
ATOM	23113	C5	c	E	86	30.805	76,794	22.507	1,00	80,44	c
ATOM	23114	C6	c	E	86	30,572	77,982	21,950	1.00	81.81	c
ATOM	23115	02	c	E	86	32,431	77.801	18,965	1,00	77.95	0
ATOM	23116	N4	c	E	86	31.925	74,706	22.283	1,00	79,69	N
ATOM	23117	05'	G	E	87	26.795	77,822	18.014	1.00	88.54	0
ATOM	23118	C4'	G	E	87	28,052	77.219	16,033	1,00	83.72	c

ATOM	23119	C3'	G	E	87	28.090	75.804	15.496	1.00	79.36	c
ATOM	23120	C2'	G	E	87	29,573	75.466	15,553	1,00	80.37	C
ATOM	23121	P	G	E	87	26.218	79,141	18.691	1.00	90,94	P
ATOM	23122	OP1	G	E	87	25.280	79;728	17.697	1.00	96.11	0
ATOM	23123	OP2	G	E	87	25,795	78.839	20,090	1,00	85.69	0
ATOM	23124	C5'	G	E	87	26.730	77,659	16.608	1.00	86,71	C
ATOM	23125	04'	G	E	87	29.074	77,229	17.062	1,00	85,28	0
ATOM	23126	03'	G	E	87	27,528	75.693	14,201	1,00	88.67	0
ATOM	23127	02'	G	E	87	30.265	76;019	14;447	1,00	76.48	0
ATOM	23128	CI'	G	E	87	30.003	76,189	16.827	1,00	83,15	c
ATOM	23129	N9	G	E	87	30,017	75.281	17,999	1,00	81.21	N
ATOM	23130	C8	G	E	87	29.350	75.449	19;197	1,00	82.18	C
ATOM	23131	N7	G	E	87	29.549	74,480	20.058	1,00	72,75	N
ATOM	23132	C5	G	E	87	30.408	73;617	19;384	1.00	74.14	c
ATOM	23133	C4	G	E	87	30,707	74.092	18,120	1,00	72.56	C
ATOM	23134	Ul	G	E	87	31.776	71,827	18.825	1.00	61,13	N
ATOM	23135	C2	G	E	87	32.011	72;378	17.596	1,00	70.48	c
ATOM	23136	N3	G	E	87	31,495	73.526	17,181	1,00	75,39	N
ATOM	23137	C6	G	E	87	30.974	72,381	19.807	1.00	66,50	C
ATOM	23138	06	G	E	87	30.826	71,806	20.894	1,00	63,03	O
ATOM	23139	N2	G	E	87	32,823	71.693	16,787	1,00	66.24	N
ATOM	23140	05'	A	E	88	27.828	73;248	13;730	1,00	82.91	O
ATOM	23141	C4'	A	E	88	29.931	72,257	12.988	1,00	80,89	c
ATOM	23142	C3'	A	E	88	29,352	70.987	12,393	1,00	77.02	C
ATOM	23143	C2'	A	E	88	28.813	70.264	13;615	1,00	73.21	C
ATOM	23144	P	A	E	88	26.702	74,373	13.791	1,00	86,45	P
ATOM	23145	OP1	A	E	88	26,217	74.513	12,393	1,00	82.93	0
ATOM	23146	OP2	A	E	88	25,722	74.098	14,876	1,00	79.82	0
ATOM	23147	C5'	A	E	88	28.996	73,441	12.931	1,00	82,14	c
ATOM	23148	04'	A	E	88	30;266	71.939	14;371	1.00	74.49	0
ATOM	23149	03'	A	E	88	30,406	70.233	11,819	1,00	74.59	0
ATOM	23150	02'	A	E	88	28.650	68,874	13.443	1.00	68,75	0
ATOM	23151	CI'	A	E	88	29.872	70;613	14.657	1,00	73.09	c
ATOM	23152	N9	A	E	88	29,397	70.541	16,042	1,00	69.68	N
ATOM	23153	C8	A	E	88	28.568	71,353	16.780	1.00	70,84	c
ATOM	23154	N7	A	E	88	28.361	70,937	18.013	1,00	68,18	N
ATOM	23155	C5	A	E	88	29,117	69.771	18,084	1,00	66.35	c
ATOM	23156	C4	A	E	88	29.752	69;524	16;876	1,00	70.39	c
ATOM	23157	N1.	A	E	88	30.156	67,797	18.801	1,00	68,16	N
ATOM	23158	C2	A	E	88	30,701	67.693	17,578	1,00	65.94	c
ATOM	23159	N3	A	E	88	30,561	68.501	16,539	1,00	65.40	N
ATOM	23160	C6	A	E	88	29.343	68,832	19.103	1,00	59,72	C
ATOM	23161	N6	A	E	88	28;825	68;871	20.331	1.00	53.99	N
ATOM	23162	P	G	E	89	30,076	69.314	10,560	1,00	83.94	P
ATOM	23163	OP1	G	E	89	30.468	70,001	9.302	1.00	82,69	O
ATOM	23164	OP2	G	E	89	28.672	68;883	10.801	1.00	78.81	O
ATOM	23165	05'	G	E	89	31,054	68.074	10,709	1,00	80.20	O
ATOM	23166	C5'	G	E	89	31..374	67,537	11.987	1,00	78,63	C
ATOM	23167	C4'	G	E	89	32.015	66,182	11.849	1,00	73,78	c
ATOM	23168	04'	G	E	89	31,159	65..347	11,027	1,00	74.43	0
ATOM	23169	C3'	G	E	89	33.370	66.189	11;162	1,00	69.31	C
ATOM	23170	03'	G	E	89	34.103	65,072	11.636	1,00	72,51	0
ATOM	23171	C2'	G	E	89	32,999	65.960	9,704	1,00	73.60	C
ATOM	23172	02'	G	E	89	34.044	65.442	8;907	1,00	75.79	0
ATOM	23173	C1'	G	E	89	31.844	64,975	9.843	1,00	75,23	c
ATOM	23174	N9	G	E	89	30,871	65.026	8,758	1,00	76.61	N
ATOM	23175	C8	G	E	89	30,462	66.132	8,056	1,00	83.53	c
ATOM	23176	N7	G	E	89	29.546	65,863	7.159	1,00	80,86	N
ATOM	23177	C5	G	E	89	29;330	64;498	7.292	1.00	83.33	c
ATOM	23178	C4	G	E	89	30,139	63.966	8,278	1,00	78.65	c
ATOM	23179	Ul	G	E	89	28.544	62,313	7.045	1.00	72,67	N
ATOM	23180	C2	G	E	89	29.376	61;897	8;042	1.00	66.40	c
ATOM	23181	N3	G	E	89	30,208	62.687	8,703	1,00	66.91	N

ATOM	23182	C6	G	E	89	28.444	63.627	6.593	1.00	81.55	c
ATOM	23183	06	G	E	89	27.648	63.900	5.686	1.00	77.16	0
ATOM	23184	N2	G	E	89	29.307	60.592	8.319	1.00	69.41	N
ATOM	23185	P	U	E	90	35.650	65.221	12.009	1.00	75.56	P
ATOM	23186	OP1	U	E	90	36.376	64.554	10.900	1.00	63.51	0
ATOM	23187	OP2	U	E	90	35.959	66.630	12.378	1.00	77.65	0
ATOM	23188	05'	U	E	90	35.807	64.349	13.324	1.00	65.11	0
ATOM	23189	C5'	U	E	90	35.111	64.642	14.531	1.00	61.22	c
ATOM	23190	C4'	U	E	90	35.166	63.444	15.446	1.00	73.56	c
ATOM	23191	04'	U	E	90	33.937	62.699	15.231	1.00	69.27	0
ATOM	23192	C3'	U	E	90	36.336	62.478	15.136	1.00	70.71	c
ATOM	23193	03'	U	E	90	37.194	62.051	16.237	1.00	66.08	0
ATOM	23194	C2'	U	E	90	35.681	61.313	14.397	1.00	61.67	c
ATOM	23195	02'	U	E	90	36.262	60.049	14.633	1.00	75.63	0
ATOM	23196	CI '	U	E	90	34.224	61.360	14.865	1.00	68.26	c
ATOM	23197	Ul	U	E	90	33.325	60.959	13.770	1.00	69.81	N
ATOM	23198	C2	u	E	90	32.577	59.811	13.949	1.00	60.02	c
ATOM	23199	N3	u	E	90	31.813	59.452	12.859	1.00	51.13	N
ATOM	23200	C4	U	E	90	31.747	60.105	11.633	1.00	58.03	c
ATOM	23201	C5	u	E	90	32.572	61.267	11.517	1.00	57.90	c
ATOM	23202	C6	u	E	90	33.326	61.633	12.563	1.00	66.00	c
ATOM	23203	02	u	E	90	32.591	59.213	15.017	1.00	58.46	0
ATOM	23204	04	u	E	90	31.006	59.675	10.739	1.00	56.40	0
ATOM	23205	P	C	E	91	36.723	61.666	17.726	1.00	67.32	P
ATOM	23206	OP1	c	E	91	35.278	61.874	17.868	1.00	74.39	0
ATOM	23207	OP2	c	E	91	37.272	60.370	18.157	1.00	74.34	0
ATOM	23208	05'	c	E	91	37.417	62.749	18.635	1.00	62.25	0
ATOM	23209	C5'	c	E	91	36.691	63.916	18.973	1.00	69.09	c
ATOM	23210	C4'	c	E	91	36.989	65.042	18.024	1.00	71.06	c
ATOM	23211	04'	C	E	91	35.743	65.750	17.746	1.00	68.09	0
ATOM	23212	C3'	c	E	91	37.959	66.065	18.607	1.00	72.12	c
ATOM	23213	03'	c	E	91	38.875	66.573	17.638	1.00	71.33	0
ATOM	23214	C2'	C	E	91	37.034	67.159	19.115	1.00	71.59	c
ATOM	23215	02'	c	E	91	37.588	68.455	19.207	1.00	80.19	0
ATOM	23216	CI '	c	E	91	35.857	67.100	18.145	1.00	67.56	c
ATOM	23217	Nl	c	E	91	34.655	67.534	18.872	1.00	69.20	N
ATOM	23218	C2	c	E	91	34.022	68.733	18.529	1.00	64.98	c
ATOM	23219	N3	c	E	91	32.987	69.189	19.278	1.00	56.48	N
ATOM	23220	C4	c	E	91	32.621	68.514	20.362	1.00	60.86	c
ATOM	23221	C5	c	E	91	33.276	67.307	20.770	1.00	62.10	c
ATOM	23222	C6	c	E	91	34.293	66.876	20.018	1.00	63.78	c
ATOM	23223	02	c	E	91	34.419	69.310	17.514	1.00	66.11	0
ATOM	23224	N4	C	E	91	31.603	68.966	21.080	1.00	53.64	N
ATOM	23225	05'	G	E	92	39.411	68.980	17.501	1.00	76.80	0
ATOM	23226	C4'	G	E	92	39.262	70.460	15.611	1.00	85.76	c
ATOM	23227	C3'	G	E	92	40.377	71.205	16.337	1.00	90.78	c
ATOM	23228	C2'	G	E	92	39.630	71.889	17.465	1.00	86.83	c
ATOM	23229	P	G	E	92	39.990	67.638	18.112	1.00	72.76	P
ATOM	23230	OF1	G	E	92	41.277	67.405	17.405	1.00	76.98	0
ATOM	23231	OP2	G	E	92	39.955	67.737	19.605	1.00	50.98	0
ATOM	23232	C5'	G	E	92	39.085	69.057	16.114	1.00	82.07	c
ATOM	23233	04'	G	E	92	38.038	71.199	15.880	1.00	77.71	0
ATOM	23234	03'	G	E	92	40.986	72.177	15.494	1.00	92.66	0
ATOM	23235	02'	G	E	92	40.288	73.000	18.037	1.00	87.81	0
ATOM	23236	C1'	G	E	92	38.301	72.238	16.799	1.00	83.52	c
ATOM	23237	N9	G	E	92	37.242	72.254	17.796	1.00	83.77	N
ATOM	23238	C8	G	E	92	37.221	71.375	18.846	1.00	77.60	c
ATOM	23239	N7	G	E	92	36.245	71.587	19.667	1.00	73.89	N
ATOM	23240	C5	G	E	92	35.603	72.687	19.127	1.00	77.96	c
ATOM	23241	C4	G	E	92	36.212	73.130	17.972	1.00	79.49	c
ATOM	23242	Ul	G	E	92	34.143	74.429	18.774	1.00	78.23	N
ATOM	23243	C2	G	E	92	34.821	74.794	17.636	1.00	81.51	c
ATOM	23244	N3	G	E	92	35.892	74.165	17.174	1.00	81.00	N

ATOM	23245	C6	G	E	92	34.469	73.364	19.606	1.00	74.96	c
ATOM	23246	06	G	E	92	33,807	73.099	20,617	1,00	72,10	O
ATOM	23247	N2	G	E	92	34.327	75,858	16.983	1.00	81,48	N
ATOM	23248	05'	G	E	93	42.006	74.447	15.696	1.00	93.62	O
ATOM	23249	C4'	G	E	93	40,467	76.183	16,350	1,00	93.82	C
ATOM	23250	C3'	G	E	93	40.412	77,492	17.109	1.00	94,25	C
ATOM	23251	C2'	G	E	93	38.935	77,854	17.080	1,00	91,44	c
ATOM	23252	P	G	E	93	42,328	72.918	15,975	1,00	92.59	P
ATOM	23253	OP1	G	E	93	43.439	72.507	15.068	1,00	91.32	0
ATOM	23254	OF2	G	E	93	42.455	72,782	17.455	1,00	83,02	0
ATOM	23255	C5'	G	E	93	41,609	75.292	16,755	1,00	92.48	C
ATOM	23256	04'	G	E	93	39.200	75.539	16.632	1,00	87.55	0
ATOM	23257	03'	G	E	93	41.255	78,456	16.513	1,00	94,54	0
ATOM	23258	02'	G	E	93	38.597	78.451	15.838	1.00	96.39	0
ATOM	23259	CI '	G	E	93	38,281	76.476	17,145	1,00	87.99	c
ATOM	23260	N9	G	E	93	37.949	76,059	18.519	1,00	87,30	N
ATOM	23261	C8	G	E	93	38.524	74.991	19.164	1.00	85.58	c
ATOM	23262	N7	G	E	93	38,067	74.788	20,365	1,00	84.89	N
ATOM	23263	C5	G	E	93	37.119	75,781	20.523	1.00	85,52	c
ATOM	23264	C4	G	E	93	37.025	76,584	19.395	1,00	86,55	c
ATOM	23265	N1	G	E	93	35,472	77.153	21,404	1,00	84.48	N
ATOM	23266	C2	G	E	93	35.443	77.894	20.236	1,00	85.60	C
ATOM	23267	N3	G	E	93	36.217	77,651	19.184	1,00	84,63	N
ATOM	23268	C6	G	E	93	36,299	76.049	21,643	1,00	86.17	C
ATOM	23269	06	G	E	93	36.272	75.423	22.715	1,00	82.53	O
ATOM	23270	N2	G	E	93	34.573	78,926	20.203	1,00	87,28	N
ATOM	23271	05'	U	E	94	41,855	80.115	18,270	1,00	94.08	O
ATOM	23272	C4'	U	E	94	39,929	81.517	18,844	1,00	95.16	C
ATOM	23273	C3'	U	E	94	40.567	81,856	20.180	1,00	95,98	C
ATOM	23274	C2'	U	E	94	39.353	81.913	21.101	1.00	96.07	c
ATOM	23275	P	U	E	94	42,518	79.018	17,318	1,00	92.15	P
ATOM	23276	OP1	υ	E	94	43.070	77,942	18.172	1.00	96,82	0
ATOM	23277	OP2	U	E	94	43.409	79.639	16.298	1.00	94.67	0
ATOM	23278	C5'	U	E	94	40,837	80.974	17,763	1,00	94.01	c
ATOM	23279	04'	υ	E	94	38.898	80,551	19.204	1.00	94,55	0
ATOM	23280	03'	u	E	94	41.353	83,036	20.171	1,00	95,59	0
ATOM	23281	02'	u	E	94	38,623	83.119	20,913	1,00	92.19	0
ATOM	23282	CI '	u	E	94	38.515	80.753	20.557	1,00	90.98	c
ATOM	23283	Nl	u	E	94	38.733	79,513	21.349	1,00	93,66	N
ATOM	23284	C2	u	E	94	37,997	79.391	22,526	1,00	92.80	c
ATOM	23285	N3	u	E	94	38,218	78.252	23,263	1,00	87.88	N
ATOM	23286	C4	u	E	94	39.094	77,235	22.947	1,00	91,82	c
ATOM	23287	C5	u	E	94	39.830	77.433	21.727	1.00	90.60	c
ATOM	23288	C6	u	E	94	39,637	78.535	20,987	1,00	90.41	c
ATOM	23289	02	υ	E	94	37.191	80,230	22.894	1.00	90,36	0
ATOM	23290	04	u	E	94	39.182	76.264	23.708	1.00	92.62	0
ATOM	23291	05'	G	E	95	41,882	83.539	22,583	1,00	92.32	0
ATOM	23292	C4'	G	E	95	40.125	84,575	23.883	1.00	90,86	c
ATOM	23293	C3'	G	E	95	40.813	84,408	25.225	1,00	96,01	c
ATOM	23294	C2'	G	E	95	39,700	83.821	26,086	1,00	98.66	c
ATOM	23295	P	G	E	95	42.583	83.179	21.200	1,00	98.41	P
ATOM	23296	OF1	G	E	95	43.438	84,308	20.761	1,00	98,86	0
ATOM	23297	OP2	G	E	95	43,208	81.841	21,357	1,00	102.66	0
ATOM	23298	C5'	G	E	95	41.024	84.663	22.681	1,00	90.38	c
ATOM	23299	04'	G	E	95	39.270	83,407	23.786	1,00	89,99	0
ATOM	23300	03'	G	E	95	41,349	85.622	25,723	1,00	99.59	0
ATOM	23301	02'	G	E	95	38,775	84.828	26,483	1,00	94.33	0
ATOM	23302	CI '	G	E	95	39.004	82,900	25.080	1,00	95,25	c
ATOM	23303	N9	G	E	95	39.495	81.507	25.167	1.00	95.35	N
ATOM	23304	C8	G	E	95	40,255	80.825	24,241	1,00	91.84	c
ATOM	23305	N1	G	E	95	40.530	79,604	24.605	1.00	89,35	N
ATOM	23306	C5	G	E	95	39.919	79.461	25.848	1.00	94.81	c
ATOM	23307	C4	G	E	95	39,274	80.627	26,209	1,00	95,37	c

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ATOM  23308  Nl    G  E  95    39.147  78.649  27.889  1.00 91.35    N
ATOM  23309  C2    G  E  95    38,538  79.845  28,154  1,00 92.37    C
ATOM  23310  N.3   G  E  95    38.572  80,885  27.338  1.00 93,00    N
ATOM  23311  C6    G  E  95    39.873  78.352  26.743  1.00 94.63    C
ATOM  23312  06    G  E  95    40,374  77.223  26,623  1,00 92.26    O
ATOM  23313  N2    G  E  95    37.882  79,917  29.318  1.00 89,73    N
ATOM  23314  05'   C  E  96    42.161  85,860  28.100  1,00 95,56    O
ATOM  23315  C4'   C  E  96    41,623  84.691  30,131  1,00104.32    C
ATOM  23316  C3'   C  E  96    42.073  84.021  31.421  1,00109.86    C
ATOM  23317  C2'   C  E  96    40.868  83,166  31.779  1,00109,30    C
ATOM  23318  P     C  E  96    42,688  85.626  26,614  1,00 95.15    P
ATOM  23319  OP1   C  E  96    43.466  86.818  26.190  1,00 99.14    0
ATOM  23320  OP2   C  E  96    43.324  84,284  26.557  1,00103,94    0
ATOM  23321  C5'   C  E  96    42.712  85.155  29.201  1.00 99.04    C
ATOM  23322  04'   C  E  96    40,822  83.678  29,468  1,00100.85    0
ATOM  23323  03'   C  E  96    42.406  84,948  32.431  1.00113,64    0
ATOM  23324  02'   C  E  96    39.831  83.966  32.329  1.00112.42    0
ATOM  23325  C1'   C  E  96    40,433  82.688  30,398  1,00106.44    C
ATOM  23326  Nl    C  E  96    41.109  81,418  30.043  1.00106,73    N
ATOM  23327  C2    C  E  96    40.728  80,237  30.694  1,00101,91    C
ATOM  23328  N3    C  E  96    41,360  79.089  30,368  1,00 99.86    N
ATOM  23329  C4    C  E  96    42.322  79.087  29.446  1,00 99.60    C
ATOM  23330  C5    C  E  96    42.731  80,268  28.772  1,00100,32    C
ATOM  23331  C6    C  E  96    42,103  81.398  29,102  1,00104.02    C
ATOM  23332  02    C  E  96    39.827  80.263  31.551  1,00102.01    0
ATOM  23333  N4    C  E  96    42.910  77,926  29.163  1,00100,03    N
ATOM  23334  P     u  E  97    43,284  84.510  33,707  1,00126.52    P
ATOM  23335  OP1   u  E  97    42,839  85.364  34,844  1,00123.78    O
ATOM  23336  OP2   u  E  97    44.703  84,526  33.258  1,00124,59    O
ATOM  23337  05'   u  E  97    42.865  82.999  34.045  1.00125.95    O
ATOM  23338  C5'   u  E  97    42,402  82.631  35,346  1,00126.76    C
ATOM  23339  C4'   u  E  97    43.316  81,643  36.050  1.00129,14    C
ATOM  23340  04'   u  E  97    43.339  80.376  35.337  1.00120.40    O
ATOM  23341  C3'   u  E  97    44,787  82.040  36,178  1,00130.68    C
ATOM  23342  03'   u  E  97    45.039  82,902  37.280  1.00128,80    0
ATOM  23343  C2'   u  E  97    45.501  80,698  36.292  1,00124,21    C
ATOM  23344  02'   u  E  97    45,467  80.209  37,624  1,00121.51    0
ATOM  23345  CI '  u  E  97    44.627  79.799  35.412  1,00124.67    C
ATOM  23346  Nl    u  E  97    45.127  79,599  34.022  1,00128,68    N
ATOM  23347  C2    u  E  97    46,403  79.938  33,533  1,00128.45    C
ATOM  23348  N3    u  E  97    46,603  79.623  32,206  1,00127.17    N
ATOM  23349  C4    u  E  97    45.730  79.on   31.329  1,00118,08    C
ATOM  23350  C5    u  E  97    44.465  78.678  31.901  1.00111.86    C
ATOM  23351  C6    u  E  97    44,228  78.971  33,182  1,00117.52    C
ATOM  23352  02    u  E  97    47.315  80,492  34.132  1.00128,73    0
ATOM  23353  04    u  E  97    46.080  78.799  30.167  1.00118.62    0
TER
ATOM  23354  P     DG F   1    36.387  20,424  20.252  1.00 75,89    P
ATOM  23355  OF1   DG F   1    35.674  21,057  19.098  1,00 71,24    0
ATOM  23356  OP2   DG F   1    36,897  21.240  21,385  1,00 60.36    0
ATOM  23357  OP3   DG F   1    37.523  19.606  19.744  1,00 63.64    0
ATOM  23358  05'   DG F   1    35.363  19,382  20.866  1,00 65,62    0
ATOM  23359  C5'   DG F   1    34,771  19.641  22,111  1,00 62.89    C
ATOM  23360  C4'   DG F   1    33.731  18.592  22.402  1,00 60.01    C
ATOM  23361  04'   DG F   1    34.382  17,381  22.856  1,00 50,49    0
ATOM  23362  C3'   DG F   1    32,714  18.985  23,482  1,00 56.00    C
ATOM  23363  03'   DG F   1    31,417  19.Oil  22,932  1,00 61.01    0
ATOM  23364  C2'   DG F   1    32.828  17,890  24.527  1,00 52,79    C
ATOM  23365  CI '  DG F   1    33.536  16.767  23.776  1.00 51.94    C
ATOM  23366  N9    DG F   1    34,289  15.934  24,694  1,00 44.00    N
ATOM  23367  C8    DG F   1    35.280  16,323  25.558  1.00 45,62    C
ATOM  23368  N7    DG F   1    35.686  15.366  26.344  1.00 42.38    N
ATOM  23369  C5    DG F   1    34,895  14.277  25,967  1,00 48.32    C
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ATOM	23370	C4	DG	F	1	34.015	14.634	24.981	1.00	46.33	C
ATOM	23371	Nl	DG	F	1	33.881	12.186	25.804	1.00	43.81	N
ATOM	23372	C2	DG	F	1	33.050	12.652	24.799	1.00	40.37	C
ATOM	23373	N3	DG	F	1	33.093	13.866	24.336	1.00	43.25	N
ATOM	23374	C6	DG	F	1	34.872	12.940	26.440	1.00	44.38	C
ATOM	23375	06	DG	F	1	35.573	12.429	27.321	1.00	49.11	O
ATOM	23376	N2	DG	F	1	32.169	11.789	24.281	1.00	38.56	N
ATOM	23377	05'	DC	F	2	29.593	17.762	24.160	1.00	53.16	O
ATOM	23378	C4'	DC	F	2	28.658	15.656	23.563	1.00	53.87	C
ATOM	23379	C3'	DC	F	2	27.658	15.684	24.696	1.00	50.96	C
ATOM	23380	C2'	DC	F	2	27.812	14.291	25.279	1.00	51.55	C
ATOM	23381	P	DC	F	2	30.147	19.225	23.891	1.00	63.03	P
ATOM	23382	OP1	DC	F	2	29.160	19.919	23.032	1.00	58.68	0
ATOM	23383	OP2	DC	F	2	30.586	19.780	25.193	1.00	57.44	0
ATOM	23384	C5'	DC	F	2	29.128	17.004	23.087	1.00	51.87	C
ATOM	23385	04'	DC	F	2	29.767	14.958	24.132	1.00	49.28	0
ATOM	23386	03'	DC	F	2	26.343	15.848	24.208	1.00	59.40	0
ATOM	23387	C1'	DC	F	2	29.245	13.903	24.901	1.00	52.40	C
ATOM	23388	Nl	DC	F	2	30.092	13.677	26.088	1.00	44.36	N
ATOM	23389	C2	DC	F	2	30.034	12.436	26.725	1.00	39.89	C
ATOM	23390	N3	DC	F	2	30.792	12.240	27.831	1.00	42.21	N
ATOM	23391	C4	DC	F	2	31.584	13.212	28.287	1.00	42.90	C
ATOM	23392	C5	DC	F	2	31.648	14.494	27.643	1.00	44.28	C
ATOM	23393	C6	DC	F	2	30.885	14.681	26.562	1.00	42.91	C
ATOM	23394	02	DC	F	2	29.273	11.551	26.270	1.00	37.21	0
ATOM	23395	N4	DC	F	2	32.323	12.962	29.378	1.00	36.28	N
ATOM	23396	P	DC	F	3	25.151	16.120	25.251	1.00	58.90	P
ATOM	23397	OP1	DC	F	3	24.Oil	16.547	24.418	1.00	65.70	0
ATOM	23398	OP2	DC	F	3	25.735	16.895	26.375	1.00	46.31	0
ATOM	23399	05'	DC	F	3	24.782	14.706	25.897	1.00	52.05	0
ATOM	23400	C5'	DC	F	3	24.169	13.697	25.118	1.00	56.24	C
ATOM	23401	C4'	DC	F	3	24.137	12.387	25.877	1.00	53.21	C
ATOM	23402	04'	DC	F	3	25.491	11.940	26.176	1.00	48.14	0
ATOM	23403	C3'	DC	F	3	23.483	12.455	27.240	1.00	50.30	C
ATOM	23404	03'	DC	F	3	22.088	12.420	27.095	1.00	60.19	0
ATOM	23405	C2'	DC	F	3	23.986	11.164	27.853	1.00	48.55	C
ATOM	23406	C1'	DC	F	3	25.428	11.102	27.324	1.00	47.13	C
ATOM	23407	Nl	DC	F	3	26.419	11.548	28.329	1.00	41.57	N
ATOM	23408	C2	DC	F	3	26.700	10.709	29.406	1.00	39.47	C
ATOM	23409	N3	DC	F	3	27.587	11.104	30.331	1.00	38.87	N
ATOM	23410	C4	DC	F	3	28.173	12.292	30.229	1.00	42.11	C
ATOM	23411	C5	DC	F	3	27.867	13.195	29.147	1.00	42.57	C
ATOM	23412	C6	DC	F	3	26.993	12.781	28.230	1.00	41.02	C
ATOM	23413	02	DC	F	3	26.131	9.612	29.478	1.00	46.33	0
ATOM	23414	N4	DC	F	3	29.055	12.634	31.184	1.00	33.74	N
ATOM	23415	05'	DA	F	4	21.405	12.032	29.546	1.00	53.15	0
ATOM	23416	C4'	DA	F	4	21.453	9.968	30.836	1.00	54.66	C
ATOM	23417	C3'	DA	F	4	21.138	10.561	32.183	1.00	48.49	C
ATOM	23418	C2'	DA	F	4	22.119	9.771	33.047	1.00	48.52	C
ATOM	23419	P	DA	F	4	21.104	12.955	28.259	1.00	59.81	P
ATOM	23420	OP1	DA	F	4	19.757	12.689	27.694	1.00	62.43	0
ATOM	23421	OF2	DA	F	4	21.531	14.309	28.664	1.00	44.43	0
ATOM	23422	C5'	DA	F	4	20.906	10.714	29.618	1.00	53.31	C
ATOM	23423	04'	DA	F	4	22.900	9.937	30.828	1.00	52.48	0
ATOM	23424	03'	DA	F	4	19.794	10.264	32.552	1.00	54.52	0
ATOM	23425	CI'	DA	F	4	23.352	9.719	32.152	1.00	46.32	C
ATOM	23426	N9	DA	F	4	24.313	10.753	32.491	1.00	46.78	N
ATOM	23427	C8	DA	F	4	24.562	11.907	31.802	1.00	41.96	C
ATOM	23428	N7	DA	F	4	25.489	12.658	32.361	1.00	43.58	N
ATOM	23429	C5	DA	F	4	25.852	11.945	33.502	1.00	38.49	C
ATOM	23430	C4	DA	F	4	25.142	10.778	33.599	1.00	38.83	C
ATOM	23431	Nl	DA	F	4	26.892	11.281	35.506	1.00	44.84	N
ATOM	23432	C2	DA	F	4	26.131	10.201	35.472	1.00	35.39	C

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ATOM   23433   N3    DA  F   4      25..230    9,861    34..569   1,00  37.65       N
ATOM   23434   C6    DA  F   4      26,,764   12..203   34.,520   1,00  40..16      C
ATOM   23435   N6    DA  F   4      27.520    13.,287   34..550   1,00  34,07       N
ATOM   23436   05'   DA  F   5      19..812   10.,386   35.,118   1,00  57.75       O
ATOM   23437   C4'   DA  F   5      20.,395    8.805    36.,770   1,00  41.99       C
ATOM   23438   C3'   DA  F   5      19.887     9,743    37..829   1,00  47,58       C
ATOM   23439   C2'   DA  F   5      21.046     9,720    38..834   1,00  47,74       C
ATOM   23440   P     DA  F   5      19.,111   10. 990   33.,818   1,00  57.73       P
ATOM   23441   OP1   DA  F   5      17.700    10.,555   33.,751   1,00  63..66      0
ATOM   23442   OF2   DA  F   5      19..610   12.,366   33..912   1,00  42,48       0
ATOM   23443   C5'   DA  F   5      19.,739    9.007    .35.,438  1,00  47.11       C
ATOM   23444   04'   DA  F   5      21..776    9,194    36,651    1,00  40..28      0
ATOM   23445   03'   DA  F   5      18. 676    9,265    38. 381   1,00  53,66       0
ATOM   23446   CI'   DA  F   5      22..261    9,616    37..912   1,00  39..40      C
ATOM   23447   N9    DA  F   5      22.,989   10..867   37.,716   1,00  41.81       N
ATOM   23448   C8    DA  F   5      22..904   11,712    36..634   1,00  42,42       C
ATOM   23449   N7    DA  F   5      23..680   12.,768   36.,721   1,00  39..80      N
ATOM   23450   C5    DA  F   5      24.,328   12.606    37.,937   1,00  38..57      C
ATOM   23451   C4    DA  F   5      23..919   11,434    38..563   1,00  39,.67      C
ATOM   23452   Nl    DA  F   5      25..737   12.,929   39..802   1,00  44,01       N
ATOM   23453   C2    DA  F   5      25,241    11.782    40.,282   1,00  38..40      C
ATOM   23454   N3    DA  F   5      24..326   10.,972   39.,749   1,00  34.28       N
ATOM   23455   C6    DA  F   5      25..296   13.,375   38..604   1,00  41,25       C
ATOM   23456   N6    DA  F   5      25.,798   14.500    .38.,113  1,00  38..4.1     N
ATOM   23457   05'   DG  F   6      18.,455   10.,615   40,510    1,00  56..24      O
ATOM   23458   C4'   DG  F   6      19. 587   10.,173   42.540    1,00  51,45       C
ATOM   23459   C3'   DG  F   6      19.,132   11.414    4.3.,259  1,00  51.4.3      C
ATOM   23460   C2'   DG  F   6      20.,449   11.886    43.,859   1,00  52..48      C
ATOM   23461   P     DG  F   6      17.695    10.,270   39. 162   1,00  63,41       P
ATOM   23462   OP1   DG  F   6      16.,514    9,445    39.,436   1,00  65..82      O
ATOM   23463   OP2   DG  F   6      17,622    11.618    38.,552   1,00  44.20       O
ATOM   23464   C5'   DG  F   6      18..631    9,645    41.494    1,00  48,.86      C
ATOM   23465   04'   DG  F   6      20.,793   10.,619   41,896    1,00  50..21      0
ATOM   23466   03'   DG  F   6      18.,205   11.090    44,277    1,00  62.65       0
ATOM   23467   CI'   DG  F   6      21..447   11,529    42.765    1,00  50,.04      C
ATOM   23468   N9    DG  F   6      21.924    12.,687   42..007   1,00  44,03       N
ATOM   23469   C8    DG  F   6      21.,530   13. 075   40.,759   1,00  39..96      C
ATOM   23470   N7    DG  F   6      22.,143   14,147    40,339    1,00  44.62       N
ATOM   23471   C5    DG  F   6      22.998    14,493    41.376    1,00  4.1 ,24     C
ATOM   23472   C4    DG  F   6      22.,881   13..604   42.,408   1,00  41.62       C
ATOM   23473   Nl    DG  F   6      24.,614   15..517   42.,690   1,00  42.98       N
ATOM   23474   C2    DG  F   6      24.426    14,576    43. 664   1,00  44,10       C
ATOM   23475   N3    DG  F   6      23.,551   13.,589   43.,578   1,00  43..22      N
ATOM   23476   C6    DG  F   6      23..922   15..558   41,485    1,00  44.75       C
ATOM   23477   06    DG  F   6      24..169   16.,459   40..663   1,00  45,.12      O
ATOM   23478   N2    DG  F   6      25.,187   14,694    44,759    1,00  44.86       N
ATOM   23479   05'   DC  F   7      18.,433   13. 178   45,745    1,00  59..63      O
ATOM   23480   C4'   DC  F   7      19.791    13.,917   47.593    1,00  56,.09      C
ATOM   23481   C3'   DC  F   7      19..166   15.,286   4,' .715  1,00  57,26       C
ATOM   23482   C2'   DC  F   7      20.,410   16. 165   47,837    1,00  54.23       C
ATOM   23483   P     DC  F   7      17,358    12..259   45.,000   1,00  66..61      P
ATOM   23484   OF1   DC  F   7      16..519   11,602    46..025   1,00  72,14       0
ATOM   23485   OP2   DC  F   7      16.,789   13..106   4.3.,949  1,00  54.50       0
ATOM   23486   C5'   DC  F   7      18.,886   12.,833   47,036    1,00  53..94      C
ATOM   23487   04'   DC  F   7      20. 893   14,148    46. 691   1,00  56,23       0
ATOM   23488   03'   DC  F   7      18.,357   15.. .367 48.,876   1,00  61.97       0
ATOM   23489   CI'   DC  F   7      21.,395   15..458   46.,909   1,00  55..75      C
ATOM   23490   Nl    DC  F   7      21.546    16.,131   45. 611   1,00  49,37       N
ATOM   23491   C2    DC  F   7      22.,505   17.118    45.,473   1,00  45..54      C
ATOM   23492   N3    DC  F   7      22.,650   17.724    44,287    1,00  43..75      N
ATOM   23493   C4    DC  F   7      21..863   17,389    43..274   1,00  4.3,.15     C
ATOM   23494   C5    DC  F   7      20.,870   16.,381   43.,397   1,00  42.47       C
ATOM   23495   C6    DC  F   7      20.,749   15. 782   44,573    1,00  45..83      C
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ATOM  23496  02   DC F  7    23.204  17.410  46.437  1.00  50.96   O
ATOM  23497  N4   DC F  7    22.038  18.027  42.117  1.00  41.51   N
ATOM  23498  05'  DG F  8    18.289  17.839  49.377  1.00  47.18   O
ATOM  23499  C4'  DG F  8    20.054  18.988  50.522  1.00  48.34   C
ATOM  23500  C3'  DG F  8    19.443  20.381  50.414  1.00  47.87   C
ATOM  23501  C2'  DG F  8    20.611  21.190  49.852  1.00  47.99   C
ATOM  23502  P    DG F  8    17.342  16.602  49.048  1.00  63.80   P
ATOM  23503  OP1  DG F  8    16.469  16.261  50.192  1.00  64.71   0
ATOM  23504  OP2  DG F  8    16.773  16.912  47.724  1.00  58.51   0
ATOM  23505  C5'  DG F  8    19.060  17.846  50.552  1.00  47.72   C
ATOM  23506  04'  DG F  8    20.889  18.871  49.354  1.00  47.05   0
ATOM  23507  03'  DG F  8    19.073  20.834  51.697  1.00  49.79   0
ATOM  23508  C1'  DG F  8    21.326  20.160  48.952  1.00  47.81   C
ATOM  23509  N9   DG F  8    21.036  20.314  47.528  1.00  47.09   N
ATOM  23510  C8   DG F  8    20.136  19.582  46.780  1.00  46.24   C
ATOM  23511  N7   DG F  8    20.089  19.938  45.524  1.00  44.78   N
ATOM  23512  C5   DG F  8    21.025  20.973  45.435  1.00  41.36   C
ATOM  23513  C4   DG F  8    21.601  21.225  46.655  1.00  44.72   C
ATOM  23514  Nl   DG F  8    22.381  22.674  44.662  1.00  38.79   N
ATOM  23515  C2   DG F  8    22.901  22.845  45.915  1.00  41.42   C
ATOM  23516  N3   DG F  8    22.545  22.140  46.966  1.00  44.24   N
ATOM  23517  C6   DG F  8    21.421  21.737  44.325  1.00  43.10   C
ATOM  23518  06   DG F  8    21.001  21.669  43.159  1.00  52.65   0
ATOM  23519  N2   DG F  8    23.818  23.806  46.047  1.00  42.17   N
ATOM  23520  05'  DC F  9    18.604  23.295  51.390  1.00  48.45   O
ATOM  23521  C4'  DC F  9    20.232  25.070  51.433  1.00  48.37   C
ATOM  23522  C3'  DC F  9    19.314  26.187  50.885  1.00  47.21   C
ATOM  23523  C2'  DC F  9    20.144  26.729  49.726  1.00  42.11   C
ATOM  23524  P    DC F  9    17.917  21.929  51.878  1.00  56.04   P
ATOM  23525  OP1  DC F  9    17.658  21.970  53.329  1.00  67.09   O
ATOM  23526  OP2  DC F  9    16.803  21.613  50.973  1.00  51.30   O
ATOM  23527  C5'  DC F  9    19.556  23.954  52.207  1.00  42.98   C
ATOM  23528  04'  DC F  9    20.867  24.509  50.260  1.00  47.17   0
ATOM  23529  03'  DC F  9    19.103  27.210  51.883  1.00  50.10   0
ATOM  23530  CI ' DC F  9    20.822  25.449  49.187  1.00  47.52   C
ATOM  23531  Nl   DC F  9    20.104  24.842  48.034  1.00  40.92   N
ATOM  23532  C2   DC F  9    20.375  25.299  46.753  1.00  39.51   C
ATOM  23533  N3   DC F  9    19.716  24.759  45.712  1.00  38.61   N
ATOM  23534  C4   DC F  9    18.802  23.805  45.922  1.00  41.47   C
ATOM  23535  C5   DC F  9    18.495  23.339  47.230  1.00  41.39   C
ATOM  23536  C6   DC F  9    19.167  23.878  48.248  1.00  42.14   C
ATOM  23537  02   DC F  9    21.223  26.172  46.605  1.00  40.94   0
ATOM  23538  N4   DC F  9    18.170  23.288  44.860  1.00  39.20   N
ATOM  23539  05'  DA F 10    18.299  29.194  50.468  1.00  41.87   0
ATOM  23540  C4'  DA F 10    19.731  30.538  49.133  1.00  42.47   C
ATOM  23541  C3'  DA F 10    18.632  31.355  48.520  1.00  42.31   C
ATOM  23542  C2'  DA F 10    18.917  31.211  47.027  1.00  46.13   C
ATOM  23543  P    DA F 10    17.914  28.315  51.725  1.00  48.28   P
ATOM  23544  OF1  DA F 10    18.026  29.251  52.867  1.00  44.89   0
ATOM  23545  OP2  DA F 10    16.674  27.566  51.414  1.00  44.47   0
ATOM  23546  C5'  DA F 10    19.423  30.034  50.519  1.00  42.12   C
ATOM  23547  04'  DA F 10    19.846  29.407  48.238  1.00  49.28   0
ATOM  23548  03'  DA F 10    18.741  32.717  48.949  1.00  60.36   0
ATOM  23549  CI ' DA F 10    19.547  29.816  46.926  1.00  41.47   C
ATOM  23550  N9   DA F 10    18.683  28.824  46.300  1.00  39.91   N
ATOM  23551  C8   DA F 10    17.972  27.834  46.910  1.00  42.50   C
ATOM  23552  N7   DA F 10    17.258  27.092  46.068  1.00  46.50   N
ATOM  23553  C5   DA F 10    17.522  27.653  44.822  1.00  44.18   C
ATOM  23554  C4   DA F 10    18.395  28.720  44.955  1.00  41.46   C
ATOM  23555  Nl   DA F 10    17.572  28.095  42.510  1.00  46.48   N
ATOM  23556  C2   DA F 10    18.406  29.091  42.803  1.00  46.08   C
ATOM  23557  N3   DA F 10    18.875  29.480  43.982  1.00  43.01   N
ATOM  23558  C6   DA F 10    17.097  27.334  43.502  1.00  48.23   C
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ATOM   23559  N6    DA F  10      16.249  26.332  43.188  1.00 43.63          N
ATOM   23560  05'   DC F  11      17.281  33.890  47.217  1.00 49.91          O
ATOM   23561  C4'   DC F  11      17.848  34.600  45.001  1.00 57.62          C
ATOM   23562  C3'   DC F  11      16.483  35.183  44.649  1.00 49.73          c
ATOM   23563  C2'   DC F  11      16.063  34.364  43.433  1.00 53.33          c
ATOM   23564  P     DC F  11      17.495  33.743  48.778  1.00 55.52          P
ATOM   23565  OF1   DC F  11      18.017  35.036  49.259  1.00 56.84          0
ATOM   23566  OP2   DC F  11      16.288  33.078  49.297  1.00 56.13          0
ATOM   23567  C5'   DC F  11      18.208  34.651  46.464  1.00 57.86          c
ATOM   23568  04'   DC F  11      17.765  33.225  44.613  1.00 49.37          0
ATOM   23569  03'   DC F  11      16.610  36.560  44.292  1.00 55.92          0
ATOM   23570  CI'   DC F  11      16.960  33.122  43.471  1.00 50.47          c
ATOM   23571  N1    DC F  11      16.170  31.898  43.562  1.00 46.38          N
ATOM   23572  C2    DC F  11      15.625  31.364  42.400  1.00 48.89          c
ATOM   23573  N3    DC F  11      14.862  30.261  42.487  1.00 46.42          N
ATOM   23574  C4    DC F  11      14.628  29.715  43.668  1.00 49.36          c
ATOM   23575  C5    DC F  11      15.154  30.272  44.878  1.00 46.20          c
ATOM   23576  C6    DC F  11      15.911  31.352  44.775  1.00 41.39          c
ATOM   23577  02    DC F  11      15.859  31.914  41.316  1.00 51.46          0
ATOM   23578  N4    DC F  11      13.875  28.613  43.699  1.00 50.23          N
ATOM   23579  05'   DC F  12      14.600  37.012  42.785  1.00 57.51          0
ATOM   23580  C4'   DC F  12      14.341  36.613  40.473  1.00 63.22          c
ATOM   23581  C3'   DC F  12      12.861  36.948  40.485  1.00 60.88          c
ATOM   23582  C2'   DC F  12      12.294  35.801  39.651  1.00 62.34          c
ATOM   23583  P     DC F  12      15.300  37.495  44.121  1.00 69.03          P
ATOM   23584  OP1   DC F  12      15.765  38.889  43.988  1.00 67.25          0
ATOM   23585  OP2   DC F  12      14.297  37.125  45.136  1.00 64.15          0
ATOM   23586  C5'   DC F  12      15.171  37.265  41.555  1.00 56.50          c
ATOM   23587  04'   DC F  12      14.348  35.194  40.650  1.00 52.01          0
ATOM   23588  03'   DC F  12      12.646  38.198  39.844  1.00 72.91          0
ATOM   23589  CI'   DC F  12      13.276  34.657  39.914  1.00 55.76          c
ATOM   23590  Nl    DC F  12      12.688  33.572  40.681  1.00 51.90          N
ATOM   23591  C2    DC F  12      11.876  32.670  40.031  1.00 58.43          c
ATOM   23592  N3    DC F  12      11.329  31.652  40.734  1.00 53.67          N
ATOM   23593  C4    DC F  12      11.574  31.537  42.030  1.00 50.76          c
ATOM   23594  C5    DC F  12      12.401  32.462  42.720  1.00 50.11          c
ATOM   23595  C6    DC F  12      12.937  33.457  42.009  1.00 52.51          c
ATOM   23596  02    DC F  12      11.675  32.822  38.817  1.00 62.14          0
ATOM   23597  N4    DC F  12      11.010  30.522  42.682  1.00 52.75          N
ATOM   23598  05'   DC F  13      10.213  38.172  39.134  1.00 66.35          0
ATOM   23599  C4'   DC F  13       9.523  36.964  37.159  1.00 71.91          c
ATOM   23600  C3'   DC F  13       8.072  37.213  37.506  1.00 78.38          c
ATOM   23601  C2'   DC F  13       7.457  35.817  37.349  1.00 75.88          c
ATOM   23602  P     DC F  13      11.259  39.002  40.024  1.00 75.86          P
ATOM   23603  OP1   DC F  13      11.510  40.310  39.383  1.00 69.16          0
ATOM   23604  OP2   DC F  13      10.885  38.961  41.465  1.00 64.33          0
ATOM   23605  C5'   DC F  13      10.502  37.947  37.761  1.00 64.50          c
ATOM   23606  04'   DC F  13       9.807  35.634  37.642  1.00 75.91          0
ATOM   23607  03'   DC F  13       7.520  38.145  36.566  1.00 88.18          0
ATOM   23608  C1'   DC F  13       8.604  34.893  37.766  1.00 71.10          c
ATOM   23609  Ml    DC F  13       8.508  34.368  39.186  1.00 70.34          N
ATOM   23610  C2    DC F  13       7.812  33.191  39.432  1.00 64.03          c
ATOM   23611  02    DC F  13       7.266  32.615  38.487  1.00 63.39          0
ATOM   23612  N3    DC F  13       7.741  32.722  40.703  1.00 61.02          N
ATOM   23613  C4    DC F  13       8.347  33.383  41.695  1.00 59.70          c
ATOM   23614  N4    DC F  13       8.252  32.882  42.927  1.00 62.49          N
ATOM   23615  C5    DC F  13       9.079  34.579  41.466  1.00 55.72          c
ATOM   23616  C6    DC F  13       9.130  35.035  40.212  1.00 64.02          c
ATOM   23617  05'   DA F  14       5.052  38.327  37.039  1.00 86.83          0
ATOM   23618  C4'   DA F  14       3.476  36.674  36.257  1.00 87.96          c
ATOM   23619  C3'   DA F  14       2.450  37.479  37.072  1.00 90.40          c
ATOM   23620  C2'   DA F  14       2.539  36.878  38.461  1.00 83.55          c
ATOM   23621  P     DA F  14       6.388  39.204  37.007  1.00 97.39          P
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ATOM	23622	OP1	DA	F	14	6.295	40.211	35.925	1.00	91.70	O
ATOM	23623	OP2	DA	F	14	6.655	39.661	38.389	1.00	93.74	O
ATOM	23624	C5'	DA	F	14	4.734	37.454	35.941	1.00	85.97	C
ATOM	23625	04'	DA	F	14	3.819	35.511	37.065	1.00	82.10	O
ATOM	23626	03'	DA	F	14	1.131	37.362	36.538	1.00	90.00	O
ATOM	23627	CI '	DA	F	14	2.940	35.441	38.160	1.00	82.36	C
ATOM	23628	N9	DA	F	14	3.609	34.842	39.299	1.00	75.57	N
ATOM	23629	C8	DA	F	14	4.619	35.395	40.032	1.00	71.33	C
ATOM	23630	N7	DA	F	14	4.988	34.662	41.054	1.00	71.60	N
ATOM	23631	C5	DA	F	14	4.142	33.571	41.004	1.00	67.85	C
ATOM	23632	C4	DA	F	14	3.275	33.669	39.935	1.00	73.02	C
ATOM	23633	Ml	DA	F	14	3.076	31.533	41.494	1.00	69.25	N
ATOM	23634	C2	DA	F	14	2.296	31.761	40.431	1.00	68.69	C
ATOM	23635	N3	DA	F	14	2.318	32.790	39.587	1.00	70.67	N
ATOM	23636	C6	DA	F	14	4.026	32.439	41.812	1.00	67.21	C
ATOM	23637	N6	DA	F	14	4.811	32.220	42.870	1.00	69.98	N
ATOM	23638	05'	DA	F	15	-0.931	37.587	37.995	1.00	85.01	O
ATOM	23639	C4'	DA	F	15	-2.608	35.909	38.457	1.00	85.17	C
ATOM	23640	C3'	DA	F	15	-3.046	36.421	39.815	1.00	82.60	C
ATOM	23641	C2'	DA	F	15	-3.055	35.121	40.609	1.00	81.52	C
ATOM	23642	P	DA	F	15	0.006	38.415	36.998	1.00	92.15	P
ATOM	23643	OP1	DA	F	15	-0.767	38.750	35.779	1.00	96.58	0
ATOM	23644	OF2	DA	F	15	0.669	39.475	37.798	1.00	81.55	0
ATOM	23645	C5'	DA	F	15	-2.089	36.957	37.493	1.00	84.96	C
ATOM	23646	04'	DA	F	15	-1.561	34.963	38.766	1.00	83.96	0
ATOM	23647	03'	DA	F	15	-4.349	36.994	39.726	1.00	85.99	0
ATOM	23648	CI '	DA	F	15	-1.805	34.418	40.056	1.00	80.68	C
ATOM	23649	N9	DA	F	15	-0.627	34.634	40.879	1.00	75.46	N
ATOM	23650	C8	DA	F	15	0.360	35.560	40.683	1.00	74.08	C
ATOM	23651	N7	DA	F	15	1.296	35.535	41.602	1.00	73.13	N
ATOM	23652	C5	DA	F	15	0.894	34.522	42.458	1.00	72.20	C
ATOM	23653	C4	DA	F	15	-0.294	33.959	42.030	1.00	74.52	C
ATOM	23654	Nl	DA	F	15	0.800	32.986	44.244	1.00	71.54	N
ATOM	23655	C2	DA	F	15	-0.346	32.540	43.711	1.00	71.16	C
ATOM	23656	N3	DA	F	15	-0.975	32.957	42.615	1.00	72.41	N
ATOM	23657	C6	DA	F	15	1.457	33.996	43.631	1.00	70.29	C
ATOM	23658	N6	DA	F	15	2.593	34.447	44.162	1.00	70.15	N
ATOM	23659	05'	DT	F	16	-5.144	37.242	42.111	1.00	75.84	O
ATOM	23660	C4'	DT	F	16	-6.232	35.527	43.430	1.00	77.90	C
ATOM	23661	C3'	DT	F	16	-6.097	36.404	44.664	1.00	80.57	C
ATOM	23662	C2'	DT	F	16	-5.757	35.350	45.705	1.00	77.00	C
ATOM	23663	P	DT	F	16	-4.852	38.091	40.792	1.00	77.39	P
ATOM	23664	OP1	DT	F	16	-6.160	38.571	40.286	1.00	88.33	0
ATOM	23665	OP2	DT	F	16	-3.767	39.069	41.042	1.00	75.53	0
ATOM	23666	C5'	DT	F	16	-6.150	36.246	42.094	1.00	72.79	C
ATOM	23667	04'	DT	F	16	-5.121	34.598	43.560	1.00	84.27	0
ATOM	23668	03'	DT	F	16	-7.312	37.092	44.966	1.00	87.33	0
ATOM	23669	CI '	DT	F	16	-4.719	34.542	44.930	1.00	82.32	C
ATOM	23670	Nl	DT	F	16	-3.325	35.105	45.076	1.00	72.85	N
ATOM	23671	C2	DT	F	16	-2.597	34.792	46.200	1.00	73.04	C
ATOM	23672	N3	DT	F	16	-1.357	35.366	46.248	1.00	71.21	N
ATOM	23673	C4	DT	F	16	-0.787	36.207	45.315	1.00	69.22	C
ATOM	23674	C5	DT	F	16	-1.598	36.502	44.171	1.00	71.02	C
ATOM	23675	C6	DT	F	16	-2.816	35.948	44.104	1.00	71.85	C
ATOM	23676	02	DT	F	16	-3.010	34.054	47.088	1.00	71.96	O
ATOM	23677	04	DT	F	16	0.331	36.674	45.451	1.00	73.52	O
ATOM	23678	C7	DT	F	16	-1.075	37.414	43.098	1.00	70.84	C
ATOM	23679	P	DT	F	17	-7.252	38.573	45.601	1.00	84.83	P
ATOM	23680	OP1	DT	F	17	-6.054	39.249	45.056	1.00	84.10	0
ATOM	23681	OP2	DT	F	17	-8.581	39.204	45.421	1.00	84.10	0
ATOM	23682	05'	DT	F	17	-7.012	38.315	47.157	1.00	73.60	0
ATOM	23683	03'	DT	F	17	-7.886	38.885	50.766	1.00	80.41	0
ATOM	23684	C1'	DT	F	17	-5.104	36.600	50.061	1.00	76.43	C

```
ATOM   23685  C2'  DT  F  17     -5.791  37.604  51.001  1.00  76.07       C
ATOM   23686  C3'  DT  F  17     -6.774  38.296  50.055  1.00  76.65       C
ATOM   23687  C4'  DT  F  17     -7.242  37.107  49.222  1.00  81.96       C
ATOM   23688  C5'  DT  F  17     -7.856  37.450  47.873  1.00  73.06       C
ATOM   23689  04'  DT  F  17     -6.038  36.303  49.032  1.00  77.08       0
ATOM   23690  Nl   DT  F  17     -3.830  37.151  49.453  1.00  75.25       N
ATOM   23691  C2   DT  F  17     -2.645  37.Oil  50.147  1.00  70.20       C
ATOM   23692  N3   DT  F  17     -1.550  37.569  49.540  1.00  69.20       N
ATOM   23693  C4   DT  F  17     -1.519  38.238  48.332  1.00  70.23       C
ATOM   23694  C5   DT  F  17     -2.792  38.356  47.651  1.00  69.28       C
ATOM   23695  C6   DT  F  17     -3.876  37.819  48.239  1.00  69.90       C
ATOM   23696  02   DT  F  17     -2.565  36.430  51.212  1.00  69.47       0
ATOM   23697  04   DT  F  17     -0.481  38.697  47.866  1.00  74.62       0
ATOM   23698  C7   DT  F  17     -2.877  39.063  46.328  1.00  67.42       C
ATOM   23699  P    DT  F  18     -7.898  40.450  51.179  1.00  76.25       P
ATOM   23700  OP1  DT  F  18     -9.211  40.667  51.824  1.00  88.44       0
ATOM   23701  OP2  DT  F  18     -7.525  41.307  50.028  1.00  70.66       0
ATOM   23702  05'  DT  F  18     -6.747  40.586  52.284  1.00  68.29       0
ATOM   23703  C5'  DT  F  18     -6.857  39.892  53.497  1.00  70.66       C
ATOM   23704  C4'  DT  F  18     -5.577  39.998  54.302  1.00  70.71       C
ATOM   23705  04'  DT  F  18     -4.524  39.206  53.684  1.00  79.76       0
ATOM   23706  C3'  DT  F  18     -4.964  41.380  54.382  1.00  68.39       C
ATOM   23707  03'  DT  F  18     -5.664  42.208  55.303  1.00  70.95       0
ATOM   23708  C2'  DT  F  18     -3.566  41.015  54.876  1.00  68.90       C
ATOM   23709  CI'  DT  F  18     -3.261  39.796  53.988  1.00  70.96       C
ATOM   23710  K1   DT  F  18     -2.542  40.180  52.700  1.00  66.81       N
ATOM   23711  C2   DT  F  18     -1.165  40.169  52.674  1.00  67.14       C
ATOM   23712  N3   DT  F  18     -0.614  40.579  51.491  1.00  64.49       N
ATOM   23713  C4   DT  F  18     -1.277  41.001  50.361  1.00  68.15       C
ATOM   23714  C5   DT  F  18     -2.717  41.013  50.459  1.00  66.68       C
ATOM   23715  C6   DT  F  18     -3.270  40.609  51.607  1.00  66.93       C
ATOM   23716  02   DT  F  18     -0.476  39.813  53.625  1.00  67.36       0
ATOM   23717  04   DT  F  18     -0.684  41.345  49.347  1.00  68.19       0
ATOM   23718  C7   DT  F  18     -3.553  41.457  49.299  1.00  57.91       C
ATOM   23719  P    DC  F  19     -5.544  43.809  55.187  1.00  70.57       P
ATOM   23720  OF1  DC  F  19     -6.582  44.387  56.065  1.00  81.94       0
ATOM   23721  OP2  DC  F  19     -5.518  44.247  53.776  1.00  61.69       0
ATOM   23722  05'  DC  F  19     -4.119  44.101  55.836  1.00  58.15       0
ATOM   23723  C5'  DC  F  19     -3.296  45.091  55.285  1.00  55.51       C
ATOM   23724  C4'  DC  F  19     -1.891  44.965  55.832  1.00  63.89       C
ATOM   23725  04'  DC  F  19     -1.229  43.787  55.259  1.00  69.82       0
ATOM   23726  C3'  DC  F  19     -0.991  46.127  55.491  1.00  64.58       C
ATOM   23727  03'  DC  F  19     -1.095  47.119  56.485  1.00  62.39       0
ATOM   23728  C2'  DC  F  19      0.388  45.470  55.467  1.00  65.41       C
ATOM   23729  CI'  DC  F  19      0.066  44.138  54.801  1.00  63.73       C
ATOM   23730  Nl   DC  F  19      0.050  44.206  53.282  1.00  65.29       N
ATOM   23731  C2   DC  F  19      1.264  44.295  52.561  1.00  63.88       C
ATOM   23732  N3   DC  F  19      1.218  44.365  51.208  1.00  68.15       N
ATOM   23733  C4   DC  F  19      0.046  44.340  50.571  1.00  69.38       C
ATOM   23734  C5   DC  F  19     -1.195  44.249  51.278  1.00  68.43       C
ATOM   23735  C6   DC  F  19     -1.145  44.180  52.615  1.00  64.37       C
ATOM   23736  02   DC  F  19      2.340  44.322  53.166  1.00  58.88       0
ATOM   23737  N4   DC  F  19      0.063  44.412  49.238  1.00  64.31       N
ATOM   23738  05'  DC  F  20      0.798  48.634  55.803  1.00  65.56       0
ATOM   23739  C4'  DC  F  20      3.169  48.768  56.377  1.00  64.07       C
ATOM   23740  C3'  DC  F  20      3.471  50.066  55.635  1.00  63.25       C
ATOM   23741  C2'  DC  F  20      4.631  49.658  54.746  1.00  63.66       C
ATOM   23742  P    DC  F  20     -0.790  48.636  56.097  1.00  62.64       P
ATOM   23743  OP1  DC  F  20     -1.037  49.473  57.289  1.00  67.96       0
ATOM   23744  OP2  DC  F  20     -1.487  48.913  54.825  1.00  63.76       0
ATOM   23745  C5'  DC  F  20      1.736  48.619  56.886  1.00  60.12       C
ATOM   23746  04'  DC  F  20      3.471  47.705  55.428  1.00  58.83       0
ATOM   23747  03'  DC  F  20      3.872  51.069  56.546  1.00  65.04       0
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ATOM    23748   CI'   DC  F   20          4.278   48..211   54..391   1.00  57.63              C
ATOM    23749   Nl    DC  F   20          3..548  48..087   53..133   1,00  58,.52             N
ATOM    23750   C2    DC  F   20          4,201   48..362   51.,931   1.00  6.3..12            C
ATOM    23751   N3    DC  F   20          3..516  48..243   50..776   1.00  65..41             N
ATOM    23752   C4    DC  F   20          2,,246  47,859    50,.786   1,00  63,,29             C
ATOM    23753   C5    DC  F   20          1,559   47.564    52..002   1.00  62.40              C
ATOM    23754   C6    DC  F   20          2.245   47.689    53..142   1,00  62.76              C
ATOM    23755   02    DC  F   20          5,390   48.,709   51,,949   1,00  62,36              0
ATOM    23756   N4    DC  F   20          1.622   47.757    49..607   1,00  63..79             N
TER
HETATM2  3757   O    HOH  S    3         28..258  -10.,786   36..710   1,00  49.68              0
HETATM2  3758   0    HOH  S    5         52..598   29..337   31..629   1,00  44.36              0
HETATM2  3759   0    HOH  S    8         20.,912   -0,.705   37.,229   1,00  50..62             0
HETATM2  3760   0    HOH  S   12        -26..744   77.531   -13..678   1.00  52.18              0
HETATM2  3761   0    HOH  S   16         18..633   24.061    39..010   1,00  56,.87             0
HETATM2  3762   0    HOH  S   17         43.,996   .34..071  29.,891   1.00  44.67              0
HETATM2  3763   0    HOH  S   19         26..844    6..726   27..881   1.00  47.77              0
HETATM2  3764   0    HOH  S   22        -11,897    90..858  -12,.266   1,00  41,90              0
HETATM2  3765   0    HOH  S   24         -5.,108   98..270  -13.,.393  1.00  59..19             0
HETATM2  3766   0    HOH  S   26        --25..174  91..323   -4.262    1,00  39..06             0
HETATM2  3767   0    HOH  S   28         23,.944    0,317    42,.413   1,00  47,34              0
HETATM2  3768   0    HOH  S   29         49..118   30..034   32..173   1,00  46..34             0
HETATM2  3769   0    HOH  S   30        --9..681   97..245   -9..548   1,00  39..58             0
HETATM2  3770   0    HOH  S   31         24..274    3,908    29..296   1,00  46..04             0
HETATM2  3771   0    HOH  S   34         22..123   23..201   38..032   1,00  55..73             0
HETATM2  3772   0    HOH  S   49         27,847    30,.581   29.,661   1,00  47.72              0
HETATM2  3773   0    HOH  S   58         17.600    27,178    62..121   1,00  53..78             0
HETATM2  3774   0    HOH  S   63         24..402   21.173    39..663   1,00  38,.04             0
HETATM2  3775   0    HOH  S   66         20.,436   88,.920  -50.,935   1,00  51..17             0
HETATM2  3776   0    HOH  S   83         15..057   63..506   46..203   1.00  54.19              0
HETATM2  3777   0    HOH  S   84        --11.677   53..438   -23..776  1,00  56,.42             0
HETATM2  3778   0    HOH  S   85         -1,.355   70..085  -13.,656   1.00  71.89              0
HETATM2  3779   0    HOH  S   86        -39..078   55..902   -27..104  1,00  73..87             0
HETATM2  3780   0    HOH  S   87        -12,.500   80.,709    4,150    1,00  58,,06             0
HETATM2  3781   0    HOH  S   88         -5.,235  115..444  -11 ,711   1.00  61.83              0
HETATM2  3782   0    HOH  S   89         -5..307  114 .195   -6..818   1,00  50..26             0
HETATM2  3783   0    HOH  S   90          0,,014  110.,207    1,744    1,00  74,93              0
HETATM2  3784   0    HOH  S   91        -16..938  116..582  -12..733   1,00  38..02             0
HETATM2  3785   0    HOH  S   92        -24 ,198  122,.431  -18.,017   1,00  43..60             0
HETATM2  3786   0    HOH  S   93        -22..551  121.,930  -15..210   1,00  42.18              0
HETATM2  3787   0    HOH  S   94        -22..832  116..900  -22..076   1,00  33,.71             0
HETATM2  3788   0    HOH  S   95        -16.,276  118,.948  -24 ,048   1,00  42..23             0
HETATM2  3789   0    HOH  S   96         -7.529   117.399   -24..460   1.00  54.18              0
HETATM2  3790   0    HOH  S   97         -3..004  102..312   -27..221  1,00  51,81              0
HETATM2  3791   0    HOH  S   98        -25,937   112..773   -28,012   1.00  4.3..62             0
HETATM2  3792   0    HOH  S   99        -31..786  120..707  -21..586   1.00  44.43              0
HETATM2  3793   0    HOH  S  100        -29,.993  122 ,705   -19,294   1,00  36,,89             0
HETATM2  3794   0    HOH  S  102        -13.,125  100..496  -15.,326   1.00  35..52             0
HETATM2  3795   0    HOH  S  103        -17 .536   94..769  -21 .737   1,00  41.03              0
HETATM2  3796   0    HOH  S  104        -15,.396   95.,088   -19,009   1,00  46,,13             0
HETATM2  3797   0    HOH  S  105        -10..516   97..199  -19..846   1,00  36..06             0
HETATM2  3798   0    HOH  S  106         -6..613   94..605  -19..389   1,00  55..42             0
HETATM2  3799   0    HOH  S  107        -17.725    96..110  -15..125   1,00  44.51              0
HETATM2  3800   0    HOH  S  108        -16..802   85..471  -12..906   1,00  50..83             0
HETATM2  3801   0    HOH  S  109        -14 ,860  106,.226  -25.,142   1,00  37..21             0
HETATM2  3802   0    HOH  S  110        -12..684  105.,000   -25..088  1,00  34.34              0
HETATM2  3803   0    HOH  S  111         -5..064  Ill .567   -46..540  1,00  70..85             0
HETATM2  3804   0    HOH  S  112        -18.,884  105,.302  -26.,112   1,00  45..87             0
HETATM2  3805   0    HOH  S  113         16..417   79..779  -72..486   1.00  73..75             0
HETATM2  3806   0    HOH  S  114          2..632   72.459   -58..182   1,00  65,.38             0
HETATM2  3807   0    HOH  S  115         51.,072   .3..945   29.,467   1.00  48..41             0
HETATM2  3808   0    HOH  S  116         41.217    21..541   14.226    1.00  66..44             0
HETATM2  3809   0    HOH  S  117         24,.484   -4,498    29,.329   1,00  64,75              0
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HETATM2 3810  0    HOH  S  118    28.328   -1.772   19.345  1.00 44.30      O
HETATM2 3811  0    I-IOH S 119    21.127    0.031   29,041  1,00 54.51      O
HETATM2 3812  0    HOH  S  120    14.483   -4.692   35.415  1,00 67,64      O
HETATM2 3813  0    HOH  s  121    -8.347   76.414   -3.222  1.00 62.56      O
HETATM2 3814  0    HOH  S  122   -13,881   80.057   -9,160  1,00 42,17      O
HETATM2 3815  0    HOH  S  123   -18.249   68.882  -12.545  1,00 44,76      O
HETATM2 3816  0    HOH  s  124    -7.559   67.810   -5.810  1,00 63,53      O
HETATM2 3817  0    HOH  S  125   -19,838   81.249  -11,789  1,00 39,05      O
HETATM2 3818  0    I-IOH s 126   --23.667  84.109  -17.042  1,00 47.01      O
HETATM2 3819  0    HOH  s  127   —22.890   76.088  -21.812  1,00 42,36      O
HETATM2 382 0 0    HOH  s  128   -21,611   71.658  -21,954  1,00 50.94      O
HETATM2 382 1 0    I-IOH s 129    11.999   54.335   17.093  1,00 60.05      O
HETATM2 3822  0    HOH  s  130    43.901    5.482   32.290  1,00 41,35      O
HETATM2 382 3 0    HOH  s  131    40.151   31.967   35.033  1.00 54.44      O
I-IETATM2 382 4 0  I-IOH S 132   -14,850   92.402   -5,571  1,00 42.60      O
HETATM2 382 5 0    HOH  S  133   -13.001   97.969   -2.552  1,00 54,55      O
HETATM2 382 6 0    HOH  s  134   -15.027   85.491  -15.679  1.00 45.50      O
HETATM2 3827  0    HOH  S  135   -18,765   89.579  -11,650  1,00 54,10      O
HETATM2 382 8 0    HOH  S  136   -14.647   95.855   -8.577  1,00 43,28      O
HETATM2 382 9 0    HOH  s  137    -9.041   99.586  -16.055  1,00 42,72      O
HETATM2 3830  0    HOH  S  138   -19,396  111.754  -21,489  1,00 48,31      O
HETATM2 3831  0    I-IOH s 139   -35.173  117.162  -32 .786  1,00 55.38      O
HETATM2 3832  0    HOH  s  140   -31.387  115.184  -25.096  1,00 38,04      O
HETATM2 3833  0    HOH  s  141   -35,689  119.074  -26,998  1,00 58.80      O
HETATM2 3834  0    I-IOH s 142   -51.531  110.751  -14.476  1,00 61.44      O
HETATM2 3835  0    HOH  s  143    -3.492  104.729   -5.040  1,00 59,82      O
HETATM2 3836  0    HOH  s  144   -11,961   68.255   -0,557  1,00 45.06      0
I-IETATM2 3837 0   I-IOH S 145    40,043   -0.361   23,104  1,00 39.02      0
HETATM2 3838  0    HOH  s  146    37.771   -1.554   23.774  1,00 31,44      0
HETATM2 3839  0    HOH  s  147    33.883    4.703   30.376  1.00 35.17      0
I-IETATM2 3840 0   I-IOH S 148    39,536   -2.026   17,974  1,00 51.83      0
HETATM2 3841  0    HOH  S  149    42.442    3.270   20.744  1,00 42,88      0
HETATM2 3842  0    HOH  S  150    27.281   19.616   38.577  1.00 38.65      0
HETATM2 3843  0    HOH  S  151    23,899   25.411   36,341  1,00 44,94      0
HETATM2 3844  0    HOH  S  152    29.242   27.507   31.270  1,00 40,97      0
HETATM2 3845  0    HOH  s  153    32.277   27.994   32.791  1,00 42,53      0
HETATM2 3846  0    HOH  S  154    37,267   25.650   39,359  1,00 38,64      0
HETATM2 3847  0    I-IOH s 155    39.977   20.825   40.592  1,00 41.38      0
HETATM2 3848  0    HOH  s  157    60.092   -6.383   31.497  1,00 54,89      0
HETATM2 3849  0    HOH  s  158    32,016   30.136   41,114  1,00 56.65      0
HETATM2 3850  0    I-IOH S 159    38,784   66.437   33,999  1,00 63.08      0
HETATM2 3851  0    HOH  s  160    36.587   72.974   27.965  1,00 81,92      0
HETATM2 3852  0    HOH  s  161    41.786   66.203   31.813  1.00 53.74      0
I-IETATM2 3853 0   I-IOH S 162    62,657   37.974   32,271  1,00 62.54      0
HETATM2 3854  0    HOH  S  163    47.674   47.151   27.536  1,00 54,19      0
HETATM2 3855  0    HOH  S  164     1.867   35.930   55.550  1.00 51.99      0
HETATM2 3856  0    HOH  S  165   -29,552  110.441  -24,068  1,00 48,11      0
HETATM2 3857  0    HOH  S  166    37.281   13.304   29.079  1,00 45,93      0
TER
HETATM2 3858  02   EDO  G    1   -18,620  112.623  -31,738  1,00 42,29      0
HETATM2 3859  C2   EDO  G    1   -19.259  113.704  -32 .442  1,00 47.67      c
HETATM2 3860  CI   EDO  G    1   -20.770  113.455  -32 .474  1,00 52,14      c
HETATM2 3861  01   EDO  G    1   -21,297  113.414  -31,130  1,00 47,34      0
HETATM2 3862  02   EDO  G    2   -23.869  122.514  -27.072  1,00 54.91      0
HETATM2 3863  C2   EDO  G    2   -22.904  122.612  -26.025  1,00 43,42      c
HETATM2 3864  CI   EDO  G    2   -23,244  123.768  -25,104  1,00 47,39      c
I-IETATM2 3865 01  EDO  G    2   -22,901  125.014  -25,704  1,00 46.57      0
HETATM2 3866  02   EDO  G    3   -16.327  113.930  -21.535  1,00 53,44      0
HETATM2 3867  C2   EDO  G    3   -17.456  114.819  -21.322  1.00 48.59      c
I-IETATM2 3868 CI  EDO  G    3   -18,318  114.734  -22,572  1,00 50.17      c
HETATM2 3869  01   EDO  G    3   -18.468  113.321  -22.818  1,00 51,48      0
TER
END
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Example 9: S. pyogenes (Sp) SpCas9 truncations from Crystal Structure

[00602] Figures 25A-B pertain to SpCas9 truncations from full length SpCas9. These figures show Surveyor gel test results of SpCas9 truncation mutants from the crystal structure that retain cleavage activity (A) and a table showing the amino acid truncations and flexible (GGGS) or rigid (A(EAAAK)) linker substitutions of the lanes of the gels of Figure 25A (B)

[00603] In this Example, SpCas9 sequences were analyzed by 1. Comparing against orthologs *(S. aureus, S. thermophilus* CRISPR1, *S. thermophilus* CRISPR3, and *N. meningiditis),* including smaller Cas9s (*S. aureus, S. thermophilus* CRISPR1, and *N. meningiditis)* for regions that are conserved or variable, and 2. Boundaries identified by crystallography as being potentially non-critical for contacting target DNA:sgRNA duplex. A region of SpCas9 (helical domain 2) was not present in many smaller Cas9 orthologs, and predicted to be dispensable for function. Two similar sets of truncations were made, one by sequence alignment with smaller Cas9s, one by crystal prediction. In addition, several sets of flexible glycine-serine (GlyGlyGlySer) or rigid alpha-helical linkers (Ala(GluAlaAlaAlaLys)Ala) in groups of 3, 6, 9, or 12 repeats were also used to replace helical domain 2 for potential structural stabilization and/or aiding of retaining SpCas9:sgRNA specificity. All of the helical region 2 truncations and linker substitutions retained SpCas9 activity. SpCas9 was truncated systematically in Helical 1, 2, and 3 domains, as well as the C'-terminal putative PAM-recognizing domain. Truncation mutants were transfected into HEK 293FT cells as follows: 400ng of truncation Cas9 plasmid and 100ng of sgRNA co-transfected into 200,000 cells by Lipofectamine 2000. DNAs from cells were harvested for SURVEYOR analysis.

[00604] Below: full length SpCas9 DNA sequence and sequences of the subdomains; followed by helical domain 2 truncation and variants.

[00605] > Full length NLS-SpCas9-NLS

[00606] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG
CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGCTGGGCC
GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC
CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCG
AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG
**GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG
ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG**

CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA
GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG
ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCC
TGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAG
CTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGT
GGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATC
TGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCC
CTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGC
CAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCC
AGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCC
ATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAG
CGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAG
CTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCA
AGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAG
TTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCT
GAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCC
ACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTAC
CCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCC
CTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAA
AGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCT
TCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGA
GAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCT
GACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCG
AGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTG
AAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAAT
CTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAA
AATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAG
ATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTG
AAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAG
ATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGC
AGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAAC

TTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGC

CCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCA

GCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTG

AAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGA

ACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGA

AGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAAC

ACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATAT

GTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATA

TCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGA

AGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGA

AGA1XGAAGAAC1 AC1 GGCXGCAGC1 XGC1 GAACXGCXAAGC1 GATTACXXAGAGAAAG

TTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGG

C1 1 XATGAAGAGACAGC1XGGTGGAAACCCGGCAGATCACΛAΛGCΛCXGTGGCACΛ(∃Λ

TCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAA

GTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAG

TTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAA

CGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCG

TGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAG

GAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTC

AAGACXXGAGATTACXX1 GGCXAACGGCGAGATCCXGGAAGCXGGiCXTCTGATCXGAGAC

AAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGC

⩿GGAAAGTCX1 GAGCATG CCCXAA(iTGAATΛ1 CXGTGAAAAAGACXXGA(iGTGCΛ(GACA

GGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGC

CAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGG

CCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAG

AGTGTG AA AGAGCTG CTGG GGATC ACC ATC ATGGA AAGA AGC AGCTTCG AGAA GA A

TXXXA !XXiA{r!T(TG{iAA⩿CXAAG{iG{rA(AAA(;AA (GTxGAAAAA(GGA(XTX∃AT(-A

TCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTG

⩿iC(!(!GCXXxiCGAAC!xXA(GAAGCXGAAAcXiAA(TGGCXXixicXXT(XA AATATGT

GAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATA

ATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATC

GAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAA AGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGA ATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTT TGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCA CCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGC TGGGAGGCGACAAAAGGCCGGCGGCCACGAAAAAGGCCGGCCAGGCAAAAAAGAA AAAGtaa

[00607] **>N'terminal NLS**

[00608] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG **CC**

[00609] >RuvCI domain

[00610] **GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTG GGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGC^** ACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGC **GGCGAAACA**

[00611] >Bridging helix

[00612] **GCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGAC GGAAGAACCGGATCTGCTATCTGCAAGAGATCTTC**

[00613] >Helical domain 1

[00614] AGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAG AGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAAC **ATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACC^^**CTGAGAAA GAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGG **CCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGAC**

[00615] >Helical domain 2 (dispensable)

[00616] CTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCA GACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCA **AGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCC** CAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCT GGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGC **AGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGC**

GACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTG AGCGACATCCTGAGAGTGAACACCGAG

[00617] >Helical domain 3

[00618] ATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCA CCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGT ACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGC GGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGA **CGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGC GGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCC** ATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACA ACCGGGAAAAGAT [illegible] CAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACT [illegible] AACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTA CGAGTACTTCACCGTGTATAACGAGCTGACCAA AGTGAAATACGTGACCGAGGGAA TGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTG TTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAA **AATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTC** CCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACA [illegible] **GACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAA** [illegible] AAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCT GAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCC TGACCTTTAAAGAGGACATCCAGAAAGCC

[00619] >Flexible linker

[00620] CAGGTGTCCGGCCAGGGCGAT

[00621] >RuvC II

[00622] ATCGTGATCGAAATGGCCAGAGAG

[00623] **>HNH**

[00624] GACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGACTC CATCGACAACAAGGTGCTGACCAGAAGCGACAAGAAC

[00625] >RuvCm

[00626] CACCACGCCCACGACGCCTACCTG

[00627] >C-terminal (PAM recognizing domain)

[00628] ACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGA GGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGG CGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAA GGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGG AAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAA GAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGA AAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAA CTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAG CTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAA GCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCC TGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAG CCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGA GCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGC ACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGA GACACGGATCGACCTGTCTCAGCTGGGAGGCGAC

[00629] C'-NLS

[00630] AAAAGGCCGGCGGCCACGAAAAAGGCCGGCCAGGCAAAAAAGAAAAAG

[00631] 6. Sp_A_hel 2(174-311) helical domain 2 deletion (from ortholog alignment)

[00632] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCG AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA

GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG
ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCC
TGATCGAGGGCGACATCACCAAGGCaCCaCTGAGCGCCTCTATGATCAAGAGATACG
ACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCT
GAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACAT
TGACXGGCGGAGCCAGC(A GGAAGAGTTCTACAAGTTGATCAAGCCCATCCGTGGAAA
AGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGG
AAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCT
GCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGG
AAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCA
GGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCAGC^C
CTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGC
GGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCC^AAGCACAGC
CTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACC
GAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGG
ACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTAC
TTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTC
AACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTT
CCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACAC
TGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTC
GACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGC
TGAGCXXXiAAGC TGATCAACGGCATCXX}GGACAAGCA GTCXXXGCAAGA(A ATCXTG
GATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGAC
GACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGA
TAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCA
TCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAG
CCX^GAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGAC
AGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGG
(AGiCCAGATCXT XGAAA GAACACCXXXriXiGAAAAi CA(XXCAGCTGCAGAACXGAGAAG
CTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGA
CATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAA

GGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAG
AGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCA
GCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCG
AGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTG
GAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACAC
TAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGT
CCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCA
ACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTG
ATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTA
CGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCC
AAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCC
AACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGA
TCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCC
CAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTC
TATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACC
CTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGG
CCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGG
GATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAG
CCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCC
CTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCA
GAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCA
GCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTT
GTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTC
CAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACA
AGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACC
CTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGG
AAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCAT
CACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACAAAGGC
CGGCGGCCACGAAAAAGGCCGGCCAGGCAAAAAAGAAAAAGtaa

[00633] **7. Sp_Δ_hel 2-(GGGGS)3 helical domain 2 deletion (from ortholog alignment)**

[00634] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG
CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC
GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC
CGACCGGCAGAGCA TCAAGAA(∃AA(CCTGA'!XGGiAGi(XCTXGCTXGTT(XGA(CAG{{iG{CG
AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG
GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG
ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG
CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA
GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG
ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCC
TGATCGAGGGCGACGGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGQcg
ATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCA
⩿GiA(X'IGACXX'[xï(C'iXiAAAGC'iC'ixCG'IxGCXGGCAGCAGCTXGCX'IGAGAΛ(GTΛCA ΛA(G
AGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCC
**AGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCAC
CGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCT
TCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTG**
CGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAA
GATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAG
ATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGACTTCGAGG
AAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTC
GATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTA
CTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAA
AGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAG
ACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGA
GTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGG
CΛCΛTΛCCA(XGΛ'IX'I XGC'I XGAAAA'J'·ΓΛ'Iχ·AΛ(XGΛ(A A⩿GAC'I 'I XX'I XGGA(·AΛ'I'GA⩿G
AAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGA
GAGATGATXXGAGGAACXGGC'I X∃AAACX'I 'ATXGCXχ'ACX'I 'GT'I XX∃ACXGACAAAGTXiA'!
GAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTG
ATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTC

CGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTT
TAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGC
ACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTG
AAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGT
GATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGC
GAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGA
AAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTAC
CTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTC
CGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGA
CAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCC
TCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAA
GCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGA
GCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATC
ACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAA
TGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCG
ATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACG
CCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCT
AAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGAT
GATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACA
GCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGG
AAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGG
GCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTG
AAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAG
GAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGC
GGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAG
GGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACC ATCATGGA
AAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTAC CAAAG
AAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAA
AACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAAC
TGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGC
TGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAG

CACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCT
GGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGC
CCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGA
GCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGC
ACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGA
GACACGGATCGACCTGTCTCAGCTGGGAGGCGACAAAAGGCCGGCGGCCACGAAA
AAGGCCGGCCAGGCAAAAAAGAAAAAGtaa

[00635] 8. Sp_Δ_hel 2-(GGGGS)6 helical domain 2 deletion (from ortholog alignment)

[00636] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG
CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC
GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC
CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCG
AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGG
GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG
ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG
CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA
GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG
ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCC
TGATCGAGGGCGACGGTGGCGGTGGCtcgGGTGGCGGTGGCtegGGTGGCGGTGGCtcg
GGrGGCGGrGGacg^GTGGCGGTGGCtcgQGTGGCGGTGGCicgArCACCAAGGCCCCC
CTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCT
GAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAG^TTTTCTTCGACC
AGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTC
TACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGT
GAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGC
ATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGA
TTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCG
CATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGA
CCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAA
GGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGC
CCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTAT

AACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCT
GAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAA
GTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTC
CGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACG
ATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGAC
ATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGA
GGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGA
AGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATC
CGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGC
CAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACA
TCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAAT
CTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGA
CGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGG
CCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAA
GCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCC
GTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGG
GCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATG
TGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGC
TGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGT
CGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCC
AGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGAT
AAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGT
GGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGA
TCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAG
GATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCC
TACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAG
CGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGA
GCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATG
AACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCT
GATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTG
CCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAG

GTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAA
GCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCC
CCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAG
AAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTT
CGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGG
ACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAG
AGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTC
CAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCC
CGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACG
AGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAAT
CTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCA
GGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTT
CAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGC
TGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGAC
CTGTCTCAGCTGGGAGGCGACAAAAGGCCGGCGGCCACGAAAAAGGCCGGCCAGG
CAAAAAAGAAAAAGtaa

[00637] 9. **Sp**_A_hel **2-(GGGGS)9** helical domain 2 deletion (from ortholog alignment)

[00638] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG
CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC
GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC
CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCG
AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG
GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG
ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG
CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA
GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG
ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCC
TGATCGAGGGCGACGGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGCtcg
GGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGQcgG
GTGGCGGTGGCtcgGGTGGCGGTGGCtcgATCACCAAGGCCCCCCTGAGCGCCTCTATG
ATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCG

GCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCT
ACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAG
CCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGA
GGA£CTGCrGCGGAAGCAGCGGACCrrCGA£AACGGCAGCA:TCCCCCACCAGA:TCC
ACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGA
AGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTG
GGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGG
AAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAG
AGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCT
GCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAG
TGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAA
AAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCT
GAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCG
TGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCA
AGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTG
CTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTA
TGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCG
GCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGC
AAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAG
CTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTC
CGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA
ITAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATG
GGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCA
CCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCAT
CAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGC
AGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGAC
CAGGAMJTGGACATCAACCGGCrGTCCGACTAGGATGTGGACCATATCGTGCCTCA
GAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGA
ACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAA
CTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATC
TGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAG

AGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTC CCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGA TCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAG TGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTG GGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGA CTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCA AGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGA TTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAA ACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCT GAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCA GCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAG GACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTG CTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAG AGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGAC TTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCC TAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCG GCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTG TACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAA ACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCA GCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCG CCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCAC CTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACC ATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCA CCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCG ACAAAAGGCCGGCGGCCACGAAAAAGGCCGGCCAGGCAAAAAAGAAAAAGtaa

[00639] 10. Sp_Δ_hel 2-(GGGGS)12 helical domain 2 deletion (from ortholog alignment)

[00640] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCG AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG

GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG
ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG
CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA
GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG
ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCC
TGATCGAGGGCGACGGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGQcg
GGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGCtcgG
GTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGGTGGCGGTGGCtcgGG
TGGCGGTGGCtcgATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGAC
GAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGA
GAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTG
ACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAG
ATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAA
GCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGC
ACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAA
AAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGG
GGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTG
GAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGA
TGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTG
CTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGA
GGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACC
TGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTC
AAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAA
CGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCT
GGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGT
TTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGAC
GACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGA
GCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGAT
TTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGAC
AGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAG
CCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCC

TGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCC
GAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGA
AGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAG
CCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGT
ACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATC
AACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGC^CTGAAGGAC
GACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCG
ACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTG
CTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAG
AGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAA
CCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACAAG
TACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAA
GCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTCACAAAGTGCGCGAGATCAACAA
CTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCA
AAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGAC
GTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGT
ACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACG
GCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGT
GTGGGATAAGGGCCGGGA1TTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAG
TGAATATCCTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATC
CTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTA
AGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCA
AAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGAT
CACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCA
AGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTG
TTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAA
GGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCA
CTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGG
AACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAG
AGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCA
CCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGA

CCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGA
GGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACC
GGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACAAAAGGCCGGC
GGCCACGAAAAAGGCCGGCCAGGCAAAAAAGAAAAAGtaa

[00641] 11. Sp_A_hel 2-A(EAAAK)3A helical domain 2 deletion (from ortholog alignment)

[00642] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG
CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC
GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC
CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCG
AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG
GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG
ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG
CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA
GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG
ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCC
TGATCGAGGGCGACgctGAAGCTGCTGCTAAAGAAGCTGCTGCTAAAGAAGCTGCTG
CTAAAgctATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGC
ACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAG
TACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGG
CGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGG
ACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCA
GCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACG
CCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAG
ATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGA
AACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAA
CTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGA
CCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTG
TACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGG
AATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTG
TGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAG
AAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCC

TCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGAC
AATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGA
GGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACA
AAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCG
GAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCC
TGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGC
CTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCT
GCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGC
AGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGA
GAACATCGTGATCGAAATGGCCAGAGAGAACCAGACC ACCCAGAAGGGACAGAAG
AACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCC
AGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTAC
CTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAA
CCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGA
CTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGAC
AACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCT
GAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAG
GCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACC
CGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTA
CGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGC
TGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACT
ACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCrc^ GATCAAA
AAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGT
GCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTAC
TTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGC
GAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTG
GGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGA
ATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTG
CCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGA
AGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAG
TGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCAC

CATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGG
GCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTC
GAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGG
GAAACGAA(CTGGCXXT `G(XXT XXAAATATXGTGAACT T XCT XGTACCT XGG CXAGCCACY
ATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAA
CA GCACA AGCACTA CCTGGACXGAGATCATCC=AGCAGATCAGCXGAGTT TCT TCC-AACG=AC=
AGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACC
GGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACC
AATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAG
GTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCG
GCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACAAAAGGCCGGCG
GCCACGAAAAAGGCCGGCCAGGCAAAAAAGAAAAAGtaa

[00643] 12. Sp_A_hel 2-A(EAAAK)3ALEA(EAAAK)3A helical domain 2 deletion (from ortholog alignment)

[00644] **ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG**
CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC
GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC
CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCG
AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG
GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG
ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG
CACGAGCGGCACCCCATCTTCXGGCA ACA TCXGTGGACGAGGTXiGCXTACXA(X=A(GAA
GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG
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AAAgctATCAC(CAA(i(G(XXXXXT TGAGCXGCXTCTATGATCAAGAGATA(XGACXGAxGCAC
CACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTA
CAAAGAGKTTFTCrrCGA£CAGAGCAAGAACGGCTACGCCGGCrACKr'TGACGGCG
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[00645] 13. Sp_A_hel 2-A(EAAAK)3ALEA(EAAAK)3ALEA(EAAAK)3A helical domain 2 deletion (from ortholog alignment)

[00646] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG CCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC CrTGATxCACCXiACXGAGTACAAGCrTGCCXAGCA AGAAA'I'IXCAAGGTGC'IGGGCA ACAC CGAC(GG(A(A(GCATX'AAGAAGAACXT!(GATC(iGAG(CX'IXGCT!(GTT(GA(A(i(XiGCXi AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG

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[0647] 14. Sp_del_hel 2-A(EAAAK)3LE(EAAAK)3LE(EAAAK)3LE(EAAAK)312A helical domain 2 deletion (from ortholog alignment)

[0648] ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAG
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TGA CsGAAAACXGA GGΛCATTCTXsGAACGATATCXGT (G(''TGACX(TGA(A CTGTTTGAG(G

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[00649] 30. Sp_del **(175-307)** (Hiroshi's prediction)

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[00651] 31. Sp_del (1098-end)

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[00653] 32. Sp_del (175-307)-(GGGGS)3

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[0655] 33. Sp_del (175-307)-(GGGGS)6

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[00657] 34. Sp_del (175-307)-(GGGGS)9

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[0659] 35. Sp_del **(175-307)-(GGGGS)12**

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[00669] *Example 10: New nickases*

[00670] Figures 24A-C pertain to new SpCas9 nickases and provide A. Schematic showing catalytic domains of SpCas9, and sites of mutagenesis for putative new nickases. RuvC domains I, II, and III are shown in orange, HNH domain in white between RuvCII and RuvCIII. Domain sizes not drawn to scale. B. Schematic showing locations of sgRNAs used for testing double nicking: when sgRNAs are transfected singly (A1 or C1 alone) with SpCas9 nickases, no indels should result. The combination of A1 + C1, used in combination with RuvC III mutation nickases result in 5'-overhang, where as D1 + A1 and C7 + A1 would result in 3'-overhangs. Conversely, those three combinations used with HNH mutation nickases would result in 3'-, 5'-, and 5'-overhangs, respectively. C. Surveyor test showing 1 HNH mutant that retains nuclease activity (N854A), and 1 HNH mutant that shows nickase activity (N863A), as well as 2 RuvCIII mutants that show nickase activity (H983A, D986A).

[00671] In this Example, five potential nicking mutation sites were chosen based on sequence homology between Cas9 orthologs. And three additional sites were chosen based on herein crystallography data. A subset of these sets of nickase mutant Cas9s were re-cloned to incorporate both N' and C'-NLS sequences that are identical to those of optimized SpCas9. Sequences are below.

[00672] Nickase mutants were re-cloned to incorporated designated mutations into pAAV-vector under Cbh promoter and sequence validated.

[00673] Nuclease and double-nicking activities for all potential nickases were tested in HEK 293FT cells as follows: co-transfection of 400ng of nickase and 100 ng of U6-driven sgRNA (100ng for one guide, or 50ng each for a pair of sgRNAs) by Lipofectamine 2000 into -200,000 cells. DNAs from transfected cells were collected for SURVEYOR analysis. Nickases do not result in indel mutations when co-transfected with a single sgRNA, but do when co-transfected with a pair of appropriately off-set sgRNAs. Based on data from the original D10A SpCas9 nickase, the pair of sgRNA chosen (A1/C1) for RuvC domain mutants have 0-bp offset and 5'-overhang for maximal cleavage.

[00674] Homology set:	Mutant domain	Functional?
Cbh-hSpCas9 (D10A)-NLS	RuvCI	nickase activity
Cbh-hSpCas9(E762A)-NLS	RuvCn	
Cbh-hSpCas9(H840A)-NLS	HNH	no activity
Cbh-hSpCas9(N854A)-NLS	HNH	wt nuclease activity
Cbh-hSpCas9(N863A)-NLS	HNH	nickase activity
Cbh4iSpCas9(D986A)~NLS	RuvCIII	

[00675] Crystal set set:	Mutant domain	Functional?
NLS-S15A-NLS	RuvCI	wt nuclease activity
NLS-E762A-NLS	RuvC II	catalytically dead
NLS-H982A-NLS	RuvC III	wt nuclease activity
NLS-H983A-NLS	RuvCIII	nickase activity
NLS-D986A-NLS	RuvCIII	nickase activity

[00676] >NLS-S15A-NLS

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ĵGAGCA<iAAA(CAG{CTGTΓΠ XGTGGAACA(XCACAAG(CACTΛ{CCl XXiA(XGAGΛTXA TCXG
AGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAA
(GTGCl XGTXXXGCXl A iCΛΛCAAGCACCGGGATAAGCCXA TCAGAGAGC-ACXGCXXGAGAA
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AAAGtaa

[00682] >NLS-H983A-NLS

[00683] ATCXGCXXXCAAAGAAiiAAGi **XiGA**A**(X**GT**XXX**GT**A**T**(XA** CCX=A(=TCCXA **(X**-AG
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[00684] **>NLS-D986A-NLS**

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AAAG

Example 11: Truncating and Creating Chimeric Cas9s based on S. pyogenes Cas9 Crystal Structure Herein

[00686] Figures 27A-C pertain to truncating and creating chimeric Cas9s based on the herein crystal structure. These figures provide schematics illustrating A. SpCas9 mutants designed for mapping out essential functional domains of Cas9 for truncation of protein. B. chimeric Cas9s that contain sequences (regions in pink) from Cas9 from *S. thennophilus CRISPR /, S. thermophilus CRISPR 3, Staphylococcus aureus, Neisseria meningiditis,* or other Cas9 orthologs. C. Designs for creating chemically inducible dimerization of SpCas9. The chemically inducible SpCas9 functions.

[00687] DNA sequences for chimeric Cas9s are optimized for human expression by GenScript and synthesized de novo. Chimeric Cas9 proteins can be constructed by cloning and ligating individual functional domains from Cas9 orthologs (i.e. by PCR-amplifying individual functional domains from a desired Cas9 ortholog, then assemblying the pieces together by either Gibson or Golden Gate-cloning). Additionally, a set of chemically-inducible Cas9s were constructed as two-component systems, where one portion of the Cas9 protein is fused to FKBP, and the remainder fused to FRB (e.g. FKBP-Cas9(amino acids 1-1098), FRB-Cas(l 099-1368)). In absence of chemical induction, co-transfection of the two inducible Cas9 components have no catalytic activity, but the functional assembly of the components may be induced using Rapamycin [5 nM to 10μM].

Example 12: Crystal Structure ofCas9 in complex with guide RNA and Target DNA

[00688] Cas9 is an RNA-guided nuclease from the microbial CRISPR-Cas system that can be targeted to specific genomic loci by single guide RNAs (sgRNAs). Applicants report the crystal structure of *Streptococcus pyogenes* Cas9 in complex with sgRNA and its target DNA at 2.4 A resolution. The structure revealed a biiobed architecture composed of target recognition and nuclease lobes, accommodating a sgRNA:DNA duplex in a positively-charged groove at their interface. Whereas the recognition lobe is essential for sgRNA and DNA binding, the nuclease lobe contains the HNH and RuvC nuclease domains, which are properly positioned for the cleavage of complementary and non-complementary strands of the target DNA, respectively. This high-resolution structure and accompanying functional analyses elucidate the molecular mechanism of RNA-guided DNA targeting by Cas9, paving the way for rational design of new and versatile genome-editing technologies.

[00689] The CRISPR (clustered regularly interspaced palindromic repeat)-Cas system is a naturally occurring microbial adaptive immune system for defense against invading phages and other mobile genetic elements (Deveau et al., 2010; Horvath and Barrangou, 2010; Marraffini and Sontheimer, 2010; Terns and Terns, 2011). Three types (I- III) of CRISPR-Cas systems have been functionally identified across a wide range of microbial species (Barrangou et al., 2007;

Brouns et al., 2008; Marraffini and Sontheiraer, 2008), each containing a cluster of CRISPR-associated (Cas) genes and its corresponding CRISPR array. These characteristic CRISPR arrays consist of repetitive sequences (direct repeats, referred to as repeats) interspaced by short stretches of non-repetitive sequences (spacers) derived from short segments of foreign genetic material (protospacers). The CRISPR array is transcribed and processed into short CRISPR RNAs (erRNAs), which direct Cas proteins to the target nucleic acids, DNA or RNA, via Watson-Crick base pairing to facilitate the nucleic acid destruction.

[00690] Type I and III CRISPR systems utilize ensembles of Cas proteins in complex with crRNA to mediate recognition and subsequent degradation of target nucleic acids (Spilman et al., 2013; Wiedenheft et al, 2011). In contrast, the Type II CRISPR system achieves recognition and cleavage of the target DNA (Garneau et al., 2010) via a single enzyme called Cas9 (Sapranauskas et aL, 2011) along with two non-coding RNAs, the crRNA and a trans-activating crRNA (tracrRNA) (Deltcheva et al., 2011). The crRNA hybridizes with the tracrRNA to form a crRNA:tracrRNA duplex, which is then loaded onto Cas9 to direct cleavage of cognate DNA sequences bearing appropriate protospacer adjacent motifs (PAM) (Mojica et al., 2009).

[00691] The Type II CRISPR system was the first to be adapted for facilitating genome editing in eukaryotic cells (Cong et al., 2013; Mali et al, 2013b). The Cas9 protein from *Streptococcus pyogenes*, along with a single guide RNA (sgRNA), a synthetic fusion of crRNA and minimal tracrRNA (Jinek et aL, 2012), could be programmed to instruct cleavage of virtually any sequence preceding a 5'-NGG PAM sequence in mammalian cells (Cong et al., 2013; Mali et al., 2013b). This unprecedented flexibility has enabled a broad range of applications including rapid generation of genetically modified cells and animal models (Gratz et al., 2013; Hwang et al., 2013; Wang et aL, 2013; Yang et al., 2013), and genome-scale genetic screening (Qi et aL, 2013; Shalem et al., 2014; Wang et aL, 2014).

[00692] However, despite brisk progress in the development of the Cas9 technology, the mechanism of how the Cas9-sgRNA complex recognizes and cleaves its target DNA remains to be elucidated. Up to date, biochemical analyses at the domain levels have enabled site-specific engineering to convert the native Cas9 into a DNA nicking enzyme (Gasiimas et al., 2012; Jinek et al., 2012; Sapranauskas et al., 2011) that facilitates homology-directed repair in eukaryotic cells (Cong et al., 2013; Mali et aL, 2013b) and further cleaves DNA with improved specificity given appropriately paired sgRNAs (Mali et aL, 2013a; Ran et aL, 2013). Moreover, a

catalytically inactive Cas9 can serve as a RNA-guided DNA-binding platform to target effector domains and modulate endogenous transcription (Gilbert et al., 2013; Konermann et al., 2013; Maeder et al., 2013; Perez-Pinera et al., 2013; Qi et al, 2013). These Cas9 engineering advances represent just the first steps of what is possible in fully realizing the potential of this flexible RNA-guided genome positioning system. A precise structural information on Cas9 will thus not only enhance the understanding of how this elegant RNA-guided microbial adaptive immune system functions, but also inform further improvements of Cas9 targeting specificity, simplification of in vitro and in vivo delivery, and engineering of Cas9 for novel functions and optimized features.

[00693] In this example, Applicants report the crystal structure of *S. pyogenes* Cas9 in complex with sgRNA and its target DNA at 2.4 A resolution. This high-resolution structure along with functional analysis reveals the key functional interactions that integrate the guide RNA, target DNA, and Cas9 protein, paving the way towards enhancing Cas9 function as well as engineering novel applications.

[00694] Overall structure of the Cas9-sgRNA-DNA ternary complex: Applicants solved the crystal structure of full-length *S. pyogenes* Cas9 (residues 1-1368; D10A/C80L/C574E/H840A) in complex with a 98-nucleotide (nt) sgRNA and a 23-nt target DNA, at 2.4 Aresolution, by the SAD (single-wavelength anomalous dispersion) method using a SeMet-labeled protein (Figs. 1, 37 and Table 1). To improve the solution behavior of Cas9, Applicants replaced two less conserved cysteine residues (Cys80 and Cys574) with leucine and glutamic acid, respectively. This C80L/C574E mutant retained the ability to efficiently cleave genomic DNA in human embryonic kidney 293FT (HEK293FT) cells, confirming that these mutations have no effects on Cas9 nuclease function (Fig. 38). Additionally, to prevent cleavage of the target DNA during crystallization, Applicants replaced the two catalytic residues, Asp10 from the RuvC domain and His840 from the HNH domain, with alanine.

Table 1: Data collection and refinement statistics

	Native Cas9	SeMet Cas9
Data collection		
Beamline	SPring-8 BL32XU	SPring-8 BL41XU
Wavelength (A)	1.000	0.9791
Space group	$P1$	$P1$
Cell dimensions		
a, b, c (A)	76.7, 105.7, 126.8	76.2, 104.5, 125.5

α, β, γ (°)	97.7, 98.4, 100.3	97.0, 98.2, 101.1
Resolution (Å)	50–2.4	50–2.6
	(2.54–2.4)	(2.67–2.6)
R_{sym}	0.07 (1.53)	0.167 (1.96)
$I/\sigma I$	22.53 (1.45)	12.62 (1.44)
Completeness (%)	98.2 (96.3)	99.9 (99.9)
Redundancy	7.93 (7.88)	19.1 (15.9)
CC(1/2)	0.999 (0.671)	0.999 (0.736)
Refinement		
Resolution (Å)	50–2.4	
No. reflections	146,862	
R_{work}/ R_{free}	0.241 / 0.276	
No. atoms		
Protein	19,021	
Nucleic acid	5,013	
Solvent	200	
B-factors		
Protein	72.6	
Nucleic acid	72.6	
Solvent	53.3	
R.m.s deviations		
Bond lengths (Å)	0.002	
Bond angles (°)	0.454	
Ramachandran plot		
Favored region	96.8%	
Allowed region	3.2%	
Outlier region	0.0%	
*Highest resolution shell is shown in parenthesis.		

[00695] The crystallographic asymmetric unit contained two Cas9-sgRNA-DNA ternary complexes (Mol A and Mol B). Although there are conformational differences between the two complexes, sgRNA and DNA are recognized by Cas9 in a similar manner. Most notably, while the HNH domain in Mol A is connected with the RuvC domain by a disordered linker, the HNH domain in Mol B is not visible in the electron density map, indicating the flexible nature of the HNH domain. Thus, Applicants first describe the structural features of Mol A unless otherwise stated, and then discuss the structural differences between the two complexes, which suggest the conformational flexibility of Cas9.

[00696] The crystal structure revealed that Cas9 consists of two lobes, a recognition (REC) lobe and a nuclease (NUC) lobe (Fig. 30A-C). The REC lobe can be divided into three regions, a long a-helix referred to as Bridge helix (BH) (residues 60-93), the RECl (residues 94-179 and 308-713), and REC2 (residues 180-307) domains (Fig. 30A-C). The NUC lobe consists of the RuvC (residues 1-59, 718-769, and 909-1098), HNH (residues 775-908), and PAM-interacting (PI) (residues 1099-1368) domains (Fig. 30A-C). The negatively-charged sgRNA:DNA hybrid duplex is accommodated in a positively-charged groove at the interface between the REC and NUC lobes (Fig. 30D). In the NUC lobe, the RuvC domain is assembled from the three split RuvC motifs (RuvC I-III), which interfaces with the PI domain to form a positively-charged surface that interacts with the 3' tail of the sgRNA (Fig. 30D). The HNH domain lies in between the RuvC II-III motifs and forms only a few contacts with the rest of the protein.

[00697] The REC lobe of Cas9 interacted with the repeat:anti-repeat duplex: The REC lobe comprises the RECl and REC2 domains. RECl adopted an elongated, a-helical structure comprising 26 a-helices (a2--a5 and α12--α33) and two β-sheets (β6/β10 and β7-β9), whereas REC2 adopted a six-helix bundle structure (a6-al1) (Figs. 31A and 39). A Dali search (Holm and Rosenstrom, 2010) revealed that the REC lobe did not share structural similarity with other known proteins, indicating that it is a Cas9-specific functional domain.

[00698] The REC lobe is one of the least conserved regions across the three families of Cas9 within the Type II CRISPR system (IIA, IIB and IIC) and many Cas9s contain significantly shorter REC lobes (Figs. 40, 41). Applicants hypothesized that truncations in the REC lobe could be tolerated. As expected, and consistent with the observation that the REC2 domain does not contact the bound sgRNA:DNA hybrid duplex, a Cas9 mutant lacking the REC2 domain (Δ175-307) showed ~50% of the wild-type Cas9 activity (Fig. 3IB), indicating that the REC2 domain is not critical for DNA cleavage. The lower cleavage efficiency may be attributed in part to the reduced levels of Cas9 (Δ175-307) expression relative to that of the wild-type protein (Fig. 31C). In striking contrast, deletion of the crRNA repeat-interacting region (Δ97-150) or cracrRNA anti-repeat-interacting region (Δ312-409) of the RECl domain abolished DNA cleavage activity (Fig. 3IB), indicating that the recognition of the repeat:anti-repeat duplex by the RECl domain is critical for Cas9 function.

[00699] The PAM-interacting (Pi) domain confers PAM specificity: The NUC lobe contains the PI domain, which adopts an elongated structure comprising seven a-helices (a47-a53), a

three-stranded antiparailel β-sheet (β18-β20), a five-stranded aiitiparallel β-sheet (β21-β23, β26 and β27), and two-stranded antiparailel β-sheet (β24 and β25) (Figs. 31D and 39). Similar to the REC lobe, the PI domain also represents a novel protein fold unique to the Cas9 family.

[00700] The locations of the bound complementary strand DNA and the active site of the RuvC domain in the present structure suggest that the PI domain is positioned to recognize the PAM sequence on the non-complementary strand of the target DNA. Applicants tested whether replacement of the *S. pyogenes* Cas9 (SpCas9; Cas9 in this study) PI domain with that of an orthologous Cas9 protein recognizing a different PAM would be sufficient to alter SpCas9 PAM specificity. The Streptococcus thermophilus CRISPR-3 Cas9 (St3Cas9) shares -60% sequence identity with SpCas9; furthermore, their crRNA repeats and tracrRNAs are interchangeable (Fonfara et al., 2013). However, SpCas9 and St3Cas9 require different PAM sequences (5'-NGG for Cas9 and 5'-NGGNG for St3Cas9) for target DNA cleavage (Fonfara et al, 2013).

[00701] Applicants swapped the two PI domains to generate two chimeras, Sp-St3Cas9 (SpCas9 with the PI domain of St3Cas9) and St3-SpCas9 (St3Cas9 with the PI domain of SpCas9), and examined their cleavage activities for target DNA sequences bearing 5'-NGG PAM (5'-GGGCT) or 5'-NGGNG PAM (5'-GGGCG) (Fig. 31E). SpCas9 and St3-SpCas9, but not St3Cas9, cleaved the target DNA with 5'-NGG PAM (Fig. 3IE), indicating that the PI domain of SpCas9 is required for the recognition of 5'-NGG PAM and is sufficient to alter the PAM recognition of St3Cas9. Sp-St3Cas9 retained cleavage activity for the target DNA with 5'-NGG PAM, albeit at a lower level than that of SpCas9 (Fig. 3IE). Additionally, deletion of the PI domain (Δ1099-1368) abolished the cleavage activity (Fig. 31E), indicating that the PI domain is critical for Cas9 function. These results reveal that the PI domain is a major determinant of PAM specificity.

[00702] The RuvC domain targets the non-complementary strand DNA: The RuvC domain consists of a six-stranded mixed β-sheet (β1, β2, β5, β11, β14 and β17) flanked by α-helices (α34, α35 and α40-α46) and two additional two-stranded antiparailel β-sheets (β3/β4 and β15/β16) (Figs. 32A and 39). It shares structural similarity with retroviral integrase superfamily members characterized by an RNase H fold, such as *Escherichia coli* RuvC (PDB code IHJR, 13% identity, root-mean-square deviation (rmsd) of 3.4 A for 123 equivalent Ca atoms) (Ariyoshi et al, 1994) and *Thermus thermophilus* RuvC (PDB code 4LD0, 17% identity, rmsd of

3.4 **A** for 129 equivalent Ca atoms) (Ariyoshi et al, 1994) and Themms thermophilus RuvC (PDB code 4LDQ, 17% identity, rmsd of 3.4 **A** for 129 equivalent *Ca* atoms) (Gorecka et al., 2013) (Fig. 32B). RuvC nucleases have four catalytic residues (e.g., Asp7, Glu70, His 143 and Asp 146 in *T. thermophilus* RuvC), and cleave Hoiliday junctions through a two-metal mechanism (Ariyoshi et al., 1994; Chen et al, 2013; Gorecka et al., 2013). Asp 10 (Ala), Glu762, His983 and Asp986 of the Cas9 RuvC domain are located at positions similar to those of the catalytic residues of *T. thermophilus* RuvC (Fig. 32A, B), consistent with the previous results that the D10A mutation abolished cleavage of the non-complementary DNA strand and that Cas9 requires Mg2+ ions for cleavage activity (Gasiunas et al., 2012; Jinek et al., 2012). Moreover, alanine substitution of Glu762, His983 or Asp986 also converted Cas9 into nickases (Fig. 32C, D). Each nickase mutant was able to facilitate targeted double strand breaks using pairs of juxtaposed sgRNAs (Fig. 32C, D), as demonstrated with the D10A nickase previously (Ran et al, 2013). This combination of structural observations and mutational analysis suggest that the Cas9 RuvC domain cleaves the non-complementary strand of the target DNA through the two-metal mechanism previously observed for other retroviral integrase superfamily nucleases.

[00703] It is important to note that there are key structural dissimilarities between the Cas9 RuvC domain and RuvC nucleases, explaining their functional differences. Unlike the Cas9 RuvC domain, RuvC nucleases forms a dimer and recognize a Hoiliday junction (Gorecka et al, 2013) (Fig. 32B). In addition to the conserved RNase H fold, the RuvC domain of Cas9 has additional structural elements involved in the interactions with the guide:DNA duplex (an end-capping loop between a43 and a44), and the PI domain/stem loop 3 (β-hairpin formed by β3 and β4) (Fig. 32A).

[00704] The HNH domain targets the complementary strand DNA; The HNH domain comprises a two-stranded antiparallel β-sheet (β12 and β13) flanked by four a-helices (a36-a42) (Fig. 32E). Likewise, it shares structural similarity with HNH endonucleases characterized by a ββα-metal fold, such as the phage T4 endonuclease VII (Endo VII) (Biertumpfel et al, 2007) (PDB code 2QNC, 8% identity, rmsd of 2.6 **A** for 60 equivalent Ca atoms) (Fig. 32F) and Vibrio vulnificus nuclease (Li et al, 2003) (PDB code 10UP, 8% identity, rmsd of 2.9 **A** for 78 equivalent Ca atoms). HNH nucleases have three catalytic residues (e.g., Asp40, His41, and Asn62 in Endo VII), and cleave nucleic acid substrates through a single-metal mechanism

(Biertumpfel et al., 2007; Li et al., 2003). In the structure of the Endo VII N62D mutant in complex with a Hoiliday junction, a Mg2+ ion is coordinated by Asp40, Asp62, and oxygen atoms of the scissile phosphate group of the substrate, while His41 acts as a general base to activate a water molecule for catalysis (Fig. 32F). Asp839, His840, and Asn863 of the Cas9 HNH domain correspond to Asp40, His41, and Asn62 of Endo VII, respectively (Fig. 32E), consistent with the observation that His840 is critical for the cleavage of the complementary DNA strand (Gasiunas et al., 2012; Jinek et al., 2012). The N863A mutant functions as a nickase (Fig. 32C, D), indicating that Asn863 participates in catalysis. These observations suggest that the Cas9 HNH domain may cleave the complementary strand of the target DNA through a single-metal mechanism as observed for other HNH supertamily nucleases. However, in the present structure, Asn863 of Cas9 is located at a position different from that of Asn62 in Endo VII (Biertumpfel et al., 2007), whereas Asp839 and His840 (Ala) of Cas9 are located at positions similar to those of Asp40 and His41 of Endo VII, respectively (Fig. 32E, F). This might be due to the absence of divalent ions, such as Mg2+, in Applicants' crystallization solution, suggesting that Asn863 can point towards the active site and participate in catalysis. Whereas the HNH domain shares a ββα-metal fold with other HNN endonuclease, their overall structures are different (Fig. 32E, F), consistent with the differences in their substrate specificities.

[00705] sgRNA recognizes target DNA via Watson-Crick base pairing: The sgRNA consists of crRNA- and tracrRNA-derived sequences connected by an artificial tetraloop (Fig. 33A). The crRNA sequence can be subdivided into guide (20-nt) and repeat (12-nt) regions, and the tracrRNA sequence likewise into anti-repeat (14-nt) and three tracrRNA stem loops (Fig. 33A). The crystal structure reveals that the sgRNA binds the target DNA to form a T-shaped architecture comprising a guide:DNA duplex, repeatanti-repeat duplex and stem loops 1-3 (Fig. 33A, B). The repeatanti-repeat duplex and stem loop 1 are connected by a single nucleotide (A51), and stem loops 1 and 2 are connected by a 5-nt single-stranded linker (nucleotides 63-67).

[00706] The guide (nucleotides 1-20) and target DNA (nucleotides 3'-23') form the guide:DNA hybrid duplex via 20 Watson-Crick base pairs, with the conformation of the duplex distorted from a canonical A-form RNA duplex (Figs. 33B and 42). The crRNA repeat (nucleotides 21-32) and tracrRNA anti-repeat (nucleotides 37-50) form the repeat:anti-repeat duplex via nine Watson-Crick base pairs (U22:A49-A26:U45 and G29:C40-A32:U37) (Fig.

33A, B). Within this region, G27, A28, A41, A42, G43, and U44 are unpaired, with A28 and U44 flipped out from the duplex (Fig. 33C). The nucleobases of G27 and A41 stack with the A26:U45 and G29:C40 pairs, respectively, and the 2-amino group of G27 interacts with the backbone phosphate group between G43 and U44, stabilizing the duplex structure (Fig. 33C). G21 and U50 form a wobble base pair at the three-way junction between the guide:DNA/repeat:anti-repeat duplexes and stem loop 1, stabilizing the T-shaped architecture (Fig. 33C).

[00707] As expected from the RNA-fold predictions of the nucleotide sequence, the tracrRNA 3' tail (nucleotides 68—81 and 82-96) form stem loops 2 and 3 via four and six Watson-Crick base pairs (A69:U80-U72:A77 and G82:C96-G87:C91), respectively (Fig. 33A, B). Previously-unappreciated, nucleotides 52-62 also form a stem loop (stem loop 1) via three Watson-Crick base pairs (G53:C61, G54:C60 and C55:G58), with U59 flipped out from the stem (Fig. 33A, B). Stem loop 1 is stabilized by the G62-G53:C61 stacking interaction and the G62-A51/A52 polar interactions (Fig. 33C).

[00708] The guide: DNA and repeatanti-repeat duplexes are accommodated and deeply buried in a positively-charged groove at the interface of the two lobes, while the rest of the sgRNA extensively interacts with the positively-charged surface on the back side of the protein (Fig. 30D). in Mol A, the 3'-terminal bases of the target DNA (3'-ACC complementary to the PAM) are not visible in the electron density map. In contrast, the two adjacent bases (3'-AC) in Mol B are not recognized by Cas9, although they are structurally ordered due to the crystal packing interactions and are visible in the electron density map. These observations suggest that the 3'-ACC sequence complementary to the PAM (5'-TGG) is not recognized by Cas9, consistent with the previous biochemical data demonstrating that Cas9-catalyzed DNA cleavage requires the 5'-NGG PAM on the non-complementary strand, but not the 3'-NCC sequence on the complementary strand (Jinek et al., 2012).

[00709] Previous studies showed that although sgRNA with a 48-nt tracrRNA tail (referred to as sgRNA(+48)) is a minimal region for the Cas9-catalyzed DNA cleavage *in vitro* (jinek et al., 2012), sgRNAs with extended tracrRNA tails, sgRNA(+67) and sgRNA(+85), dramatically improved Cas9 cleavage activity *in vivo* (Hsu et al., 2013). The present structure revealed that sgRNA(+48), sgRNA(+67) and sgRNA(+85) contain stem loop 1, stem loops 1-2 and stem loops 1-3, respectively (Fig. 33A, B). These observations indicated that, whereas stem loop 1 is

essential for the formation of the functional Cas9-sgRNA complex, stem loops 2 and 3 further support the stable complex formation as well as enhance sgRNA stability, thus improving the *in vivo* activity.

[00710] To confirm the significance of each sgRNA structural component on Cas9 function, Applicants tested a number of sgRNAs with mutations in the repeat:anti-repeat duplex, stem loops 1-3, and the linker between stem loops 1 and 2. Applicants' results revealed that, whereas stem loops 2 and 3 as well as the linker region can tolerate a large number of mutations, the repeat:anti-repeat duplex and stem loop 1 are critical for Cas9 function (Fig. 33D). Moreover, the sgRNA sequence can tolerate a large number of mutations (Fig. 33D, reconstructed sgRNA). These results highlight the functional significance of the structure-dependent recognition of the repeat:anti-repeat duplex by Cas9.

[00711] Conserved arginine cluster on Bridge helix play a critical role in sgRNA:DNA interaction: The crRNA guide region is primarily recognized by the REC lobe (Fig. 34A). The backbone phosphate groups of the crRNA guide region (nucleotides 4-6 and 13-20) interact with the REC1 domain (Arg165, Gly166, Arg403, Asn407, Lys510, Tyr515 and Arg661) and Bridge helix (Ala59, Arg63, Arg66, Arg70, Arg71, Arg74 and Arg78) (Fig. 34B), and the 2'-hydroxyl groups of C15, U16 and G19 hydrogen bond with Tyr450, Arg447/Ile448 and Thr404 in the REC1 domain (Fig. 34B), respectively. These observations suggested that the Watson-Crick faces of eight PAM-proximal nucleotides of the Cas9-bound sgRNA are exposed to the solvent, thus serving as a nucleation site for pairing with the target complementary strand. This is consistent with previous reports that the 10-12 bp PAM-proximal "seed" region is critical for Cas9-catalyzed DNA cleavage (Cong et al., 2013; Fu et al., 2013; Hsu et al., 2013; Jinek et al, 2012; Mali et al., 2013a; Pattanayak et al., 2013).

[00712] Mutational analysis demonstrated that the R66A, R70A and R74A mutations on Bridge helix markedly reduced DNA cleavage activities (Fig. 34C), highlighting the functional significance of the recognition of the sgRNA "seed" region by the Bridge helix. Although Arg78 and Arg165 also interact with the "seed" region, the R78A and R165A mutants showed only moderately decreased activities (Fig. 34C). These results may reflect that, whereas Arg66, Arg70 and Arg74 form bifurcated salt bridges with the sgRNA backbone, Arg78 and Arg165 form a single salt bridge with the sgRNA backbone. A cluster of arginine residues on the Bridge helix are highly conserved among Cas9 proteins in the Type II-A-C systems (Figs. 40, 41), suggesting

that the Bridge helix is a universal structural feature of Cas9 proteins involved in recognition of the sgRNA and target DNA. This notion is supported by a previous observation that a strictly conserved arginine residue, equivalent to Arg70 of *S. pyogenes* Cas9, is essential for the function of *Francisella novicida* Cas9 in the Type II-B system (Sampson et al., 2013). Moreover, the alanine mutation of the repeat:anti-repeat duplex-interacting residues (Arg75 and Lysl63) and stem loop 1-interacting residue (Arg69) resulted in decreased DNA cleavage activity (Fig. 34C), confirming the functional importance of the recognition of the repeatanti-repeat duplex and stem loop 1 by Cas9.

[00713] The crRNA guide region is recognized by Cas9 in a sequence-independent manner except for the U16-Arg447 and G18-Arg71 interactions (Fig. 34A, B). This base-specific G18-Arg71 interaction may partly explain the observed preference of Cas9 for sgRNAs having guanines in the four PAM-proximal guide sequences (Wang et al., 2014).

[00714] The RECl and RuvC domains facilitate RNA-guided DNA targeting: Cas9 recognizes the 20-bp DNA target site in a sequence-independent manner (Fig. 34A). The backbone phosphate groups of the target DNA (nucleotides 1', 9'-11', 13', and 20') interact with the RECl (Asn497, Trp659, Arg661 and Gln695), RuvC (Gln926), and PI (Giul 1O8) domains. The C2' atoms of the target DNA (nucleotides 5', 7', 8', *IV*, 19', and 20') form van der Waals interactions with the RECl domain (Leul69, Tyr450, Met495, Met694 and His698) and RuvC domain (Ala728) (Fig. 34D). These interactions are likely to contribute towards discriminating between DNA vs. RNA targets by Cas9. The terminal base pair of the guide:DNA duplex (Gl:C20') is recognized by the RuvC domain via end-capping interactions (Fig. 34D); the nucleobases of sgRNA Gl and target DNA C20' interact with the side chains of Tyrl013 and VallOlS, respectively, whereas the 2'-hydroxyl and phosphate groups of sgRNA Gl interact with Val1009 and Gln926, respectively. These end-capping interactions are consistent with the previous observation that Cas9 recognizes a 17-20-bp guide:DNA duplex, and that extended guide sequences are degraded in cells and do not contribute to improving sequence specificity (Mali et al., 2013a; Ran et al, 2013). Taken together, these structural findings explain the RNA-guided DNA targeting mechanism of Cas9.

[00715] The repeatanti-repeat duplex is recognized by the REC and NUC lobes in a sequence-dependent manner: The repeatanti-repeat duplex is extensively recognized by the REC and NUC lobes (Fig. 34A). The backbone phosphate groups of the crRNA repeat (nucleotides

24, 26, and 27) and anti-repeat (nucleotides 41, 45, 46, and 48-50) interact with the REC1 domain (Argl 15, His116, His160, Lysl63, Arg340, and Arg403), PI domain (LysllllS), and Bridge helix (Lys76) (Fig. 34E, F). The 2'~hydroxyl groups of the crRNA repeat (nucleotides 22-24) and anti-repeat (nucleotides 43-45 and 47) hydrogen bond with the REC1 domain (LeulOl, Serl04, Phel05, Ilel35, Tyr359, and Gln402) and the PI domain (Ilel 110 and Tyr1131).

[00716] In contrast to the sequence-independent recognition of the guide region, there are sequence-dependent interactions between Cas9 and the repeatanti-repeat duplex. The nucleobase of the flipped U44 is sandwiched between the side chains of Tyr325 and His328, with its N3 atom hydrogen bonded with the carbonyl group of Tyr325, while that of unpaired G43 stacks with the side chain of Tyr359 and hydrogen bonds with the side chain of Asp364 (Fig. 34A, F). Finally, the nucleobases of U23/A49 and A42/G43 hydrogen bond with the side chain of Argl 122 and the main-chain carbonyl group of Phe351, respectively.

[00717] In the present structure, the repeatanti-repeat duplex is recognized primarily by the REC lobe, which is divergent in sequence and length among Cas9 orthologs within the Type II-A-C systems (Figs. 40, 41), consistent with the previous observation that Cas9 and sgRNA are interchangeable only between closely related Type II systems (Fonfara et al., 2013). The three PAM-distal base pairs (C30:G39-A32:U37) are not recognized by Cas9 and protrude from the complex (Fig. 34A), consistent with a proposed model in which a Cas9-bound repeatanti-repeat duplex is processed by the host RNase III enzyme (Deltcheva et al., 2011).

[00718] The nucleobases of G21 and U50 in the G21 :U50 wobble pair stack with the terminal C20:G1 ' pair in the guide:DNA duplex and the side chain of Tyr72 on Bridge helix, respectively, with the U50 0 4 atom hydrogen bonded with the side chain of Arg75 (Fig. 34E). Notably, A51 adopts the syn-conformation, and is oriented in the direction opposite to U50 (Figs. 33C and 34G). The nucleobase of A51 is sandwiched between the Phel 105 side chain in the PI domain and the U63 nucleobase in the linker, with its N7 and N1 atoms hydrogen bonded with the main-chain amide group of Phel 105 and the G62 2'-hydroxyl group in stem loop 1, respectively (Fig. 34G). Whereas a repeat: anti-repeat duplex is diverse in sequence and length among the Type II-A---C systems, the G21 :U50 base pair is highly conserved among Cas9s (Fonfara et al., 2013), suggesting that this wobble pairing is a universal structural feature involved in the three-way junction formation.

[00719] To verity the sequence-dependent recognition of the repeat:anti-repeat duplex, Applicants evaluated the effect of repeatanti-repeat mutations on Cas9-meditated DNA cleavage, and found multiple mutations that significantly reduce **Cas9** activity (Fig. 34C). Notably, replacement of G43, which forms a base-specific hydrogen bond with **Asp364,** with adenine reduced Cas9 activity by over 3-fold. In addition, replacement of the flipped U44 in the repeat:anti-repeat duplex with adenine resulted in over a 5-fold drop in cleavage activity, whereas replacement of U44 with another pyrimidine base (cytosine) did not significantly affect cleavage activity (Fig. 34C). These results suggest that base-specific recognition of G43 and U44 could play an important role in **sgRNA** recognition by Cas9.

[00720] sgRNA stem loops **1-3** interact with Cas9: Stem loop **1** is primarily recognized by the **REC** lobe together with the PI domain (Fig. 34A). The backbone phosphate groups of stem loop 1 (nucleotides 52, 53, and 59-61) interact with the REC1 domain (Leu455, Ser460, Arg467, **Thr472,** and **Ile473),** PI domain (Lys1123 and Lys1124), and Bridge helix **(Arg70** and Arg74), with the **2**'-hydroxy 1 group of G58 hydrogen bonded with Leu455 in the REC1 domain. A52 interacts with Phe1105 through a face-to-edge π--π stacking interaction (Fig. 34G), and the flipped U59 nucleobase hydrogen bonds with the side chain of Asn77 (Fig. 34F1).

[00721] Stem loops 2 and 3, and the single-stranded linker are primarily recognized by the NUC lobe (Fig. 34A); this contrasts with stem loop **1** and the guide:DNA/repeat:anti~repeat duplexes, which are recognized by both of the NUC and REC lobes. The backbone phosphate groups of the linker (nucleotides 63-65 and 67) interact with the RuvC domain (Glu57, Lys742, and Lysl 097), PI domain (Thr1102), and Bridge helix (Arg69), with the 2'-hydroxyl groups of **U64** and A65 hydrogen bonded with Glu57 and His721, respectively (Fig. 341). The nucleobase of C67 hydrogen bonds with the main-chain amide group of Vail 100 (Fig. **341).**

[0G722] Stem loop 2 is recognized by Cas9 via the interactions between the NUC lobe and the non- **Watson-Crick** A68:G81 pair, which is formed by direct (between the A68 N6 and G81 0 6 atoms) and water-mediated (between the A68 N1 and G81 N1 atoms) hydrogen-bonding interactions (Fig. 34J). The nucleobases of A68 and G81 contact the side chains of Serl351 and Tyrl356, respectively, with the A68:G81 pair recognized by Thrl358 via a water-mediated hydrogen bond (Fig. 34J). The 2'-hydroxy! group of A68 hydrogen bonds with the side chain of His! 349, and the 2-amino group of G81 hydrogen bonds with the main-chain carbonyl group of Lys33 (Fig. 34J).

[00723] Stem loop 3 interacts with the NUC lobe more extensively relative to stem loop 2 (Fig. 34K). The backbone phosphate groups of C91 and G92 interact with the RuvC domain (Arg40 and Lys44) (Fig. 34K), while the nucleobases of G89 and U90 hydrogen bond with Glnl272 and Glul225/Alal227, respectively (Fig. 34K). The nucleobases of A88 and C91 are recognized by the side chain of Asn46 via multiple hydrogen-bonding interactions (Fig. 34K).

[00724] Structural flexibility of Cas9 and sgRNA: Although the HNH domain cleaves the complementary strand of the target DNA at a position three nucleotides upstream of the PAM sequence (Gasiunas et al., 2012; Jinek et al., 2012), in the present structure the HNH domain is positioned away from the scissile phosphate group of the bound complementary strand (Fig. 35A). A structural comparison of Mol A and Mol B provided mechanistic insights into the complementary strand cleavage by the HNH domain. In Mol A, the HNH domain is followed by the α40 helix of the RuvC domain, which is connected with the a41 helix by an α40- α41 linker (residues 919-925) (Fig. 35A). Whereas in Mol A residues 913-925 form the C-terminal portion of the a43 helix and α43--α44 linker, in Mol B these residues form an extended a-helix, which is directed toward the cleavage site of the complementary strand (Fig. 35A). These observations suggest that the HNH domain can approach and cleave the target DNA through conformational changes in the segment connecting the HNH and RuvC domains.

[00725] Moreover, the structural comparison revealed a conformational flexibility between the REC and NUC lobes (Fig. 35B). Compared to Mol A, Mol B adopts a more open confomiation, in which the two lobes are rotated by 15° at a hinge loop between Bridge helix and the strand β5 in the RuvC domain (Fig. 35B). The bound sgRNA also undergoes an accompanying conformational change at the single-stranded linker, which interacts with the hinge loop (Fig. 35C). Applicants also observed an accompanying displacement of the β17–β18 loop of the PI domain, which interacts with the repeatanti-repeat duplex and the α2- α3 loop of the REC1 domain (Fig. 35B). Notably, there is no direct contact between the two lobes in the present structure, except for the interactions between the α2- α3 and β17–β18 loops (Fig. 35D), suggesting that Cas9 is highly flexible in the absence of the sgRNA. The flexible nature of Cas9 is likely to play a role in the assembly of the Cas9--sgRNA--DNA ternary complex.

[00726] The crystal structure of Cas9 in complex with guide RNA and target DNA reveals that the 20-bp heteroduplex formed by the crRNA guide region and the complementary strand of

the target DNA is accommodated in the positively-charged groove at the interface between the REC and NUC lobes of Cas9, with the scissile phosphate group of the target properly positioned for cleavage by the HNH domain. Although the present structure does not contain the non-complementary DNA strand, the position of the bound complementary strand suggests that the scissile phosphate of the non-complementary strand is located in the vicinity of the active site of the RuvC domain, consistent with previous biochemical data (Gasiunas et al., 2012; Jinek et al., 2012). Furthermore, Applicants' structural and functional analyses indicate that the PI domain participates in the recognition of the PAM sequence of the non-complementary strand.

[00727] Based on these observations, Applicants propose a model for the Cas9-catalyzed RNA-guided DNA cleavage (Fig. 36). Cas9 recognizes the PAM-proximal guide region and repeat:anti-repeat duplex of sgRNA to form a Cas9-sgRNA binary complex. The binary complex subsequently recognizes the DNA sequence complementary to the 20-nt guide region of the bound sgRNA, forming the final Cas9-sgRNA-target DNA ternary complex. During the ternary complex formation, the PI domain recognizes the PAM sequence of the non-complementary strand, facilitating the R-loop formation. Upon assembly of the ternary complex, the mobile HNH domain approaches and cleaves the complementary strand in the guide:DNA duplex, whereas the RuvC domain cleaves the single-stranded, non-complementary strand.

[00728] Applicants' crystal structure provides a critical step towards understanding the molecular mechanism of RNA-guided DNA targeting by Cas9. Further structural and functional studies with *S. pyogenes* Cas9 or related orthologs, including the structural determination of the Cas9-sgRNA-DNA ternary complex containing the non-complementary strand, may be important for illuminating details such as Cas9~mediated recognition of PAM sequences on the target DNA or mismatch tolerance between the sgRNA:DNA duplex. However, the present structural and functional analyses already provide a useful scaffold for rational engineering of Cas9-based genome modulating technologies. Applicants reported, for example, an *S. pyogenes* Cas9 truncation mutant (Fig. 31B) that will facilitate packaging of Cas9 into size-constrained viral vectors for *in vivo* and therapeutic applications. Similarly, future engineering of the PI domain allows for programming of PAM specificity, improving target site recognition fidelity, and increasing the versatility of the Cas9 genome engineering platform.

[00729] Experimental Procedures

Protein preparation: The gene encoding full-length *S. pyogenes* Cas9 (residues 1-1368) was cloned between the *NdeI* and *XhoI* sites of the modified pCold-GST vector (TaKaRa). The protein was expressed at 20°C in *Escherichia coli* Rosetta 2 (DE3) (Novagen), and was purified by Ni-NTA Superflow resin (QIAGEN). The eluted protein was incubated overnight at 4°C with TEV protease to remove the GST-tag, and further purified by chromatography on Ni-NTA, Mono S (GE Healthcare) and HiLoad Superdex 200 16/60 (GE Healthcare) columns. The SeMet-labeled protein was prepared using a similar protocol for the native protein. The sgRNA was *in vitro* transcribed by T7 polymerase using a PCR-amplified template, and was purified on 10% denaturing polyacrylamide gel electrophoresis. The target DNA was purchased from Sigma-Aldrich. The purified Cas9 protein was mixed with sgRNA and DNA (molar ratio 1:1.5:2), and then the complex was purified using a Superdex 200 Increase column (GE Healthcare) in a buffer containing 10 mM Tris-HCl, pH 8.0, 150 mM NaCl and 1 mM DTT.

[00730] Crystallography: The purified Cas9-sgRNA---DNA complex was crystallized at 20°C by the hanging-drop vapor diffusion method. Crystals were obtained by mixing 1 µl of complex solution ($A_{260\ nm}$ = 15) and 1 µl of reservoir solution (12% PEG 3,350, 100 mM Tris-HCl, pH 8.0, 200 **mM** ammonium acetate, 150 mM NaCl and 100 mM NDSB-256).The SeMet-labeled protein was crystallized under conditions similar to those for the native protein. X-ray diffraction data were collected at 100 K on the beamlines BL32XU and BL41XU at SPring-8 (Hyogo, Japan). The crystals were cryoprotected in reservoir solution supplemented with 25% ethylene glycol. X-ray diffraction data were processed using XDS (Kabsch, 2010) . The structure was determined by the SAD method, using the 2.8 Å resolution data from the SeMet-labeled crystal. Forty of the potential 44 Se atoms were located using SHELXD (Sheldrick, 2008) and autoSHARP (delaForteile and Bricogne, 1997). The initial phases were calculated using autoSHARP, and further improved by 2-fold NCS averaging using DM (Winn et al., 2011). The model was automatically built using PHENIX AutoSol (Adams et al, 2002), followed by manual model building using COOT (Erasley and Cowtan, 2004) and refinement using PHENIX (Adams et al., 2002). The resulting model was further refined using for native 2.4 Å resolution data.

[00731] Cell culture and transfection: Human embryonic kidney (HEK) cell line 293FT (Life Technologies) or mouse Neuro 2a (Sigma-Aldrich) cell line was maintained in Dulbecco's modified Eagle's Medium (DMEM) supplemented with 10% fetal bovine serum (HyClone), 2 **mM** GlutaMAX (Life Technologies), 100 U/ml penicillin, and 100 µg/ml streptomycin at 37°C with 5% CO_2 incubation. Cells were seeded onto 24-well plates (Corning) at a density of 120,000 cells/well, 24 h prior to transfection. Cells were transfected using Lipofectamine 2000 (Life Technologies) at 70-80% confluency following the manufacturer's recommended protocol. A total of 400 ng Cas9 plasmid and 100 ng of U6::sgRNA PCR product was transfected.

[00732] SURVEYOR nuclease assay for genome modification: 293FT cells were transfected with DNA as described above. Cells were incubated at 37°C for 72 h post-transfection prior to genomic DNA extraction. Genomic DNA was extracted using the QuickExtract DNA Extraction Solution (Epicentre) following the manufacturer's protocol. Briefly, pelleted cells were resuspended in QuickExtract solution and incubated at 65°C for 15 min, 68°C for 15 min, and 98°C for 10 min.

[00733] The genomic region flanking the CRISPR target site for each gene was PCR amplified, and products were purified using QiaQuick Spin Column (Qiagen) following the manufacturer's protocol. 400 ng total of the purified PCR products were mixed with 2 μl 10X Taq DNA Polymerase PCR buffer (Enzymatics) and ultrapure water to a final volume of 20 μl, and subjected to a re-annealing process to enable heteroduplex formation: 95°C for 10 min, 95°C to 85°C ramping at - 2°C/s, 85°C to 25°C at - 0.25°C/s, and 25°C hold for 1 min. After re-annealing, products were treated with SURVEYOR nuclease and SURVEYOR enhancer S (Transgenomics) following the manufacturer's recommended protocol, and analyzed on 4-20% Novex TBE poly-acrylamide gels (Life Technologies). Gels were stained with SYBR Gold DNA stain (Life Technologies) for 30 min and imaged with a Gel Doc gel imaging system (Bio-rad). Quantification was based on relative band intensities. Indel percentage was determined by the formula, $100 \times (1 - (1 - (b + c) / (a + b + c))^{1/2})$, where a is the integrated intensity of the undigested PCR product, and b and c are the integrated intensities of each cleavage product.

[00734] Western blot: HEK 293FT cells were transfected and lysed in 1X RIPA buffer (Sigma-Aldrich) supplemented with Protease Inhibitor (Roche). Lysates were loaded onto Bolt 4-12% Bis-Tris Plus Gel (Invitrogen) and transferred to nitrocellulose membranes. Membranes were blocked in Tris-buffered saline containing 0.1% Tween-20 and 5% blocking agent (G-Biosciences). Membrane was probed with rabbit anti-FLAG (1:5000, Abeam), HRP-conjugated anti-GAPDH (1:5,000 Cell Signaling Technology), and HRP-conjugated anti-rabbit (1:1000). Blots were visualized on Gel Doc XR+ System (Bio-rad).

[00735] Sequence information:

Italic: 3XFLAG sequence
Underlined: NLS sequences

Wildtype SpCasS
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Sp_del(97-1 50)

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Sp_de! (175-307)
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Sp_des(312-409)
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(iGGA(JCCCXTCCC(itC(Ti CAAGiiAt Γπ iiA(AACCA (tAT CXiACXCXJA A.GA Cx.JTACA (tA GitA CXAAAG
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Sp_del (1098-ersd)

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St3Cas9

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SpGas9(C80L, C574A)
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Sp_St3 Cas9 chimera (St3 in bold)

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GCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGT
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CGAGACAA^VCGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCC'GGGATTTTGC'CACCGTGCGGAAA
GTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGTGGAAGAACAGAACCACGGCCTGGAT
**CGGGGCAAGCCCAAGGGCCTGTTCAACGCCAACCTGTCCAGCAAGCCTAAGCCCAACTCCAACG
AGAATCTCGTGGGGGCCAAAGAGTACCTGGACCCTAAGAAGTACGGGTACGGCGGATACGCCG
GCATCTCCAATAGCTTCACCGTGCTCGTGAAGGGCACAATCGAGAAGGGCGCTAAGAAAAAGAT
CACAAACGTGCTGGAATTTCAGGGGATCTCTATCCTGGACCGGATCAACTACCGGAAGGATAAG**

CTGAACTTTCTGCTGGAAAAAGGCTACAAGGACATTGAGCTGATTATCGAGCTGCCTAAGTACT
CCCTGTTCGAACTGAGCGACGGCTCCAGACGGATGCTGGCCTCCATCCTGTCCACCAACAACAA
GCGGGGCGAGATCCACAAGGGAAACCAGATCTTCCTGAGCCAGAAATTTGTGAAACTGCTGTAC
CACGCCAAGCGGATCTCCAACACCATCAATGAGAACCACCGGAAATACGTGGAAAACCACAAGA
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AGCTCCTTCATCGGCCCTACCGGCAGCGAGCGGAAGGGACTGTITGAGCTGACCTCCAGAGGCT
CTGCCGCCGACTTTGAGTTCCTGGGAGTGAAGATCCCCCGGTACAGAGACTACACCCCCTCTAG
TCTGCTGAAGGACGCCACCCTGATCCACCAGAGCGTGACCGGCCTGTACGAAACCCGGATCGAC
CTGGCTAAGCTGGGCGAGGGAAAAAGGCCGGCGGCCACGAAAAAGGCCGGCCAGGCAAAAAAGAA
AAAG

St3 Sp Cas9 chimera **(St3 in** bold)
ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAGCCatgACCAAGCCCTACA
GCATCGGCCTGGACATCGGCACCAATAGCGTGGGCTGGGCCGTGACCACCGACAACTACAAGG
TGCCCAGCAAGAAAATGAAGGTGCTGGGCAACACCTCCAAGAAGTACATCAAGAAAAACCTGCT
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GGGACAGCAi GTACCCCATCTTCGGCAACCTGGTGGAAGAGAi GGCCTACCACGACGAGTTCCC
CACCATCTACCACCTGAGAAAGTACCTGGCCGACAGCACCAAGAAGGCCGACCTGAGACTGGTG
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TACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACAAAAGGCCGGCGGCCACGAAAAAGGCCG
GCCAGGCAAAAAAGAAAAAG

SpCasS rsickases
Mutated residues (changed ь GCC) bo!ded in order: D10, E762, N863, H983, D988

ATeGACrATAAGGACCACGACGGAGACTACAAGGATCATGAA WGATTACA\AAGACGATGACGATAAGA3XXKX£CAAAGAAGAAGCG
GAAGGTCGGTATCCACGGAGTCCCAGCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGC
CGTGATCACXXJACGAGTAC AAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCT
GATCGGAGCCCTGCT GTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG
GAAGAACCGGATCTGCTATCTGCAAGAGATCT^ AGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGA
GTCCTTCCT GGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCA TC ITCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA
GTACCCCACCATCTACCACCTGAGAAAGAAACTC GTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCC
CACATGATGAAGLTCCGGGGCCACLTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACG IGGACAAGCTGTTCATCCAGC
TGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCC AGACT
GAGCAAGACK:AGACGGCTGGAAAATCTGATCG^^ CAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGCAACCTGATTGCCCT
GAGCCTGGGCCTGACCCCCAACTT CAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGA
CGACGACCTGGACAACCT(X:TGGCXX^^ ATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATC
CTGCTGAGCGACA ICCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTAIGATCAAGAGATACGACGAGCAC
CACCAGGACCTGACCCTGCTGAY\IKGCTCTCGTGCGGCAGCACK^TGCCTGAGAAGTACAA,^GAGATTTTCTTCGACCAGAGCAAGA
ACGGCTACGC CGGCTACATRGACGGCGGAGCCAGCCAGGAAGAGTFCTACAAGTRCATCAAGC CCATCCTGGAAAAGATGGACG
GCACCGAGGAACTCX;TCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTC GACAACGGCAGCATCCCCCACC
AGATCCACCTGGGAGAGCTGCACGCCALTCTGCGGCGGCAGGAAGALTLTRACCCATTCCTGAAGGACA^CCGGGAAAAGATCG
AGAAGATCCTG ACCTTCCGC ATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGARFCGCCTGGATGACCAGAAAGAG
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AGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATC^ AGGAACGGCTGAAAA
CCTATGCCCACCTGIT CGACGACAAAGTG ATGAAGCAGCTGAA GCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGC
TGATCAACGGCATCCGGGACAAGCAGTCCGCX:^^^ GACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCAT
GCAGCTGATCCACGACGACAGCCTGACCTITAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGC GATAGCCTGCACGA
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GCGAGAGAA IIGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCC AG
CTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCACXJAACTGGACATCAY^CCGGCTGT
CCGACTACGATG7 GGACCATATCG IGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGIGCTGACCAGAAGCGACAA
GAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCA
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AGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAG TACGACGAGA

ATGACAAGCTGATCC(X¾JAAGTGAAAG TGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAA
AGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCC
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AGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTG
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CCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACC
AAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCrCAGCTGGGAGGC
GACAAAAGGCCGGCGGCCACGAAAAAGGCCGGCCAGGCAAAAAAGAAAAAG

SpCasd point mutants

Mutated residues (changed b GCC) **bo!ded** in order: R63A, R66A, R69A, R70A, R74A, R75A, R78A, K163A, R165A, K510A

A TGGA CTA TAA GGA CCA CGACGGA GA CTA CAA GGA TCA TG-A TA TTGA TTA CM A GA CGA TGACGA TAA GATGGCCCCAAAGAAGAAGCG
GAAGGTCGGTATCCACGGAGTCCCAGCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGC
CGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAAITCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCT
GATCGGAGCCCTGCTGTTCGACAGCGGCGAAA^ ;CCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGAC
GGAAGAACCGGATCTGCTATCTGCAAGAGATCTrCAGCAACGAGATGGCCAAGGTGGACGACAGCTTC ITCCACAGACTGGAAG
AGTCCTTCCTGGTCKTAAGACKTATAAGAAGCACG AGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGA
AGTACCCX^ACCATCTACCACCTGAGAAAGAAA CTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGC
CCACATGATCAAGTTCC'CKXJGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCA
GCTGGTGCAGACCTACA\CCAGCTGTTCGAGGA^ AAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGA
CTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTRCGGCAACCTGALTGCC
CTGAGCCTGGGCCTGACCCCCAACTTCAAGAGC^^^ CTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACG
ACGACGACCTGGACAACCTGCTGGC CCAGATCGGCGACCAGTACGCCGACCTGTTRCTGGCCGCCAAGAACCTG RCCGACGCCAT
CCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCA
CCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGC GGCAGCAGCTGCC RGAGAAGTACAAAGAGATTRTC LTCGACCAGAGCAAG
AACGGCTACGCCGGC IACALTGACGGCGGAGCCAGCCAGGAAGAG ITCTACAAGTTCATCAAGCCCA ICCTGGAAAAGATGGAC
CKK^ACCGAGGAACTGCTCGTGAAGCTGAYKCAGAGAGGACCTGCTCK^ GGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCAC
CAGATCCACCTGGGAGAGCTGCACGCCATRCTGCGGCGGCAGGAAGATTNTACCCATRCCTGAAGGACAACCGGGAAAAGATCG
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AAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTC^ \GCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTC
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GACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCAC
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AAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCrCAGCTGGGAGGC
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sgRNA sequences:

guide sequence underlined

i-83

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AAA AAGUGGCACCGAGUCGGXXiCXUUXJ

+47

GAGUCCGAGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGUIJAAAAUAAGGCUAGUCCGUUUU

+67

GAGUCCGAGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU
GAA AAAGUGUI/UU

mutate proximal crRNA:tracrRNA dup!ex

GAGUCCGAGC$_A$GAAGAAGAAGCCCCAGAGCUAGAAAUAGCAAGUUGGGGUAAGGCUAGUCCGUUAUCAACUUG
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truncate dista! crRNA:tracrRNA duplex

GAGUCCGAGCAGAAGAAGAAGUUUUAGAGACAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUG
(X: ACCGAGUCGC XXX:UχUU;

remove crRMA:tracrRNA dup!ex bulge

GAGUCXG AGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCUUUAAAAUAAGGCUAGUCCGUUAUCAACUUGA
AAAAGUGGCACCGAGUCGGUGCUUUU

abolish siem!oop 1

GAGUCCGAGCAGA AGAAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAUUCUAGUAAGUUAUCAACUU
GAAAAAGUGGC A.CCGAG-UCGGUGCUXJUU

mutate stem!oop 1

GAGUGCGAGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGCCAUGUGCGUUAUCAACUU
GAAAAAGIXXCXACCGAGUCGGUGCUIIXjX;

truncate linker

GA GUCCGAGGAGAAGA AGAAGIJUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUAACUUGAAA
AAGLXGCACCGAGUCGGUGCUUUXJ

replace stemloop 2

GAGUCCGAGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCACGCC
GAAACXiCCXiGCACXjGAGUCGGUGClJIJUU

lengthen stem!oop 2

GAGJ C« AGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU
GAGAAAUCAAGXXCAXXiAGXX GGUGCUUXU

mutate stem!oop 3

GAGUCCXGAGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU
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lengthen stemloop 3

GAGUCCGAGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU
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reconstructed sgRNA

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CCCGXACCGAXJCGXXUUUX

G43A

GAXUCCGAGCAGAAGA AGAAGUUUUAGAGCUAGAAAUAGCAACUUAAAAUAAGGCUAGUCCGUUAUCAACUU
GAAA AAGUGGC ACCGAGXXGG5GCU UU!J

U44G

GAGUCCGAGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGGUAAAAUAAGGCUAGUCCGUUAUCAACUU
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U44C

GAGUCCGAGCAGAAGAAGAAGUUUUAGAGCUAGAAAUAGCAAGCUAAAAUAAGGCUAGUCCGUUAUCAACUU
GAAAAAGLXX;AXXAGi XXXUX X3XX

Primers

Cas9	Target	PAM	SURVEYOR primer F	SURVEYOR PRIMER R
Sp	GAGTCCGAGC AGAAG AA GAA	GGG	CCATXXXTTCTGTGAAT GT	GGAGATTGGAGACACGG AGA
St3	GCTCCCATCACATCAACC GG	TGGC G	*same*	*same*

Example 13: Generation of optimized functional CRISPR-Cas systems targeting the Neurog2 gene by modifying sgRNA architecture with the insertion ofMS2 loops into loops of the sgRNA

[00736] The crystal structure information (described in U.S. provisional applications 61/915,251 filed December 12, 2013, 61/930,214 filed on January 22, 2014, 61/980,012 filed April 15, 2014) provides structural information to modify sgRNA architecture. Applicants detemiinded that there was potentially room for extension of both the tetraloop and ioop2 of the sgRNA (without collision with the Cas9 protein). Applicants showed that insertion of MS2 loops at these positions enabled recruitment of MS2 binding proteins to these two locations, and thereby mediated locus specific recruitment of any effector fusions (such as transcriptional activator domains vp64, p65, transcriptional repressor domains SID4X, KRAB, or any epigenetic effector domains). The Examples are interesting. There is a focus on the identification of two 4nt stretches in the guides that are exposed "outside" of Cas9-guide-target DNA complex (no contact between these 4 nt stem terminations and Cas9 amino acids were identified in the crystal). One 4nt stretch falls in the tetraloop, the other 4nt stretch falls in the stem loop 2. Either or both of these 4nt stretches can be replaced by aptamer sequence. Each or both can either be replaced completely or partial!)', or that either or both may be retained completely and a noncoding loop can be added after the 4 nts. The aptamers is a polynucleotide and may be DNA or RNA, but RNA is preferred. The aptamer has a corresponding RNA-binding protein that recognises a specific RNA sequence. Recruitment of these effector domains to the tetraloop and loop 2 of the sgRNA potentially led to a more favorable positioning relative to the targeted DNA (compared to C-term fusions of effector domains to the Cas9 proteins or addition of Ms2 loops after loop 3 of the sgRNA).

[00737] Neuro 2a cells (Sigma-Aldricb) were grown in media containing a 1:1 ratio of OptiMEM (Life Technologies) to high-glucose DMEM with GlutaMax and sodium pyruvate (Life Technologies) supplemented with 5% HyClone heat-inactivated FBS (Thermo Scientific), 1% penicillin/streptomycin (Life Technologies), and passaged at 1:5 every 2 days. 120,000 cells were plated in each well of a 24-well plate 18-20 h before transfection. Cells were transfected with Lipofectamine transfection reagent (Life Technologies) according to the manufacturer's instructions. Plasmid DNA was used for transfection of MS2-VP64 and Cas9 constructs, while PCR product was transfected for the guide RNA expression cassette.

[00738] RNA was extracted using the RNeasy kit (Qiagen) according to manufacturer's instructions and lmg of RNA per sample was reverse-transcribed using qScript (Quanta Biosystems). Relative mRNA levels were measured by reverse transcription andquantitative PGR (qRT-PCR) using TaqMan probes specific for the targeted gene as well as GAPDH as an endogenous control (Life Technologies). ddCt analysis was used to obtain fold-changes relative to negative controls transfected with GFP only.

[00739] Results indicated that both insertions in the tetraloop and loop 2 are effective and that the most efficient combination uses an insertion of MS2 loops in both in the tetraloop and in loop 2 of the sgRNA in combination with a dCas9-vp64 and MS2-vp64 construct. This new activator design (illustrated in Fig. 44 and shown as red bar for the TL + L2: Ms2 guide in Fig. 45) was found to mediate much higher target gene upreguiation compared to the previous design (illustrated in Fig. 43 and shown as the green bar for the regular guide in Fig. 45).

[00740] MS2 Pilot Sequences are indicated below:

Neurog2 target sequence

GATACGATGAAAAGAATAAGC

Tetraloop MS2 stem loop msertion sgRNA scaffold

NNNNNNNNNNNNNNNNNNNNgttttagagctaggccAACATGAGGATCACCCATGTCTGCAGggcctagcaagttaaaataaggctagtccgttatcaCGCCGAAAGGCGggcaccgAGTcggtgcTTTTT

Loop 2 MS2 stem loop msertion sgRNA scaffold

NNNNNNNNNNNNNNNNNNNNgttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttggccAACATGAGGATCACCCATGTCTGCAGggccaagtggcacegAGTcggtgcTTTTT

Tetraloop and Loop 2 MS2 stem loop insertion sgRNA scaffold

NNNNNNNNNNNNNNNNNNNNgttttagagctaggccAACATGAGGATCACCCATGTCTGCAGggcctagcaagttaaaataaggctagtccgttatcaacttggccAACATGAGGATCACCCATGTCTGCAGggccaagtggcaccgAGTcggtgcTTTTT

Standard guide scaffold

NNNNNNNNNNNNNNNNNNNNgtttiagagctaGAAAiagcaagitaaaataaggctagtccgttai caacttGAAAaagtggcaccgAGTcggtgcTTTTT

M82-vp64 sequence

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGG [illegible] CAACTCACGGAGCCAGGCCTACAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCC **AGAAGAGAAAGTATACCATCAAGGTGGAGGTCCCCAAAGTGGCTACCCAGACAGTG** GGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCTACCTGAACATGGAGCTCACT **ATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAAGGCAATGCAGGGG** [illegible] gcgctGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCggacctaaga aaaagaggaaggtggcggccgctggatccGGACGGGCTGACGCATTGGACGATTTTGATCTGGATAT GCTGGGAAGTGACGCCCTCGATGATTTTGACCTTGACATGCTTGGTTCGGATGCCCT **TGATGACTTTGACCTCGACATGCTCGGCAGTGACGCCCTTGATGATTTCGACCTGGA** CATGCTGATTAAC

Example 14: Further optimization of functional CRISPR-Cas systems by modifying sgRNA backbone or architecture

[00741] Applicants tested the efficiency of the tetrafoop and !oop2 MS2 loop insertions on two additional gene targets (human ASCLl and human MYODl) and confirmed the increased effectiveness of sgRNA design as described in Example 13 compared to the standard C-terminal fusion of VP64 to Cas9 (See Figs. 46 and 47). Applicants further tested the hypothesis that a combination of two different activation domains (for e.g. VP64 and P65) could lead to synergy and therefore increased efficiency of target gene upregulation compared to using the same total number of a single type of activation domain. Applicants also tested an alternative guide architecture optimized for CRISPR/Cas9 imaging in: Chen, Baohui, et al. "Dynamic Imaging of Genomic Loci in Living Human Cells by an Optimized CRISPR/Cas System." Ceil 155.7 (2013): 1479-1491 in the context of gene activation.

[00742] Methods:

Target Sequences

ASCL1

GCAGCCGCTCGCTGCAGCAG

MYOD1

GGGCCCCTGCGGCCACCCCG

[00743] Cell Culture and Transfection and Gene Expression Analysis

Human HEK293FT cells were maintained in high-glucose DMEM with GlutaMax and sodium pyruvate (Life Technologies) supplemented with 10% heat-inactivated characterized HyClone fetal bovine serum (Thermo Scientific) and 1% penicillin/streptomycin (Life Technologies). Cells were passaged daily at a ratio 1 to 2 or 1 to 2.5. For MS2/dCas9 activator experiments, 20,000 HEK293FT cells were plated in 100 µL of culture medium in poly-d-lysine coated 96-well plates (BD biosciences). 24 hours after plating, cells were transfected with a 1:1:1 mass ratio of:

- sgRNA backbone plasmid with gene specific targeting sequence or pUC19 control plasmid
- MS2-VP64 plasmid or MS2-p65 plasmid or pUC19 control plasmid
- dCas9 plasmid or dCas9-VP64 plasmid or dCas9-p65 plasmid or pUC19 control plasmid

[00744] Total plasmid mass per well was 0.3 micrograms. Transfection was performed with 1.5 µL Lipfectamine 2000 (Life Technologies), according to the manufacturer's instructions. Culture medium was changed 5 hours after transfection. 48 hours after transfection, cell lysis and reverse transcription were performed using a Cells-to-Ct kit (Life Technologies). Gene expression levels were quantified by using Taqman qPCR probes (Life technologies) and Fast Advanced Master Mix (Life Technologies). ASCL1 and MYOD1 expression levels were calculated relative to GAPDH expression level. Fold gene expression levels were determined by comparison to samples transfected with GFP plasmid only.

[00745] The results indicate that the Applicants validated the efficiency of the tetraloop and loop2 MS2 loop insertions on two additional gene targets and confirmed the increased effectiveness of this design compared to the standard C-terminal fusion of VP64 to Cas9. Applicants further confirmed the hypothesis that a combination of two different activation domains could improve target gene activation (via synergy, e.g. by recruiting different epigenetic modulators, general transcription factors and co-activators). Applicants also determined that the

alternative guide architecture optimized for CRISPR/Cas9 imaging in: Chen, Baohui, et al. "Dynamic Imaging of Genomic Loci in Living Human Cells by an Optimized CRISPR/Cas System." Cell 155.7 (2013): 1479-1491 did not exhibit any improvement over the standard architecture.

[00746] In conclusion, these experiments showed that an improved Cas9 activator architecture consists of a sgRNA with MS2 loop insertions in the tetraloop and loop 2 in combination with either M82-VP64 and dCas9-P65 or MS2-P65 and dCas9-VP64.

[00747] MS2 sgRNA Scaffold Sequence Information

In all sequences below, NNNNNNNNNNNNNNNNNNNN represents the locus-specific targeting sequence of each sgRNA.

pSAMca006 standard sgRNA backbone

NNNNNNNNNNNNNNNNNNNNgttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaecgagtcggtgcTTTTTTT

+83 nucleotide chimeric backbone used in Zhang Lab CRISPR/Cas9 publications

pSAMca002 Tetraloop stem extension + AU flip sgRNA backbone

NNNNNNNNNNNNNNNNISiNNNgtttaagagctatgctgGAAAcagcatagcaagtttaaataaggctagtccgttatcaacttgaaaaagtggcaecgagtcggtgcTTTTTTT

[00748] Backbone optimized for CRISPR/Cas9 imaging in:

Chen, Baohui, et al. "Dynamic Imaging of Genomic Loci in Living Human Cells by an Optimized CRISPR/Cas System." Cell 155.7 (2013): 1479-1491.

T in location +5 (5th nucleotide after target sequence) exchanged with A in location +36. Authors suggest this change should increase sgRNA concentration by removing putative U6 termination site at location +2 to+5.

TGCTG is added after location +12 of standard backbone and CAGCA is added after location +21 of standard backbone. These insertions pair with one another to created an extended stem at the base of the tetraloop. Authors suggest that this stem extension may help stabilize the sgRNA.

[00749] pSAMca009 MS2-binding loop on tetraloop and stemloop 2 sgRNA backbone

NNNNNNNNNNNNNNNNNNNNgtttiagagctaggccAACATGAGGATCACCCATGTCTGCAGggcctagcaagttaaaataaggctagtccgttatcaacttggccAACATGAGGATCACCCATGTCTGCAGggccaagtggcaccgagtcggtgcTTTTTTT

MS2-binding loop ggccAACATGAGGATCACCCATGTCTGCAGggcc replaces nucleotides +13 to +16 and nucleotides +53 to +56 of the standard sgRNA backbone. The resulting structure is an sgRNA scaffold in which the tetraloop and stemloop 2 sequences have been replaced by an MS2 binding loop. The tetraloop and stemloop 2 were selected for replacement based on information obtained from the Cas9/RNA/DNA crystal structure. Specifically, the tetraloop and stemloop 2 were found to protrude from the Cas9 protein in such a way which suggested that adding an MS2 binding loop would not interfere with any Cas9 residues. Additionally, the proximity of the tetraloop and stemloop 2 sites to the DNA suggested that localization to these locations would result in a high degree of interaction between the DNA and any recruited protein, such as a transcriptional activator.

[00750] pSAMcaOlO MS2-binding loop on tetraloop and stemloop 2 + tetraloop stem extension + AU flip sgRNA backbone

NNNNNNNNNNNNNNNNNNNNgtttaagagctatgctgggccAACATGAGGATCACCCATGTCTGCAGggcccagcatagcaagtttaaataaggctagtccgttatcaacttggccAACATGAGGATCACCCATGTCTGCAGggccaagtggcaccgagtcggtgcTTTTTTT

T in location +5 of standard sgRNA backbone exchanged with A in location +36 of standard sgRNA backbone. The stem loop extension and MS2-binding loop sequence tgctgggccAACATGAGGATCACCCATGTCTGCAGggcccagca replaces nucleotides +13 to +16 of the standard sgRNA backbone. The MS2-bindmg loop sequence ggccAACATGAGGATCACCCATGTCTGCAGggcc replaces nucleotides +53 to +56 of the standard sgRNA backbone. The resulting structure combines the hypotheses described for pSAMca002 and pSAMca009.

[00751] pSAMcaOl l MS2-bindmg loop on tetraloop and stemloop 2 + AU flip sgRNA backbone

NNNNNNNNNNNNNNNNNNNNgtttaagagctaggccAACATGAGGATCACCCATGTCTGCAGggcctagcaagtttaaataaggctagtccgttatcaacttggccAACATGAGGATCACCCATGTCTGCAGggccaagtggcaccgagtcggtgcTTTTTTT

T in location +5 of standard sgRNA backbone exchanged with A in location +36 of standard sgRNA backbone. The MS2-binding loop sequence **ggccAACATGAGGATCACCCATGTCTGCAGggcc** replaces nucleotides +13 to +16 and nucleotides +53 to +56 of the standard sgRNA backbone. The resulting structure combines the hypothesis described for pSAMca009 with the AUflip hypothesis of pSAMcaG02 (removing putative U6 termination). This construct differs from pSAMcaOlO in that it does not include the additional tgctg tetraioop stem extension from pSAMca002, to determine whether overextending the tetraioop stem would diminish sgRNA functionality in the case of pSAMcaOlO.

[00752] pSAMca003 MS2-binding loop on tetraioop + stemloop 2 GC tract switch sgRNA backbone

NNNNNNNNNNNNNNNNNNNNgttttagagctaggccAACATGAGGATCACCCATG TCTGCAGggcctagcaagttaaaataaggctagtccgttatcaCGCCgaaaGGCGggcaccgagtcggtgcTTTTTTT

The MS2-binding loop sequence **ggccAACATGAGGATCACCCATGTCTGCAGggcc** replaces nucleotides +13 to +16 **of** the standard sgRNA backbone. The sequence CGCC replaces nucleotides +49 to +52 of the standard sgRNA backbone. The sequence GGCG replaces nucleotides +57 to +60 of the standard sgRNA backbone. The tetraioop MS2-binding loop insertion was designed with the same rationale as described for pSAMca009 above. The CGCC and GGCG sequences replace the stem portion of stemloop 2. The increased base-pairing strength of the CGCC-GGCG stem compared to the original ACTT-AAGT stem was hypothesized to provide additional stability to the stemloop 2 structure, thereby increasing sgRNA performance or longevity.

[00753] pSAMcaOB MS2-binding loop on tetraioop No stemloop 2 GC tract switch sgRNA backbone

NNNNNNNNNNNNNNNNNNNNgttttagagctaggccAACATGAGGATCACCCATG TCTGCAGggcctagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtgcTTTTTTT

The MS2~bindmg loop sequence ggccAACATGAGGATCACCCATGTCTGCAGggcc replaces nucleotides +13 to +16 of the standard sgRNA backbone. The tetraioop MS2-binding loop insertion was designed with the same rationale as described for pSAMca009 above.

[00754] pSAMca025 MS2-binding loop on tetraioop and stemloop 2 + 2 MS2 binding loops on 3' tail sgRNA backbone

NNNNNNNNNNNNNNNNNNNNgtttiagagctaggccAACATGAGGATCACCCATG TCTGCAGggcctagcaagttaaaataaggctagtccgttatcaacttggccAACATGAGGATCACCCATGTCTG CAGggccaagtggcaccgagtcggtgcTAACATGAGGATCACCCATGTCTGCAGTGCAGGTCGAC TCTAGAAACATGAGGATCACCCATGTTTTTTT

The sequence TAACATGAGGATCACCCATGTCTGCAGTGCAGGTCGACTCTAGAAACATGAGGATC ACCCATGT comprising two MS2-binding loops separated by a short linker was inserted between nucleotide +76 and +77 of the standard sgRNA backbone. We hypothesize that adding 2 additional MS2-binding loops to the 3' tail of the sgRNA will increase the activity of the MS2/CRISPR/dCas9 activator system by providing a greater number of MS2 domain binding sites and facilitating increased recruitment of activation domains.

[00755] pSAMca026 MS2-binding loop on tetraioop and stemloop 1 and stemloop 2 sgRNA backbone

NNNNNNNNNNNNNNNNNNNNgttttagagctaggccAACATGAGGATCACCCATG TCTGCAGggcctagcaagttaaaataaggggccAACATGAGGATCACCCATGTCTGCAGggcctccgttat caacttggccAACATGAGGATCACCCATGTCTGCAGggccaagtggcaccgagtcggtgcTTTTTTT

MS2-binding loop ggccAACATGAGGATCACCCATGTCTGCAGggcc replaces nucleotides +13 to +16 and nucleotides +35 to +38 and nucleotides +53 to +56 of the standard sgRNA backbone. In addition to the tetraioop and stemloop 1 MS2-binding loop replacements described for pSAMcaOG9, this structure replaces the loop of stem loop 1 with an MS2-binding loop. The exposed state of stemloop 1, as observed in the Cas9/RNA/DNA crystal structure, suggests that adding an MS2-binding loop at this location would not disrupt the Cas9/RNA/DNA interaction. Further, an MS2-binding loop inserted at this location would allow for recruitment of MS2-activator protein in a region local to the target DNA.

[00756] MS2-activator Protein Information

MS2-VP64

DNA sequence

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGG GGATGTGACAGTGGCTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTC CAACTCACGGAGCCAGGCCTACAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCC **AGAAGAGAAAGTATACCATCAAGGTGGAGGTCCCCAAAGTGGCTACCCAGACAGTG**

GGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCTACCTGAACATGGAGCTCACT
ATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAAGGCAATGCAGGGG
CTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGTATCTACa
gcgctGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCggacctaaga
aaaagaggaaggtggcggccgctggatccGGACGGGCTGACGCATTGGACGATTTTGATCTGGATAT
GCTGGGAAGTGACGCCCTCGATGATTTTGACCTTGACATGCTTGGTTCGGATGCCCT
TGATGACTTTGACCTCGACATGCTCGGCAGTGACGCCCTTGATGATTTCGACCTGGA
CATGCTGATTAAC

Amino acid sequence

MASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQ
SSAQKRKYTIKVEVPKVATQTVGGVELPVAAWRSYLNMELTIPIFAIT^SDCELIVKAMQ
GLLKDGNPIPSAIAANSGIYSAGGGGSGGGGSGGGGSGPKKKRKVAAAGSGRADALDD
FDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLIN

Description

The M82-VP64 activator protein consists of the following domains from N-term to C-term: the N55K mutant of the MS2 bacteriophage coat protein (shown to have higher binding affinity than wild type MS2 in Lim, F., M. Spingola, and D. S. Peabody. "Altering the RNA binding specificity of a translational repressor." Journal of Biological Chemistry 269.12 (1994): 9006-9010.), 3X GGGGS linker, SV40 nuclear localization signal, and VP64 activation domain. Functionally, the MS2 domain binds to its specific RNA aptamer, the 3XGGGGS linker provides mechanical flexibility between the MS2 and VP64 domains, the SV40 nuclear localization signal facilitates transport of the protein into the nucleus, and the VP64 activation domain promotes transcriptional activation.

[00757] **MS2-p65**

DNA sequence

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGG
GGATGTGACAGTGGCTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTC
CAACTCACGGAGCCAGGCCTACAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCC
AGAAgAGAAAGTATACCATCAAGGTGGAGGTCCCCAAAGTGGCTACCCAGACAGTG
GGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCTACCTGAACATGGAGCTCACT
ATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAAGGCAATGCAGGGG

CTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGTATCTACa
gcgctGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCggacctaaga
aaaagaggaaggtggcggccgctggatccCCTTCAGGGCAGATCAGCAACCAGGCCCTGGCTCTGG
CCCCTAGCTCCGCTCCAGTGCTGGCCCAGACTATGGTGCCCTCTAGTGCTATGGTGC
CTCTGGCCCAGCCACCTGCTCCAGCCCCTGTGCTGACCCCAGGACCACCCCAGTCAC
TGAGCGGCTCCAGTGCCCAAGTCCTACAGGCCCCGGGCCCAGGGGACTCTGAGTGA AGCT
CTGCTGCACCTGCAGTTCGACGCTGATGAGGACCTGGGAGCTCTGCTGGGGAACAG
CACCGATCCCGGAGTGTTCACAGATCTGGCCTCCGTGGACAACTCTGAGTTTCAGCA
GCTGCTGAATCAGGGCGTGTCCATGTCTCATAGTACAGCCGAACCAATGCTGATGGA
GTACCCCGAAGCCATTACCCGGCTGGTGACCGGCAGCCAGCGGCCCCCCGACCCCG
CTCCAACTCCCCTGGGAACCAGCGGCCTGCCTAATCGGCTGTCCGGAGATGAAGAC
TTCTCAAGCATCGCTGATATGGACTTTAGTGCCCTGCTGTCACAGATTTCCTCTAGTG
GGCAG

Amino acid sequence

MASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQ
SSAQKEXYTIKVEVPKVATQTVGGVELPVAAWRSYLNMELTIPIFATNSDCELIVKAMQ
GLLKDGNPIPSAIAANSGIYSAGGGGSGGGGSGGGGSGPKKKRKVAAAGSPSGQISNQA
LALAPSSAPVLAQTMVPSSAMVPLAQPPAPAPVLTPGPPQSLSAPVPKSTQAGEGTLSEA
LLHLQFDADEDLGALLGNSTDPGVFTDLASVDNSEFQQLLNQGVSMSHSTAEPMLMEY
PEAITRLVTGSQRPPDPAPTPLGTSGLPNGLSGDEDFSSIADMDFSALLSQISSSGQ

Description

The MS2-VP64 activator protein consists of the following domains from N-term to C-term: the N55K mutant of the MS2 bacteriophage coat protein (shown to have higher binding affinity than wild type MS2 in Lim, F., M. Spingola, and D. S. Peabody. "Altering the RNA binding specificity of a translational repressor." Journal of Biological Chemistry 269.12 (1994): 9006-9010.), 3X GGGGS linker, SV40 nuclear localization signal, and p65 activation domain. Functionally, the MS2 domain binds to its specific RNA aptamer, the 3XGGGGS linker provides mechanical flexibility between the MS2 and p65 domains, the SV40 nuclear localization signal facilitates transport of the protein into the nucleus, and the p65 activation domain promotes transcriptional activation.

Example 15: Further optimization of functional CRISPR-Cas systems by multiplexing to mediate distinct effects at different genomic loci simultaneously

[00758] PP7 is the RNA-binding coat protein of the bacteriophage Pseudomonas. Like MS2, it binds a specific RNA sequence and secondary structure. The PP7 RNA-recognition motif is distinct from that of MS2. Consequently, PP7 and MS2 may be multiplexed to mediate distinct effects at different genomic loci simultaneously. For example, an sgRNA targeting locus A may be modified with MS2 loops, recruiting MS2-VP64 activators, while another sgRNA targeting locus B may be modified with PP7 loops, recruiting PP7-SID4X repressor domains (Fig. 48). In the same cell, dCas9 may thus mediate orthogonal, locus-specific modifications. This principle may be extended to incorporate other orthogonal RNA-binding proteins such as Q-beta.

[00759] PP7-effector Protein Information

Applicants construct PP7-effector constructs as previously described in Examples 13 and 14. Sequence information on these contracts are provided below:

[00760] PP7-VP64

DMA sequence

ATGTCCAAAACCATCGTTCTTTCGGTCGGCGAGGCTACTCGCACTCTGACTGAGATC
CAGTCCACCGCAGACCGTCAGATCTTCGAAGAGAAGGTCGGGCCTCTGGTGGGTCG
GCTGCGCCTCACGGCTTCGCTCCGTCAAAACGGAGCCAAGACCGCGTATCGCGTCA
ACCTAAAACTGGATCAGGCGGACGTCGTTGATTCCGGACTTCCGAAAGTGCGCTACA
CTCAGGTATGGTCGCACGACGTGACAATCGTTGCGAATAGCACCGAGGCCTCGCGC
AAATCGTTGTACGATTTGACCAAGTCCCTCGTCGCGACCTCGCAGGTCGAAGATCTT
GTCGTCAACCTTGTGCCGCTGGGCCGTagcgctGGAGGAGGTGGAAGCGGAGGAGGAG
GAAGCGGAGGAGGAGGTAGCggacctaagaaaaagaggaaggtggcggccgctggatccGGACGGGCTG
ACGCATTGGACGATTTTGATCTGGATATGCTGGGAAGTGACGCCCTCGATGATTTTG
ACCTTGACATGCTTGGTTCGGATGCCCTTGATGACTTTGACCTCGACATGCTCGGCA
GTGACGCCCTTGATGATTTCGACCTGGACATGCTGATTAAC

Amino acid sequence

MSKTIVLSVGEATRTLTEIQSTADRQIFEEKVGPLVGRLRLTASLRQNGAKTAYRVNLKL
DQADWDSGLPKVRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLVVNLV
PLGRSAGGGGSGGGGSGGGGSGPKKKRKVAAAGSGRADALDDFDLDMLGSDALDDFD
LDMLGSDALDDFDLDMLGSDALDDFDLDMLIN

Description

The PP7-VP64 activator protein consists of the following domains from N-term to C-term: the PP7 Pseudomonas bacteriophage coat protein (with amino acids 68-69 mutated to SG and amino acids 70-75 deleted from the wild type protein as described in Wu, Bin, Jeffrey A. Chao, and Robert H. Singer. "Fluorescence fluctuation spectroscopy enables quantitative imaging of single mRNAs in living cells."Biophysical journal 102.12 (2012): 2936-2944. and Chao, Jeffrey A., et al. "Structural basis for the coevolnfion of a viral RNA-protein complex." Nature structural & molecular biology 15.1 (2007): 103-105.), 3X GGGGS linker, SV40 nuclear localization signal, and VP64 activation domain. Functionally, the PP7 domain binds to its specific RNA aptamer, the 3XGGGGS linker provides mechanical flexibility between the MS2 and VP64 domains, the SV4Q nuclear localization signal facilitates transport of the protein into the nucleus, and the VP64 activation domain promotes transcriptional activation.

[00761] PP7-SID4X

DNA sequence

ATGTCCAAAACCATCGTTCTTTCGGTCGGCGAGGCTACTCGCACTCTGACTGAGATC
CAGTCCACCGCAGACCGTCAGATCTTCGAAGAGAAGGTCGGGCCTCTGGTGGGTCG
GCTGCGCCTCACGGCTTCGCTCCGTCAAAACGGAGCCAAGACCGCGTATCGCGTCA
ACCTAAAACTGGATCAGGCGGACGTCGTTGATTCCGGACTTCCGAAAGTGCGCTACA
CTCAGGTATGGTCGCACGACGTGACAATCGTTGCGAATAGCACCGAGGCCTCGCGC
AAATCGTTGTACGATTTGACCAAGTCCCTCGTCGCGACCTCGCAGGTCGAAGATCTTY
GTCGTCAACCTTGTGCCGCTGGGCCGTagcgctGGAGGAGGTGGAAGCGGAGGAGGAG
GAAGCGGAGGAGGAGGTAGCggacctaagaaaaagaggaaggtggcggccgctggatccATGAACATCC
AGATGCTGCTGGAGGCCGCTGACTACCTGGAACGGAGAGAGCGCGAAGCCGAGCAC
GGATATGCTTCAATGCTGCCCGGAAGCGGCATGAATATTCAGATGCTGCTGGAGGCT
GCTGATTACCTGGAAAGGCGCGAACGGGAGGCCGAACATGGCTATGCTTCCATGCT
GCCTGGGTCTGGAATGAATATCCAAATGCTGCTGGAGGCAGCCGATTACCTGGAAC
GGAGAGAAAGAGAAGCCGAGCACGGATACGCCAGCATGCTGCCAGGCAGCGGGAT
GAACATACAAATGCTGCTGGAGGCTGCCGATTACCTGGAGAGGCGCGAGAGAGAAG
CTGAACATGGCTATGCCTCTATGCTGCCC

Amino acid sequence

MSKTIVL8VGEATRTLTEIQSTADRQIFEEKVGPLVGRLRLTASLRQNGAKTAYRVNLKL
DQADVVDSGLPKVRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLVVNLV
PLGRSAGGGGSGGGGSGGGGSGPKKKRKVAAAGSMNIQMLLEAADYLERREREAEHG
YASMLPGSGMNIQMLLEAADYLERREREAEHGYASMLPGSGMN1QMLLEAADYLERR
EREAEHGYASMLPGSGMNIQMLLEAADYLERREREAEHGYASMLP

Description

The PP7-SID4X repressor protein consists of the following domains from N-term to C-term: the PP7 Pseudomonas bacteriophage coat protein (with amino acids 68-69 mutated to SG and amino acids 70-75 deleted from the wild type protein as described in Wu, Bin, Jeffrey A. Chao, and Robert H. Singer. "Fluorescence fluctuation spectroscopy enables quantitative imaging of single mRNAs in living cells."Biophysical journal 102.12 (2012): 2936-2944. and Chao, Jeffrey A., et al. "Structural basis for the coevolution of a viral RNA-protem complex." Nature structural & molecular biology 15.1 (2007): 103-105.), 3X GGGGS linker, SV40 nuclear localization signal, and SID4X repressor domain. Functionally, the PP7 domain binds to its specific RNA aptamer, the 3XGGGGS linker provides mechanical flexibility between the MS2 and S1D4X domains, the SV40 nuclear localization signal facilitates transport of the protein into the nucleus, and the SID4X domain represses transcriptional activity.

[00762] PP7-KRAB

DNA sequence

ATGTCCAAAACCATCGTTCTTTCGGTCGGCGAGGCTACTCGCACTCTGACTGAGATC
CAGTCCACCGCAGACCGTCAGATCTTCGAAGAGAAGGTCGGGCCTCTGGTGGGTCG
GCTGCGCCTCACGGCTTCGCTCCGTCAAAACGGAGCCAAGACCGCGT^^ CGCGTCA
ACCTAAAACTGGATCAGGCGGACGTCGTTGATTCCGGACTTCCGAAAGTGCGCTACA
CTCAGGTATGGTCGCACGACGTGACAATCGTTGCGAATAGCACCGAGGCCTCGCGC
AAATCGTTGTACGATTTGACCAAGTCCCTCGTCGCGACCTCGCAGGTCGAAGATCTT
GTCGTCAACCTTGTGCCGCTGGGCCGTagcgctGGAGGAGGTGGAAGCGGAGGAGGAG
GAAGCGGAGGAGGAGGTAGCggacctaagaaaaagaggaaggtggcggccgctggatccgctttgtctcctcagcac
tctgctgtcactcaaggaagtatcatcaagaacaaggagggcatggatgctaagtcactaactgcctggtcccggacactggtgaccttcaa
ggatgtatttgtggacttcaccagggaggagtggaagctgctggacactgctcagcagatcgtgtacagaaatgtgatgctggagaactata
agaacctggtttccttgggttatcagcttactaagccagatgtgatcctccggttggagaagggagaagagccctggctggtggagagaga
aattcaccaagagacccatcctgattcagagactgcatttgaaatcaaatcatcagtt

Amino acid sequence

MSKTIVLSVGEATRTLTEIQSTADRQIFEEKVGPLVGRLRLTASLRQNGAKTAYRVNLKL
DQADWDSGU»KWYTQWSHDWIVANSTEASRKSLYDLTKSLVATSQVEDLVVNLV
PLGRSAGGGGSGGGGSGGGGSGPKKKRKVAAAGSALSPQHSAVTQGSIIKNKEGMDAK
SLTAWSRTLVTFKXIVFVDFTREEWKL-LDTAQQIVYRNVMLENYKNLVSLGYQLTKPDV
ILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSV

Description

The PP7-KRAB repressor protein consists of the following domains from N-term to C-term: the PP7 Pseudomonas bacteriophage coat protein (with amino acids 68-69 mutated to SG and amino acids 70-75 deleted from the wild type protein as described in Wu, Bin, Jeffrey A. Chao, and Robert H. Singer. "Fluorescence fluctuation spectroscopy enables quantitative imaging of single mRNAs in living cells/'Biophysical journal 102.12 (2012): 2936-2944. and Chao, Jeffrey A., et al. "Structural basis for the coevolution of a viral RNA-protein complex." Nature structural & molecular biology 15.1 (2007): 103-105.), 3X GGGGS linker, SV40 nuclear localization signal, and KRAB repressor domain. Functionally, the PP7 domain binds to its specific RNA aptamer, the 3XGGGGS linker provides mechanical flexibility between the MS2 and KRAB domains, the SV40 nuclear localization signal facilitates transport of the protein into the nucleus, and the KRAB domain represses transcriptional activity.

[00763] PP7-NUE

DNA sequence

ATGTCCAAAACCATCGTTCTTTCGGTCGGCGAGGCTACTCGCACTCTGACTGAGATC
CAGTCCACCGCAGACCGTCAGATCTTCGAAGAGAAGGTCGGGCCT CTGGTGGGTCG
GCTGCGCCTCACGGCTTCGCTCCGTCAAAACGGAGCCAAGACCGCGTATCGCGTCA
ACCTAAAACTGGATCAGGCGGACGTCGTTGATTCCGGACTTCCGAAAGTGCGCTACA
CTCAGGTATGGTCGCACGACGTGACAATCGTTGCGAATAGCACCGAGGCCTCGCGC
AAATCGTTGTACGATTTGACCAAGTCCCTCGTCGCGACCTCGCAGGTCGAAGATCTT
GTCGTCAACCTGGTGCCGCTGGGCCGTagcgctGGAGGAGGTGGAAGCGGAGGAGGAG
GAAGC GGAGG AGGAGGT AGCggacctaagaaaaagaggaaggtggcggcc gctggatcc ACT ACCAACT
CCACTCAGGACACACCTGTACCTGCAGCCTCCACCGGCGGAATCCGACTCCCGCCATCCCAT
ACCCCGTGAGGAGAGTCGAGCAGCTGCTCCAGTTCTCTTTTCTGCCCGAACTCCAGT
TCCAGAACGCCGCTGTGAAACAGAGAATCCAGCGCCTGTGCTATAGAGAGGAAAAG

CGGCTGGCTGTCAGCTCCCTCGCAAAGTGGCTGGGCCAGCTCCACAAACAGAGGCT
GAGAGCACCAAAGAACCCCCCTGTGGCCATTTGTTGGATCAATAGTTACGTGGGCTA
TGGAGTCTTTGCCCGGGAGTCTATTCCCGCTTGGAGTTACATCGGCGAATATACCGG
CATCCTGCGGCGCCGACACIGCTCIXGTGGCI(X=ACGAGAACGAITACIGCIIXXGCTA
TCCTGTGCCACGCTACTCATTCCGATATTTACCATCGACAGCGGGATGCAGGTAA
CGT[XACAAGGTI(CA[XAAIXAC!CCGATAACCCTAAIXTXGGAGGCAAICGGGGCCCTT
CGAAAACGGTATCTTCCATATCATCATCAGGGCCATCAAGGATATCCTGCCCGGGGA
GGAACTCTGTTACCACTATGGACCTCTGTACTGGAAGCATCGAAAGAAAAGGGAGG
AGTTCGTGCCACAGGAGGAA

Amino acid sequence

MSKTIVLSVGEATRTLT EIQSTADRQIFEEKVGPL VGRLRLT ASLRQNGAKTAYRVN LKL
DQADVVDSGLPKVRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLVVNLV
PLGRSAGGGGSGGGGSGGGGSGPKXK-RKVAAAGSTTNSTQDTLYLSLHGGIDSAIPYPV
RRVEQLLQFSFLPELQFQNAAVKQRIQRLCY REEKRLAVSSLAKWLGQLHKQRLRAPK
NPPVAICWINS YVGYGVFARES IPAWSYIGE YTGILRRRQALWLDEND YCFRYPVPRYSF
RYFTIDSGMQGNVTRFINHSDNPNLEAIGAFENGIFHIIIRAIKDILPGEELCYHYGPLYWK
HRKKREEFVPQ EE

Description

The PP7-NUE histone effector protein consists of the following domains from N-term to C-term: the PP7 Pseudomonas bacteriophage coat protein (with amino acids 68-69 mutated to SG and amino acids 70-75 deleted from the wild type protein as described in Wu, Bin, Jeffrey A. Chao, and Robert H. Singer. "Fluorescence fluctuation spectroscopy enables quantitative imaging of single mRNAs in living cells."Biophysical journal 102.12 (2012): 2936-2944. and Chao, Jeffrey A., et al. "Structural basis for the revolution of a viral RNA-protein complex." Nature structural & molecular biology 15.1 (2007): 103-105.), 3X GGGGS linker, SV40 nuclear localization signal, and the NUE histone methyltransferase domain from Chlamydia trachomatis. Functionally, the PP7 domain binds to its specific RNA aptamer, the 3XGGGGS linker provides mechanical flexibility between the MS2 and NUE domains, the SV40 nuclear localization signal facilitates transport of the protein into the nucleus, and the NUE domain increases repressive histone methylation.

[00764] PP7-NcoR

DNA sequence

ATGTCCAAAACCATCGTTCTTTCGGTCGGCGAGGCTACTCGCACTCTGACTGAGATC
CAGTCCACCGCAGACCGTCAGATCTTCGAAGAGAAGGTCGGGCCTCTGGTGGGTCG
GCTGCGCCTCACGGCTTCGCTCCGTCAAAACGGAGCCAAGACCGCGTATCGCGTCA
ACCTAAAACTGGATCAGGCGGACGTCGTTGATTCCGGACTTCCGAAAGTGCGCTACA
CTCAGGTATGGTCGCACGACGTGACAATCGTTGCGAATAGCACCGAGGCCTCGCGC
AAATCGTTGTACGATTTGACCAAGTCCCTCGTCGCGACCTCGCAGGTCGAAGATCTT
GTCGTCAACCTTGTGCCGCTGGGCCGTagcgctGGAGGAGGTGGAAGCGGAGGAGGAG
GAAGCGGAGGAGGAGGTAGCggacctaagaaaaagaggaaggtggcggccgctggatccAACGGGCTGA
TGGAGGACCCAATGAAAGTCTACAAGGACAGGCAGTTTATGAACGTGTGGACCGAC
CACGAGAAGGAAATCTTTAAGGATAAGCCCATCCAGCATCCCAAAAATTTCGGCCT
GATCGCCAGCTACCTGGAGAGGAAGTCGGTGCCTGACTGTGTCCTGTACTATTACCT
CACAAAGAAAAACGAAAATTACAAA

Amino acid sequence

MSKTIVLSVGEATRTLTEIQSTADRQIFEEKVGPLVGRLRLTASLRQNGAKTAYRVNLKL
DQADWDSGLPKVRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLWNLV
PLGRSAGGGGSGGGGSGGGGSGPiGCKRKVAAAGSNGLMEDPMKVYKDRQFMNVWT
DHEKEIFKDKPIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYK

Description

The PP7-NcoR histone effector protein consists of the following domains from N-term to C-term: the PP7 Pseudomonas bacteriophage coat protein (with amino acids 68-69 mutated to SG and amino acids 70-75 deleted from the wild type protein as described in Wu, Bin, Jeffrey A. Chao, and Robert H. Singer. "Fluorescence fluctuation spectroscopy enables quantitative imaging of single mRNAs in living cells."Biophysical journal 102.12 (2012): 2936-2944. and Chao, Jeffrey A., et al. "Structural basis for the coevolution of a viral RNA-protein complex." Nature structural & molecular biology 15.1 (2007): 103-105.), 3X GGGGS linker, SV40 nuclear localization signal, and the HDAC recruiter domain of the human NcoR protein (amino acids 420-488 of wild type). Functionally, the PP7 domain binds to its specific RNA aptamer, the 3XGGGGS linker provides mechanical flexibility between the MS2 and NcoR domains, the SV40 nuclear localization signal facilitates transport of the protein into the nucleus, and the NcoR domain recruits histone deacetylases leading to repressive histone modifications.

[00765] Other potential orthogonal RNA-binding proteins: Additional orthogonal RNA-binding proteiiVaptamer combinations exist within the diversity of bacteriophage coat proteins. These alternative combinations may be used to develop transcriptional modulators or DNA-effectors analogous to those Applicants have described for MS2 and PP7. A list of such coat proteins includes, but is not limited to: Qβ, F2, GA, fr, JP50I, M12, R17, BZ13, JP34, JP500, KU1, Mil, MX1, TW18, VK, SP, FI, ID2, NL95, TW19, AP205, φi¾5, <|>Cb8r, <|>Cbl2r, <|>Cb23r, 7s, PRR1.

Example 16: MS2 CasLITE

[00766] Further embodiments of the invention include modification of sgRNA architecture with MS2 loops as described in Examples 13 and 14 with further application in inducible CRISPR-Cas systems as decribed in PCT Application PCT/US2013/051418, entitled "INDUCIBLE DNA BINDING PROTEINS AND GENOME PERTURBATION TOOLS AND APPLICATIONS THEREOF" filed on July 21, 2013 and published as PCT Publication WQ2014018423A2 on January 30, 2014, the contents of which are incorporated herein by reference in their entirety.

[00767] Applicants previously showed that CRY2 and CIB1 proteins may be fused to transcription activation domains and DNA-binding domains, respectively, in order to allow locus-specific light-indueibie control of endogenous transcription (Konermann S, Brigham MD, Trevino AE, Hsu PD, Heidenreich M, Cong L, Piatt RJ, Scott DA, Church GM, Zhang F.. 'Optical control of endogenous mammalian transcription and epigenetic states." Nature. 2013 Aug 22;5Q0(7463):472-6). Applicants further showed that this system may be extended to dCas9 transcriptional effectors. Applicants generate an analogous dCas9-based light-indueibie MS2-effector, characterized by an MS2-CIB1 recruitment component bound to dCas9-sgRNA, and a CRY2-VP64 transcriptional activator domain. Upon activation with blue light, CRY2-VP64 associate with MS2-CIB1, enabling the recruitment of the transcriptional machinery to the target locus.

[00768] The novel MS2-CIB1 inducible recruitment complex consists of the following domains from N-term to C-term: the N55K mutant of the MS2 bacteriophage coat protein (shown to have higher binding affinity than wild type MS2 in Lim, F., M. Spingola, and D. S. Peabody. "Altering the RNA binding specificity of a translational repressor." Journal of Biological Chemistry 269.12 (1994): 9006-9010.), 3X GGGGS linker, SV40 nuclear localization

signal, and p65 activation domain. Functionally, the MS2 domain binds to its specific RNA aptamer, the 3XGGGGS linker provides mechanical flexibility between the MS2 and CIB1 domains, the SV40 nuclear localization signal facilitates transport of the protein into the nucleus, and the CIB1 domain is a heterodimeric binding partner of the light-sensitive Cryptochrome 2 (CRY2).

[00769] The alternative sgRNA designs, orthogonal RNA-binding proteins, and MS2 fusion architectures discussed in previous Examples are entirely compatible with the MS2-CIB1 fusion, with CIB1 acting as the "effector" domain. dCas9-CIBl, which are previously described, may also be compatible with MS2-CIB1 - i.e., using dCas9-CIBl and M82-CIB1 fusions in tandem may provide functional advantages for inducible manipulation of target gene expression. Finally, optimized LITE architectures may be employed as described in Konermann et al 2013.

[00770] Sequence information for MS2 CasLITE constructs are provided below:

MS2-CIB1 DNA Sequence

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTG
ACAGTGGCTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCA
CGGAGCCAGGCCTACAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAgAG
AAAGTATACCATCAAGGTGGAGGTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAG
TCGAACTGCCTGTCGCCGCTTGGAGGTCCTACCTGAACATGGAGCTCACTATCCCAA
TTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAAGGCAATGCAGGGGCTCCTCA
AAGGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCCGGTATCTACagcgctGGA
GGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCggacctaagaaaaagaggaa
ggtggcggccgctggatccAACGGCGCGATTGGTGGGGATTTGCTGCTTAACTTTCCCGACATG
TCCGTGTTGGAACGTCAGCGCGCACATTTGAAGTATCTTAACCCCACCTTCGACTCC
CCGTTGGCCGGGTTCTTTGCGGACTCATCTATGATTACGGGAGGGGAAATGGACAGC
TACCTCTCAACGGCCGGATTGAATCTTCCGATGATGTATGGAGAAACCACTGTAGAA
GGCGACTCGCGACTCTCGATTTCGCCTGAAACGACGCTGGGAACAGGGAACTTCAA
GAAACGGAAATTCGGACAGCGCTAGACAAAAGATTGCAACGAAAAGAAGAAGAAAATG
ACCATGAATCGCGATGATCTGGTAGAGGAGGGAGAGGAGGAAAAGTCGAAGATTA
CTCGAACAGAACAATGGGTCTACCAAAAGTATCAAAAAGATGAAGCACAAAGCTAAG
AAAGAAGAGAACAATTTCAGCAATGACAGCAGTAAAGTCACAAAAGAACTGGAGA
AAACGGATTACATTCACGTGAGGGCGCGACGAGGGCAGGCTACAGATTCACATTCA

ATTGCGGAGAGAGTACGGAGAGAGAAAATCTCAGAAAGGATGAAGTTCCTCCAAGA
CCTTGTGCCAGGTTGTGACAAGATCACAGGCAAAGCAGGAATGCTGGATGAGATCA
TCAACTACGTCCAATCGTTGCAAAGACAAATTGAGTTTCTCTCGATGAAACTGGCCA
1XGTGAATCCTAGACCGGATTTCGACATGGATGACATCm GCGAAAGAAGTGGCAT
CCACl CCCATGACGGTTGTGC(C(1 CA (C(GGAGATxGGTCl 1 GTx1 GGTTACA(GC(A(Xi
AAATGGTGCATTCGGGTTATTCAAGCGAGATGGTCAATTCGGGATACCTTCACGTCA
ATCCCATGCAGCAGGTGAATACTTCCAGTGATCCACTCTCCTGCTTTAACAACGGCG
AGGCCCCTTCGATGTGGGACTCCCACGTACAGAATCTCTATGGAAATCTCGGAGTC

[00771] **MS2-CIB1** Amino Acid Sequence:

MASNFTQFVLVDNGGTGDVTVAPSNFANGVAEW1SSNSRSQAYKVTCSVRQSSAQKRK
YTIKVEVPKVATQTVGGVELPVAAWRSYLNMELTIPIFATNSDCELIViCAMQGLLKDGN
PIPSAIAANSGIYSAGGGGSGGGGSGGGGSGPKKKRKVAAAGSNGAIGGDLLLNFPDMS
VLERQRAHLKYLNPTFDSPLAGFFADSSMITGGEMDSYLSTAGLNLPMMYGETTVEGD
SRLSISPETTLGTGNFKXRKFDTETKDCNEKKKKMTMNRDDLVEEGEEEKSKITEQNNG
STKSIKKMKHKAKKEENNFSNDSSKVTKEi EKTDYIHVRARRGQATDSHSIAERVRREK
ISERMKFLQDLVPGCDKJTGKAGMLDEIINYVQSLQRQIEFLSMK1AWNPRPDFDMDDI
FAKrA^ASTPMTVA^SPEAdVLSGYSeEAdVHSGYSSEMVNSGYLHANPMQQVNTSSDPLS
CFNNGEAPSMWDSHVQNLYGNLGV

Example 17: New dCas9 activator constructs informed by crystal structure information

[00772] An optimized CRISPR/Cas9 activator system requires improvements not only in the sgRNA backbone, but in the dCas9-activator fusion constructs. The **Cas9/RNA/DNA** crystal structure has led to the generation of several hypotheses for improving dCas9-activator function. The crystal structure showed that the C-terminus of dCas9, where the activation domain of the standard dCas9-activator is fused, is poorly localized to the target DNA. Most, but not all, of these hypotheses seek to improve dCas9-activator function by finding preferable locations for the activation domain within the dCas9 protein, rather than at the C-terminus.

[00773] In brief:

- Replace dCas9 Rec2 domain with transcriptional effector domain,
- Replace dCas9 HNH domain with transcriptional effector domain,
- Insert transcriptional effector domain at sites of flexible linkers within dCas9: amino acid 553, 575, or 1153

- Create catalytically inactive dCas9 by combination of D10A and N863A mutations, rather than D10A and H840A mutations.

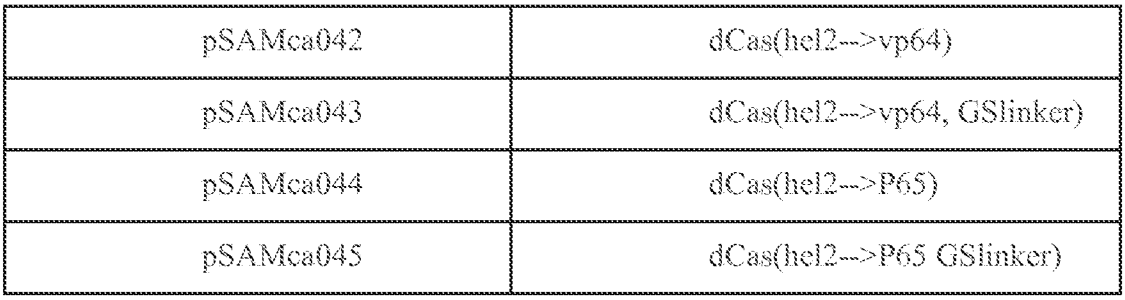
[00774] Replacing the dCas9 Rec2 domain with transcriptional effector domain:

The Cas9/RNA/DNA crystal structure experiments showed that a Cas9 mutant from which the Rec2 domain had been deleted maintained a significant level of nuclease activity. This finding suggests that the Rec2 domain is not essential for the formation of the Cas9/RNA/DNA complex. We hypothesize that replacing the Rec2 domain in dCas9 with a transcriptional effector domain would not inhibit formation of the dCas9/RNA/DNA complex and could facilitate a more efficient interaction between the transcriptional effector domain and the target DNA. Several constructs have been synthesized to investigate this theory.

[00775] In each case amino acids 175-306 of dCas9 were replaced with one of the following inserts, with subdomains listed from N- to C-terminus:

- VP64 activation domain
- 3X GGGGS linker, VP64 activation domain, 3X GGGGS linker
- p65 activation domain
- 3X GGGGS linker, p65 activation domain, 3X GGGGS linker

[00776] Corresponding constructs



pSAMca042	dCas(hel2-->vp64)
pSAMca043	dCas(hel2-->vp64, GSlinker)
pSAMca044	dCas(hel2-->P65)
pSAMca045	dCas(hel2-->P65 GSlinker)

[00777] Replacing the HNH domain with a transcriptional effector domain:

Based on the crystal structure, the HNH domain is located close to the DNA/RNA hybrid. In addition, it was found that it is a flexible domain that can move as a consequence of conformational changes while Cas9 is binding target DNA. It is flanked by a disordered linker on the N-term and the a39-a40 linker on the C-term, which can undergo a conformational change to an extended a-helix, moving the HNH domain closer to its target DNA bases. The proximity to target DNA and the flexibility identified in the crystal make a replacement of this nuclease domain with a transcriptional effector domain promising. See Fig. 49 for illustration.

[00778] Applicants replace AA775-901 (of the HNH domain) with either vp64 or P65 flanked by a (GGGGS)3 or a (GGGGS)6 linker on both sides of the inserted transcriptional effector domain.

[00779] Corresponding constructs

pSAMca050	dCas9(HNH-->vp64, 3XGS)
pSAMca051	dCas9(HNH-->vp64, 6XGS)
pSAMca052	dCas9(HNH-->P65, 3XGS)
pSAMca053	dCas9(HNH-->P65, 6XGS)

[00780] insertions of transcriptional domains into 3 loops of dCas9:
in addition to replacing an existing domain (e.g. HNH, Rec2) with a transcriptional effector domain, it may be possible to insert a transcriptional effector domain at different positions in the Cas9 protein. The crystal structure helps in identifying promising loops for such an insertion (favorable properties for a place for insertion include low secondary structure complexity (loop versus helix or sheet, unobstructed space for the additional domain, proximity to target DNA and no current interactions with either target DNA or sgRNA (as these may be disrupted by the addition of the transcriptional effector domain)).

[00781] Applicants identified three favorable positions: G533, F575 and K1153. The locations of G533 and K1153 in the Cas9 protein is indicated in the corresponding Fig. 49. Applicants insert either vp64 or P65 flanked by a (GGGGS)1 or a (GGGGS)3 linker on both sides of the inserted transcriptional effector domain at these three locations.

[00782] Corresponding constructs

pSAMca054	dCas9(G533-vp64, 1XGS)
pSAMca055	dCas9(G533-vp64, 3XGS)
pSAMca056	dCas9(G533-P65, 1XGS)

pSAMca057	dCas9(G533-P65, 3XGS)
pSAMca058	dCas9(F575-vp64, 1XGS)
pSAMca059	dCas9(F575-vp64, 3XGS)
pSAMca060	dCas9(F575-P65, 1XGS)
pSAMca061	dCas9(F575-P65, 3XGS)
pSAMca062	dCas9(K1 153-vp64, 1XGS)
pSAMca063	dCas9(K1 153-vp64, 3XGS)
pSAMca064	dCas9(K1 153-P65, 1XGS)
pSAMca065	dCas9(K1 153-P65, 3XGS)

[00783] dCas activator sequence information is provided below:

Replacing the dCas9 Rec2 domain with transcriptional effector domain

pSAMca042 dCas(hel2->vp64) - DNA

atgGACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGC
TGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGG
CAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACA
GCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACAC
CAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCA
AGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGAT
AAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCA
CGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACA
AGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCC
ACTTCCTGATCGAGGGCGACCTGAACGGACGGGCTGACGCATTGGACGATTTTGATC
TGGATATGCTGGGAAGTGACGCCCTCGATGATTTTGACCTTGACATGCTTGGTTCGG
ATGCCCTTGATGACTTTGACCTCGACATGCTCGGCAGTGACGCCCTTGATGATTTCG
ACCTGGACATGCTGATTAACAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGC
GCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGC
TCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCA

AGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAG
TTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCT
GAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCC
ACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGTTTTTAC
CCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCC
CTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAA
AGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCT
TCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGA
GAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCT
GACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCG
AGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTG
AAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAAT
CTCCGGCXGTGGAAGAiCGGTTGAACGCCl XCCTGGGCAGATYACVACGATCl XGCTGAA
AATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAG
ATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTG
AAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAG
ATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGC
AGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAAC
TTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGC
CCAGGTG\XXC]GCCAGGG(: GATAG(: CYGCAGGAGCACATVTGCCAAICl XGGCXCXGCA
GCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTG
AAAGTGATGGGCCGGCACA AGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGA
ACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGA
AGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAAC
ACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATAT
GTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACgcTAT
CXriXGCXTCAGAGCiTIXl XGAAGGACXGACl XCATCXGACAACAAGGTGCl TGACχCAC=AA
GCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAA
<GATGAAGAA(l ACTXiGCXGGCAGCl GCl XGAACGCχCAAGCl GATl ACXCAGAGAAAGT
TCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGC
TTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGAT

CCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAG
TGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGT
TTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAAC
GCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGT
GTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGG
ΛΛΑ ΊΧ'GGcΆAGGCTΑCΧG(ΧΆΑ <ΞΤΑ CΙ Ί ΧΤ ΓCTΑCΑG<Α ΑC/VΙΧΆΤGΑΑCΠΥ ΓΤCVΛ
AGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACA
AACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCG
GAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAG
GCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCC
Α<ΞΑΛΑ<ΞΑΛ<i(ΞΑC"iΧΪ(Ξ(ΞΑ(:(C'ΤΑΛ(ΞΛΑGΊ ΆΑ{ΧΧΞCΧΞG<Ί Ί ΧΧΞΑ<ΑGCΧΧΧ'Λ(ΧΧΞΊ GG<
CTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGA
(ΞΤGΊΧΞΛΑΛ(ΞΛ(ΞCΊ ΧΞCΊ ΧΧΞ(ΧΞΑΊΧ'Λ {CCΑΊΧΑΊ'GGΑΑΑGΑΑGCΑGCΊ Ί ΧΧΞΑC=ΑΑGΑΑΊ'
CCCΛΊΧΧΞΛCΊΠ Χ:ΓGGΑΛG(ΧΆΑGGGC-ΤΑCΑΑΑGΑΑGΤGΑΑΑΑΑGGΑCCΤGΑΤCΑΤ
CAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGG
CCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTG
AACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAA
TGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCG
AGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAA
GΊΧΞC-ΤGΊΧΧ'GCΧ'ΤΑ CΑΑCΑ ΑGC-ΑiΧ'GGGΑΤΑΑGCΧΧ'ΑΊ](Α (ΞΑ(ΞΑ(ΞC-ΑG(ΞCΧΧ=Α(=ΑΑ
TATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTT
GACACCA(X:ATCGAC(XK}AAGAGGTAC ΆCCΑGCΑCCΑΑΑGΑGGΤGCΤGGΑCGCCΑC
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pSAMca042 dCas(hel2—>vp64) - amino acid

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pSAMca043 dCas(hel2->vp64, GSlinker) - DNA

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pSAMca043 dCas(hel2— >vp64, GSlinker) - amino acid

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pSAMca044 dCas(hel2->P65) - DNA

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GC1 XGGGGC-AGGC1 `C=AGCCGGAAGC1 `GA1 X-AACGGCATCX`GGGACAAGCA(=·TCχ`GGC
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C(XGGAT(GAA(CA(`!AA(GTA (`(GA(`GAGAATXiACAAGCTGATx`CGGGAAGTGAAAGTGA
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pSAMca044 dCas(hel2~>P65) - amino acid

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pSAMca045 dCas(hel2->P65 GSlinker) - DNA

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GAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCC
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GATCXT XGAAAGAACACXXXXGTGGAAAA CA(CCCAGCTGCAGAAi CGiACiAAGCTxGTACC
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pSAMca045 dCas(hel2~>P65 GSlinker) - amino acid

MDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRfiSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDiCK HERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEG DLNGGGGSGGGGSGGGGSPSGQISNQALALAPSSAPVLAQTMVPSSAMVPLAQPPAPAP VLTPGPPQSLSAPVPKSTQAGEGTLSEALLHLQFDADEDLGALLGNSTDPGVFTDLASV DNSEFQQLLNQGVSMSHSTAEPMLMEYPEAITRLVTGSQRPPDPAPTPLGTSGLPNGLSG DEDFSSIADMDFSALLSQISSSGQGGGGSGGGGSGGGGSRVNTEITKAPLSASM1KRYDE HHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTE ELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKJLTFRIP YYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKV LPiMSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFE DREMIEERLKIYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSD GFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVD ELVKVMGRHKPENIVffiMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENT QLQNEKLYLYYLQNGRDMYV^ QELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDK NRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQ LVETRQITKHVAQ1LDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVRE1NN YHHAHDAYLNAVVGTALIKKYPKLESEFVYODYKVYOVRKMIAKSEQEIGKATAKYTF YSNIMNFFKTEITIANGEERK-RPLIETOGETGEIVWDKGRDFATVRKVLSMPQVNIViCKT EVQTGGFSKESILPKRNSDKXIARKKDWDPKKYGGFDSPWAYS\^LVVAKVEKGKSKK LKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLlIKLPKYSLFELENGRKRMLASA GELQKGNELALPSKY\TSTLYLASFIYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFS KRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYT STKEVLDATLIHQSITGLYETRIDLSQLGGDSAGGGGSGGGGSGGGGSGPKKKRKVAAA

Replacing the HNH domain with a transcriptional effector domain

pSAMca050 dCas9(HNH-->vp64, 3XGS) - DNA

atgGACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGC TGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGG CAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACA

GCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACAC
CAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCA
AGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGAT
AAGAAGC\\{]GAGCXGCX ACXX CAI Cl Y CXXGCAACAI XGTXGGACXGAGGTGGCXTACCA
CGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACA
AGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCC
ACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTC
ATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAG
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(GGCXXA GATXXGGCXGA(XA G]A{(XCCiACCI XGTl l Xl XGGCXXGCCAAGAAi]Cl XGT(XX
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AGCggacctaagaaaaagaggaaggtggc ggccgct

pSAMcaOSO dCas9(HNH-->vp64, 3XGS) **- AA**

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pSAMcaOSl dCas9(HNH-->vp64, 6XGS) - DNA

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pSAMcaOSl dCas9(HNH->vp64, 6XGS) **- AA**

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\\¾TEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTV\"NELTKVKY\^TEG
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VSGQGDSLHEHIANLAGSPAIKKGILQTVKWDELVKVMGRHKPENIVffiMARENQTTQ KGQKGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGRADALDDFDLDMLGSDALDDF DLDMLGSDALDDFDLDMLGSDALDDFDLDMLINGGGGSGGGGSGGGGSGGGGSGGG GSGGGGSTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIRE VKVITLKSKLVSDFRKDFQFYK\^REINNYHHAHDAYLNAVA^GTALIKKYPKLESEFVYG **DYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEI** VWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKK YGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGS PEDNEQKQLFVEQHKHYLDEilEQISEFSKRVILADANLDKYLSAYNKHRDKPIREQAENI iHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKLEVLDATLlHQSITGLYETRIDLSQLGGDSA GGGGSGGGGSGGGGSGPKJOCRKVAAAASG

pSAMca052 **dCas9(HNH->P65,** 3XGS) - DNA

GACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCTG GGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCA **ACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGC GGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCA GACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAG GTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAA GAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACG** AGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGG **GCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCAC TTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCAT** CCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCG GCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAA AATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGCAACCTGAT TGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGG ATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGG GCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGAC **GCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCT**

GAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGA
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AGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTA
CAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGA
AGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATC
CCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGAT^^
TTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCA
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CTCCAACTCCCCTGGGAACCAGCGGCCTGCCTAATGGGCTGTCCGGAGATGAAGAC
TTCTCAAGCATC(GCI ⊲AΛ]ΛTGGΛ(TI A GTXGCCXI XGCI XG](ΛCΛ (GΛTI XCI (I Λ{GTXG
GGCAGGGCGGGGGAGGCTCCGGTGGTGGGGGCAGCGGAGGGGGGGGCAGCACCAA
GGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAG
CTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGAT
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GCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAA
GGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCT
Λ({XGc**XAAGTACT**TCTTCTΛCAGCΛΛCΛIXATGAACI I TΠX ΛΛGΛCXXGAGATTACX
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GGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCA
TGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAA
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GGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGT
GGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTG
(I XGGGGAI XACxATxATXGGAAAGAAGCAGCTTXXGAGAAGAATCXXATXXGACTTTXY
GGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGT
ACixCXI XGTI XXGAG(!GCλΛΛΛACXGG(XXGGAAGAGAAixG(I XG(GC(](]G{CGG(XGAA
CTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTG
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GTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGT
TCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACA
ACΛ AGCACXX}GGATAACXXXAT](AGAGAGCAGGa GAGAATATCATCXACXTGIY T
ACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGAC
CGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAG
CATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGAC

pSAMca052 dCas9(HNH-->P65, 3XGS) - AA

DKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFD
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GDEDFSSIADMDFSALLSQISSSGQGGGGSGGGGSGGGGSTKAERGGLSELDKAGFIKR
QLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREIN
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FYSNIIVINFFKTEITLANGEIRKJ^LJETNGETGEIVWDKGRDFATVRKVLSMPQV NIVKK
TEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSK
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pSAMca053 dCas9(HNH->P65, 6XGS) - DNA

gGACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCT
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GGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATA
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AAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGCAACCTGA
TTG(XX'l XÏA G(:i'TXG(G(XXl 'G ACCX'{X'AACΠ'CAAGAGCAAG l XXïA C(:TG(GCC*GAGG*
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(XX:X'ACCAGATCCA CCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTT
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CXGiCGAGCA(iAAAAA (GGCX'A'l'CXGTXGGA(X'lXG(:TGTTCAAGACCAACX'(GGAAA(G'!<GA
CCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTG
*G*AAA'l'(:T(XX=G(XGTXGGAAGA'iX'GG'iT'Ix'Aa CCX'C'iC(CCTGGG CACA'iAiX'A(X=A'lX'l'G
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pSAMca053 **dCas9(HNH-->P65,** 6XGS) - AA

DKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFD
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NGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAA
KNLSDAn .LSDiLRVNTElTKAPLSASMiKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQ
SKJ^GYAGYIDGGASQEEFYKFIKPILEKJVIDGTEELLVKLNREDLLRKQRTFDNGSIPHQI
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NDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKL
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AKGYKEVKKDLJIKIPKYSLFELENGRKRMLASAGELQKGNELAL-PSKYVNFLYLASHY
EKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ
LGGD

Insertions of transcriptional domains into 3 loops of dCas9

pSAMca054 dCas9(G533-vp64, 1XGS) - DNA

GACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCTG
GGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCA
ACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGC
GGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCA
GACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAG
GTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAA
GAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACG
AGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAG
GCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCAC
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GCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAA
AATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGCAACCTGAT
TGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGG
ATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTG

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GCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCT
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pSAMca054 dCas9(G533-vp64, 1XGS) **- AA**

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pSAMca055 dCas9(G533~vp64, 3XGS) - DNA

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pSAMca055 dCas9(G533-vp64, 3XGS) - AA

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pSAMca056 dCas9(G533-P65, 1XGS) - DNA

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pSAMca056 dCas9(G533-P65, 1XGS) - AA

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pSAMca057 dCas9(G533-P65, 3XGS) - DNA

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pSAMca057 dCas9(G533-P65, 3XGS) - AA

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pSAMca058 dCas9(F575-vp64, 1XGS) - DNA

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AAAGTGA'**e** AAGCΛ(jCT(jAA(jC**GG**(X**G**i**A**(jATA**(**CA**(**(**X**G**i**(CTXG**G(jC**i**(AGG('TGAGCC
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pSAMca058 dCas9(F575-vp64, 1XGS) - AA

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pSAMca059 dCas9(F575-vp64, 3XGS) - DMA

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CXGC{CA\CGiACGCC1 A CX1 'GAAC(XX'GTCGTGGGAACXGCXX'TGATC-AA A AA GTACX-
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pSAMca059 dCas9(F575-vp64, 3XGS) - AA

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pSAMca060 dCas9(F575-P65, 1XGS) - DNA

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GT**GA**T CG**AAA**TG**G**CC**A(**GA(GA(GAAi CC**A**<i**A(X**'**AC**X**X**'**A**<i**AAGGGA**CA G A **A(}A**AC**AG{X**'
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A(A AC**AA**GGTGCTG**i**ACC-AGAAGCG**A**G-AAGAACCGGGGCAAGAGG-G**A**G-AAC**X**GTGC**X**'
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ΛGCA ΛiA !XA TXGΛΛ(TTTT CΛΛGΛ{C{**GAGAr** !**A** (C**X**T**X**GGCCAΛC(GGC**Xi**A**GA iXX**'**G**
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(XGGCTY **(**XGΛ**{A G**C**XXXA** C**XX**T**GG**CX' A Π X**T G**Txx**TGG**T**X**G']XCXX**AAAGTGGAAAA**
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Λ**A**Λ<**i**Λ**AG**C**AG**CΠ **XX**G**A**G**A**ΛGΛΛTX**X**CΛ' X**Xi**Λ(CTTTCT**G**G**A**ΛG(CCΛΛGGG(CT**A(**C**A**A**A**
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pSAMca060 dCas9(F575-P65, 1XGS) - AA

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pSAMca061 dCas9(F575-P65, 3XGS) - DNA

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pSAMca061 dCas9(F575-P65, 3XGS) - AA

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pSAMca062 dCas9(K1 153-vp64, 1XGS) - DNA

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pSAMca062 dCas9(Kl 153-vp64, 1XGS) - AA

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pSAMca063 dCas9(K1153-vp64, 3XGS) - DNA

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pSAMca063 dCas9(Kl 153-vp64, 3XGS) - AA

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pSAMca064 **dCas9(Kl** 153-P65, 1XGS) - DNA

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CCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTG
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GGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGACCGAGGAAC
GGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGG
CGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGA
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AAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGC
CGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGC
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cTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCA
GAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAA
GAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAA
AGTʹlʹCGACA ATCʹlʹGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATA AGGCCG-
GGCTTCAʹlʹCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAG(ʹA(ʹGT(iG(ʹA(ʹA
GATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGG
AAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCC
AGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTG
AA(XiGXXT!XGTGGGAACCXiCCCʹlʹGAʹlʹCA AAAAGTACCCʹlʹAAGCʹlʹGGAAAGCXiAGTʹlʹ
CGTXiT!A(XKiCXiA(ʹTACAAGGTGTACGACXiTGCGGAAGATGATCGC(ʹAA(iA(iCGAGC
AGGAAAT{ʹG(iCV\ AGGCTACCXiCXAAGTACTΠCT!T](ʹTA cV\(iCΛAXʹAʹlʹXATGAAcʹlʹʹlʹʹlʹ
TCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAG
ACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGT
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GGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGGGAGGGGGAGGCA
GCXXTTxʹACiGCiCA GATXA(iCΛ A(X-A(iGCXXʹlʹ(iGCʹlʹ(ʹlʹ(iG(XCCTA GCTXXXiCTCCA(=
TGCTGGCCCAGACTATGGTGCCCTCTAGTGCTATGGTGCCTCTGGCCCAGCCACCTG
CTXXA(i(XX Xʹlʹ XiTXiCʹlʹC=ΛCXXXA{iGA(XV\(XXX ʹAGTCA(ʹTGA(iCXiCTXXAG!XiCXXA
AGTCTACACAGGCCGGCGAGGGGACTCTGAGTGAAGCTCTGCTGCACCTGCAGTTC
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GCTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGA
AGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGT

GAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACG
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CTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAG
GGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAAC^^ CACAAGCACTA
CCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCG
ACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATC
AGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCT
GCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAA
AGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACAC
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AGGAAGCGGAGGAGGAGGTAGCggacctaagaaaaagaggaaggtggcggccgct

pSAMca064 dCas9(Kl 153-P65, 1XGS) - AA

DKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFD
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NPDNSDVDKLFIQLVQTY!SQLFEENPiNASGVDAKAILSARLSKSRRLENLIAQLPGEKK
NGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAA
KNLSDAILLSDILRWTEITKAPLSASMIKRYDEHHQDLTLLK,\LVRQQLPEKYKEIFFDQ
SKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKXNREDLLRKQRTFDNGSIPHQI
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WNFEEVVDKGASAQSF!ERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEG
MRKPAFLSGEQKKAWDLLFKTNRKVTVKQLK^^ YFKKIECFDSVEISGVEDRFNASLG
TYHDLLK1IKDKDFLDNEENEDILED1VLTLTLFEDREM1EERLKTYAHLFDDKVMKQLK
RRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQ
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NRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKK¾4KNYWRQLLN
AKLITQRKFDNLTKAERGGLSELDKAGFlKRQLVETRQITKHVAQ!LDSRMNTKYDEND
KLJREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLES
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GETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKD

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PSSAMVPLAQPPAPAPVLTPGPPQSLSAPVPKSTQAGEGTLSEALLHLQFDADEDLGALL

GNSTDPGVFTDLASVDNSEFQQLLNQGVS MSHSTAEPM LMEYPEAITRLVTGSQRPPDP

APTPLGTSGLPNGLSGDEDFSSIADMDFSALLSQISSSGQGGGGSSKKLKSVKELLGITIM

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SKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

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SITGLYETRIDLSQLGGDSAGGGGSGGGGSGGGGSGPKKKRKVAAA

pSAMca065 dCas9(K1 153-P65, 3XGS) - DNA

atgGACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGC

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CAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACA

GCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACAC

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ACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTC

ATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAAC^ CCAG

CGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGG

AAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGCAACCTG

ATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAG

GATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCT

GGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCG

ACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCC

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CATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGA
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GTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAA
GCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCC
CXACXXGTGGCCTA TTCTGTXGCTXGGTGGTXGGCXAAAGTXGCAAAAGCGCAAGGGCXGG
GGAGGCTCCGGTGGTGGGGGCAGCGGAGGGGGGGGCAGCCCTTCAGGGCAGATCA
GCAACCAGGCCCTGGCTCTGGCCCCTAGCTCCGCTCCAGTGCTGGC^ CAGACTATGG
TGCCCTCTAGTGCTATGGTGCCTCTGGCCCAGCCACCTGCTCCAGCCCCTGTGCTGA
CCCCAGGACCACCCCAGTCACTGAGCGCTCCAGTGCCCAAGTCTACACAGGCCGGC
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GGGAGCTCTGCTGGGGAACAGCACCGATCCCGGAGTGTTCACAGATCTGGCCTCCG
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CAGCCGAACCAATGCTGATGGAGTACCCCGAAGCCATTACCCGGCTGGTGACCGGC
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GGGCTGTCCGGAGATGAAGACTTCTCAAGCATCGCTGATATGGACTTTAGTGCCCTG
CTGTCACAGATTTCCTCTAGTGGGCA GGGCGGGGGAGGCTCCGGTGGTGGGGGCAG
CGGAGGGGGGGGCAGCTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATC
ACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAA
GGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGT
TCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAG
(XGAAA iXGAA(T XG(GCXXT XXXXT XXCAAAT AT XGTXGAA(T T XXT XGT A(XT G(GCχCA(GCXAC
TATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGA
ACA(GCA{CAA(GCA(TACXTXG(GA(XGA(GAT(CAT[CXGAGCAGATxCAGCXGAGTTCTCCAAGA
GAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCAC
CGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGAC

CAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAG
GTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCG
GCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACagcgctGGAGGAGG
TGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCggacctaagaaaaagaggaaggtggcg
gccgct

pSAMca065 dCas9(Kl 153-P65, 3XGS) - AA

MDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF
DSGETAEATRLKRTARRRYTRRKNRSCYLQEIFSNEMAKVODSFFHRLEESFLAEEDKK
HERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEG
DLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGE
KKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFL
AAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFF
DQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPH
QIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRPAWMTRKSEETI
TPWNFEEVVDKGASAQSFIERMTNFDKINLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE
GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASL
GTYHDLLKIIKDKDFLDNEENEDILEDrVLTLTLFEDREMIEERLKTYAHLFDDKVMKQL
KRRRYTGWGRLSRKLLNGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKA
QVSGQGDSLHEHIANI-AGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTT
QKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL
DINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQL
LNAKLITQRKPDNLTKLAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDE
NDKLIREVKViTLKSKLVSDFRKDFQFYKVREINNYHFIAFIDAYLWAVVGTALIKKYPKL
ESEFVYGDYKVYDVRKMIAKSEQE1GKATAKYFFYSNIMNFFKTEITLANGEIRKRPL1ET
NGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESIL-PKRNSDKLIARKK
DWDPKKYGGFDSPTVAYSVLVVAKVEKGKGGGGSGGGGSGGGGSPSGQISNQALALA
PSSAPVLAQTMVPSSAMVPLAQPPAPAPVLTPGPPQSLSAPVPKSTQAGEGTLSEALLHL
QFDADEDLGALLGNSTDPGVFTDLASVDNSEFQQLLNQGVSMSHSTAEPMLMEYPEAIT
RLVTGSQRPPDPAPTPLGTSGLPNGLSGDEDFSSIADMDFSALLSQISSSGQGGGGSGGG
GSGGGGSSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELE

NGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKH YLDEIIEQISEFSKRV1LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKY FDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSAGGGGSGGGGSGGGGSG **PKKKRKVAAA**

Example 18: New catalytically inactive dCas9 proteins

[00784] In another aspect of the invention, novel dCas9 mutants are created. Catalytically inactive dCas9 are generated by combination of DIOA and N863A mutations, rather than DIOA and H840A mutations.

[00785] The catalytically inactive dCas9 mutant used in the literature and Applicants' previous experiments was generated by mutations DIOA and H840A within the wildtype Cas9 protein. From the crystal structure, Applicants made the observation that H840A fails to form a functional DNA-nickase. This result suggests that the H840A mutation has a greater dysfunctional effect on the Cas9 protein that originally hypothesized; the original theory being that H840A would result in loss of a single nucieopytic site, with no other effects. If the H840A mutation is disrupting other functions or conformational properties of the dCas9 protein, it stands to reason that a dCas9-activator fusion might be partially compromised by H840A. Thus, Applicants are interested in finding other mutations within the HNH domain which could knock out HNH nuclease activity, without disrupting other Cas9 functions. The Cas9/RNA/DNA crystal structure manuscript identifies mutation N863A as precisely such a mutation: N863A knocks out Cas9 double stranded nuclease activity, but permits nickase activity, suggesting that the global function of N863A Cas9 is not fully disrupted. In light of this observation, Applicants have synthesized a double knockout DIOA N863A Cas9 mutant for use as a dCas9-activator.

[00786] Corresponding constructs

pSAMca041	dCas(N863A)-vp64

[00787] Sequence information for creating catalytically inactive dCas9 by combination of DIOA and N863A mutations, rather than DIOA and H840A mutations is provided below:

[00788] **pSAMca041 dCas(N863A)-vp64** - DNA

[00789] **atgGACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGC TGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGG** CAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACA GCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACAC

CAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCA
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AAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCA
CGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACA
AGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCC
ArrTCCTGAJTCGAGGGCGACCTGAACCCCGACAACAGCGACarGGACAAGCmrTC
ATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAG
CGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGG
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GATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCT
GGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCG
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CTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCT
GAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACC
AGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTC
TACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGT
GAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGC
ATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGA
TVYTTACCCAYTCCmAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCYTCCG
CATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGA
CCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAA
GGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGC
CCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTAT
AACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCT
GAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAA
GTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTC
CGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACG
ATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGAC
ATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGA
GGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGA

AGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATC
CGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGC
CAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACA
1X'C-AGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCl 'GCΛ(C⋿A(GCΛ{ΛΊ1 'GCCΛΛT
CTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGA
CGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGG
CCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAA
GCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCC
GTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGG
GCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATG
TGGACCACATCGTGCCTCAGAGCTTTCTGAAGGACGACT^CATCGACAACAAGGTG
CTGACCAGAAGCGACAAGGCCCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGG
1XXGTGAAGAAGA'**r** **A**AGAA**A**Cl 'ACl 'C**X**GCGGCAGCl 'GCl 'GA**A(X**GCχ'A**A**GCl 'GATl 'ACX'
CAGAGAAAGTTCGACA ATCTGACCAAGG(C(XGAGAGAG(G**(X**GC**X**'!(iA(i(XiAA('TGG
ATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCAC
GTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCT
GATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGA
AGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGAC
GCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGA
AAGC**X**G**AG**TT(**X**GT**X**GTΛ {XiGC**GA**(C'T'**A**CΛ **A**(**X**G'!**X**G'T**A** (**X**⋿**A**CXGTXGCXGGAAGATGATCGCX'**A**
AGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATC
ΛT**]**(GΛΛ{ΊΊΊΊ X'Λ A(GΛ(XX⋿Λ(GΛ1'1 'Λ{XX'l XGGCXA Λ(XXGCXiAGiATCC(GGAAGCXXGCX-
TX'TXiATCXiAiiACAAAC(iGCXiAAACXXGiiGGiAGiATXXGTGT'**G G**G**A**T**AAG**G(i**C XX**G**i iG**AT'**r**
TTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACC
GAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGA
TAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACA
GCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCC
AAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCA
GCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAA
AAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCG
GAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGC

CCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCT
CCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTG
GACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGC
TAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAG
AGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCG
CCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAG
GTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGAT
CGACCTGTCTCAGCTGGGAGGCGACagcgctGGAGGAGGTGGAAGCGGAGGAGGAGG
AAGCGGAGGAGGAGGTAGCggacctaagaaaaagaggaaggtggcggccgctggatccGGACGGGCTGA
CGCATTGGACGATTTTGATCTGGATATGCTGGGAAGTGACGCCCTCGATGATTTTGA
CCTTGACATGCTTGGTTCGGATGCCCTTGATGACTTTGACCTCGACATGCTCGGCAGT
GACGCCCTTGATGATTTCGACCTGGACATGCTGATTAAC

[00790] pSAMca041 dCas(N863A)-vp64 - amino acid

MDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETA
EATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIF
GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNS
DVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG
NLIALSLGLTPNFKSNFDLAEDAKLQL5KDTYDDDLDNLLAQIGDQYADLFLAAKNLSD
AILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGY
AGYIDGGASQEEFYKLFIKLPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGEL
HAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPTOFEE
VVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPA
FLSGEQKKA1VDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLL
KIIKDKDFLDNEENEDILEDlVLTLTLFEDREMffiERLKTYAHLFDDKVMKQLKRRRYTG
WGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQG
DSLFIEFIIANLAGSPAIKKGILQTVKVVDELV^MGRFIKPENIVIEMARENQTTQKGQKN
SRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDnSfRLSD
YDVDHIVPQSFLK11DSIDNKVLTRSDK,ARGKSDNVPSEEVVKKMKNYWRQLLNAKLJT
QRKFDNLTKAERGGLSELDKAGF1XRQLVETRQJTKHVAQILDSRMNTKYDENDKLIRE
VKVITLKSKLVSDFRKDFQFYKVRELNNYHHAHDAYLNA\^VGTALIKKYPKLESEFVYG
DYKVYDVRKMLAKSEQEIGKATAKYFFYSNIMNFFKTE1TLANGEIRKRPLIETNGETGEI

VWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKK
YGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKJ>iPIDFLEAKGYKE
VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGS
PEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENI
IHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSA
**GGGGSGGGGSGGGGSGPKKKRKVAAAGSGRADALDDFDLDMLGSDALDDFDLDMLG
SDALDDFDLDMLGSDALDDFDLDMLIN**

Example 19: MS2 sgRNA sequence architecture- new MS2/dCas9/sgRNA Versions

[00791] Applicants generated additional 3' MS2 constructs and other MS2 sgRNA modifications to understand the effects of MS2 sgRNA sequence architecture. The experiments performed focused on two further ideas regarding the MS2 sgRNA sequence architecture.

[00792] First, the idea of placing the MS2 binding stems at the 3' end of the sgRNA, rather than inserting these binding sites into the native stemloops of the sgRNA. The use of a pair of 3' MS2 binding sites had previously been described in Mali, Prashant, et al. "CAS9 transcriptional activators for target specificity screening and paired nickases for cooperative genome engineering." *Nature biotechnology* (2013)), though the system was found to perform more poorly than the standard dCas9-VP64/sgRNA activation system. Applicants found that an sgRNA, of their own design, with 2 MS2 binding sites at the 3' end of the sgRNA, as well as MS2 sites at both the tetraloop and stemloop 2, activated both ASCLl and MYODl at a higher level than the 3' MS2 sgRNA from Mali et al. *{see* Fig. 50) However, Applicants' MS2 1.0, with MS2 sites only at the tetraloop and stemloop 2, was more potent than either of the 3' MS2 sgRNA architectures. *(see* Fig. 50)

[00793] Second, Applicants tested variations within the MS2 1.0 architectures. These modifications included but were not limited to removing the bulge from the MS2 1.0 binding site stem, removing the stabilizing GC tract that had been added to MS2 1.0, shortening the engineered stem by replacing the natural sgRNA stem with the stem of the MS2 binding site, as well as combinations of these approaches. These modifications had little effect on activation level for either ASCLl or MYODl, suggesting that the MS2 stemloops are somewhat robust to structural alterations within the MS2/dCas9/sgRNA activation context. In addition to the tetraloop modifications shown in Fig. 51, equivalent modifications were also tested for the MS2 binding site at stemloop 2, with similar results.

[00794] dCas9 protein modifications (NLS, N863A): Applicants tested two hypotheses for improvement of the dCas9-activator protein. First, the addition of a second SV40 nuclear localization signal, in addition to the NLS contained in the dCas9 to VP64 linker, was examined as a method of improving dCas9 nuclear localization and transcriptional modulation activity. Placement of the second NLS at the N-terminus of the dCas9 was observed to increase activation in several contexts. The effect was diminished when the second NLS was placed at the C-terminus of the VP64 activation domain. Later experiments (Figs. 54 and 55) would confirm these effects and suggest a possible improvement by use of an N-terminal alpha-importin NLS, rahter than a second SV40 signal.

[00795] Second, Applicants created a version of dCas9 using the N863A mutation, demonstrated in Nishimasu et a!., "Crystal structure of Cas9 in complex with guide RNA and target DNA." Ceil. 2014 Feb 27;156(5):935-49, to be a functional nickase-creating mutation site. This mutation replaces the H840A mutation which was observed to be a suboptimal nickase-creating mutation, suggesting that the H840A mutation, though it can be used with the D10A mutation to abolish nuclease activity, is detrimental in some way to the conformation or functionality of the nickase or dCas9 protein. Applicants observed that the N863A dCas9 acted as a more potent activator protein in certain contexts as shown in Figs. 52 and 53 for ASCL1 and MYODl, respectively.

[00796] New MS2 activator fusions proteins (HSFL MyoTAD): Based on Applicants' previous finding that a combination of two different activation domains (P65 and VP64) in the same activator complex (dCas and MS2) yielded greater activation than either domain simply used twice, Applicants wanted to test the potential for synergy between different activation domains further. Applicants constructed fusion proteins of MS2 with two distinct activation domains - either P65 in combination with HSF1 activation domain or P65 in combination with MyoD transactivation domain. Applicants observed the fold upregulation in both ASCL1 and MYODl using constructs with different NLS and point mutation dCas-VP64 architectures in combination with MS2 fused to individual or combined activation domains. It was noticed that the addition of an a-importin NLS had a favorable effect on localizing the Cas9 to the nucleus and that the N863A mutation was an advantageous mutation to generate a potent activator (Figs. 53 and 55). Applicants also determined that a combination of different activator domains had an

increased effect. E.g., The construct with a p65-HSFl fusion was found to be a more potent activator than the construct with p65 alone (Figs. 56 and 57).

[00797] PP7-VP64 activation: In addition to the MS2 phage coat protein, which Applicants have employed, a number of phage coat proteins exhibit RNA sequence specific binding. Applicants designed and tested an orthogonal activation system using the RNA binding domain from the PP7 phage. This new system includes the usual (previously described) dCas9-activator protein, a PP7-activator fusion protein, and an sgRNA with PP7 binding sites integrated at the tetraloop and stemloop 2. Applicants observed that the PP7 system functions equally as well as the MS2/dCas9/sgRNA activation system. These results suggest that the sgRNA RNA aptamer approach is generalizable and points to the future possibility of orthogonal modulation modalities using dCas9 and mutually exclusive RNA-binding proteins (such as M82, PP7, qBeta, GA, and others).

[00798] Target Diversity:

[00799] Difficult activation targets and sgRNA TSS proximity: Applicants' early work on CRISPR/Cas9 transcriptional modulation, as well as the published literature has found the majority of targets to be unamenable to activation by single sgRNA guides. Applicants selected 12 gene targets from the literature and Applicants own work which had previously proven difficult or intractable to dCas9 mediated activation. *(see* Fig. 58) Applicants attempted to activate each of these genes with the MS2-p65-HSF l/SV40-dCas9-VP64/sgRNA system using I of 8 guide sequences. Applicants observed significant activation for each of these difficult gene targets, with activation levels for the best guide ranging from 2 fold for MYC to >10,000 for IL1B. 8 of the 12 genes exhibited at least 15 fold expression. *(see* Fig. 58) For each guide sequence tested, the MS2/dCas9 system performed better than the standard dCas9-VP64 architecture, and no standard system fold expression was greater than 2 for any gene. *(see* Fig. 58) Additionally, Applicants observed that the success rate of guide sequences typically increased with closer proximity to the transcriptional start site (TSS) of the target gene. In a preferred embodiment of the invention, for particular targets, within 200bp of the TSS is deemed to be an advantageous window to select guide RNAs. This information could be useful for selection of sgRNA guide sequences for future experiments.

[00800] Activation vs. Basal expression: An open question in the field of artificial endogenous transcriptional modulation is why are some genes more amenable to activation than

others'? For the difficult targets listed above, Applicants plotted the fold expression of the best guide sequence against the deltaCt value from qPCR for that gene in control samples. These results suggest a strong inverse correlation between basal gene expression (higher deltaCt corresponds to lower basal expression) and maximal transcriptional activation by the MS2/dCas9/sgRNA system. *(see* Fig. 59)

[00801] Multiplexed activation: One important possible advantage of the ability of Applicants' system to provide robust activation with a single guide would be the capacity to easily activate a panel of genes simultaneously (by co-delivery to multiple guides for these genes), which would be intractable if a large number of guides would be required for activation of each gene alone.

[00802] In order to test the ability of Applicants' system (NLS-dCAS(D10,H840A)-NLS-VP64 in combination with MS2-NLS-P65-HSF1) to activate multiple genes simultaneously, Applicants co-transfected guides targeting 2, 4, 6, 8 or 10 genes at once. Activation of multiple genes was highly successful, as even for a combination of 10 genes each gene was activated significantly. *(see* Figs. 60-63)

Example 20: Structure-guided engineering of a CRISPR-Cas9 complex for genome-scale gene activation

Systematic interrogation of the functional organization of genomes requires the ability to perturb gene expression in a robust and generalizable manner. Structure-guided engineering of the CRISPR-Cas9 complex to mediate efficient transcriptional activation at endogenous genomic loci is described. Engineered Cas9 activators are used to investigate sgRNA-targeting rules for effective transcriptional activation, to demonstrate efficient multiplexed activation of 10 genes simultaneously, and to upregulate long intergenic non-coding RNA (lincRNA) transcripts. A library consisting of 70,290 guides targeting all human RefSeq coding isoforms was synthesized and SAM applied in a melanoma model to screen for genes whose activation confers resistance to the RAF inhibitor PLX-4720, an analog of the therapeutic compound vemurafenib. Expected resistance genes, such as EGFR and G protein-coupled receptor proteins, were enriched in the top hits, as were potentially novel resistance genes, such as members of the integrin family. The signature of the top screening hits was significantly predictive of BRAF inhibitor-resistant states in 29 short-term patient tumor cultures as well as 27 different melanoma cell lines and 113 primary and metastatic patient melanomas, demonstrating the potential of Cas9 activators as a powerful genetics tool.

[00803] Achieving genome-scale systematic perturbations within intact biological systems is important for elucidating the function of genes and epigenetic regulation. Genetic perturbations can be broadly classified as either loss-of-function or gain-of-function (GOF) based on their mode of action. Various genome-scale loss-of-function screening methods have been developed, including RNA interference[1,2] and the RNA-guided endonuclease Cas9 from the microbial adaptive immune system CRISPR[3]. Genome-scale GOF screening approaches have largely remained limited to the use of cDNA library overexpression systems. However, it is difficult to capture the complexity of transcript isoform variance using these libraries, and large cDNA sequences are often difficult to clone into viral expression vectors. Moreover, cDNA constructs tend to overdrive gene expression and may not be reflective of physiological protein levels. More generally, the endogenous regulatory contexts of the overexpressed genes cannot be recapitulated. Therefore, methods to enable genome-scale GOF perturbations at endogenous loci remain sought-after.

[00804] Programmable DNA binding proteins have emerged as an exciting platform for modulating transcription at endogenous genomic loci[4-13]. Among the established synthetic transcription factor platforms, the CRISPR-associated endonuclease Cas9 is most easily scaled to facilitate genome-scale perturbations[3,14-16] due to the simplicity of programming and producing the system relative to zinc finger proteins and transcription activator-like effectors (TALEs). Cas9 nuclease can be easily converted into a RNA-guided DNA binding protein (dCas9) by inactivating both of its catalytic domains[17-18]. dCas9 can be fused with transcription activation domains and retargeted to the promoter region of endogenous genes to achieve targeted modulation of gene expression[7,8,10-12]. Although the current generation of dCas9-based transcription effectors are able to achieve activation of some endogenous loci, the magnitude of transcriptional up-regulation achieved by individual single-guide RNAs (sgRNAs) typically ranges from low to ineffective[8,10,12]. Targeting a combination of sgRNAs tiling to a given promoter region can result in more robust transcriptional activation[10-12], but this requirement presents enormous challenges for scalability, and in particular for establishing pooled, genome-wide GOF screens using dCas9.

[00805] In order to improve and expand applications of Cas9, crystallographic studies, elucidating the atomic structure of the Cas9-sgRNA-target DNA tertiary complex[17], were undertaken, enabling rational engineering of Cas9 and sgRNA. This example provides a series of structure-guided engineering steps resulting in a potent transcription activation complex capable of mediating robust up-regulation with a single sgRNA. Using this new activation system, activation of endogenous genes as well as non-coding RNAs is demonstrated, the design rules for effective sgRNA target sites are elucidated, and a genome-wide dCas9-based transcription activation screening system to study targeted therapy resistance in a cellular model of melanoma is established and applied. These results collectively demonstrate the potentially broad applicability of RNA-guided gain-of-function (GOF) screening for functional genomics research.

[00806] Structure-guided design of a dCas9-based transcription activation complex

[00807] A key step in transforming the Cas9-sgRNA complex into an effective transcriptional activator is finding optimal anchoring positions for the activation domains. An ideal position would be proximally located relative to the target DNA to allow efficient interaction between the transcription machinery and target DNA, as well as permit unobstructed presentation of the transactivating effector to recruit transcription machinery. The crystal structure of the *Streptococcus pyogenes* dCas9 (D10A/H840A) in complex with a single guide RNA (sgRNA) and complementary target DNA[17] revealed a ribonucleoprotein complex in which the sgRNA-target DNA heteroduplex serves as a scaffold for the three-dimensional organization of the Cas9 protein domains. The N- and C-termini of Cas9 are located at the opposite side to the sgRNA-target DNA heteroduplex-binding groove (Fig. **64a),** indicating that fusing transactivating peptides at these locations, as reported in previous dCas9-activator designs, may be suboptimal. It was observed that the tetraloop and stem-loop 2 of the sgRNA protrude outside of the Cas9-sgRNA ribonucleoprotein complex, with the distal 4 bp of each stem completely free of interactions with Cas9 amino acid sidechains (Fig. **70a).** Both tetraloop and stem-loop 2 are also more proximal to the target DNA than either the N- or C-terminus and could provide better anchoring positions for effectors. Based on these observations and functional data showing that substitutions and deletions in the tetraloop and stem-loop 2 regions of the sgRNA sequence do not affect Cas9 catalytic function[17] **(Fig. 64a),** it was reasoned that the tetraloop and stem-loop 2 can be extended to incorporate protein-interacting aptamers, facilitating the recruitment of effectors to the Cas9 complex **(Fig. 64b).**

[00808] A minimal hairpin aptamer capable of binding to the bacteriophage coat protein MS2, which is known to be capable of binding MS2 through strong sequence- and structure-specific interactions in mammalian cells[18,19], to incorporate into tetraloop and stem-loop 2 (Fig, 70b) was chosen. Tests were performed to evaluate whether MS2-mediated recruitment of VP64 to the tetraloop and stem-loop 2 could mediate transcriptional up-regulation more efficiently than a dCas9-VP64 fusion alone. Aptamer-mediated recruitment of MS2-VP64 to either tetraloop (sgRNA 1.1) or stem-loop 2 (sgRNA 1.2) mediated 3- and 5-fold higher levels of *Neurog2* up-regulation than a dCas9-VP64 fusion (sgRNA 1.0), respectively. Recruitment of VP64 to both positions (sgRNA 2.0) resulted in an additive effect, leading to 12-fold increase over dCas9-VP64 (sgRNA 1.0). Combining sgRNA 2.0 with dCas9-VP64 instead of dCas9 provided an additional 1.3-fold increase in *Neurog2* up-regulation.

[00809] To confirm that spatial positioning, and not simply the number of activation domains, is the critical factor for effective transcription activation, sgRNA2.0 was compared to a previously described sgRNA bearing two MS2-binding stem-loops at the 3` end (sgRNA + 2xMS2)[11]. sgRNA2.0 drove 14- and 8.5-fold higher levels of transcription activation than sgRNA + 2xMS2 *for ASCL1 and MYOD1,* respectively (Fig. 64d).

[00810] <u>Effector Domains Act in Synergy to Enhance Transcription Activation</u>

[00811] To further improve the potency of Cas9-mediated transcription activation, how transcription activation is achieved in natural contexts was considered. Endogenous transcription factors generally act in synergy with co-factors to stimulate transcription[20]. It was hypothesized that combining VP64 with additional, distinct activation domains could improve activation efficiency through synergy. NF-κB trans-activating subunit p65 was chosen, which, while sharing some common co-factors with VP64, recruits a distinct subset of transcription factors and chromatin remodeling complexes. For example, p65 has been shown to recruit Ap-1, ATF/CREB, and *Spi*[21], whereas VP64 recruits PC4[22], CBP/p300[23], and the SWI/SNF complex[24].

[00812] The effector domain fused to dCas9 and MS2 was varied. Hetero-effector pairing of dCas9 and MS2 fusion proteins (e.g. dCas9-VP64 paired with MS2-p65 or dCas9-p65 with MS2-VP64) provided over 2.5-fold higher transcription activation for both *ASCL1* and *MYQD1* than same-effector pairing (e.g. dCas9-VP64 paired with MS2-VP64 or dCas9-p65 with MS2-p65) (Fig, 64e). This concept of domain synergy was further explored by introducing the activation domain from human heat-shock factor 1 (HSF1) (Marinho et al., Redox Biol 2014) as

a third activation domain, and it was demonstrated that an MS2-p65-HSF1 fusion protein further improved transcriptional activation of *ASCL1* (12%) and *MYOD1* (37%). Additional modifications to the sgRNA as well as Cas9 protein provided only minor improvements (Fig. **70c-e).** Based on these results it was concluded that the combination of sgRNA2.0, NLS-dCas9-VP64, and MS2-p65-HSF1 comprises the most effective transcription activation system, and designated it SAM. For simplicity, sgRNA2.0 is referred to as sgRNA in subsequent discussions of this example, unless noted otherwise.

[00813] Characterization of SAM efficacy and determination of sgRNA efficiency rules

[00814] To thoroughly evaluate the effectiveness of SAM for activating endogenous gene transcription, 12 genes were chosen that have been found previously to be difficult to activate using dCas9-VP64 and individual sgRNA1.0 guides[8,11,12]. For each gene, 8 sgRNA target sites spread across the proximal promoter between -1000bp and the +1 transcription start site (TSS) were selected. For 9 out of 12 genes, the maximum level of activation achieved using dCas9-VP64 with any of the 8 sgRNA1.0 guides was less than 2-fold, while the remaining three genes (ZFP42, KLF4 and IL1b) were maximally activated between 2- and 5-fold (Fig. 65a). In contrast, SAM stimulated transcription at least 2-fold for all genes and more than 15-fold for 8 out of 12 genes. Consistently, SAM performed better than sgRNA 1.0+dCas9-VP64 for all 96 guides, with a median gain of 105-fold higher expression up-regulation across all 12 genes.

[00815] Previous studies have demonstrated that poor activation efficiency of single sgRNA can be overcome by combining dCas9-VP64 with a pool of sgRNAs tiling the proximal promoter region of the target gene[10-13]. Therefore the single sgRNA activation efficiency of SAM was compared with dCas9-VP64 combined with a pool of 8 same-gene targeting sgRNA 1.0 guides. For most genes, SAM with a single sgRNA performed more robustly than dCas9-VP64 with pools of 8 sgRNA 1.0 guides (Fig. 65b). On average, SAM with single sgRNAs achieved 15 times more activation than dCas9-VP64 combined with pools of 8 sgRNA 1.0 guides. For all 12 genes, SAM incorporating three distinct activation domains (dCas9-VP64 with either MS2-p65-HSF1 or MS2-p65-MyoD1, whereas MyoD1 is a transactivating peptide derived from the human *MYOD1* gene[25]) performed better than SAM incorporating only two distinct activation domains (dCas9-VP64 with MS2-p65) (Fig. **71a).** For 9 out of 12 genes, triple-domain SAM achieved between 42% to 196% greater activation than double-domain SAM ($p < 0.01$, Student's t-test

with FDR correction). Also, triple-domain SAM with a non-targeting sgRNA generated less than 1% non-specific activation compared to activation by a targeting sgRNA (Fig, 71b and c).

[00816] Next, studies were performed to determine factors that contribute inter- and intragenic variability of activation efficiency by different sgRNAs. For intergene variability, the variation in the activation levels between sgRNAs and target genes was analyzed. Differences in activation levels could stem from how tightly a given locus is regulated and/or from variation in its basal level of transcription. Thus, correlation between basal transcription and the level of transcription activation achieved using SAM was of particular interest. Using the relative transcript level of target genes in control samples, a highly significant correlation between the inverse of basal transcript level and the fold up-regulation achieved using SAM was observed (Fig, 65c; $r = 0.94$, $p < 0.0001$). Whereas highly expressed genes (e.g. *MYC, VEGFA, TERT, SOX2)* were moderately upregulated, lowly expressed genes (e.g. *HBG1, IL1B, ZFP42)* were more significantly upregulated by SAM.

[00817] For intragenic variability, the activation data was aggregated for all 96 guides and the distance between the guide RNA target site and the TSS was found to be the most significant predictor of activation efficiency (Fig. 65d; $r = 0.67$, $p < 0.0001$). The strongest guides for each gene were always located within -200 bp and +1. A high fraction of guides were efficient in this window - 85% of guides within 200 bp upstream of the TSS achieved as least 25% of the maximal activation of a given gene. This simple finding can be used to inform the selection of efficient sgRNAs for gene activation.

[00818] <u>Transcriptional activation of lincRNAs</u>

[00819] Long intergenic noncoding RNAs (lincRNAs) are a class of non-protein-coding transcripts longer than 200 bp[26]. While numerous lincRNAs have been identified by transcriptome sequencing, most of these molecules lack functional characterization. Nonetheless, some have so far been shown to play crucial roles in epigenetic regulation, cancer, and development[27]. Targeted activation of these transcripts would be a valuable tool for revealing their biological significance. To test whether SAM is able to activate lincRNAs, 3 targets with known functions (TTNCR[28], HOTTIP[29], and PCAT[30]) and 3 with unknown functions (L1NC00925, LINC00514 and LINC0Q028) were chosen. Similar to previous mRNA up-regulation experiments, RefSeq annotations were used to select 8 sgRNA target sites from the proximal promoter (-800bp to +1) of each lincRNA. SAM indeed mediated significant up-

regulation of lincRNA transcripts from 3-fold up-regulation of PCAT to 360-fold up-regulation of LINC00514 (Fig. 66a). Interestingly, and in contrast to mRNA data, no significant correlation between the distance of lincRNA-targeted guides to the TSS and fold activation was found (**Fig.66b).** Possibly, this discrepancy could arise from the complex isoform structure of non-coding transcripts - the targets all have at least 2 isoforms with a different TSS reported[31].

[00820J In order to find an effective activation domain for lincRNAs, the efficacy of different transactivator components was compared. A comparison of MS2 fusions to VP64 alone, p65 alone, p65-HSFl, and p65-MyoDl for each of the 48 lincRNA-targeting guides was conducted **(Fig.** 72). Triple domain SAMs, dCas9-VP64 coupled with MS2-p65-HSFl or MS2-p65-MyoD1, led to significantly higher activation than the dual domain SAM (dCas9-VP64 with MS2-P65) for the best guides for all 6 lincRNAs ($p < 0.01$). Single domain SAM, dCas9-VP64 with MS2-VP64, performed worst for all 6 lincRNAs, suggesting that activation with a complex of synergistic domains may be important for efficient artificial up-regulation of non-coding RNAs based on the domains tested.

[00821] SAM mediates simultaneous activation of multiple genes

[00822] In order to study the complexity of gene network and transcription regulation, tools for simultaneous modulation of gene expression at multiple loci are needed. This would enable targeting of multiple elements of a signaling pathway or sets of genes that coordinate signaling in disease states. To that end, it was sought to test whether SAM can activate multiple genes simultaneously, and characterize factors impacting multiplexing performance. Simultaneous activation of three sets of 2, 4, 6 or 8 genes and one set of 10 genes was tested (Fig. 73) by co-expressing combinations of sgRNAs. Successful activation of all genes (>2-fold) for all gene combinations tested, including simultaneous activation of 10 genes was observed (Fig. 67a and 67b). Most genes (excluding *IL1R2)* exhibited a drop in the amount of up-regulation achieved when concurrently targeted with 9 other genes (Fig. 67a and 67b). Interestingly, the relative activation levels of each gene changed between multiplex activation and single-gene activation experiments. For example, whereas *NANOG* ranked 5th among the 10 targeted genes during single-gene activation, it ranked 10th in the 10-plex activation experiment. Some genes showed no change or only a modest and gradual drop in activation when concurrently targeted alongside an increasing number of genes (e.g. *ILIR2, MYODI, ASCL1).* Others, however, displayed a steep decrease in up-regulation when combined with even a single gene partner (e.g. *L1N28A, [LIB,*

NANOG). These distinct behaviours between genes were observed generally, across different-gene pairings (Fig. 73).

[00823] It was evaluated whether reduced activation of targets during multiplexing of 10 genes was due to the reduced amounts of sgRNA or SAM protein components available per gene. Surprisingly, diluting the sgRNA expression plasmid by 10-fold in single-gene activation experiments did not reduce activation for all genes (Fig. 67d). For example, activation for 4 out of 10 genes *(IL1R2, KLF4, ASCII,* and *MYOD1)* increased by an average of 90% with 10X dilution of sgRNA expression plasmid. The remaining 6 genes were decreased by an average of 51%. Genes whose activation was reduced as a result of sgRNA dilution were also dampened by multiplexing (Fig, 67e; $r = 0.94$, $p<0.001$).

[00824] The activation efficiency of SAM was generally stable to dilution of its protein components (dCas9-VP64 and MS2-p65-HSFl). Reducing the amount of expression plasmids for both components by 10-fold led to an average drop of 26% in activation efficiency (Fig. **74a).** Activation efficiency was particularly stable when all three components (including sgRNA) were diluted, retaining on average 100% activation efficiency across a 50-fold dilution range (Fig. **74b).** The finding that SAM is highly efficient even at low transfection concentrations was particularly promising for application in genome-scale pooled screens, which rely on single copy lentiviral integration.

[00825] Development of a genome-scale pooled transcription activation screen

[00826] The ability to activate target genes using a single sgRNA opens the possibility of conducting pooled genome-scale pooled transcription activation screening. As a first step towards developing a SAM-based screen, all three components were cloned into lentiviral vectors (Fig. 68a). Each vector encodes a unique selection marker (Blast, Hygro, and Zeocin or Puromycin) to enable selection of cells co-expressing all three SAM components. To assess the efficiency of SAM when delivered via lentivirus at low multiplicity of infection (MOi), three validated genes were targeted: *MYC,* which is weakly activated; and *KLF4* and *MYOD1,* which are only moderately activated. HEK293FT cells were co-transduced with lenti-dCas9-VP64 and lenti-MS2-p65-HSFl at MOI < 1 and concurrently selected with Blast and Hygro for 7 days. dCas9-VP65- and MS2-p65-HSFl -expressing cells were then transduced with lentiviral sgRNA vectors (lenti-sgRNA) at low MOI (< 0.2) and selected for successfully transduced cells using either Puromycin or Zeocin. Target gene expression levels were measured four days post-transduction. All three genes were efficiently upregulated to levels comparable *(MYOD1)* or greater than those observed after transient SAM transfection (MFC and *KLF4).* Notably, expression levels achieved with Puromycin or Zeocin resistance markers on the sgRNA construct were not equal **(Fig.** 68b).

[0827] Having validated lentiSAM constructs (lenti-dCas9-VP64, lenti-MS2-p65-HSF1, and lenti-sgRNA), a genome-scale sgRNA library targeting every coding isoform from the RefSeq database (23430 isoforms) was designed. 3 sgRNA per isoform were designed and target sites within 200 bp upstream of the TSS, which was previously determined to provide more efficient activation (Fig. **65d),** were chosen. The final library contained 70,290 guides, and two separate libraries with Zeocin (lenti-sgRNA-Zeo) or Puromycin (lenti-sgRNA-Puro) resistance were generated. As gene activation can have both a negative and positive effect on proliferation and cell survival a genome-wide screen for effectors of cellular growth was conducated. A polyclonal A375 melanoma cell line constitutively expressing both dCas9-VP64 and MS2-p65-HSF1 components was generated and these cells were transduced with a genome-scale lenti-sgRNA-Zeo library at a MOI of 0.2 (Fig. 68c). Genomic DNA was extracted 3 and 21 days after transduction by the sgRNA lentivirus, and guide counts were determined by NGS. Log$_2$ normalized guide counts for these two timepoints were compared. As expected for a population under selection, the distribution of guide counts displayed increased variance after 21 days in culture, with a large fraction of guides exhibiting depletion (Fig. **68d)** (Wilcoxon rank sum test, $p < 0.0001$). Enrichment of functional gene categories for the top 1000 depleted sgRNAs was analyzed, as well as the top 1000 depleted genes (determined based on the average depletion of all three guides targeted to a given gene), using ingenuity pathway analysis. Categories with $p < 0.01$ after Benjamim-Hochberg FDR correction are shown in Fig. 68e. Enrichment for cancer and pluripotency related gene categories (including PTEN[32] and STAT3[33] signaling pathways, which have been implicated in cancer regulation) was observed. These results suggest that dysregulation of members of these gene categories may negatively impact melanoma proliferation and that SAM can be used for depletion screening.

Using genome-scale transcription activation screen to identify genes involved in BRAF inhibitor resistance

[0828] Previously it has been demonstrated that genome-scale screening using Cas9-mediated gene knockout can facilitate the identification of loss-of-function mutations that confer

BRAF inhibitor resistance in a cell line model of melanoma[14]. The complementary genome-scale transcription activation screen using SAM would enable the identification of gain-of-function perturbations involved in melanoma drug resistance. To test the efficiency of SAM for genome-wide positive selection screening one aim was to identify genes implicated in the development of BRAF inhibitor resistance in $BRAF^{V600E}$ mutant melanoma. The A375 melanoma cell line harbors the $BRAF^{V600E}$ mutation and is naturally sensitive to BRAF inhibitors such as PLX4720 (PLX) and the closely related commercial therapeutic Vemurafenib. Cells harboring sgRNAs that activate genes leading to PLX resistance should therefore be enriched after continued culture in the presence of the drag, whereas no such effect should be observed in cells treated with vehicle only. Normalized guide counts for the input sgRNA-zeo library at the baseline time point (3 days post infection) as well as 14 days post treatment with either PLX or vehicle were analyzed. The sgRNA distribution was significantly different between cells treated with PLX and vehicle for two independent infection replicate screens, with the majority of sgRNAs exhibiting a reduced representation and a small set of guides showing high enrichment for PLX treated cells (Wilcoxon rank sum test, $P < 0.0001$, median -1.3 for PLX vs. **DMSO)(Fig.** 69a).

[00829] For a number of gene targets, several sgRNAs for the same gene were enriched in PLX-treated cells (Fig. 69b), suggesting the importance of these genes for the formation of PLX resistance. To determine genes exhibiting consistently high enrichment across multiple sgRNAs, the RNAi Gene Enrichment Ranking (RIGER) algorithm (Fig. 69c) was employed. The 10 most significant hits were distributed throughout the genome (Fig. 69c). 50% of the top 20 RIGER hits were replicated in a validation screen using puro selection, rather than zeo, on the sgRNA library (Fig. 75). The significance of the p-values of the top 100 RIGER hits was comparable to those observed for GeCKO screening[14], indicating that the results obtained from the SAM gain-of-function activation screen have similar statistical power compared to Cas9 nuclease-based knockout screening (Fig. 69d). In addition, for the top 10 shared hits between zeo and puro screens, the fraction of effectively enriched guides per gene (present in the top 5% of all guides) was very high with 97% for zeo and 81% for puro (89% ± 10.7% overall, compared to 78% ± 27% for the top 10 GECKO hits, Fig. **69e).**

[00830] Ectopic expression of the top hit from both screens - EGFR - was previously shown to cause PLX resistance in tumor types harboring $BRAF^{V600E}$ mutations by activating AKT in a pathway parallel to BRAF[3,4]. In addition, patient-derived BRAF mutant melanomas were

sensitized to PLX when treated with EGFR and AKT inhibitors[35]. Furthermore, four out of the top 10 hits from the first screen belong to the family of G protein-coupled receptors (GPR35, LPARl, LPAR5, and P2RY8). GPCR also emerged as the top-ranked protein class conferring resistance to multiple MAP kinase inhibitors in melanoma cells in a recent screen using cDNA overexpression by Johannessen *et al.*[36] GPR35 and LPARl have previously been found to mediate PLX resistance in A375 cells when overexpressed via cDNA[36]. GPR35, LPARl and LPAR5 share Gal 3 as a downstream target[37,38] and induce cell proliferation through the ERK/GSK3 β/β-catenin pathway, leading to a growth advantage in multiple cancer types[39,40]. Although the exact molecular mechanism for P2RY8 action has not been identified, P2RY8 is abundantly expressed in leukemia cells[41]. Overexpression of P2RY8 in NIH3T3 cells with cDNA led to increased CREB, Elk-1, c-Fos, and c-Myc activity, suggesting that P2RY8, may evoke cell proliferation through the ERK pathway[41]. RAF-independent activation of ERK has previously been shown as a resistance mechanism to BRAF inhibitors[42]. A second family of proteins present in the top 20 hits of both screens are Rho guanine nucleotide exchange factors (ARHGEFl and ARHGEF2) which also act on Gal3, downstream of GPCR. The activation of the GPCR pathway was shown to act as an independent mechanism for resistance to BRAF inhibition therapy through cAMP/PKA-mediated activation of transcription through CREB and ATF1[36]. While only two of the top hits (GPR35 and LPARl) overlap with the top hits from the Johannessen screen[36], many novel members of the GPCR pathway enriched in the top hits were in agreement with a model where GPCR pathway activation can mediate resistance to MAPK pathway inhibitors. Additionally, top hits include multiple integrin genes (ITGA9, ITGB3, and 1TGB5) that have roles in tumorigenesis and malignancy. Particularly, all three integrin hits are capable of driving MAPK signaling and promoting malignancy, anchorage independence, and migration in melanoma and various carcinomas[43-46]. Additionally, ITGB3 is capable of driving cancerous cells towards a stem-like state through NF-κB pathway activation, which has been shown to mediate resistance to BRAF-inhibition therapy[47] (Fig, 69f). Therefore, these integrin top hits may play a role in circumventing BRAF inhibition by activating accessory pathways known to promote resistance and re-activate the MAPK downstream of RAF to promote malignancy.

[00831] To verify the biological relevance of the top hits from the genome-wide screen, a collection of gene expression data from BRAF^{V600}-mutant melanoma cell lines in the Cancer Cell

Line Encyclopedia (CCLE)[48], short-term cultures of patient tumors[49], and a collection of primary and metastatic patient melanoma samples from The Cancer Genome Atlas (TCGA) (https^/tcga-data.nci.nih.gov/tcga/) was examined. As shown previously[47], a distinct transcriptional state defines BRAF-inhibition sensitivity /resistance where sensitive and resistant states are described by activation of endogenous MITF/associated markers (e.g. PMEL) and NF-**KB**-pathway activity/associated markers (e.g. AXL), respectively (Fig 6f). Using gene expression profiles from 29 melanoma short-term cultures, it was found that top genes from the SAM screen were significantly co-expressed within the resistant state and that a gene expression signature representing the top hits was predictive of this BRAF-inhibitor resistant transcriptional state **(Fig 69f,** p<0.0001 for overlapping hits from zeo and pttro screens).

[00832] The expression of the top hits in 27 $BRAF^{V600}$-mutant melanoma cell lines from CCLE for which gene expression and pharmacological data were available was additionally investigated. The gene expression of the top hits from the activation screen are enriched and significantly associated with resistance to BRAF-inhibition (PLX4720) as is the top-hit signature from the SAM screens **(Fig.** 77; p = 0.007 for overlapping hits from zeo and puro screens). To confirm that the top hits were representative of a resistant state *in vivo,* gene expression data from 113 primary and metastatic melanoma samples from TCGA (Fig, 78) was analyzed. The same gene and signature markers as described above was used to define sensitive and resistant transcriptional states and found that top hits and signatures from the SAM screens were significantly associated with a BRAF-inhibitor resistant phenotype (Fig. 78, p<0.0001 for both zeo and puro screens). Thus, both *in vitro* (short-term cultures of patient melanoma samples and a panel of established melanoma cell lines) and *in vivo* (TCGA), the hits expand the understanding of the transcriptional state associated with BRAF-inhibition resistance with potentially novel therapeutic targets.

[00833] In summary, a structure-guided approach has been taken to design a dCas9-based transcription activation system for achieving robust, single sgRNA-mediated gene up-regulation. By engineering the sgRNA to incorporate protein-interacting aptamers, a synthetic transcription activation complex consisting of multiple distinct effector domains that more closely mimic natural transcription activation processes was assembled. Additional developments may be able to take advantage of the modularity and customizability of the sgRNA scaffold to establish a series of sgRNA scaffolds with different aptamers for recruiting distinct types of effectors. For

instance, replacement of the MS2 stem-loops with PP7-interacting stem-loops may be used to recruit transcription repression elements.

[00834] The exemplary steps toward defining selection rules for potent sgRNAs provided in this example allows one skilled in the art to reveal additional selection criteria, such as sequence-intrinsic properties (Fig. 79), that are useful for guide efficacy.

[00835] Further characterization and improved understanding of the targeting specificity will also be useful for continued utility of Cas9 or SAM. Recent analysis of genome-wide dCas9-binding revealed significant concentration-dependent off-target binding[57].

[00836] Application of the Cas9 transcription activation complex, either in the context of individual gene perturbation or as genome-scale gene activation libraries, further allows for the dissection of many types of genetic elements, ranging from protein-coding genes to non-coding lincRNA elements. Furthermore, combining SAM with Cas9 mediated genome editing or dCas9-mediated gene repression allows for powerful approaches for studying gene interactions in diverse biological processes in contexts spanning from development and regeneration to many diseases.

[00837] Transient transfection experiments: Neuro-2a cells (Sigma-Aldrich) were grown in media containing 1:1 ratio of OptiMEM (Life Technologies) to high-glucose DMEM with GlutaMax and sodium pyruvate (Life Technologies) supplemented with 5% HyClone heat-inactivated FBS (Thermo Scientific), 1% penicillin/streptomycin (Life Technologies), and passaged at 1:5 every 2 days.

[00838] HEK293FT cells (Life Technologies) were maintained in high-glucose DMEM with GlutaMax and sodium pyruvate (Life Technologies) supplemented with 10% heat-inactivated characterized HyClone fetal bovine serum (Thermo Scientific) and 1% penicillin/streptomycin (Life Technologies). Cells were passaged daily at a ratio 1:2 or 1:2.5. For gene activation experiments, 20,000 HEK293FT cells/well were plated in 100 µL media in poly-D-lysine coated 96-well plates (BD Biosciences). 24 hours after plating, cells were transfected with a 1:1:1 mass ratio of:

- sgRNA plasmid with gene-specific targeting sequence or pUC19 control plasmid
- MS2-effector plasmid or pUC19.
- dCas9 plasmid, dCas9-effector plasmid, or pUC19.

A total plasmid mass of 0.3 ug/well was transfected using 1.5 uL/well Lipofectamine 2000 (Life

Technologies) according to the manufacturer's instructions. Culture medium was changed 5 hours after transfection. 48 hours after transfection, cell lysis and reverse transcription were performed using a Cells-to-Ct kit (Life Technologies). Relative RNA expression levels were quantified by reverse transcription and quantitative PCR (qPCR) using Taqman qPCR probes (Life technologies) and Fast Advanced Master Mix (Life Technologies). qPCR was earned out in 5 uL multiplexed reactions and 384-well format using the LightCycler 480 Instrument Π. Data was analyzed by the AAC$_{*}$ method: target Ct values (FAM dye) were normalized to GAPDH Ct values (VIC dye), and fold changes in target gene expression were determined by comparing to GFP-transfected experimental controls.

[00839] Lentivirus production: HEK293T cells (Life Technologies) were cultured as described above for HEK293FT cells. 1 day prior to transfection, cells were seeded at ~40% confluency (12 T225 flasks for library scale production, 1 T75 flask for individual guide production). Cells were transfected the next day at -80-90% confluency. For each flask, 20 ug of plasmid containing the vector of interest, 10 ug of pVSVG, and 15 ug of psPAX2 (Addgene) were transfected using 100 uL of Lipofectamine 2000 and 200 uL Plus Reagent (Life Technologies). 5h after transfection the media was changed. Virus supernatant was harvested 48h post-trans fection, filtered with a 0.45 μm PVDF filter (Millipore), aliquoted, and stored at −80 °C.

[00840] Lentiviral transduction: A375 cells (ATCC) were cultured in RPMI 1640 (Life Technologies) supplemented with 10% FBS (Seradigm) and 1% penicillin/streptomycin (Life Technologies) and passaged every other day at a 1:4 ratio. Cells were transduced with lentivirus via spinfection in 12-well plates. 3 x 10^6 cells in 2 ml, of media supplemented with 8 ug/mL polybrene (Sigma) were added to each well, supplemented with lentiviral supernatant and centrifuged for 2h at 1000g. 24h after spinfection, cells were detached with TrypLE (Life Technologies) and counted. Cells were replated at low density (7.5 x 10^6 cells per T225 Flask) and a selection agent was added either immediately (zeocin, blasticidin and hygrornycin, all Life technologies) or 3h after plating (puromycin). Concentrations for selection agents were determined using a kill curve: 0.5 ug/ml puromycin, 200 ug/mL zeocin, 2 ug/mL blasticidin, and 300 ug/mL hygrornycin. Media was refreshed on day 2 and cells were passaged every other day starting on day 4 after replating.The duration of selection was 4 days for puromycin and 7 days for zeocin, hygrornycin and blasticidin. Lentiviral titers were determined by spinfecting cells

with 6 different volumes of lentivirus ranging from 0 to 600 uL and counting the number of surviving cells after a complete selection (3-6 days).

[00841] Design and Cloning of SAM library: RefSeq coding gene isoforms with a unique TSS (total of 23430 isoforms) were targeted with three guides each for a total library of 70300 guides. Guides were designed to target the first 200 bp upstream of each TSS and subsequently filtered for GC content >25% and minimal overlap of the target sequence. After filtering, the remaining guides were scored according to predicted off-target matches based on Hsu et al. and three guides with the best off-target scores were selected. Cloning of the SAM sgRNA libraries was performed as previously described[14] with a minimal representation of 100 transformed colonies/guide.

[00842] Depletion and PLX Screen: A375 cells stably integrated with SAM Cas9 and effector components were transduced with SAM sgRNA libraries as described above at an MOI of 0.2, with a minimal representation of 500 transduced cells/guide. Cells were maintained at > 1000 cells/guide during subsequent passaging. At 7 DPI (complete selection, see above), cells were split into vehicle (DMSO) and PLX4720 conditions (2 uM PLX dissolved in DMSO, Selleckchem). Cells were passaged every 2 days for a total of 14 days of drug treatment. >1000 cells/guide were harvested as a baseline at 3 DPI (4 days before treatment) and at 21 DPI (after 14 days of treatment) for gDNA extraction. Genomic DNA was extracted using the Zymo Quick-gDNA midi kit (Zymo Research). PGR of the virally integrated guides was performed on gDNA at the equivalent of >500cells/guide in 96 parallel reactions using NEBnext High Fidelity 2X Master Mix (New England Biolabs) in a single-step reaction of 22 cycles. Primers are listed below:

[00843] *forwardprimer:*

AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATC
TNNNNNNNN(1-10bp stagger)GCTTTATATATCTTGTGGAAAGGACGAAACACC

8 bp barcode indicated in red

[00844] *reverseprimer:*

CAAGCAGAAGACGGCATACGAGATNNNNNNNNGTGACTGGAGTTCAGACGTGTGCT
C TTCCGATCTGCCAAGTTGATAACGGACTAGCCTT

8 bp index read barcode indicated in red

[00845] PGR products from all 96 reactions were pooled, purified using Zymo-Spin™ V with

Reservoir (Zymo research) and gel extracted using the Zymoclean™ Gel DNA Recovery Kit (Zymo research). Resulting libraries were deep-sequenced on Illumina Miseq and Hiseq platforms with a total coverage of >35 million reads passing filter per library.

[00846] NGS and screen hits analysis: NGS data were demultiplexed using unique index reads. Guide counts were determined based on perfectly-matched sequencing reads only. For each condition, guide counts were normalized to the total number of counts per condition, and $\log_2$ counts were calculated based on these values. Ratios of counts between conditions were calculated as $\log_2$((count 1 + 1)/(count 2 +1)) based on normalized counts.

[00847] RIGER analysis was performed using GENE-E based on the normalized day 14 log2 ratios (PLX/DMSO) averaged over two independent infection replicates. All RIGER analysis used the Kolmogorov-Smirnov method as described previously[illegible], except for Fig. 6c, where the weighed average method was used in order to enable comparison to GeCKO values determined by that method.

[00848] Gene expression and Pharmacological Validation Analysis: Gene expression data (CCLE, TCGA, short-term cultures) and pharmacological data (CCLE, short-term cultures) were analyzed to better understand the biological relevance of the top gene hits from the SAM screens. In the CCLE dataset[48], gene expression data (RNA-sequencing) and pharmacological data (activity area for MAPK pathway inhibitors) from $BRAF^{V600}$ mutant melanoma cell lines were used to compute the association between PLX-4720 resistance and the gene expression of each of the top hits. Additionally, gene expression signatures comprised of the top hits were generated using single-sample Gene Set Enrichment Analysis (ssGSEA)[52,53], and the associations between PLX-4720 resistance and these signatures were computed.

[00849] Gene expression data (Affymetrix GeneChip HT-HGU133) and PLX-4720 pharmacological data (GI_{50}; only for a subset of the samples) from short term melanoma cultures (STC)[49] was also used for plotting the gene expression of top hits and their ssGSEA signature scores. Expression data for the STC samples were collapsed to maximum probe value per gene and preprocessed using robust spline normalization.

[00850] Gene expression (RNA-sequencing) and genotyping data were collected from 113 $BRAF^{V600}$~mutant primary and metastatic patient tumors from The Cancer Genome Atlas (https://tcga-data.nci.nih.gov/tcga/) and this data was similarly used for determining the association between resistance and the expression of top hits/ssGSEA signature scores. Because

pharmacological data was not available for the STCs (only a subset had PLX-4720 data) and the TCGA melanoma samples, a transcriptional state was plotted using marker genes and signatures[47] in order to identify which samples were resistant to BRAF-inhibition.

[00851] Single Sample Gene Set Enrichment Analysis: While there was a significant association between the overexpression of some of the top individual SAM screen hits and resistance in three external cancer datasets, a more robust scoring system independent of any single gene was sought. Gene expression signatures were generated based on the set of top hits from each of the two SAM screens and for the overlap between them. Using single-sample Gene Set Enrichment analysis (ssGSEA), a score was generated for each sample that represents the enrichment of the SAM screen gene expression signature in that sample and the extent to which those genes are coordinately up- or down-regulated. Additionally, signature gene sets from the Molecular Signature Database (MSigDB)[54] were used in order to fully map the transcriptional BRAF-inhibitor resistant/sensitive states in the short-term culture and TCGA datasets as previously described[47].

[00852] information Coefficient for Measuring Associations in External Datasets: To measure correlations between different features (signature scores, gene expression, or drug-resistance data) in the external cancer datasets, an information-theoretic approach (mformation Coefficient; IC) was used and significance was measured using a permutation test (n=10,000), as previously described[47]. The IC was calculated between the feature used to sort the samples (columns) in each dataset and each of the features plotted in the heatmap (pharmacological data, gene expression, and signature scores).

[00853] sgRNA sequence analysis: Depletion for each sgRNA was calculated as the ratio of counts (see "NGS and screen hits analysis") between day 3 and day 21. sgRNAs corresponding to genes with significant depletion (p <=.05 by RIGER analysis) in sgRNA-puro and sgRNA-zeo libraries were selected for analyses. Selected sgRNA were counted for nucleotide occurrence in the sgRNA sequence, and for each nucleotide type, the correlation and significance with the sgRNA ratio of counts was calculated by Ordinary Least Squares linear regression.

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Example 21: Inducible *Structural Design Activation Mediators Transgenic Mice*

[00855] On the basis of Piatt et al., Cell (2014), 159(2): 440-455, or PCX patent publications as herein cited, such as WO 2014/093622 (PCT/US2013/074667), an inducible structural design activation mediator transgenic mouse is established. A mouse engineered with the Lox-Stop-polyA-Lox(LSL) cassette upstream to the coding region of the SpCas9 - VP64 fusion protein is established. A second mouse enginered with the Lox-Stop-polyA-Lox(LSL) cassette upstream to the coding region of the SpCas9 - VP64 fusion protein and upstream to the coding region of the MS2-P65-HSF1 fusion protein is established.

Example 22: Screening for gain of function phenotypes using inducible structural design activation mediators in cells and transgenic mice

[00856] The mice established in Example 21 are transfected with a AAV - Cre construct coding for and expressing Cre (such as under the control of a U6 promoter) and also coding for and expressing modified sgRNA (such as U6-modified sgRNA), according to the present invention via AAV. sgRNAs are designed to target the promoter region within 1000 nucleotides upstream of the TTS of lincRNAs of unknown function. Animals are screened for aberrant phenotypes.

[00857] Human guides and mouse guides of PCX application designating, inter alia, the United States, application No. PCT/US 14/41806, filed June 10, 2014, and the applications in the lineage of this PCX application (i.e., guides in the applications as to which PCT/US 14/41806 claims priority), all incorporated herein by reference, are modified to contain an activator as herein discussed, or a repressor as herein discussed.

[00858] Human cells containing or modified to constitutively express or inducibly express Cas9 are transfected with an AAV construct coding for human sgRNA of PCT application designating, inter alia, the United States, application No. PCT/US 14/41806, filed June 10, 2014,

and the applications in the lineage of this PCX application (i.e., guides in the applications as to which PCT/US 14/41806 claims priority), wherein the guides include either at least one repressor or at least one activator, in accordance with the herein discussion, under the control of and operably linked to a promoter, such as U6~modified sgRNA, according to the present invention; and in the case of such cells wherein the Cas9 is inducibly expressed, Cre induces expression and the construct also via AAA" codes for and expresses Cre, such as by way of coding therefor operably linked to a U6 promoter. The cells as to which the sgRNA has a activator are monitored for Gain of Function and the cells as to which the sgRNA has a repressor are monitored for Loss of Function. The cells as to which the modified sgRNA has an activator show gain of function, and the cells as to which the modified sgRNA has a repressor show loss of function. In this fashion, human cells can be screened.

[00859] The Cas9 mouse of Example 21, Piatt et al, Cell (2014), 159(2): 440-455, or PCT publications as herein cited, such as WO 2014/093622 (PCT/US2013/074667), and are transfected with a AAV - Cre construct coding for and expressing Cre (such as under the control of a U6 promoter) and also coding for and expressing modified mouse sgRNA (such as U6-modified sgRNA) of PCT application designating, inter alia, the United States, application No. PCT/US 14/41806, filed June 10, 2014, and the applications in the lineage of this PCT application (i.e., guides in the applications as to which PCT/US 14/41806 claims priority), wherein the guides include either at least one repressor or at least one activator, in accordance with the herein disclosure. The mice as to which the sgRNA has a activator are monitored for Gain of Function and the mice as to which the sgRNA has a repressor are monitored for Loss of Function. The mice as to which the modified sgRNA has an activator show gain of function, and the mice as to which the modified sgRNA has a repressor show loss of function. In this fashion, mice can be screened.

[00860] In an aspect, the vector systems in the methods of the invention comprise one or more lentiviral vector(s). In a preferred embodiment, the one or more lentiviral vectors may comprise a codon optimized nuclear localization signal (NLS), a codon optimized P2A bicistronic linker sequence and an optimally placed U6 driven guide RNA cassette. In another aspect the vector system comprises two lentiviral vectors, wherein one lentiviral vector comprises the Cas9 enzyme and the other lentiviral vector comprises the guide RNA selected from the libraries of the invention. In an embodiment of the invention, each vector has a different selection marker,

e.g. a different antibiotic resistance marker. The invention also comprehends kits comprising the libraries of the invention. In certain aspects, the kit comprises a single container comprising vectors comprising the library of the invention. In other aspects, the kit comprises a single container comprising plasmids comprising the library of the invention. The invention also comprehends kits comprising a panel comprising a selection of unique CRISPR-Cas system guide sequences from the library of the invention, wherein the selection is indicative of a particular physiological condition. In preferred embodiments, the targeting is of about 100 or more sequences, about 1000 or more sequences or about 20,000 or more sequences or the entire genome. In other embodiments a panel of target sequences is focused on a relevant or desirable pathway, such as an immune pathway or cell division.

Example 23: Paired Nickase Fokl

[00861] Paired CRISPR-Cas complexes having a mutated CRISPR enzyme whereby the CRISPR enzyme is "dead" (has at most 5% nuclease activity of non-mutated Cas9 or CRISPR enzyme), and a FokI nuclease is operably linked to sgRNA are delivered to cells, whereby in the pair, a first CRISPR-Cas complex makes a cut at a first loci in the cells and a second CRISPR-Cas complex makes cut at a second loci in the cells; the two Fokl enzymes provide a double stranded break such as when the first and second loci are at or near each other but on different strands of double stranded DNA, whereby such that the CRISPR-Cas complex(es) provide(s) a particular specific cut or double stranded cut, and the CRISPR-Cas complexes have a greater reduction in off-target cutting, than unmodified CRISPR-Cas complexes. The paired CRiSPR-Cas9 complexes can cut the two strands of double stranded DNA such that HDR can occur. In embodiments template DNA is introduced into the cells whereby there is homologous recombination inserting the template DNA where the double stranded cut has been made.

Example 24: Three-Component Chimeric Cas9 Enzymes

[00862] Chimeric Cas9 enzymes were constructed and tested. The Chimeric enzymes had N' and C terminal domains from Sp Cas9, but internal domains were swapped out for Sa or St3 domains to provide Sp-St3-Sp or Sp-Sa-Sp chimeric 3 component enzymes.

[00863] A range of guides were tested with each chimeric enzyme. The guides were either pure Sp, Sa or St3 wildtype, or they were engineered such that they were hybrids of Sp with Sa or St3. Where the enzyme included one or more St3 internal domains to form an Sp-St3-Sp chimeric 3-component enzyme, the hybrid guides comprised either: an Sp BackBone (BB) and an St3 Targeting Sequence (TGS); or an St3 BackBone (BB) and an Sp Targeting Sequence (TGS). Where one or more Sa internal domains were swapped in to form Sp-Sa-Sp chimeric 3-component enzyme, the guides were engineered to comprise either: an Sp BackBone (BB) and an Sa Targeting Sequence (TGS); or an Sa BackBone (BB) and an Sp Targeting Sequence (TGS). The BackBone comprises the sgRNA scaffold (or tracr sequence and tracr mate) and the Targeting Sequence consisted of the 20bp spacer portion of the sgRNA (specific for the DNA target).

[00864] The domains swapped in or out were not necessarily complete domains in that they included full and partial domains. While complete swap of the Rec lobe is within the ambit of the instant invention, for illustrative purposes, this work focused on partial swaps of the Rec lobe. The Nuc lobe comprises the RuvCI domain, the RuvCII domain, the HNH domain, RuvCni domain and the PI domain, whilst the Rec lobe comprises the BH, REC1 and REC2 domains.

Methods

Cell culture and transfection

[00865] Human embryonic kidney (HEK) cell line 293FT (Life Technologies) or mouse Neuro 2a (Sigma-Aldrich) cell line was maintained in Dulbecco's modified Eagle's Medium (DMEM) supplemented with 10 % fetal bovine serum (HyClone), 2mM GlutaMAX (Life Technologies), 100 U/mL penicillin, and **10**(^g/mL streptomycin at 37 °C with 5 % **CO_2** incubation.

[00866] Cells were seeded onto 24-well plates (Corning) at a density of 120,000 cells/well, 24 hours prior to transfection. Cells were transfected using Lipofectamine 2000 (Life Technologies) at 80-90 % confluency following the manufacturer's recommended protocol. A total of 500 ng Cas9 plasmid and 100 ng of U6-sgRNA PGR product was transfected .

SURVEYOR nuclease assay for genome modification

[00867] 293FT and HUES62 cells were transfected with DNA as described above. Cells were incubated at 37 °C for 72 hours post-transfection prior to genomic DNA extraction. Genomic DNA was extracted using the QuickExtract DNA Extraction Solution (Epicentre) following the manufacturer's protocol. Briefly, pelleted cells were resuspended in QuickExtract solution and incubated at 65 °C for 15 minutes, 68 °C for 15 minutes, and 98 °C for 10 minutes.

[00868] The genomic region flanking the CRISPR target site for each gene was PCR amplified using primers as follows:

primer name	genomic target	primer sequence (5' to 3')
SUV901	EMX1	CCATCCCCTTCTGTGAATGT
SUV902	EMX1	GGAGATTGGAGACACGGAGA

[00869] Products were purified using QiaQuick Spin Column (Qiagen) following the manufacturer's protocol. 400 ng total of the purified PCR products were mixed with 2 microliters 10X Taq DNA Polymerase PCR buffer (Enzymatics) and ultrapure water to a final volume of 20 microliters, and subjected to a re-annealing process to enable heteroduplex formation: 95 °C for 10 min, 95 °C to 85 °C ramping at - 2 °C/s, 85 °C to 25 °C at - 0.25 °C/s, and 25 °C hold for 1 minute. After re-annealing, products were treated with SURVEYOR nuclease and SURVEYOR enhancer S (Transgenomics) following the manufacturer's recommended protocol, and analyzed on 4-20% Novex TBE poly-acrylamide gels (Life Technologies). Gels were stained with SYBR Gold DNA stain (Life Technologies) for 30 minutes and imaged with a Gel Doc gel imaging system (Bio-rad). Quantification was based on relative band intensities. Indel percentage was determined by the formula:

$$100 x (1 - (1 - (b + c) / (a + b + c))^{1/2}),$$

where 'a' is the integrated intensity of the undigested PCR product, and 'b' and 'c' are the integrated intensities of each cleavage product.

Results

[00870] The helical domains, e.g., HD2 or Helical domain 2, discussed earlier herein, are initial annotations of the 1368 amino acid Sp Cas9 and current terminology also involves a Recognition or Rec lobe with three domains: REC1 (with reference to Sp Cas9 residues 94-179), REC2 (residues 180-307, with reference to Sp Cas9) and a long alpha helix referred to as the bridge helix (residues 60-93 with reference to Sp Cas9) (see Nishimasu *et al*). The results of this Example are shown in Figure 86. Figure 86 shows testing of chimera between Sp, Sa and St3

Cas9 based on crystal structure. A) domain organization and amino acid (AA) positions of Sp Cas9. The REC lobe is a newly identified structural component of Cas9. B) Chimera maps of partial or complete swaps of the Nuc lobe, with AA positions of chimera boundaries indicated C) indel % achieved with each corresponding chimera on the left. Labels indicate the sgRNA used. TGS = targeting sequences (20bp spacer portion of the sgRNA), BB = sgRNA backbone Applicants found that it is possible to construct chimera between different Cas9 proteins (originating from different species) that consist of at least three components, thereby enabling internal domains to be swapped out. Applicants illustrated this with swaps performed on the internal REC lobe of Cas9, which was newly identified based on the crystal structure provided herein.

* * *

[00871] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

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WHAT IS CLAIMED IS:

1. A non-naturally occurring or engineered composition comprising a guide RNA (sgRNA) comprising a guide sequence capable of hybridizing to a target sequence in a genomic locus of interest in a cell, wherein at least one loop of the sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins, and wherein the adaptor protein is associated with one or more functional domains.

2. A non-naturally occurring or engineered CRISPR-Cas complex composition comprising the sgRNA of claim 1 and a CRISPR enzyme.

3. The non-naturally occurring or engineered CRISPR-Cas complex composition of claim 2, wherein:

the CRISPR enzyme comprises at least one mutation, such that the CRISPR enzyme has no more than 5% of the nuclease activity of the CRISPR enzyme not having the at least one mutation; and/or

at least one or more nuclear localization sequences.

4. The sgRNA of claim 1 or the CRISPR-Cas complex of claims 2 or 3 wherein one or more adaptor proteins associated with one or more functional domains is present and bound to the distinct RNA sequence(s) inserted into the at least one loop of the sgRNA.

5. A non-naturally occurring or engineered composition comprising:

one or more guide RNA (sgRNA) comprising a guide sequence capable of hybridizing to a target sequence in a genomic locus of interest in a cell,

a CRISPR enzyme comprising at least one or more nuclear localization sequences,

wherein the CRISPR enzyme comprises at least one mutation, such that the CRISPR enzyme has no more than 5% of the nuclease activity of the CRISPR enzyme not having the at least one mutation,

wherein at least one loop of at least one sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins, and

wherein the adaptor protein is associated with one or more functional domains.

6. The composition of any one of claims 2, 3, 4 or 5, wherein the CRISPR enzyme has a diminished nuclease activity of at least 97%, or 100% as compared with the CRISPR enzyme not having the at least one mutation.

7. The composition of any one of claims 2, 3, 4, 5 or 6, wherein the CRISPR enzyme comprises two or more mutations wherein two or more of D10, E762, H840, N854, N863, or D986 according to SpCas9 protein or any corresponding ortholog or N580 according to SaCas9 protein are mutated, or the CRISPR enzyme comprises at least one mutation wherein at least H840 is mutated.

8. The composition of claim 7, wherein the CRISPR enzyme comprises two or more mutations comprising D10A, E762A, H840A, N854A, N863A or D986A according to SpCas9 protein or any corresponding ortholog, or N580A according to SaCas9 protein, or at least one mutation comprising H840A.

9. The composition of any one of claims 2, 3, 4, 5 or 6, wherein the CRISPR enzyme comprises H840A, or D10A and H840A, or D10A and N863A, according to SpCas9 protein or any corresponding ortholog.

10. The composition of any one of claims 2, 3, 4, 5 or 6, wherein the CRISPR enzyme comprises:

N580A according to SaCas9 protein or any corresponding ortholog; or

D10A according to SpCas9 protein, or any corresponding ortholog, and N580A according to SaCas9 protein.

11. The composition of any one of claims 2-10, wherein the CRISPR enzyme is associated with one or more functional domains.

12. The composition of claim 11, wherein the one or more functional domains associated with the adaptor protein is a heterologous functional domain.

13. The composition of claim 11, wherein the one or more functional domains associated with the CRISPR enzyme is a heterologous functional domain.

14. The composition of any one of the preceding claims, wherein the adaptor protein is a fusion protein comprising the functional domain, the fusion protein optionally comprising a linker between the adaptor protein and the functional domain, the linker optionally including a GlySer linker.

15. The composition of any one of the preceding claims, wherein the at least one loop of the sgRNA is not modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins and wherein, optionally one of the unmodified sgRNA loops is either one of the tetraloop or the stem-loop 2.

16. The composition of any one of the preceding claims, wherein the one or more functional domains associated with the adaptor protein is a transcriptional activation domain.

17. The composition of any one of claims 11-16, wherein the one or more functional domains associated with the CRISPR enzyme is a transcriptional activation domain.

18. The composition of any one of the preceding claims, wherein the one or more functional domains associated with the adaptor protein is a transcriptional activation domain comprising VP64, p65, MyoDl, HSF1, RTA or SET7/9.

19. The composition of any one of claims 11-18, wherein the one or more functional domains associated with the CRISPR enzyme is a transcriptional activation domain comprises VP64, p65, MyoDl, HSF1, RTA or SET7/9.

20. The composition of any one of claims 1-15, wherein the one or more functional domains associated with the adaptor protein is a transcriptional repressor domain.

21. The composition of any one of claims 11-16, wherein the one or more functional domains associated with the CRISPR enzyme is a transcriptional repressor domain.

22. The composition of claim 20 or 21, wherein the transcriptional repressor domain is a KRAB domain.

23. The composition of claim 20 or 21, wherein the transcriptional repressor domain is a NuE domain, NcoR domain, SID domain or a SID4X domain.

24. The composition of any one of claims 1-15, wherein the one or more functional domains associated with the adaptor protein have one or more activities comprising methylase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity, DNA cleavage activity, DNA integration activity or nucleic acid binding activity.

25. The composition of any one of claims 11-15, wherein the one or more functional domains associated with the CRISPR enzyme have one or more activities comprising methylase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity, DNA cleavage activity, DNA integration activity, nucleic acid binding activity, or molecular switch activity or chemical inducibility or light inducibiiity.

26. The composition of any one of claims 24-25, wherein the DNA cleavage activity is due to a nuclease.

27. The composition of claim 26 wherein the nuclease comprises a Fold nuclease.

28. The composition of any one of claims 2-26, wherein the one or more functional domains is attached to the CRISPR enzyme so that upon binding to the sgRNA and target the functional domain is in a spatial orientation allowing for the functional domain to function in its attributed function.

29. The composition of claim 28, wherein the one or more functional domains is attached to the CRISPR enzyme via a linker, optionally a GlySer linker.

30. The composition of any one of claims 2-29, wherein the sgRNA is modified so that, after sgRNA binds the adaptor protein and further binds to the CRISPR enzyme and target, the functional domain is in a spatial orientation allowing for the functional domain to function in its attributed function.

31. The composition of any one of claims 3 or 5-27, wherein the at least one loop of the sgRNA is tetraloop and/or loop2.

32. The composition of claim 31, wherein the tetraloop and loop 2 of the sgRNA are modified by the insertion of the distinct RNA sequence(s).

33. The composition of any one of claims 31 or 32, wherein the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins is an aptamer sequence.

34. The composition of claim 33, wherein the aptamer sequence is two or more aptamer sequences specific to the same adaptor protein.

35. The composition of claim 33, wherein the aptamer sequence is two or more aptamer sequences specific to different adaptor proteins.

36. The composition of any one of the preceding claims, wherein the adaptor protein comprises MS2, PP7, Qβ, F2, GA, fr, JP5Q1, M12, R17, BZ13, JP34, JP500, KU1, M11, MX1, TW18, VK, SP, FI, ID2, NL95, TW19, AP205, ϕCb5, ϕCb8r, ϕCb12r, ϕCb23r, 7s, PRR1.

37. The composition of any one of the preceding claims, wherein the cell is a eukaryotic cell, optionally a mammalian cell.

38. The composition of claim 37, wherein the cell is a human cell or a mouse cell.

39. A mammalian cell as defined in claim 37 or 38, wherein the cell comprises a cell line and is, optionally, a human cell line or a mouse cell line.

40. A transgenic mammalian model, optionally a mouse, wherein the model has been transformed with the composition according to claim 37 or 38 or is a progeny of said transformant.

41. A method for introducing a genomic locus event comprising the administration to a host, or expression in a host, of one or more of the compositions from any of claims 1-36.

42. The method according to claim 41, wherein the genomic locus event comprises affecting gene activation, gene inhibition, or cleavage in the locus, or insertion of DNA.

43. The method according to any one of claims 41 or 42, comprising the delivery of the composition or nucleic acid molecule(s) coding therefor, wherein said nucleic acid molecule(s) are operatively linked to regulatory sequence(s) and expressed in vivo.

44. The method according to claim 42, wherein the expression in vivo is via a lentivirus, an adenovirus, or an AAA".

45. A vector comprising: a nucleic acid molecule encoding a guide RNA (sgRNA), comprising a regulatory element operable in a eukaryotic cell including a guide sequence (sgRNA) operably linked to a promoter, the sgRNA being capable of hybridizing to a target sequence in a genomic locus of interest in a cell, wherein at least one loop of the sgRNA is modified by the insertion of distinct RNA sequencers) that bind to one or more adaptor proteins.

46. A vector comprising a regulatory element operable in a eukaryotic cell including a nucleic acid molecule encoding a CRISPR enzyme operably linked to a promoter, the enzyme comprising at least one or more nuclear localization sequences, wherein the CRISPR enzyme comprises at least one mutation, such that the CRISPR enzyme has no more than 5% of the nuclease activity of the CRISPR enzyme not having the at least one mutation, and wherein the CRISPR enzyme is associated with one or more functional domains.

47. A nucleic acid molecule(s) encoding sgRNA of claim 1 or the CRISPR-Cas complex of claims 2 or 3 or the composition of claim 5.

48. A method of screening for gain of function (GOF) or loss of function (LOF) comprising the cell line of claim 39 or cells of the model of claim 40 containing or expressing Cas9 and introducing a composition of claim 1 into cells of the cell line or model, whereby the sgRNA includes either an activator or a repressor, and monitoring for GOF or LOF respectively as to those cells as to which the introduced sgRNA includes an activator or as to those cells as to which the introduced sgRNA includes a repressor.

49. The composition of any one of claims 2-15 wherein the CRISPR enzyme includes one or more functional domains.

50. The composition of any of claims 5-38 or 49 wherein there is more than one sgRNA, and the sgRNAs target different sequences whereby when the composition is employed, there is multiplexing.

51. The composition of claim 50 wherein there is more than one sgRNA modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins.

52. The composition of claim 50 or 51 wherein one or more adaptor proteins associated with one or more functional domains is present and bound to the distinct RNA sequence(s) inserted into the at least one loop of the sgRNA.

53. ACRISPR Cas complex comprising a CRISPR enzyme and a guide RNA (sgRNA), wherein

the CRISPR enzyme comprises at least one mutation, such that the CRISPR enzyme has no more than 5% of the nuclease activity of the CRISPR enzyme not having the at least one mutation and, optional, at least one or more nuclear localization sequences;

the guide RNA (sgRNA) comprises a guide sequence capable of hybridizing to a target sequence in a genomic locus of interest in a cell; and wherein:

a) the CRISPR enzyme is associated with two or more functional domains, which may be the same or different; or

b) at least one loop of the sgRNA is modified by the insertion of distinct RNA sequencers) that bind to one or more adaptor proteins, and wherein the adaptor protein is associated with two or more functional domains; or

c) the CRISPR enzyme is associated with one or more functional domains and at least one loop of the sgRNA is modified by the insertion of distinct RNA sequence(s) that bind to one or more adaptor proteins, and wherein the adaptor protein is associated with one or more functional domains

54. The composition of any of claims 5-38 or 49-52, wherein the target sequence(s) are non-coding or regulatory sequences.

55. The composition of claim 54, wherein the regulatory sequences are promoter, enhancer or silencer sequence(s).

56. (A) A non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to a CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the polynucleotide sequence comprises

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a second regulatory element operably linked to an enzyme-coding sequence encoding a CRISPR enzyme comprising at least one or more nuclear localization sequences,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein components I and II are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence,

or

(B) a non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulator}' element operably linked to

(a) a guide sequence capable of hybridizing to a target sequence in a prokaryotic cell, and

(b) at least one or more tracr mate sequences,

II. a second regulatory element operably linked to an enzyme-coding sequence encoding a CRISPR enzyme, and

III. a third regulatory element operably linked to a tracr sequence,

wherein components I, II and III are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence,

wherein the CRISPR enzyme is a Cas9 ortholog of a genus belonging to the group consisting of *Corynebacter, SuUerella, Legionella, Treponema, Filifactor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides, Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillmn, Ghiconacetobacter, Neisseria, Roseburia, Parvibaculum, Staphylococcus, Nitratifractor, Mycoplasma* and *Campylobacter,* and

wherein the Cas comprises a helical domain 2 truncation.

57. The composition according to claim 56, wherein the CRISPR enzyme has one or more mutations in any domain of the enzyme.

58. The composition according to any of claim 56 or 57, wherein the CRISPR enzyme has one or more mutations in a catalytic domain.

59. The composition according to claim 56 or 57, wherein the one or more mutations is in a RuvC I, RuvC II, RuvC III or HNH domain of the CRISPR enzyme.

60. The composition according to claim 59, wherein the CRISPR enzyme comprises one or more mutations corresponding to the position numbering of Sp Cas9 at positions D10A, E762A, D986A, S15A, E762A, H982A, H983A, D986A, H840A, N854A or N863A or any corresponding ortholog or N580 according to SaCas9 protein are mutated.

61. The composition according to claim 56, wherein the enzyme further comprises a functional domain.

62. The composition according to claim 61, wherein the functional domain is a transcriptional activator domain.

63. The composition according to claim 62, wherein the transcriptional activator domain is VP64.

64. The composition according to claim 61, wherein the functional domain is a transcriptional repressor domain.

65. The composition according to claim 64, wherein the transcriptional repressor domain is KRAB, SID or SID4X.

66. The composition according to claim 56 wherein the Cas9 ortholog is a Sutterella wadsworthensis Cas9.

67. The composition according to claim 56 wherein the Cas9 ortholog is a Filifactor alocis Cas9.

68. The composition according to claim 56 wherein the Cas9 ortholog is a Lactobacillus johnsonii Cas9.

69. The composition according to claim 56 wherein the Cas9 ortholog is a Campylobacter lari Cas9.

70. The composition according to claim 56 wherein the Cas9 ortholog is a Corynebacter diptheriae Cas9.

71. The composition according to claim 56 wherein the Cas9 ortholog is a Pambaculum lavamentivorans Cas9.

72. The composition according to claim 56 wherein the Cas9 ortholog is a Mycoplasma gailisepticum Cas9.

73. The composition according to claim 56 wherein the Cas9 ortholog is a Staphylococcus aureus subsubspecies Aureus Cas9.

74. The composition according to claim 56 wherein the Cas9 ortholog is a Legionella pneumophila Paris Cas9.

75. The composition according to claim 56 wherein the Cas9 ortholog is a Treponema denticoia Cas9.

76. The composition according to claim 56 wherein the Cas9 orthoiog is a Staphylococcus pseudintermedius Cas9.

77. The composition according to claim 56 wherein the Cas9 orthoiog is a Neisseria cinerea Cas9.

78. A method of modifying an organism or a non-human organism by manipulation of a target sequence in a genomic locus of interest comprising

delivering a non-naturally occurring or engineered composition comprising a vector system operabiy encoding a composition of claim 56 for expression thereof.

79. The method according to claim 78 wherein delivery is via one or more viral vectors.

80. A non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operabiy linked to a first CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the first polynucleotide sequence comprises

(i) a first guide sequence capable of hybridizing to a first target sequence at a first genomic locus in a cell of the organism,

(ii) a first tracr mate sequence, and

(iii) a first tracr sequence, and

II. a second regulatory element operabiy linked to a second CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the second polynucleotide sequence comprises

(i) a second guide sequence capable of hybridizing to a second target sequence at a second genomic locus in the cell of the organism,

(ii) a second tracr mate sequence, and

(iii) a second tracr sequence, and

III. a third regulator}' element operabiy linked to an enzyme-coding sequence encoding a first CRISPR enzyme comprising at least one or more nuclear localization sequences and operabiy linked to a first functional domain,

IV. a fourth regulatory element operably linked to an enzyme-coding sequence encoding a second CRISPR enzyme comprising at least one or more nuclear localization sequences and operably linked to a second functional domain,

wherein (i), (ii) and (iii) in I and II are arranged in a 5' to 3' orientation,

wherein components I, II, III and IV are located on the same or different vectors of the system,

wherein when transcribed, each tracr mate sequences hybridizes to its corresponding tracr sequence and the first and second guide sequences direct sequence-specific binding of the first and second CRISPR complex to the first and second target sequence,

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence and wherein expression of the CRISPR enzyme provides manipulation of the target sequence,

wherein the first and second CRISPR enzyme each comprise two or more mutations, and

wherein the first and second CRISPR enzyme is a Cas9 ortholog of a genus belonging to the group consisting of *Corynebacter, Sutterella, Legionella, Treponema, Filifactor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides, Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillum, Gluconacetohacter, Neisseria, Roseburia, Parvibaculum, Staphylococcus, Nitratifractor, Mycoplasma* and *Campylobacter,* and

wherein the Cas comprises a helical domain 2 truncation.

81. The composition according to claim 80, wherein the first functional domain is selected from the group consisting of a transcriptional activator, transcriptional repressor, a recombinase, a transposase, a histone remodeler, a DNA methyltransferase, a cryptochrome and a light inducible/controllable domain or a chemically inducible/controllable domain.

82. The composition according to claim 80, wherein the second functional domain is selected from the group consisting of a transcriptional activator, transcriptional repressor, a recombinase, a transposase, a histone remodeler, a DNA methyltransferase, a cryptochrome and a light inducible/controllable domain or a chemically inducible/controllable domain.

83. The composition according to claim 80, wherein the first or second functional domain is a transcriptional activator domain.

84. The composition according to claim 83, wherem the transcriptional activator domain is VP64.

85. The composition according to claim 80, wherem the first or second functional domain is a transcriptional repressor domain.

86. The composition according to claim 85, wherein the transcriptional repressor domain is KRAB, SID or SID4X.

87. The composition according to claim 80 wherein the first or second CRiSPR enzyme is a Sutterella wadsworthensis Cas9.

88. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Filifactor alocis Cas9.

89. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Lactobacillus johnsonii Cas9.

90. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Campylobacter lari Cas9.

91. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Corynebacter diptheriae Cas9.

92. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Parvibaculum lavamentivorans Cas9.

93. The composition according to claim 80 wherem the first or second CRISPR enzyme is a Mycoplasma gallisepticum Cas9.

94. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Staphylococcus aureus subsubspecies Aureus Cas9.

95. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Legionella pneumophila Paris Cas9.

96. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Treponema denticoia Cas9.

97. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Staphylococcus pseudintermedius Cas9.

98. The composition according to claim 80 wherein the first or second CRISPR enzyme is a Neisseria cinerea Cas9.

99. A method of modulating the expression of two or more genomic loci of interest in an organism comprising

delivering a non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to a first CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the first polynucleotide sequence comprises

(i) a first guide sequence capable of hybridizing to a first target sequence at a first genomic locus in a cell of the organism,

(ii) a first tracr mate sequence, and

(iii) a first tracr sequence, and

II. a second regulator}' element operably linked to a second CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the second polynucleotide sequence comprises

(i) a second guide sequence capable of hybridizing to a second target sequence at a second genomic locus in the cell of the organism,

(ii) a second tracr mate sequence, and

(iii) a second tracr sequence, and

III. a third regulatory element operably linked to an enzyme-coding sequence encoding a first CRISPR enzyme comprising at least one or more nuclear localization sequences and operably linked to a first functional domain,

IV. a fourth regulatory element operably linked to an enzyme-coding sequence encoding a second CRISPR enzyme comprising at least one or more nuclear localization sequences and operably linked to a second functional domain,

wherein (i), (ii) and (iii) in I and II are arranged in a 5' to 3' orientation,

wherein components I, II, III and IV are located on the same or different vectors of the system,

wherein when transcribed, each tracr mate sequences hybridizes to its corresponding tracr sequence and the first and second guide sequences direct sequence-specific binding of the first and second CRISPR complex to the first and second target sequence,

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence and wherein expression of the CRISPR enzyme provides manipulation of the target sequence,

wherein the first and second CRISPR enzyme each comprise two or more mutations,

wherein the first and second CRISPR enzyme is a Cas9 ortholog of a genus belonging to the group consisting of *Corynebacter, Sutterella, Legionella, Treponema, Filifactor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides, Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillum, Gluconacetobacter, Neisseria, Roseburia, Parvibaculum, Staphylococcus, Nitratifractor, Mycoplasma* and *Campylobacter,*

wherein the Cas comprises a helical domain 2 truncation, and

wherein the first genomic locus is modulated by the activity of the first functional domain and the second genomic locus is modulated by the activity of the second functional domain.

100. The method according to claim 99, wherein the first functional domain is selected from the group consisting of a transcriptional activator, transcriptional repressor, a recombinase, a transposase, a histone remodeler, a DNA methyltransferase, a cryptochrome and a light inducible/controllable domain or a chemically inducible/controllable domain.

101. The method according to claim 99, wherein the second functional domain is selected from the group consisting of a transcriptional activator, transcriptional repressor, a recombinase, a transposase, a histone remodeler, a DNA methyltransferase, a cryptochrome and a light inducible/controllable domain or a chemically inducible/controllable domain.

102. The method according to claim 99, wherein the first or second functional domain is a transcriptional activator domain.

103. The method according to claim 102, wherein the transcriptional activator domain is VP64.

104. The method according to claim 99, wherein the first or second functional domain is a transcriptional repressor domain.

105. The method according to claim 104, wherein the transcriptional repressor domain is KRAB, SID or SID4X.

106. The method according to claim 99 wherein the first or second CRISPR enzyme is a Sutterella wadsworthensis Cas9.

107. The method according to claim 99 wherein the first or second CRISPR enzyme is a Filifactor alocis Cas9.

108. The method according to claim 99 wherein the first or second CRISPR enzyme is a Lactobacillus johnsonii Cas9.

109. The composition according to claim 99 wherein the first or second CRISPR enzyme is a Campylobacter lari Cas9.

110. The method according to claim 70 wherein the first or second CRISPR enzyme is a Corynebacter diptheriae Cas9.

111. The method according to claim 99 wherein the first or second CRISPR enzyme is a Parvibaculum lavamentivorans Cas9.

112. The method according to claim 99 wherein the first or second CRISPR enzyme is a Mycoplasma gallisepticum Cas9.

113. The method according to claim 99 wherein the first or second CRISPR enzyme is a Staphylococcus aureus subsubspecies Aureus Cas9.

114. The method according to claim 99 wherein the first or second CRISPR enzyme is a Legionella pneumophila Paris Cas9.

115. The method according to claim 99 wherein the first or second CRISPR enzyme is a Treponema denticola Cas9.

116. The method according to claim 99 wherein the first or second CRISPR enzyme is a Staphylococcus pseudintermedius Cas9.

117. The method according to claim 99 wherein the first or second CRISPR enzyme is a Neisseria cinerea Cas9.

118. A method of treating or inhibiting a condition caused by a defect in a target sequence in a genomic locus of interest in a subject or a non-human subject in need thereof comprising modifying the subject or a non-human subject by manipulation of the target sequence and wherein the condition is susceptible to treatment or inhibition by manipulation of the target sequence comprising providing treatment comprising:

delivering a non-naturally occurring or engineered composition comprising an AAV vector system comprising one or more AAV vectors comprising operably encoding a composition of claim 56 for expression thereof, wherein the target sequence is manipulated by the composition when expressed.

119. A method of claim 118 including inducing expression.

120. The method of claim 118 wherem the organism or subject is a eukaryote or a non-human eukaryote.

121. The method of claim 118 wherein the organism or subject is a plant.

122. The method of claim 118 wherein the organism or subject is a mammal or a non-human mammal.

123. The method claim 118 wherein the organism or subject is algae.

124. The method of claim 118 wherein the viral vector is an AAV.

125. A modified CRISPR enzyme wherein the enzyme is a Cas9 ortholog of a genus belonging to the group consisting of *Corynebacter, Sutterella, Legionella, Treponema, Filifactor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides, Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillum, Gluconacetobacter, Neisseria, Roseburia, Parvibaculum, Staphylococcus, Nitratifractor, Mycoplasma* and *Campylobacter* and wherein differences from the corresponding wild type CRISPR enzyme comprise:

the modified CRISPR enzyme is truncated in comparison to a wild type CRISPR enzyme, or

the CRISPR enzyme has a length of at least 500 amino acids, at least 800-899 amino acids, at least 900-999 amino acids, at least 1000-1099 amino acids, at least 1100-1199 amino acids, at least 1200-1299 amino acids, at least 1300-1399 amino acids, at least 1400-1499 amino acids, at least 1500-1599 amino acids, at least 1600-1699 amino acids or at least 2000 amino acids, and/or

the CRISPR enzyme is a nuclease directing cleavage of both strands at the location of the target sequence, or the CRISPR enzyme is a nickase directing cleavage of one strand at the location of the target sequence, and/or

the CRISPR enzyme is codon-optimized or codon-optimized for expression in a eukaryotic cell, and/or

the CRISPR enzyme comprises one or more mutations,

the CRISPR enzyme comprises a chimeric CRISPR enzyme, and/or

wherein the Cas comprises a helical domain 2 truncation.

126. The modified CRISPR enzyme according to claim 70, or the composition according to claim 56, wherein the CRISPR enzyme has one or more mutations in any domain of the enzyme.

127. The modified CRISPR enzyme according to claim 125, wherein the CRISPR enzyme has one or more mutations in a catalytic domain.

128. The modified CRISPR enzyme according to claim 125, wherein the one or more mutations is in a RuvC I, RuvC II, RuvC III or HNH domain of the CRISPR enzyme.

129. The modified CRISPR enzyme according to claim 125, wherein the CRISPR enzyme comprises one or more mutations corresponding to the position numbering of Sp Cas9 at positions DIOA, E762A, D986A, S15A, E762A, H982A, H983A, D986A, H840A, N854A or N863A or any corresponding ortholog or N580 according to SaCas9 protein are mutated.

130. The modified CRISPR enzyme according to claim 56, wherein the enzyme further comprises a functional domain.

131. The modified CRISPR enzyme according to claim 125, wherein the functional domain is a transcriptional activator domain.

132. The modified CRISPR enzyme according to claim 126, wherein the transcriptional activator domain is VP64.

133. The modified CRISPR enzyme according to claim 125, wherein the functional domain is a transcriptional repressor domain.

134. The modified CRISPR enzyme according to claim 133, wherein the transcriptional repressor domain is KRAB, SID or SID4X.

135. A composition according to any of claims 56-77 or 80-98 or a CRISPR enzyme according to claims 125-134 for use in medicine.

136. A composition according to any of claims 56-77 or 80-98 or a CRISPR enzyme according to claims 125-134 for use in a method according to any of claims 78, 79, 99-134.

137. Use of a composition according to any of claims 56-77 or 80-98 or a CRISPR enzyme according to claims 125-134 in *ex vivo* gene or genome editing.

138. Use of a composition according to any of claims 56-77 or 80-98 or a CRISPR enzyme according to any of claims 125-134 in the manufacture of a medicament for *ex vivo* gene or genome editing or for use in a method according to any of claims 78, 79, 99-134.

139. A composition according to any of claims 56-77 or 80-983 or a CRISPR enzyme according to any of claims 125-134, wherein the target sequence is flanked at its 3' end by 5'-

NRG (where N is any Nucleotide), especially where the Cas9 is (or is derived from) *S. pyogenes* or *S. aureus* Cas9.

140. A method of preparing an AAV for delivery of the compositon of claim 56 or 80 or the modified enzyme of claim 125 comprising transfecting plasmid(s) containing or consisting essentially of nucleic acid molecule(s) coding for the AAV into AAV-infected cells, and supplying AAV rep and/or cap obligatory for replication and packaging of the AAV.

141. The method of claim 140, wherein the AAV rep and/or cap obligatory for replication and packaging of the AAV are supplied by transfecting the cells with helper plasmid(s) or helper virus(es).

142. The method of claim 141, wherein the helper virus is a poxvirus, adenovirus, herpesvirus or baculovirus.

143. The method of claim 142, wherein the poxvirus is a vaccinia virus.

144. The method of claim 140, wherein:
- the cells are mammalian cells; or
- the cells are insect cells and the helper virus is baculovirus.

145. A method of deliverying the CRISPR enzyme of claim 125 comprising delivering to a cell mRNA encoding the CRISPR enzyme.

146. A chimeric Cas enzyme wherein the enzyme comprises one or more fragments from a first Cas ortholog and one or more fragments from a second Cas ortholog,
wherein the Cas comprises a helical domain 2 truncation.

147. The enzyme according to claim 146 wherein the one or more fragments of the first or second Cas ortholog are from the C- or N-terminal of the first or second Cas ortholog.

148. The enzyme according to claim 146 wherein the first or second Cas ortholog is selected from a genus belonging to the group consisting of *Corynebacter, Sutterella, Legionella, Treponema, Fill/actor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides,*

Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillum, Gluconacetobacter, Neisseria, Roseburia, Parvibacuhim, Staphylococcus, Nitratifractor, Mycoplasma and *Campyiohacter.*

149. Use of the conmposition or the enzyme as defined in any preceeding claim in the preparation of a medicament for modification of a target sequence.

150. The composition according to claim 56, wherein the CRISPR enzyme is truncated in comparison to a wild type CRISPR enzyme or the CRISPR enzyme is comprised of 500-2000 amino acids.

151. The composition according to claim 56, wherein the CRISPR enzyme is a nuclease directing cleavage of both strands at the location of the target sequence, or the CRISPR enzyme is a nickase directmg cleavage of one strand at the location of the target sequence.

152. The composition according to claim 56, wherein the the guide sequence comprises at least fifteen nucleotides.

153. The composition according to claim 56, wherein the CRISPR enzyme is codon-optimized or codon-optimized for expression in a eukaryotic cell.

154. The composition according to claim 56, wherein the CRISPR enzyme comprises one or more mutations.

155. The composition according to claim 56, wherein the CRISPR enzyme comprises a chimeric CRISPR enzyme.

156. A non-naturally occurring or engineered composition comprising:

A) - I. a CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the polynucleotide sequence comprises:

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a polynucleotide sequence encoding a CRISPR enzyme comprising at least one or more nuclear localization sequences, wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence and the polynucleotide sequence encoding a CRISPR enzyme is DNA or RNA,

or

(B) I. polynucleotides comprising:

(a) a guide sequence capable of hybridizing to a target sequence in a prokaryotic cell, and

(b) at least one or more tracr mate sequences,

II. a polynucleotide sequence encoding a CRISPR enzyme, and

III. a **polynucleotide** sequence comprising a tracr sequence,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence, and the polynucleotide sequence encoding a CRISPR enzyme is DNA or RNA, and

wherein the CRISPR enzyme is a Cas9 ortho!og of a genus belonging to the group consisting of *Corynehacter, Sutterella, Legionella, Treponema, Filifactor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides, Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillum, Gluconacetobacter, Neisseria, Roseburia, Parvibaculum, Staphylococcus, Nitratifractor, Mycoplasma* **and** *Campylobacter,* **and**

wherein the Cas comprises a helical domain 2 truncation.

157. The composition according to claim 156, wherein the CRISPR enzyme is truncated in comparison to a wild type CRISPR enzyme or the CRISPR enzyme is comprised of 500-2000 amino acids.

158. The composition according to claim 156, wherein the CRISPR enzyme is a nuclease directing cleavage of both strands at the location of the target sequence, or the CRISPR enzyme is a nickase directing cleavage of one strand at the location of the target sequence.

159. The composition according to claim 156, wherein the the guide sequence comprises at least fifteen nucleotides.

160. The composition according to claim 156, wherein the CRISPR enzyme is codon-optimized or codon-optimized for expression in a eukaryotic cell.

161. The composition according to claim 156, wherein the CRISPR enzyme comprises one or more mutations.

162. The composition according to claim 156, wherein the CRISPR enzyme comprises a chimeric CRISPR enzyme.

163. A method of modifying an organism or a non-human organism by manipulation of a target sequence in a genomic locus of interest comprising delivering a non-naturally occurring or engineered composition comprising :

A) - I. a CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the polynucleotide sequence comprises:

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a polynucleotide sequence encoding a CRISPR enzyme comprising at least one or more nuclear localization sequences,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence and the polynucleotide sequence encoding a CRISPR enzyme is DNA or RNA,

or

(B) I. polynucleotides comprising:

(a) a guide sequence capable of hybridizing to a target sequence in a prokaryotic cell, and

(b) at least one or more tracr mate sequences,

II. a polynucleotide sequence encoding a CRISPR enzyme, and

III. a polynucleotide sequence comprising a tracr sequence,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence, and the polynucleotide sequence encoding a CRISPR enzyme is DNA or RNA,

wherein the CRISPR enzyme is a Cas9 ortholog of a genus belonging to the group consisting of *Corynebacter, Sutterella, Legionella, Treponema, Filifactor, Eubacterium, Streptococcus, Lactobacillus, Mycoplasma, Bacteroides, Flaviivola, Flavobacterium, Sphaerochaeta, Azospirillum, Gluconacetobacter, Neisseria, Roseburia, Parvibaculum, Staphylococcus, Nitratifractor, Mycoplasma* and *Campylobacter,* and

wherein the Cas comprises a helical domain 2 truncation.

164. The method according to claim 163, wherein the CRISPR enzyme is truncated in comparison to a wild type CRISPR enzyme or the CRISPR enzyme is comprised of 500-2000 amino acids.

165. The method according to claim 163, wherein the CRISPR enzyme is a nuclease directing cleavage of both strands at the location of the target sequence, or the CRISPR enzyme is a nickase directing cleavage of one strand at the location of the target sequence.

166. The method according to claim 163, wherein the guide sequence comprises at least fifteen nucleotides.

167. The method according to claim 163, wherein the CRISPR enzyme is codon-optimized or codon-optimized for expression in a eukaryotic cell.

168. The method according to claim 163, wherein the CRISPR enzyme comprises one or more mutations.

169. The method according to claim 163, wherein the CRISPR enzyme comprises a chimeric CRISPR enzyme.

170. A method of altering expression of one or more gene products comprising introducing into a cell containing and expressing DNA molecules encoding the one or more gene products an engineered, non-naturally occurring CRISPR-Cas system comprising a Cas protein and one or more guide RNAs that target the DNA molecules, whereby the one or more guide RNAs target the genomic loci of the DNA molecules encoding the one or more gene products and the Cas protein cleaves the genomic loci of the DNA molecules encoding the one or more gene products, whereby expression of the one or more gene products is altered; and, wherein the Cas protein and the guide RNA do not naturally occur together.

171. A method of altering expression of one or more gene products comprising introducing into a cell containing and expressing DNA molecules encoding the one or more gene products an engineered, non-naturally occurring vector system comprising one or more vectors comprising:

a) a first regulatory element operably linked to one or more CRISPR-Cas system guide RNAs that hybridize with target sequences in genomic loci of the DNA molecules encoding the one or more gene products,

b) a second regulatory element operably linked to a Cas protein,

wherein components (a) and (b) are located on same or different vectors of the system,

whereby the guide RNAs target the genomic loci of the DNA molecules encoding the one or more gene products and the Cas protein cleaves the genomic loci of the DNA molecules encoding the one or more gene products, whereby expression of the one or more gene products is altered; and, wherein the Cas protein and the guide RNAs do not naturally occur together, and

wherein the Cas comprises a helical domain 2 truncation.

172. The method of claim 170 or claim 171, wherein the expression of two or more gene products is altered.

173. A method of any preceding claim, wherein the vectors or the Cas protein of the system further comprise one or more NLS(s).

174. A method of any preceding claim, wherein the guide RNAs comprise a guide sequence fused to a tracr sequence.

175. A method of any preceding claim, wherein the cell is a eukaryotic cell.

176. The method of claim 175, wherein the eukaryotic cell is a mammalian cell.

177. The method of claim 176, wherein the mammalian cell is a human cell.

178. The method of any preceding claim, wherein the Cas protein is codon optimized for expression in a eukaryotic cell.

179. The method of any preceding claim, wherein the expression of the gene product is decreased.

180. The method of any preceding claim, wherein the gene product is a protein.

181. The method of any preceding claim, wherein the introducing into the cell is by a delivery system comprising viral particles, liposomes, electroporation, microinjection or conjugation.

182. An engineered, non-naturally occurring vector system comprising one or more vectors comprising:

a) a first regulatory element operably linked to one or more CRISPR-Cas system guide RNAs that hybridize with target sequences in genomic loci of DNA molecules encoding one or more gene products,

b) a second regulatory element operably linked to a Cas protein,

wherein components (a) and (b) are located on same or different vectors of the system, whereby the guide RNAs target the genomic loci of the DNA molecules encoding the one or more gene products in a cell and the Cas protein cleaves the genomic loci of the DNA molecules encoding the one or more gene products, whereby expression of the one or more gene products is altered; and, wherein the Cas protein and the guide RNAs do not naturally occur together, and

wherein the Cas comprises a helical domain 2 truncation.

183. An engineered, programmable, non-naturally occurring CRISPR-Cas system comprising a Cas protein and one or more guide RNAs that target the genomic loci of DNA molecules encoding one or more gene products in a cell and the Cas protein cleaves the genomic loci of the DNA molecules encoding the one or more gene products, whereby expression of the one or more gene products is altered; and, wherein the Cas protein and the guide RNAs do not naturally occur together, wherein the Cas comprises a helical domain 2 truncation.

184. The system of claim 182 or 183, wherein the expression of two or more gene products is altered.

185. The system of any of claims 182 to 183, wherein the system further comprises one or more NLS(s).

186. The system of any of claims 182 to 185, wherein the guide RNAs comprise a guide sequence fused to a tracr sequence.

187. The system of any of claims 182-186, wherein the cell is a eukaryotic cell.

188. The system of claim 187, wherein the eukaryotic cell is a mammalian cell.

189. The system of claim 188, wherein the mammalian cell is a human cell.

190. The system of any of claims 182-189, wherein the CRISPR-Cas system is a Type II CRISPR-Cas system.

191. The system of any of claims 182-190, wherein the Cas protein is a Cas9 protein.

192. The system of any of claims 182-191, wherein the Cas protein is codon optimized for expression in a eukaryotic cell.

193. The system of any of claims 182-192, wherein the expression of the gene product is decreased.

194. The system of any of claims 182-193, wherein the gene product is a protein.

195. The system of any of claims 182-194, wherein the system is introduced into the cell by a delivery system comprising viral particles, liposomes, electro poration, microinjection or conjugation.

196. A non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to a CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the polynucleotide sequence comprises

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a second regulatory element operably linked to an enzyme-coding sequence encoding a CRISPR enzyme comprising at least one or more nuclear localization sequences (NLSs) in the proximity of a terminus of the CRISPR enzyme,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein components I and II are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence,

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence,

wherein the CRISPR enzyme comprises one or more mutations in a catalytic domain thereby rendering the CRISPR enzyme to a nickase that cleaves a single DNA strand,

wherein the chimeric RNA polynucleotide sequence comprises two or more hairpins, and

wherein the Cas comprises a helical domain 2 truncation.

197. The composition of claim 196, wherein multiple chiRNA polynucleotide sequences are used, to provide a multiplexed system.

198. A multiplexed CRISPR enzyme system, wherein the system comprises a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to a CRISPR-Cas system chimeric RNA (chiRNA) polynucleotide sequence, wherein the polynucleotide sequence comprises

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a second regulatory element operably linked to an enzyme-coding sequence encoding a CRJSPR enzyme comprising at least one or more nuclear localization sequences (NLSs) in the proximity of a terminus of the CRISPR enzyme,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein components I and II are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence,

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (I) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence,

wherein the CRISPR enzyme comprises one or more mutations in a catalytic domain thereby rendering the CRISPR enzyme to a nickase that cleaves a single DNA strand,

wherein the chiRNA polynucleotide sequence comprises two or more hairpins,

wherein in the multiplexed system multiple chiRNA polynucleotide sequences are used, and

wherein the Cas comprises a helical domain 2 truncation.

199. The composition or system of claim 196, 197 or 198, wherein the first regulatory element is a polymerase III promoter.

200. The composition or system of any preceding claim, wherein the second regulatory element is a polymerase II promoter.

201. The composition or system of any preceding claim, wherein the CRISPR enzyme comprises one or more NLSs of sufficient strength to drive accumulation of said CRISPR enzyme in a detectable amount in the nucleus of a eukaryotic cell.

202. The composition or system of any preceding claim, wherein the tracr sequence exhibits at least 50% of sequence complementarity along the length of the tracr mate sequence when optimally aligned.

203. The composition or system of any preceding claim, wherein the CRISPR. enzyme is a type II CRISPR system enzyme.

204. The composition or system of any preceding claim, wherein the CRISPR enzyme is a Cas9 enzyme.

205. The composition or system of any preceding claim, wherein the CRISPR enzyme is codon-optimized for expression in a eukaryotic cell.

206. The composition or system of any preceding claim, wherein the guide sequence is at least 15 nucleotides in length.

207. The composition or system of any preceding claim, wherein the chimeric RNA polynucleotide sequence comprises two, three, four or five hairpins.

208. The composition or system of any preceding claim, wherein the catalytic domain is selected from the group comprising RuvCI, RuvCII, RuvCIII or HNH domain.

209. The composition or system of any preceding claim, wherein the CRISPR enzyme comprises a mutation in a residue selected from the group consisting of D10, E762, H840, N854, N863, or D986 of SpCas9, or corresponding residues in other CRISPR enzymes or N580 according to SaCas9 protein.

210. A non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell, and

(b) a tracr mate sequence,

II. a second regulatory element operably linked to an enzyme-coding sequence encoding a CRISPR enzyme comprising at least one or more nuclear localization sequences (NLSs) in the proximity of a terminus of the CRISPR enzyme, and

III. a third regulatory element operably linked to a tracr sequence.

wherein components I, II and III are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence,

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence, and

wherein the CRISPR enzyme comprises one or more mutations in a catalytic domain thereby rendering the CRISPR enzyme to a nickase that cleaves a single DNA strand, and

wherein the Cas comprises a helical domain 2 truncation

211. The composition of claim 210, wherein multiple guide sequences and a single tracr sequence are used, to provide a multiplexed system

212. A multiplexed CRISPR enzyme system, wherein the system comprises a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell, and

(b) a tracr mate sequence,

II. a second regulatory element operably linked to an enzyme-coding sequence encoding a CRISPR enzyme comprising at least one or more nuclear localization sequences (NLSs) in the proximity of a terminus of the CRISPR enzyme, and

III. a third regulatory element operably linked to a tracr sequence,

wherein components I, II and III are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence,

wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence,

wherein the CRISPR enzyme comprises one or more mutations in a catalytic domain thereby rendering the CRISPR enzyme to a nickase that cleaves a single DNA strand,

wherein in the multiplexed system multiple guide sequences and a single tracr sequence is used, and

wherein the Cas comprises a helical domain 2 truncation.

213. The composition or system of any of claims 210 to 212, wherein the first regulatory element is a polymerase III promoter.

214. The composition or system of any of claims 210 to 213, wherein the second regulatory element is a polymerase II promoter.

215. The composition or system of any of claims 210 to 214, wherein the third regulatory element is a polymerase III promoter.

216. The composition or system of any of claims 210 to 215, wherein the CRISPR enzyme comprises one or more NLSs of sufficient strength to drive accumulation of said CRISPR enzyme in a detectable amount in the nucleus of a eukaryotic cell.

217. The composition or system of any of claims 156 to 162, wherein the tracr sequence exhibits at least 50% of sequence complementarity along the length of the tracr mate sequence when optimally aligned.

218. The composition or system of any of claims 210 to 217, wherein the CRISPR enzyme is a type II CRISPR system enzyme.

219. The composition or system of any of claims 210 to 218, wherein the CRISPR enzyme is a Cas9 enzyme.

220. The composition or system of any of claims 210 to 219, wherein the CRISPR enzyme is codon-optimized for expression in a eukaryotic cell.

221. The composition or system of any of claims 210 to 220, wherein the guide sequence is at least 15 nucleotides in length.

222. The composition or system of any of claims 210 to 221, wherein the catalytic domain is selected from the group comprising RuvCI, RuvCII, RuvCIII or HNH domain.

223. The composition or system of any of claims 210 to 222, wherein the CRISPR enzyme comprises a mutation in a residue selected from the group consisting of D10, E762, H840, N854, N863, or D986 of SpCas9, or corresponding residues in other CRISPR enzymes or N580 according to SaCas9 protein.

224. A eukaryotic host cell comprising the composition of any of the preceding claims.

225. An organism comprising the eukaryotic host cell of claim 224.

226. A non-human organism comprising the eukaryotic host cell of claim 224.

227. A kit comprising the composition or system of any of claims 1 to 226 and instructions for using said kit.

228. A method of altering the expression of a genomic locus of interest in a eukaryotic cell comprising

contacting the genomic locus with the composition or system of any of claims 141 to 170,
determining if the expression of the genomic locus has been altered. And
wherein the Cas comprises a helical domain 2 truncation.

229. A method of altering expression of one or more gene products comprising introducing into a eukaryotic cell containing and expressing DNA molecules encoding the one or more gene products an engineered, non-naturaliy occurring vector system comprising one or more vectors comprising:

a) a first regulator}' element operably linked to one or more Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)- CRISPR associated (Cas) system guide RNAs that hybridize with target sequences in genomic loci of the DNA molecules encoding the one or more gene products,

b) a second regulatory element operably linked to a Type-II Cas9 protein,

wherein components (a) and (b) are located on same or different vectors of the system,

whereby the guide RNAs target the genomic loci of the DNA molecules encoding the one or more gene products and the Cas9 protein cleaves the genomic loci of the DNA molecules encoding the one or more gene products, whereby expression of the one or more gene products is altered; and, wherein the Cas9 protein and the guide RNAs do not naturally occur together, and

wherein the Cas comprises a helical domain 2 truncation.

230. The method of claim 229, wherein the expression of two or more gene products is altered.

231. The method of claim 229 or 230, wherein the vectors of the system further comprise one or more nuclear localization signal(s) (NLS(s)).

232. The method of any one of claims 229-231, wherein the guide RNAs comprise a guide sequence fused to a tracr sequence.

233. The method of claim 229-232, wherein the Cas9 protein is codon optimized for expression in the eukaryotic cell.

234. The method of claim 229-233, wherein the eukaryotic cell is a mammalian or human cell.

235. The method of claim 229, wherein the expression of one or more gene products is decreased.

236. An engineered, non-naturally occurring vector system comprising one or more vectors comprising:

a) a first regulatory element operably linked to one or more CRISPR-Cas system guide RNAs that hybridize with target sequences in genomic loci of DNA molecules encoding one or more gene products,

b) a second regulatory element operably linked to a Type-II Cas9 protein,

wherein components (a) and (b) are located on same or different vectors of the system,

whereby the guide RNAs target the genomic loci of the DNA molecules encoding the one or more gene products in a eukaryotic cell and the Cas9 protein cleaves the genomic loci of the DNA molecules encoding the one or more gene products, whereby expression of the one or more gene products is altered; and, wherein the Cas9 protein and the guide RNAs do not naturally occur together, and

wherein the Cas comprises a helical domain 2 truncation.

237. The vector system of claim 236, wherein the expression of two or more gene products is altered.

238. The vector system of claim 236 or 237, wherein the vectors of the system further comprise one or more NLS(s).

239. The vector system of claim 236, 237 or 238, wherein the guide RNAs comprise a guide sequence fused to a tracr sequence.

240. The vector system of claim 236, 237, 238 or 239, wherein the Cas9 protein is codon optimized for expression in the eukaryotic cell.

241. The vector system of claim 236, 237, 238, 239 or 240, wherein the eukaryotic cell is a mammalian or human cell.

242. The vector system of any one of claims 236 to 241, wherein the expression of one or more gene products is decreased.

243. An engineered, programmable, non-naturally occurring Type II CRISPR-Cas system comprising a Cas9 protein and one or more guide RNAs that target the genomic loci of

DNA molecules encoding one or more gene products in a eukaryotic cell and the Cas9 protein cleaves the genomic loci of the DNA molecules encoding the one or more gene products, whereby expression of the one or more gene products is altered; wherein the Cas9 protein and the guide RNAs do not naturally occur together, and wherein the Cas comprises a helical domain 2 truncation.

244. The CRISPR-Cas system of claim 243, wherein the expression of two or more gene products is altered.

245. The CRISPR-Cas system of claim 243 or 244, wherein the CRISPR-Cas system further comprises one or more NLS(s).

246. The CRISPR-Cas system of claim 243, 244 or 245, wherein the guide RNAs comprise a guide sequence fused to a tracr sequence.

247. The CRISPR-Cas system of claim 243, 244 or 245, wherein the Cas9 protein is codon optimized for expression in the eukaryotic cell.

248. The CRISPR-Cas system of any one of claims 243-247, wherein the eukaryotic cell is a mammalian or human cell.

249. The composition, method or use of any of the preceding claims wherein the helical domain 2 truncation is substituted with one or more sets of flexible glycine-serine (GlyGlyGlySer) or rigid alpha-helical linkers (Ala(GiuAlaAlaAlaLys)Ala) in groups of 3, 6, 9, or 12 repeats to replace helical domain 2 for potential structural stabilization and/or aiding of retaining Cas9:sgRNA specificity.

250. The composition, method or use of any of the preceding claims wherein the Cas is an SpCas.

251. The composition, method or use of claim 207 wherein the SpCas is an SpCas9.

252. A non-natural!y occurring CRISPR enzyme wherein the HD2 domain has been truncated.253. The CRISPR enzyme of claim 252 comprising a Cas9.

254. The CRISPR enzyme of claim 253 wherein the Cas9 comprises an Sp Cas9.

255. The CRISPR enzyme of claim 253 wherein the Cas9 comprises an Sa Cas9.

256. The CRISPR enzyme of any one of claims 252 to 255 wherein the truncation is replacement of the HD2 domain.

257. The CRISPR enzyme of claim 256 wherein the truncation is replacement of the HD2 domain with a linker.

258. The CRISPR enzyme of claim 257 wherein the linker is a flexible linker.

259. The CRISPR enzyme of claim 258 wherein the flexible linker comprises a GlySer linker.

260. A composition, method, system, or use of any of the preceding claims wherein the CRISPR enzyme is as in any one of claims 252 to 259.

261. A chimeric 3-component CRISPR enzyme comprising N' and C terminal components from a first CRISPR enzyme, and an internal component from a second CRISPR enzyme, the second CRISPR enzyme being an ortholog of the first CRISPR enzyme.

262. The CRISPR enzyme of claim 261 wherein the first and second CRISPR enzymes each comprise a Cas9.

263. The CRISPR enzyme of claim 262 wherein the first or second Cas9 comprises an Sp Cas9.

264. The CRISPR enzyme of claim 262 wherein the first or second Cas9 comprises an Sa Cas9.

265. The CRISPR enzyme of claim 262 wherein the first or second Cas9 comprises an St Cas9.

266. The CRISPR enzyme of claims 265 wherein the St Cas9 comprises an St3 Cas9.

267. The CRISPR enzyme of any one of claims 261 to 266 wherein an internal component from the first CRISPR enzyme is replaced by an internal component from the second CRISPR enzyme, said internal components being the same or different.

268. The CRISPR enzyme of any one of claims 261 to 267 wherein the second CRISPR enzyme is an Sa CRISPR enzyme.

269. The CRISPR enzyme of any one of claims 261 to 267 wherein the second CRISPR enzyme is an St CRISPR enzyme

270. The CRISPR enzyme of claim 269 wherein the St CRISPR enzyme is an St3 CRISPR enzyme.

271. A composition, method, system, or use of any of the preceding claims wherein the CRISPR enzyme is as in any one of claims 261 to 270.

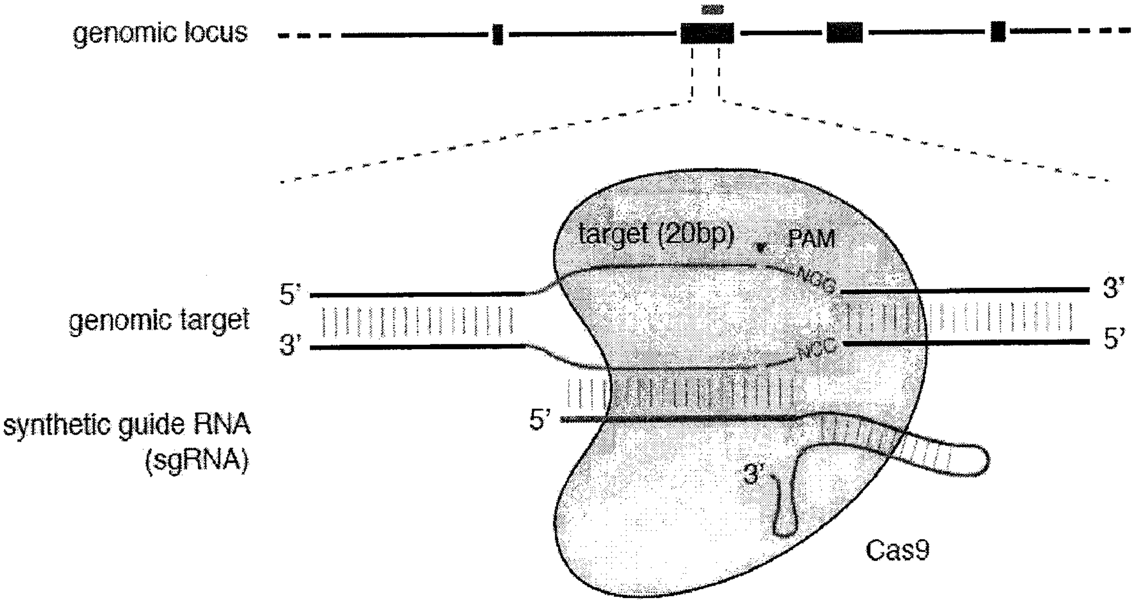

genomic locus
target (20bp)
PAM
NGG
NCC
5'
3'
genomic target
3'
5'
synthetic guide RNA
(sgRNA)
5'
3'
Cas9

FIG. 1

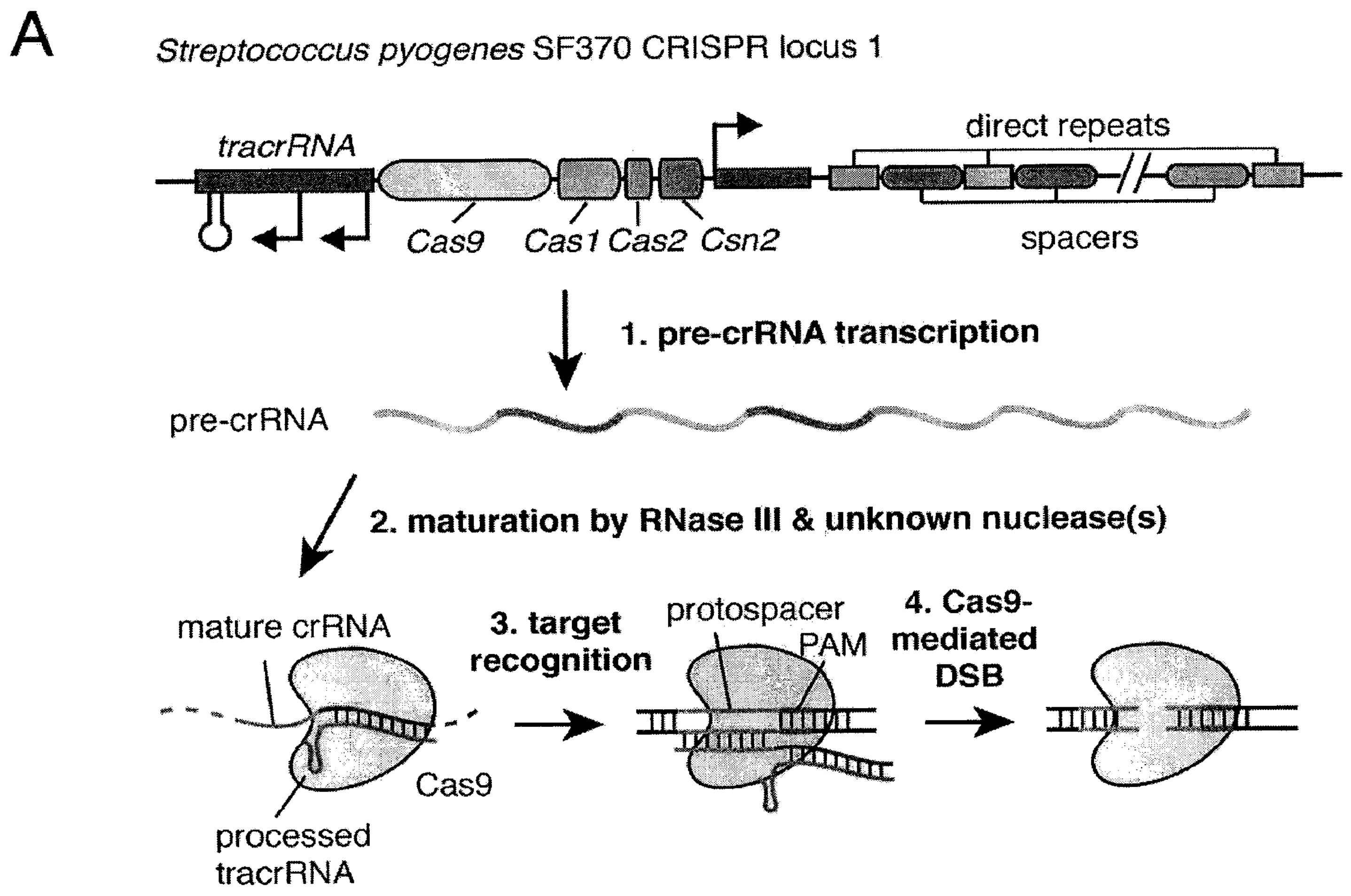

A
Streptococcus pyogenes SF370 CRISPR locus 1
tracrRNA
Cas9
Cas1
Cas2
Csn2
direct repeats
spacers
1. pre-crRNA transcription
pre-crRNA
2. maturation by RNase III & unknown nuclease(s)
mature crRNA
Cas9
processed tracrRNA
3. target recognition
protospacer
PAM
4. Cas9-mediated DSB

FIG. 2A

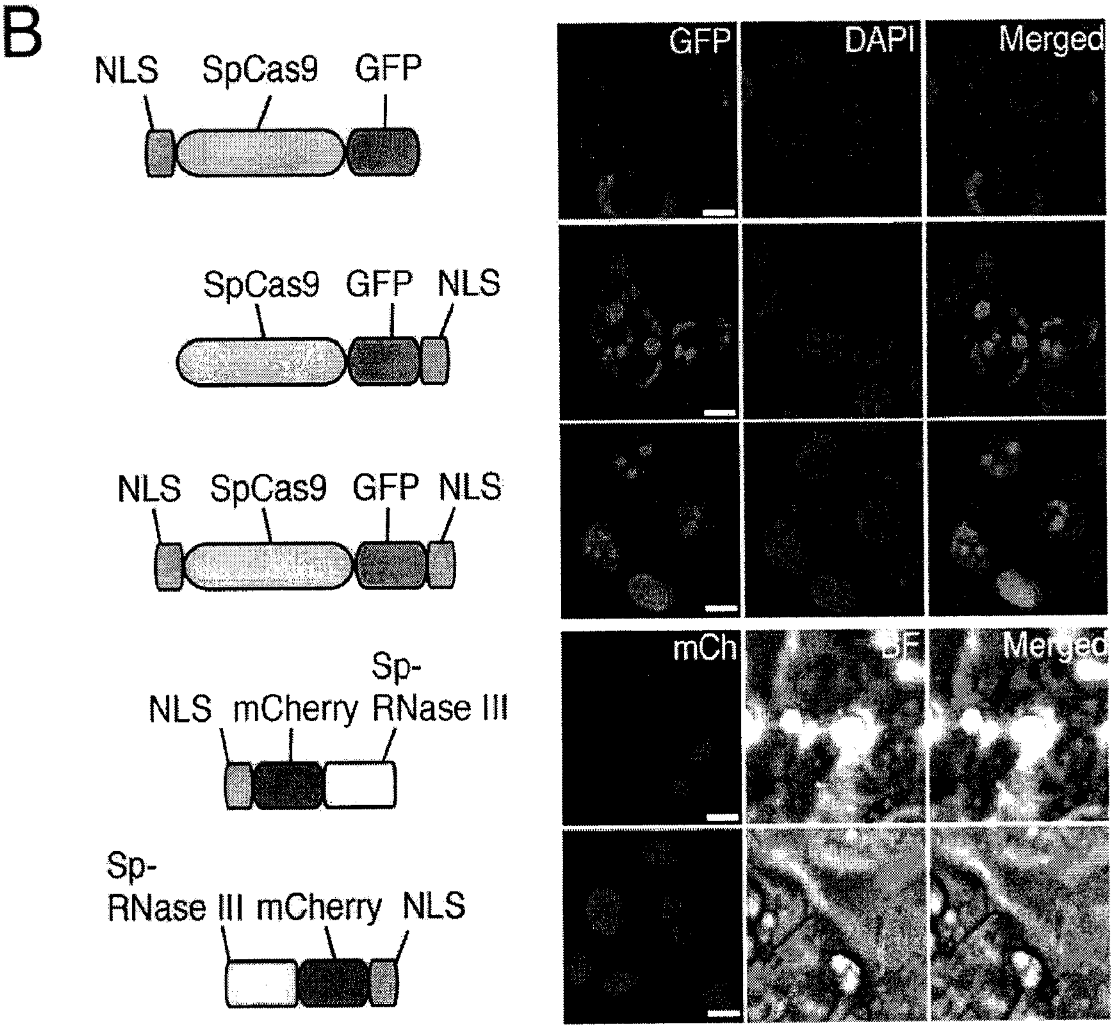

B
NLS
SpCas9
GFP
SpCas9
GFP
NLS
NLS
SpCas9
GFP
NLS
NLS
mCherry
Sp-
RNase III
Sp-
RNase III
mCherry
NLS
GFP
DAPI
Merged
mCh
BF
Merged

FIG. 2B

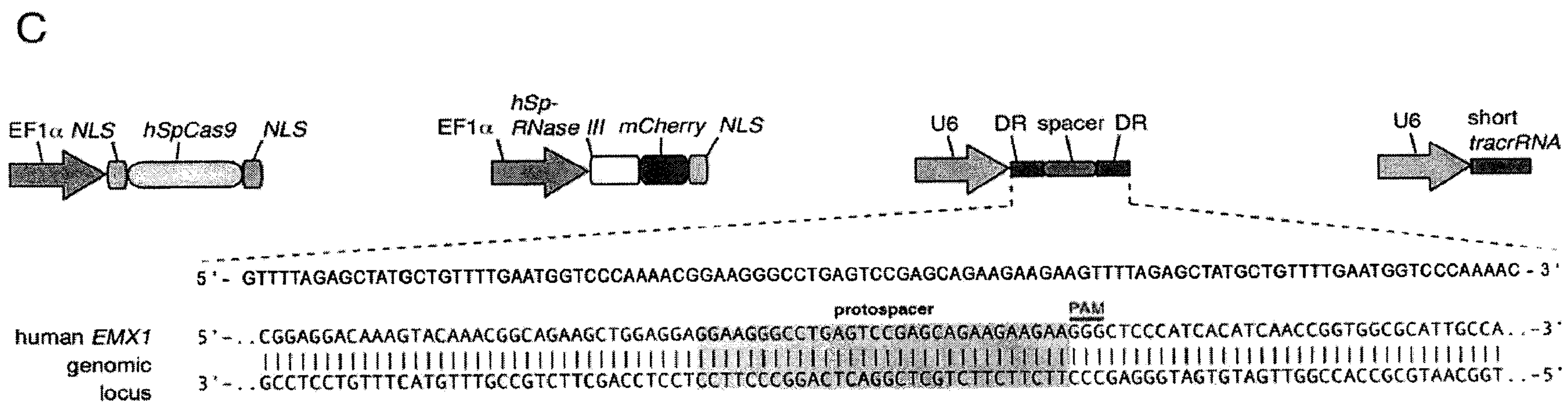

C
EF1α
NLS
hSpCas9
NLS
EF1α
hSp-RNase III
mCherry
NLS
U6
DR
spacer
DR
U6
short tracrRNA
5'- GTTTTAGAGCTATGCTGTTTTGAATGGTCCCAAAACGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGTTTTAGAGCTATGCTGTTTTGAATGGTCCCAAAAC - 3'
protospacer
PAM
human EMX1 genomic locus
5'-..CGGAGGACAAAGTACAAACGGCAGAAGCTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGGGCTCCCATCACATCAACCGGTGGCGCATTGCCA..-3'
3'-..GCCTCCTGTTTCATGTTTGCCGTCTTCGACCTCCTCCTTCCCGGACTCAGGCTCGTCTTCTTCTTCCCGAGGGTAGTGTAGTTGGCCACCGCGTAACGGT..-5'

FIG. 2C

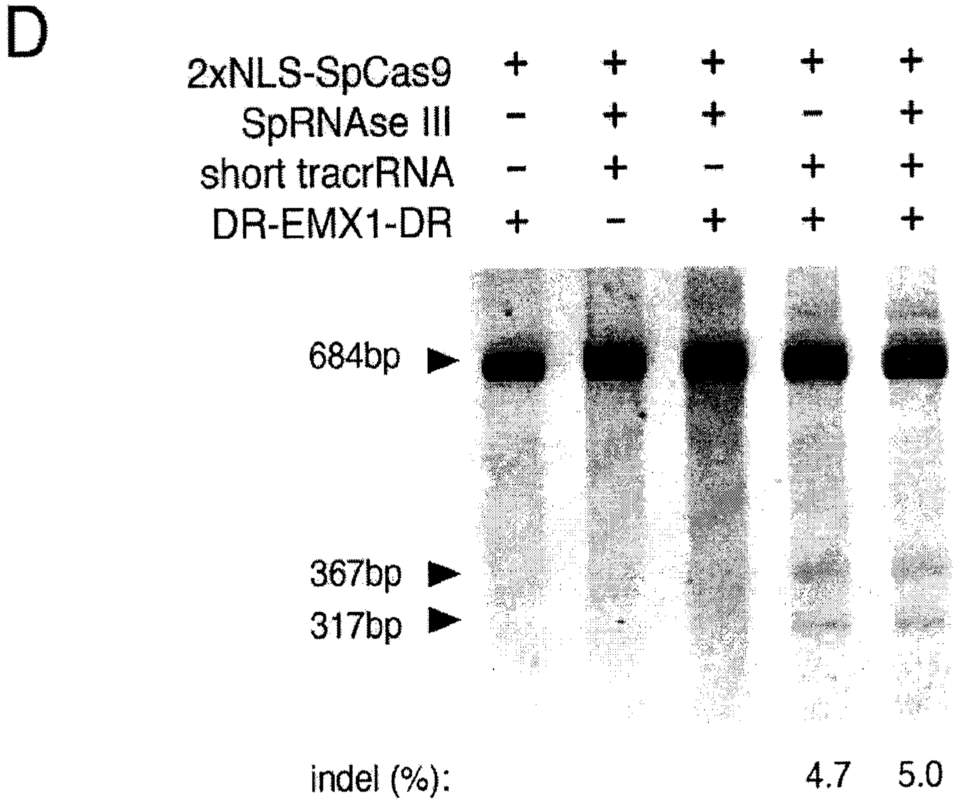

D
2xNLS-SpCas9 + + + + +
SpRNAse III − + + − +
short tracrRNA − + − + +
DR-EMX1-DR + − + + +
684bp
367bp
317bp
indel (%): 4.7 5.0

FIG. 2D

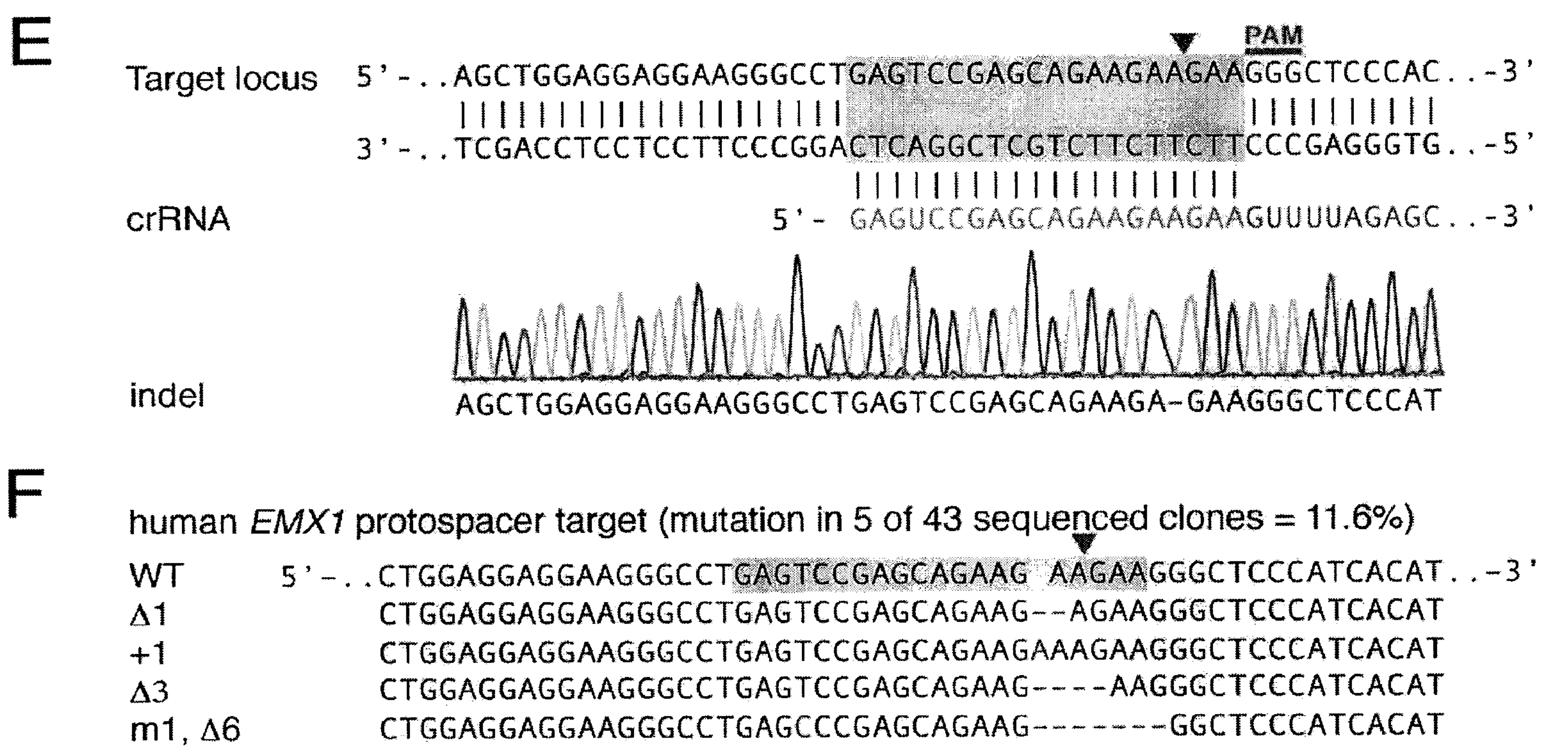

E
PAM
Target locus 5'-..AGCTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGGGCTCCCAC..-3'
3'-..TCGACCTCCTCCTTCCCGGACTCAGGCTCGTCTTCTTCTTCCCGAGGGTG..-5'
crRNA 5'- GAGUCCGAGCAGAAGAAGAAGUUUUAGAGC..-3'
indel AGCTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAGA-GAAGGGCTCCCAT
F
human *EMX1* protospacer target (mutation in 5 of 43 sequenced clones = 11.6%)
WT 5'-..CTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAG AAGAAGGGCTCCCATCACAT..-3'
Δ1 CTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAG--AGAAGGGCTCCCATCACAT
+1 CTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAGAAAGAAGGGCTCCCATCACAT
Δ3 CTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAG----AAGGGCTCCCATCACAT
m1, Δ6 CTGGAGGAGGAAGGGCCTGAGCCCGAGCAGAAG-------GGCTCCCATCACAT

FIG. 2E-F

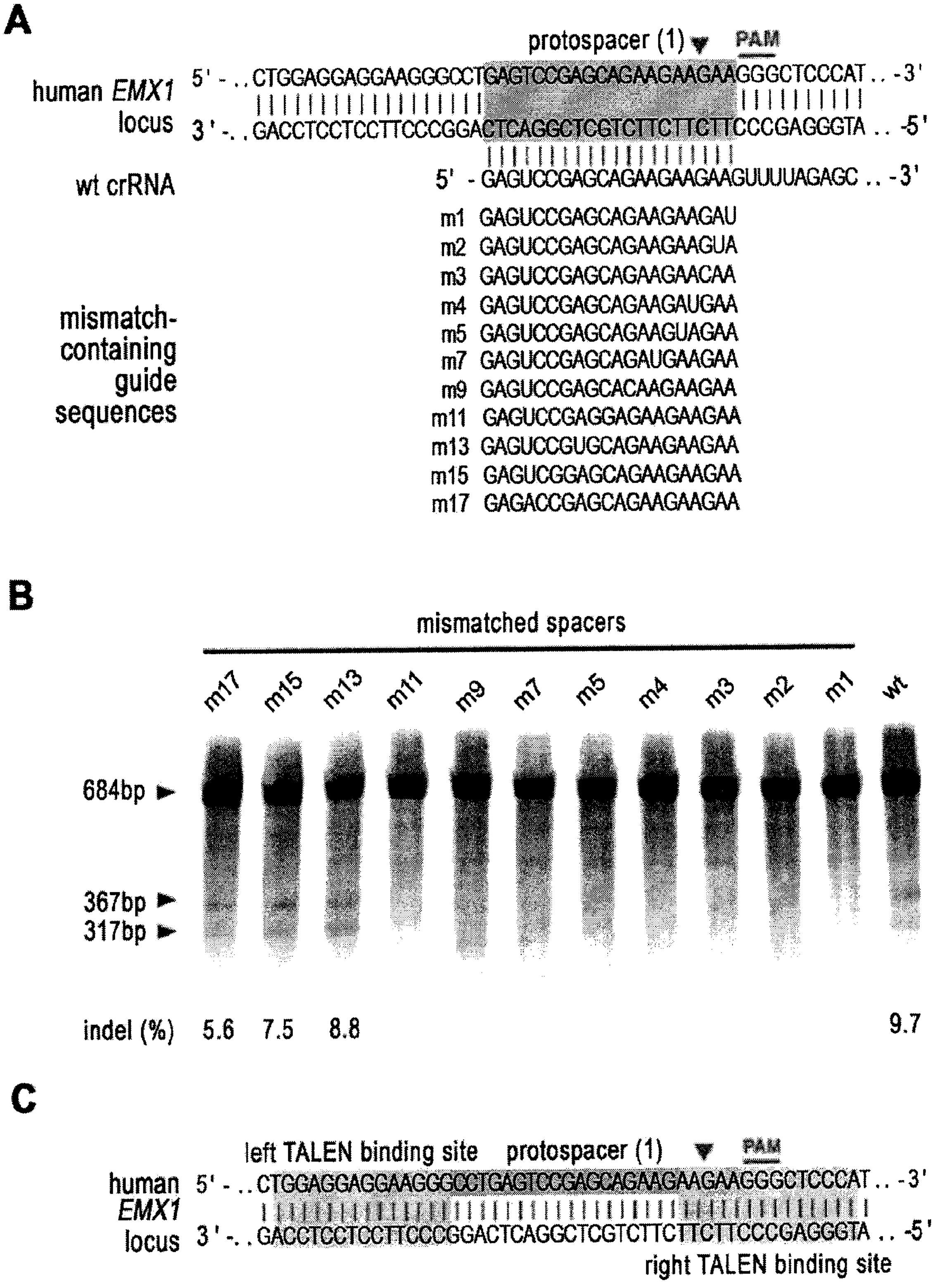

A
protospacer (1)
PAM
human EMX1 locus
5' - . . CTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGGGCTCCCAT . . -3'
3' -. . GACCTCCTCCTTCCCGGACTCAGGCTCGTCTTCTTCTTCCCGAGGGTA . . -5'
wt crRNA
5' - GAGUCCGAGCAGAAGAAGAAGUUUUAGAGC . . -3'
mismatch-containing guide sequences
m1 GAGUCCGAGCAGAAGAAGAU
m2 GAGUCCGAGCAGAAGAAGUA
m3 GAGUCCGAGCAGAAGAACAA
m4 GAGUCCGAGCAGAAGAUGAA
m5 GAGUCCGAGCAGAAGUAGAA
m7 GAGUCCGAGCAGAUGAAGAA
m9 GAGUCCGAGCACAAGAAGAA
m11 GAGUCCGAGGAGAAGAAGAA
m13 GAGUCCGUGCAGAAGAAGAA
m15 GAGUCGGAGCAGAAGAAGAA
m17 GAGACCGAGCAGAAGAAGAA
B
mismatched spacers
m17
m15
m13
m11
m9
m7
m5
m4
m3
m2
m1
wt
684bp
367bp
317bp
indel (%)
5.6
7.5
8.8
9.7
C
left TALEN binding site
protospacer (1)
PAM
human EMX1 locus
5' - . . CTGGAGGAGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGGGCTCCCAT . . -3'
3' -. . GACCTCCTCCTTCCCGGACTCAGGCTCGTCTTCTTCTTCCCGAGGGTA . . -5'
right TALEN binding site

FIG. 3A-C

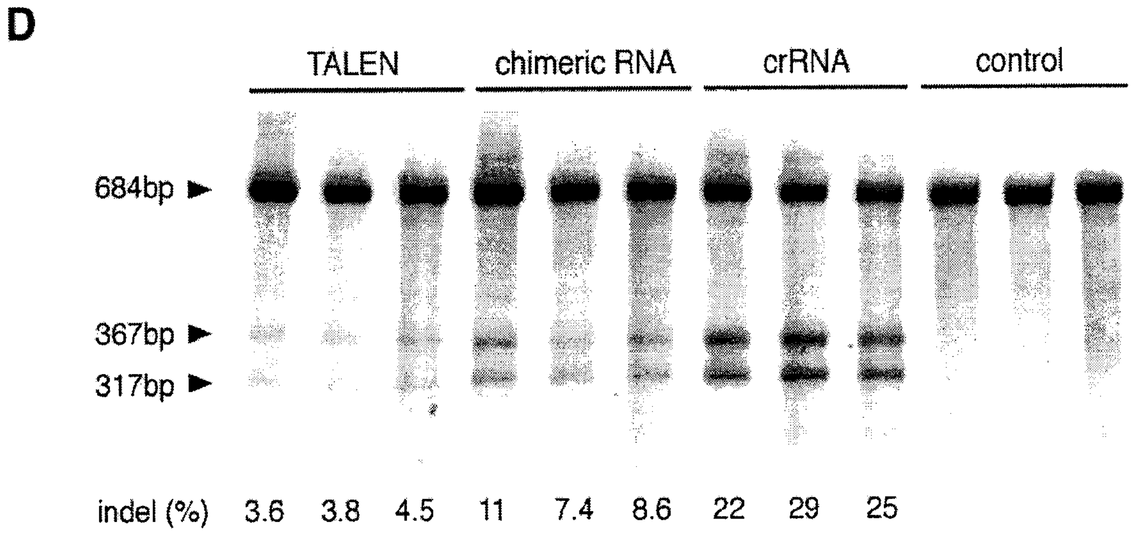

D
TALEN
chimeric RNA
crRNA
control
684bp ►
367bp ►
317bp ►
indel (%)
3.6
3.8
4.5
11
7.4
8.6
22
29
25

FIG. 3D

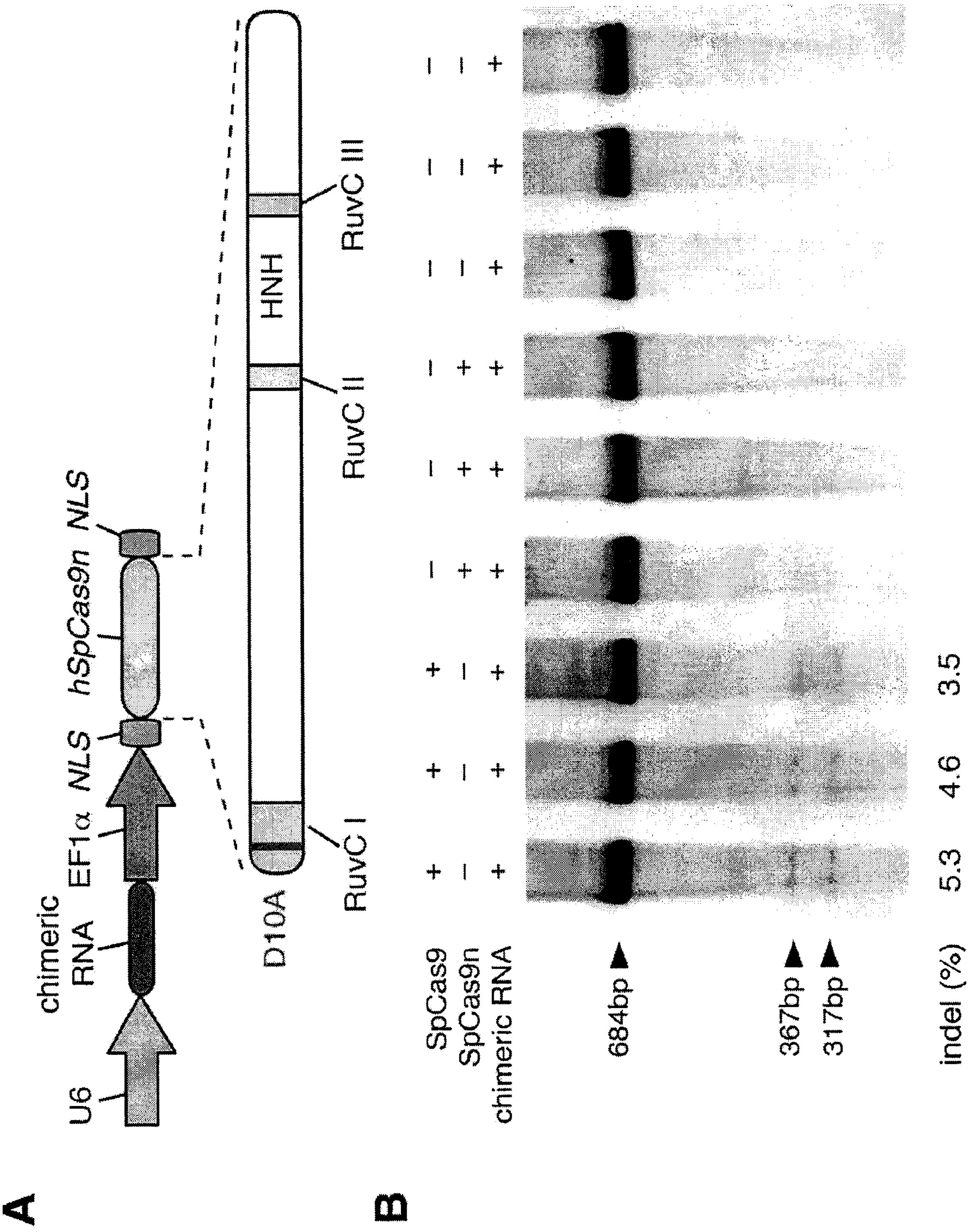

A
U6
chimeric RNA
EF1α
NLS
hSpCas9n
NLS
D10A
RuvC I
RuvC II
HNH
RuvC III
B
SpCas9 + + + − − − − − −
SpCas9n − − − + + + − − −
chimeric RNA + + + + + + + + +
684bp
367bp
317bp
indel (%) 5.3 4.6 3.5

FIG. 4A-B

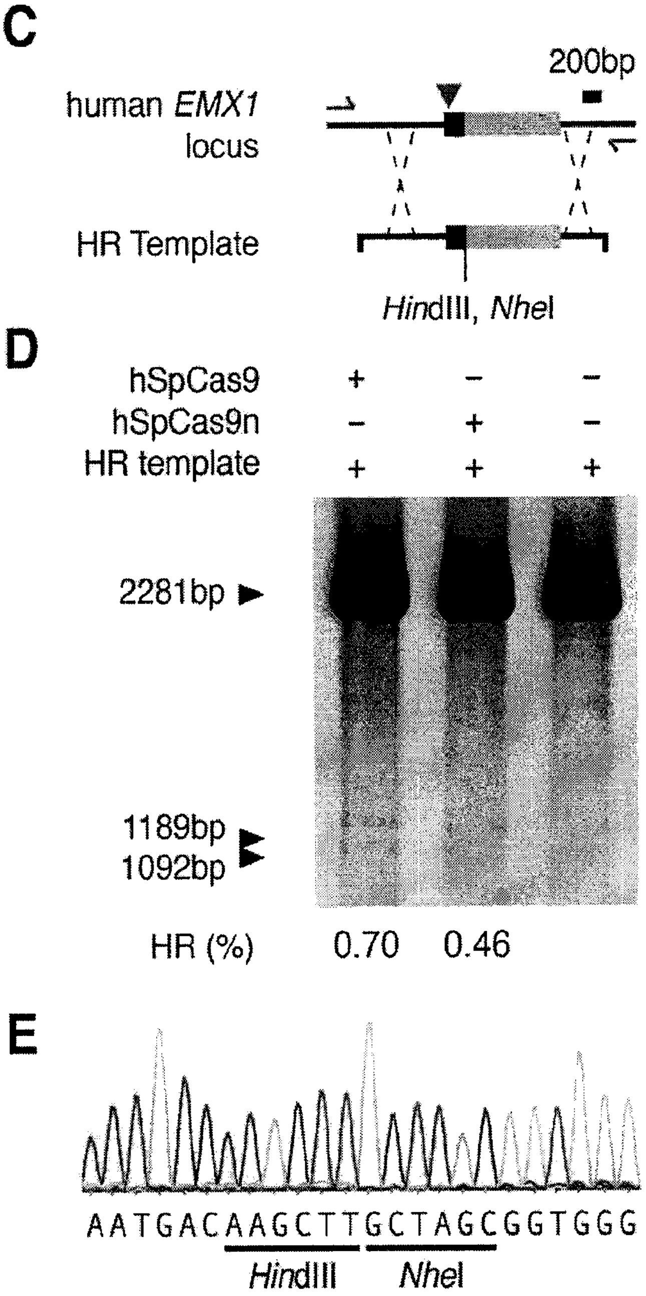

C
200bp
human *EMX1* locus
HR Template
*Hin*dIII, *Nhe*I
D
hSpCas9 + − −
hSpCas9n − + −
HR template + + +
2281bp
1189bp
1092bp
HR (%) 0.70 0.46
E
AATGACAAGCTTGCTAGCGGTGGG
*Hin*dIII
*Nhe*I

FIG. 4C-E

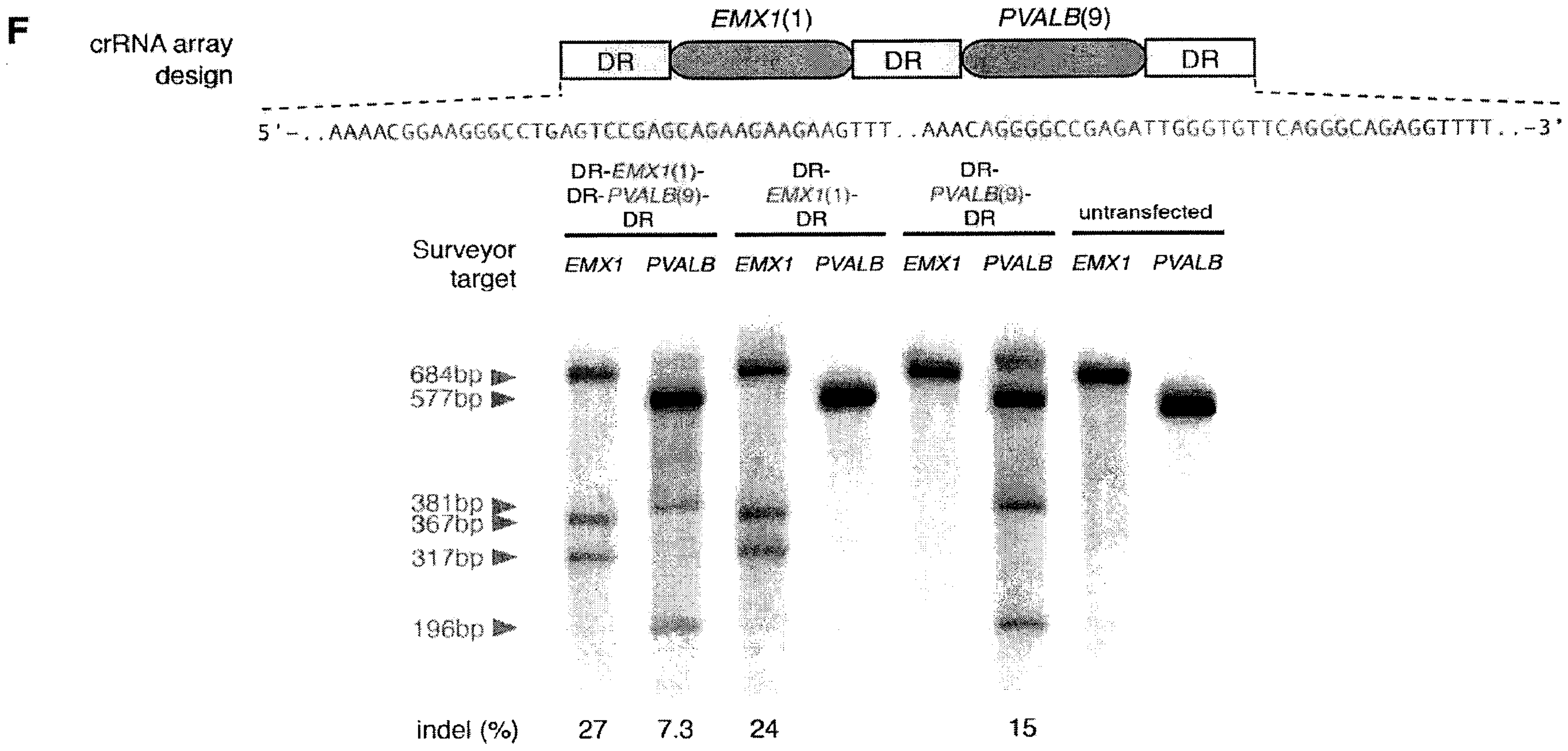

F
crRNA array design
EMX1(1)
PVALB(9)
DR
DR
DR
5'-..AAAACGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGTTT..AAACAGGGGCCGAGATTGGGTGTTCAGGGCAGAGGTTTT..-3'
DR-EMX1(1)-DR-PVALB(9)-DR
DR-EMX1(1)-DR
DR-PVALB(9)-DR
untransfected
Surveyor target
EMX1
PVALB
EMX1
PVALB
EMX1
PVALB
EMX1
PVALB
684bp
577bp
381bp
367bp
317bp
196bp
indel (%)
27
7.3
24
15

FIG. 4F

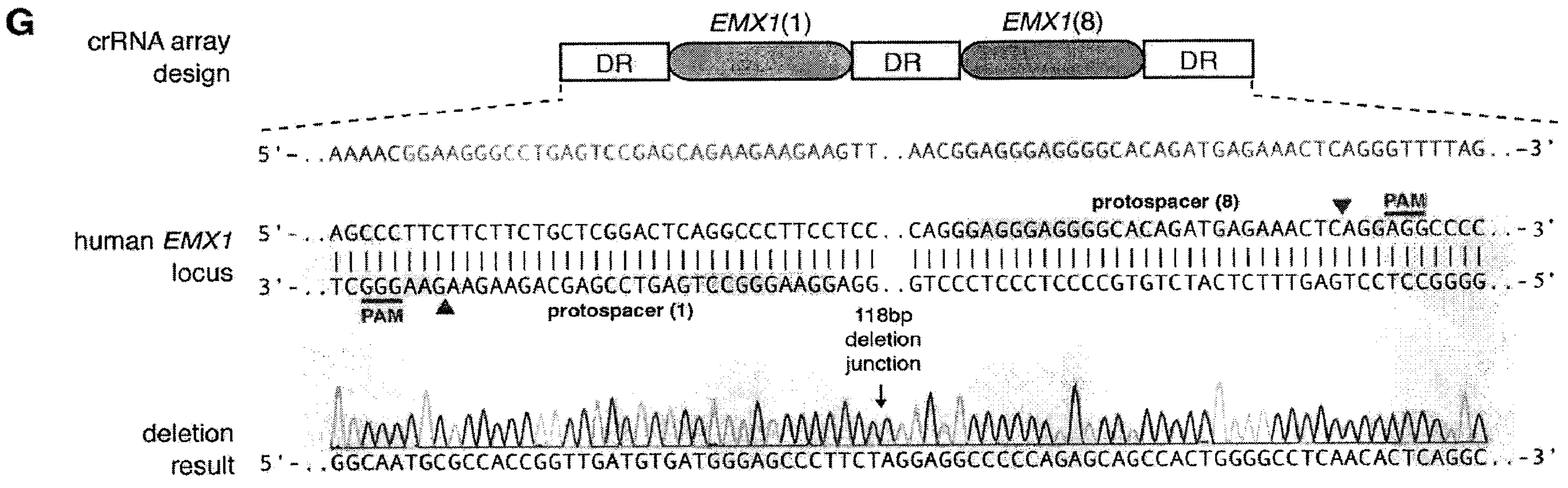

G
crRNA array design
DR
EMX1(1)
DR
EMX1(8)
DR
5'-..AAAACGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGTT..AACGGAGGGAGGGGCACAGATGAGAAACTCAGGGTTTTAG..-3'
human *EMX1* locus
protospacer (8)
PAM
5'-..AGCCCTTCTTCTTCTGCTCGGACTCAGGCCCTTCCTCC..CAGGGAGGGAGGGGCACAGATGAGAAACTCAGGAGGCCCC..-3'
3'-..TCGGGAAGAAGAAGACGAGCCTGAGTCCGGGAAGGAGG..GTCCCTCCCTCCCCGTGTCTACTCTTTGAGTCCTCCGGGG..-5'
PAM
protospacer (1)
118bp deletion junction
deletion result
5'-..GGCAATGCGCCACCGGTTGATGTGATGGGAGCCCTTCTAGGAGGCCCCCAGAGCAGCCACTGGGGCCTCAACACTCAGGC..-3'

FIG. 4G

Cas9	target species	gene	protospacer ID	protospacer sequence (5' to 3')	PAM	strand	cell line tested	% indel (pre-crRNA + tracrRNA)	% indel (chimeric RNA)
S. pyogenes SF370 type II CRISPR	*Homo sapiens*	*EMX1*	1	GGAAGGGCCTGAGTCCGAGCAGAAGAAGAA	GGG	+	293FT	20 ± 1.8	6.7 ± 0.62
		EMX1	2	CATTGGAGGTGACATCGATGTCCTCCCCAT	TGG	–	293FT	2.1 ± 0.31	N.D.
		EMX1	3	GGACATCGATGTCACCTCCAATGACTAGGG	TGG	+	293FT	14 ± 1.1	N.D.
		EMX1	4	CATCGATGTCCTCCCCATTGGCCTGCTTCG	TGG	–	293FT	11 ± 1.7	N.D.
		EMX1	5	TTCGTGGCAATGCGCCACCGGTTGATGTGA	TGG	–	293FT	4.3 ± 0.46	2.1 ± 0.51
		EMX1	6	TCGTGGCAATGCGCCACCGGTTGATGTGAT	GGG	–	293FT	4.0 ± 0.66	0.41 ± 0.25
		EMX1	7	TCCAGCTTCTGCCGTTTGTACTTTGTCCTC	CGG	–	293FT	1.5 ± 0.12	N.D.
		EMX1	8	GGAGGGAGGGGCACAGATGAGAAACTCAGG	AGG	–	293FT	7.8 ± 0.83	2.3 ± 1.2
	Homo sapiens	*PVALB*	9	AGGGGCCGAGATTGGGTGTTCAGGGCAGAG	AGG	+	293FT	21 ± 2.6	6.5 ± 0.32
		PVALB	10	ATGCAGGAGGGTGGCGAGAGGGGCCGAGAT	TGG	+	293FT	N.D.	N.D.
		PVALB	11	GGTGGCGAGAGGGGCCGAGATTGGGTGTTC	AGG	+	293FT	N.D.	N.D.
	Mus musculus	*Th*	12	CAAGCACTGAGTGCCATTAGCTAAATGCAT	AGG	–	Neuro2A	27 ± 4.3	4.1 ± 2.2
		Th	13	AATGCATAGGGTACCACCCACAGGTGCCAG	GGG	–	Neuro2A	4.8 ± 1.2	N.D.
		Th	14	ACACACATGGGAAAGCCTCTGGGCCAGGAA	AGG	+	Neuro2A	11.3 ± 1.3	N.D.
S. thermophilus LMD-9 CRISPR1	*Homo sapiens*	*EMX1*	15	GGAGGAGGTAGTATACAGAAACACAGAGAA	GTAGAAT	–	293FT	14 ± 0.88	N.T.
		EMX1	16	AGAATGTAGAGGAGTCACAGAAACTCAGCA	CTAGAAA	–	293FT	7.8 ± 0.77	N.T.

FIG. 5

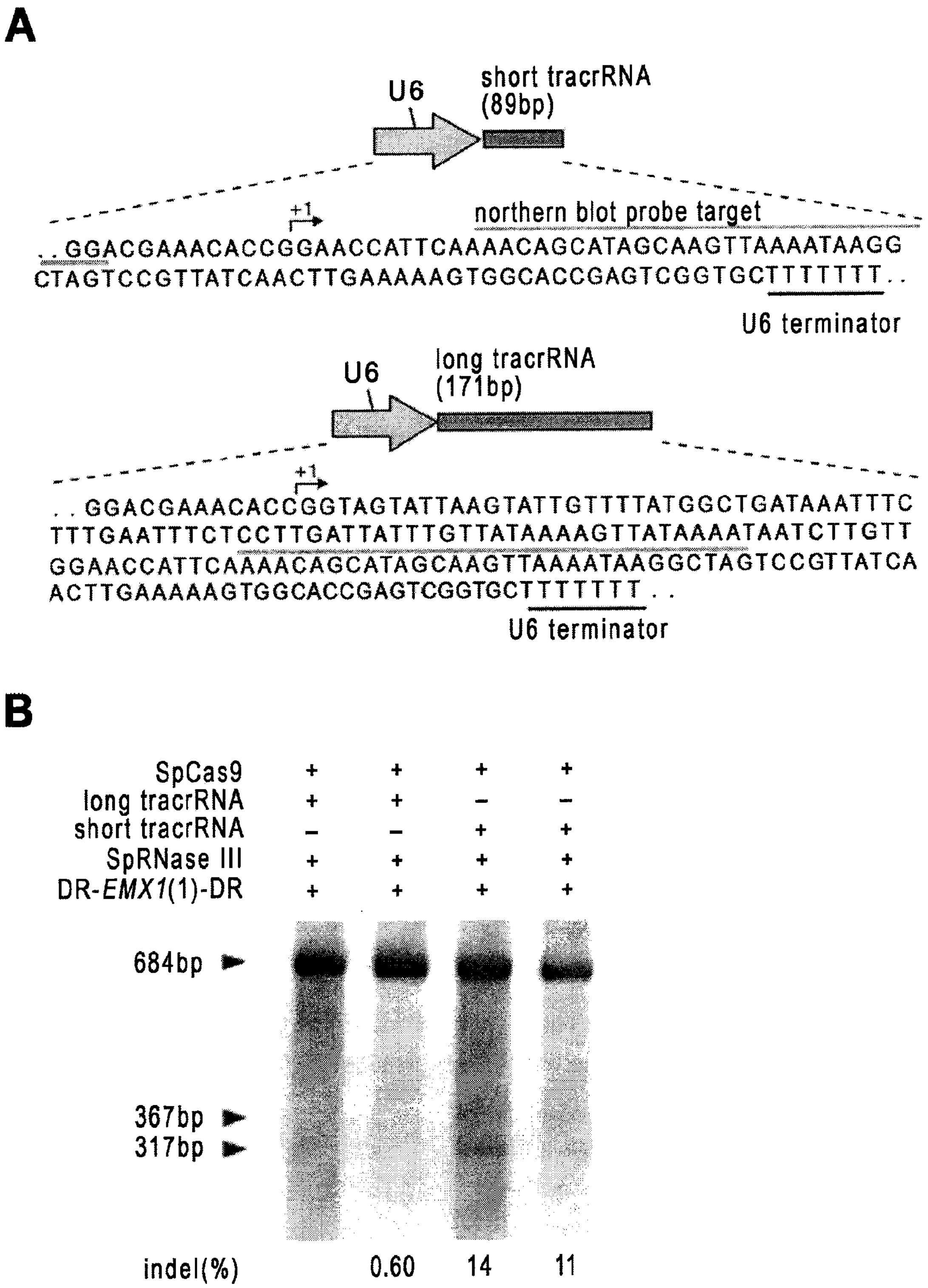

A
U6
short tracrRNA
(89bp)
+1
northern blot probe target
..GGACGAAACACCGGAACCATTCAAAACAGCATAGCAAGTTAAAATAAGG
CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTT..
U6 terminator
U6
long tracrRNA
(171bp)
+1
..GGACGAAACACCGGTAGTATTAAGTATTGTTTTATGGCTGATAAATTTC
TTTGAATTTCTCCTTGATTATTTGTTATAAAAGTTATAAAATAATCTTGTT
GGAACCATTCAAAACAGCATAGCAAGTTAAAATAAGGCTAGTCCGTTATCA
ACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTT..
U6 terminator
B
SpCas9 + + + +
long tracrRNA + + – –
short tracrRNA – – + +
SpRNase III + + + +
DR-EMX1(1)-DR + + + +
684bp
367bp
317bp
indel(%) 0.60 14 11

FIG. 6A-B

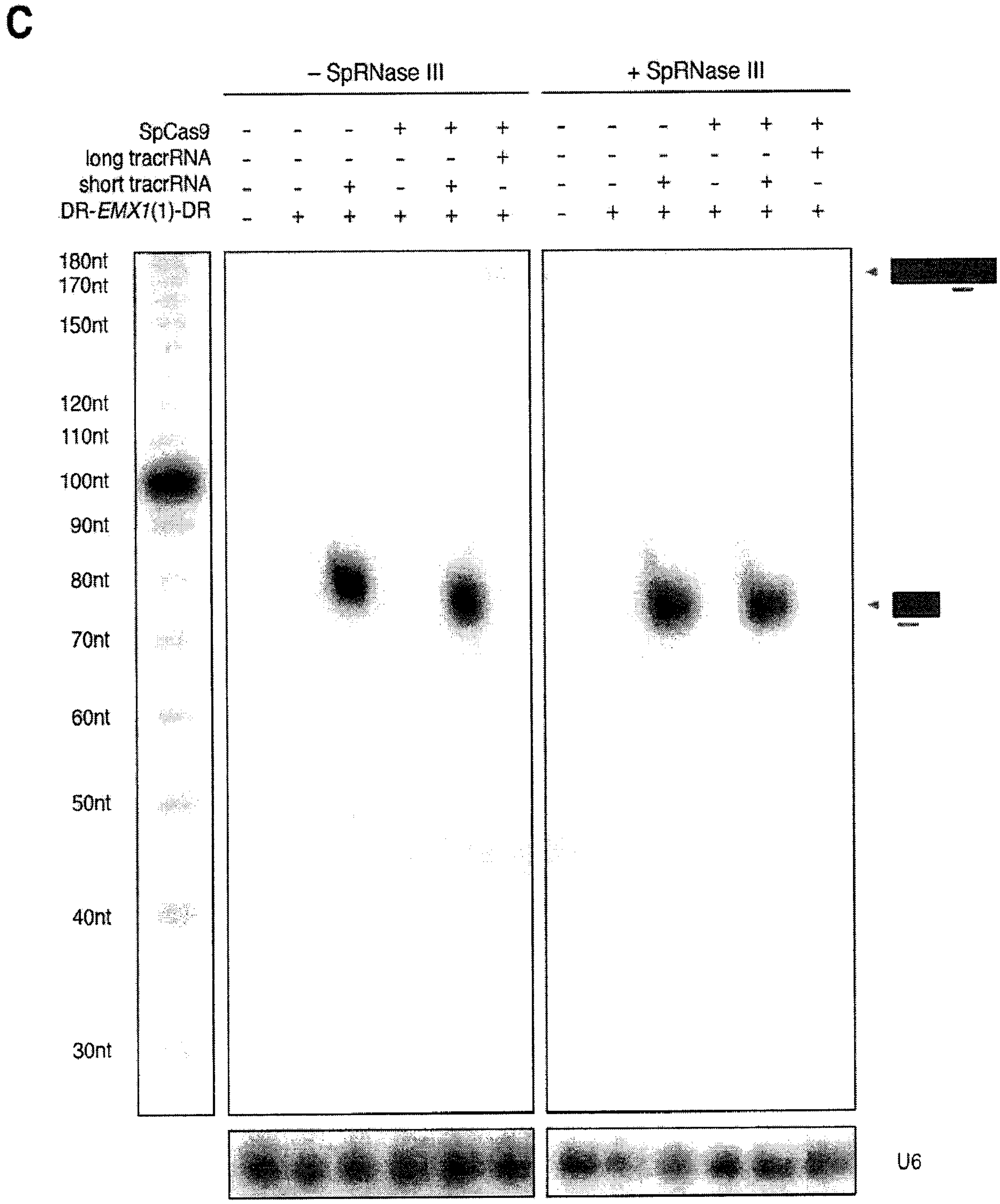

C
– SpRNase III
+ SpRNase III
SpCas9 - - - + + + - - - + + +
long tracrRNA - - - - - + - - - - - +
short tracrRNA - - + - + - - - + - + -
DR-*EMX1*(1)-DR - + + + + + - + + + + +
180nt
170nt
150nt
120nt
110nt
100nt
90nt
80nt
70nt
60nt
50nt
40nt
30nt
U6

FIG. 6C

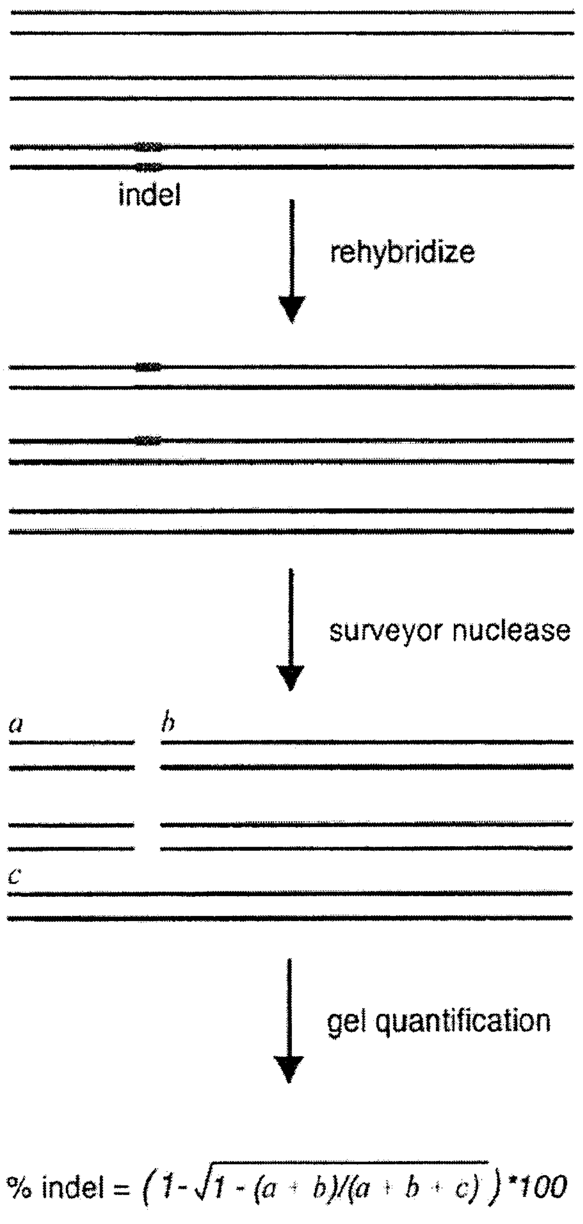

indel
rehybridize
surveyor nuclease
a
b
c
gel quantification
% indel = (1 - √1 - (a + b)/(a + b + c))*100

FIG. 7

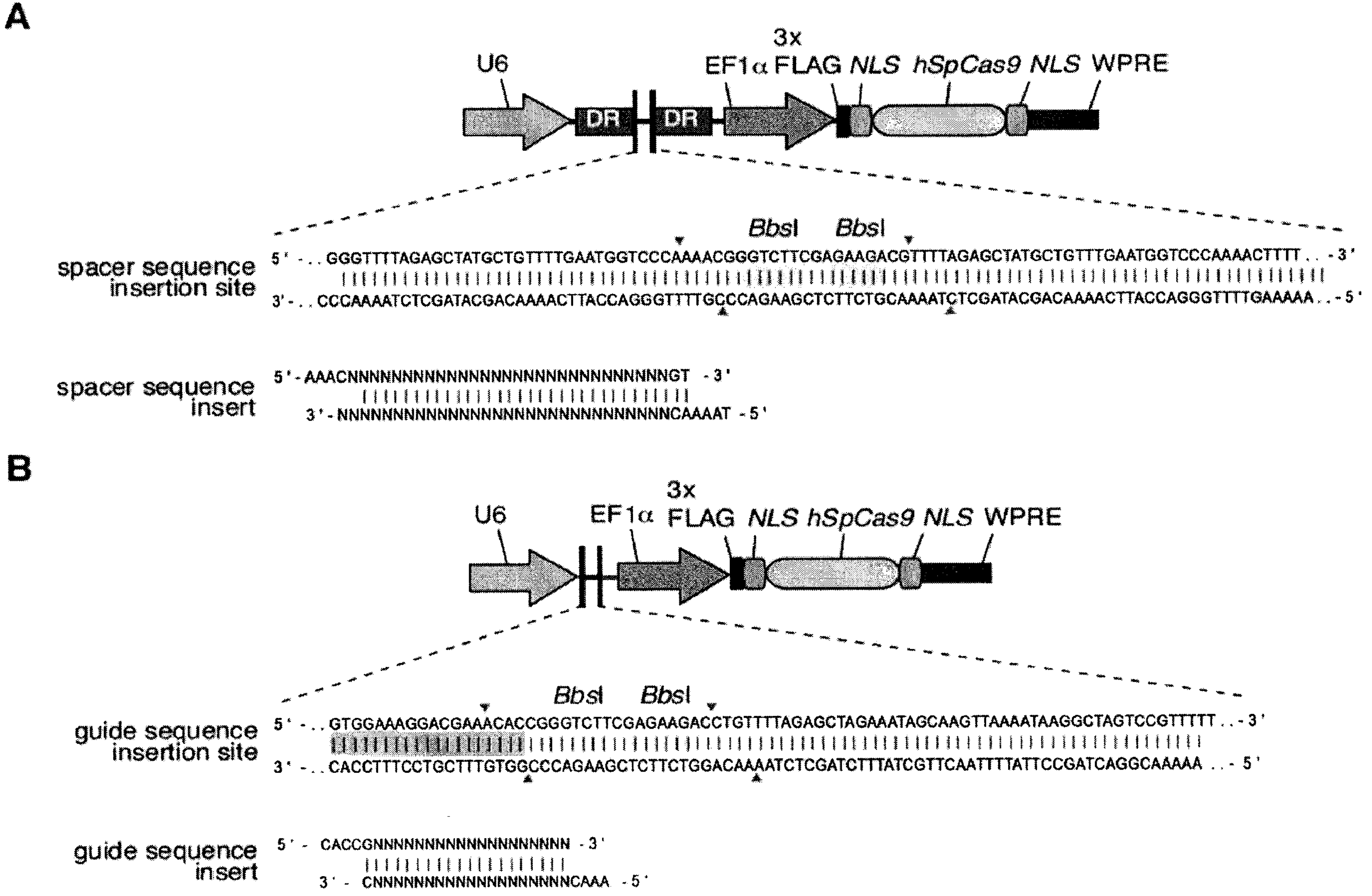
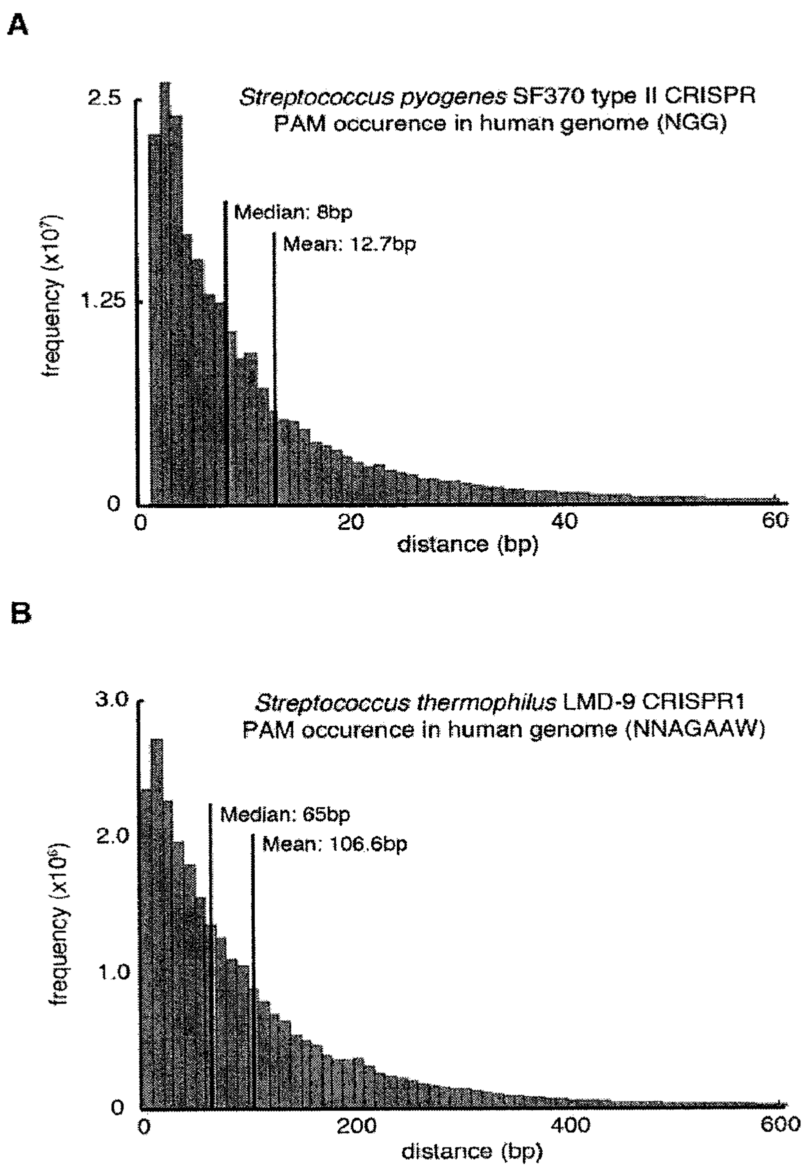

A
U6
DR
DR
3x
EF1α FLAG *NLS* *hSpCas9* *NLS* WPRE
*Bbs*I *Bbs*I
spacer sequence insertion site
5' -..GGGTTTTAGAGCTATGCTGTTTTGAATGGTCCCAAAACGGGTCTTCGAGAAGACGTTTTAGAGCTATGCTGTTTGAATGGTCCCAAAACTTTT..-3'
3'-..CCCAAAATCTCGATACGACAAAACTTACCAGGGTTTTGCCCAGAAGCTCTTCTGCAAAATCTCGATACGACAAAACTTACCAGGGTTTTGAAAAA..-5'
spacer sequence insert
5'-AAACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGT -3'
3'-NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAAAAT -5'
B
U6
3x
EF1α FLAG *NLS* *hSpCas9* *NLS* WPRE
*Bbs*I *Bbs*I
guide sequence insertion site
5' -..GTGGAAAGGACGAAACACCGGGTCTTCGAGAAGACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTTTT..-3'
3' -..CACCTTTCCTGCTTTGTGGCCCAGAAGCTCTTCTGGACAAAATCTCGATCTTTATCGTTCAATTTTATTCCGATCAGGCAAAAA ..-5'
guide sequence insert
5' - CACCGNNNNNNNNNNNNNNNNNNNN -3'
3' - CNNNNNNNNNNNNNNNNNNNNCAAA -5'

FIG. 8A-B



C

	NGG		NNAGAAW	
Chr	median	mean	median	mean
1	7	12.8	67	115.8
2	8	12.7	64	100.8
3	8	13.0	63	98.5
4	9	14.0	61	94.5
5	8	13.1	63	97.9
6	8	13.1	63	98.5
7	8	12.4	64	102.9
8	8	12.8	64	100.9
9	7	13.9	65	120.5
10	7	12.1	66	107.0
11	7	12.0	65	105.8
12	8	12.4	65	103.5
13	8	13.6	62	94.6
14	8	12.0	65	101.5
15	7	11.5	68	107.7
16	7	11.7	74	136.8
17	6	10.3	76	127.9
18	8	13.4	63	101.8
19	6	9.4	82	145.4
20	7	11.1	72	121.8
21	7	13.4	64	111.4
22	6	9.2	85	140.3
X	8	13.2	63	99.0
Y	8	29.2	62	223.7

FIG. 9A-C

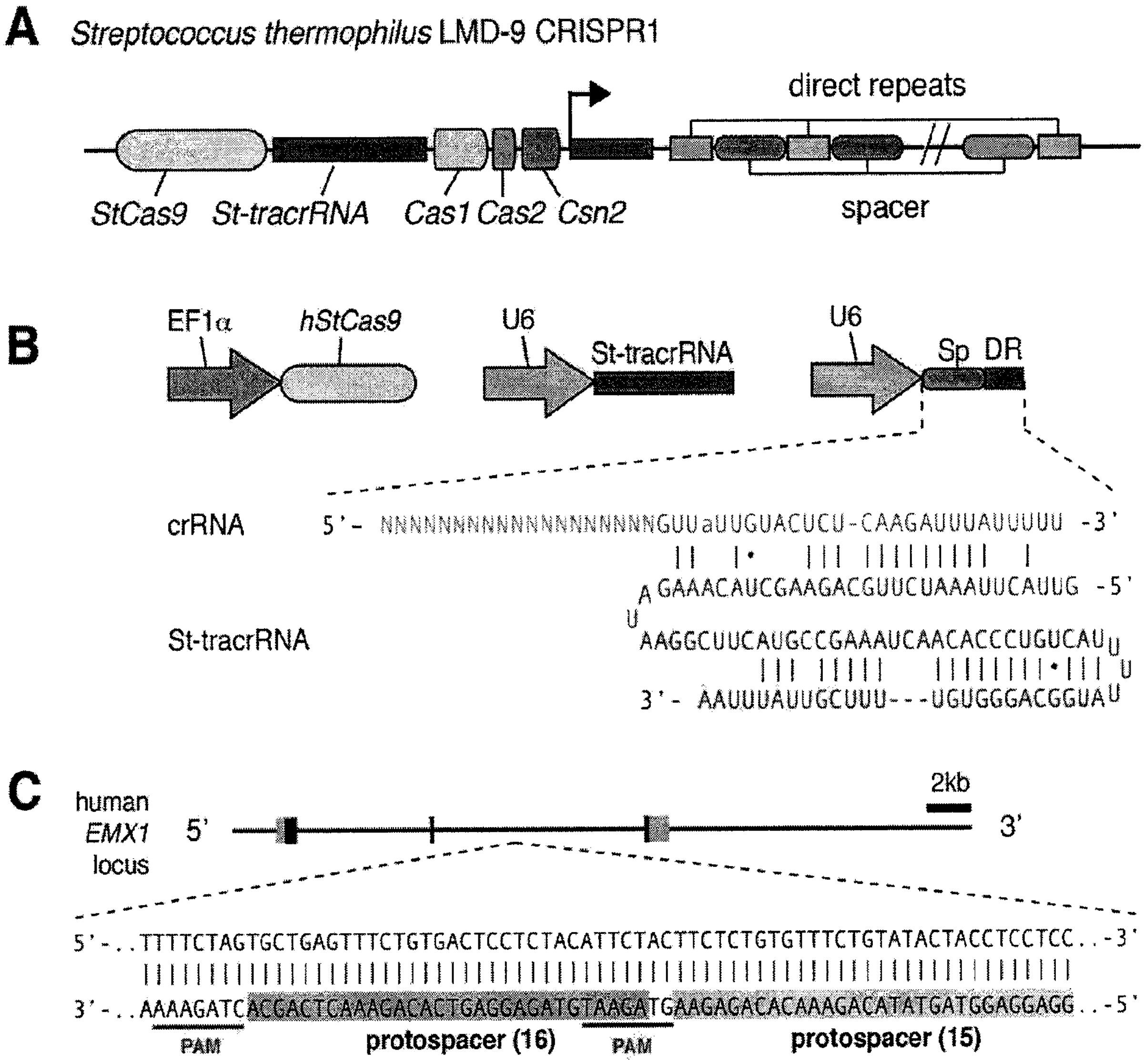

A
Streptococcus thermophilus LMD-9 CRISPR1
direct repeats
StCas9
St-tracrRNA
Cas1
Cas2
Csn2
spacer
B
EF1α
hStCas9
U6
St-tracrRNA
U6
Sp
DR
crRNA
5'- NNNNNNNNNNNNNNNNNNNNGUUaUUGUACUCU-CAAGAUUUAUUUUU -3'
AGAAACAUCGAAGACGUUCUAAAUUCAUUG -5'
U
St-tracrRNA
AAGGCUUCAUGCCGAAAUCAACACCCUGUCAUU
U
3'- AAUUUAUUGCUUU---UGUGGGACGGUAU
C
human
EMX1
locus
5'
3'
2kb
5'-..TTTTCTAGTGCTGAGTTTCTGTGACTCCTCTACATTCTACTTCTCTGTGTTTCTGTATACTACCTCCTCC..-3'
3'-..AAAAGATCACGACTCAAAGACACTGAGGAGATGTAAGATGAAGAGACACAAAGACATATGATGGAGGAGG..-5'
PAM
protospacer (16)
PAM
protospacer (15)

FIG. 10A-C

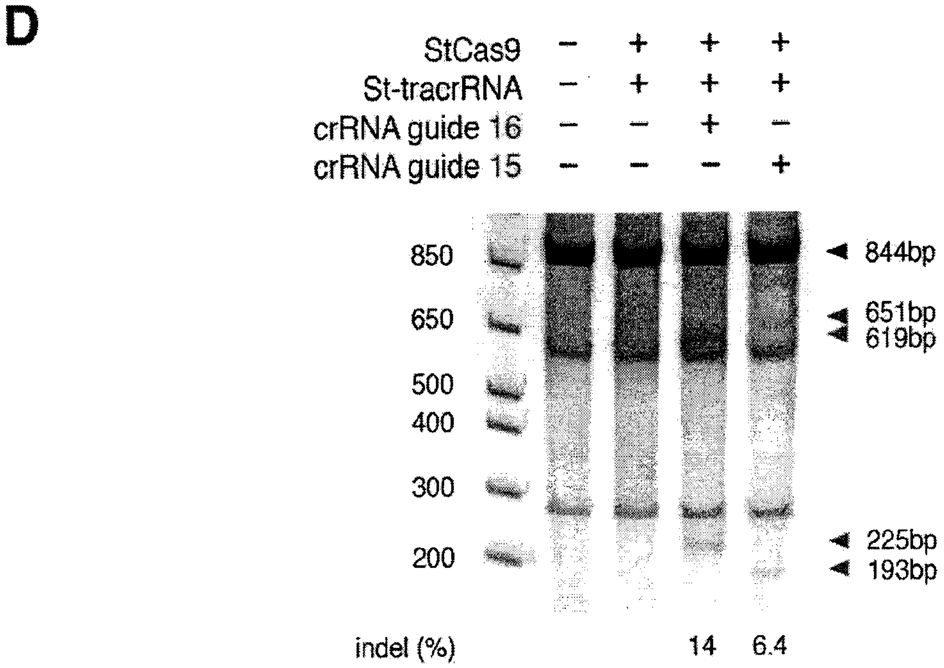

D
StCas9 − + + +
St-tracrRNA − + + +
crRNA guide 16 − − + −
crRNA guide 15 − − − +
850
650
500
400
300
200
844bp
651bp
619bp
225bp
193bp
indel (%)
14
6.4

FIG. 10D

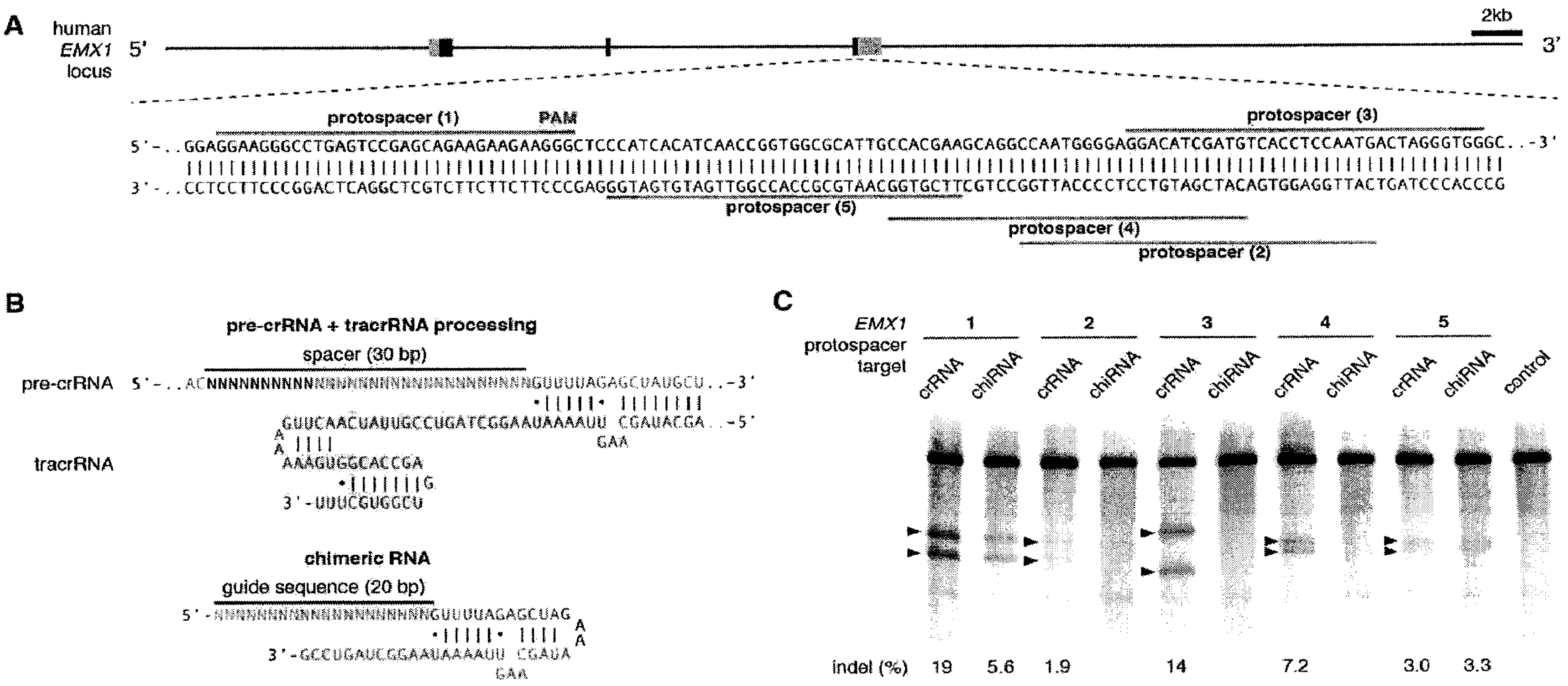

A
human
EMX1
locus
5'
3'
2kb
protospacer (1)
PAM
protospacer (3)
5'-..GGAGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGGGCTCCCATCACATCAACCGGTGGCGCATTGCCACGAAGCAGGCCAATGGGGAGGACATCGATGTCACCTCCAATGACTAGGGTGGGC..-3'
3'-..CCTCCTTCCCGGACTCAGGCTCGTCTTCTTCTTCCCGAGGGTAGTGTAGTTGGCCACCGCGTAACGGTGCTTCGTCCGGTTACCCCTCCTGTAGCTACAGTGGAGGTTACTGATCCCACCCG
protospacer (5)
protospacer (4)
protospacer (2)
B
pre-crRNA + tracrRNA processing
spacer (30 bp)
pre-crRNA
5'-..ACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAUGCU..-3'
GUUCAACUAUUGCCUGATCGGAAUAAAAUU CGAUACGA..-5'
GAA
A
A
tracrRNA
AAAGUGGCACCGA
G
3'-UUUCGUGGCU
chimeric RNA
guide sequence (20 bp)
5'-NNNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAG
A
A
3'-GCCUGAUCGGAAUAAAAUU CGAUA
GAA
C
EMX1
protospacer
target
1
2
3
4
5
crRNA
chiRNA
crRNA
chiRNA
crRNA
chiRNA
crRNA
chiRNA
crRNA
chiRNA
control
indel (%)
19
5.6
1.9
14
7.2
3.0
3.3

FIG. 11A-C

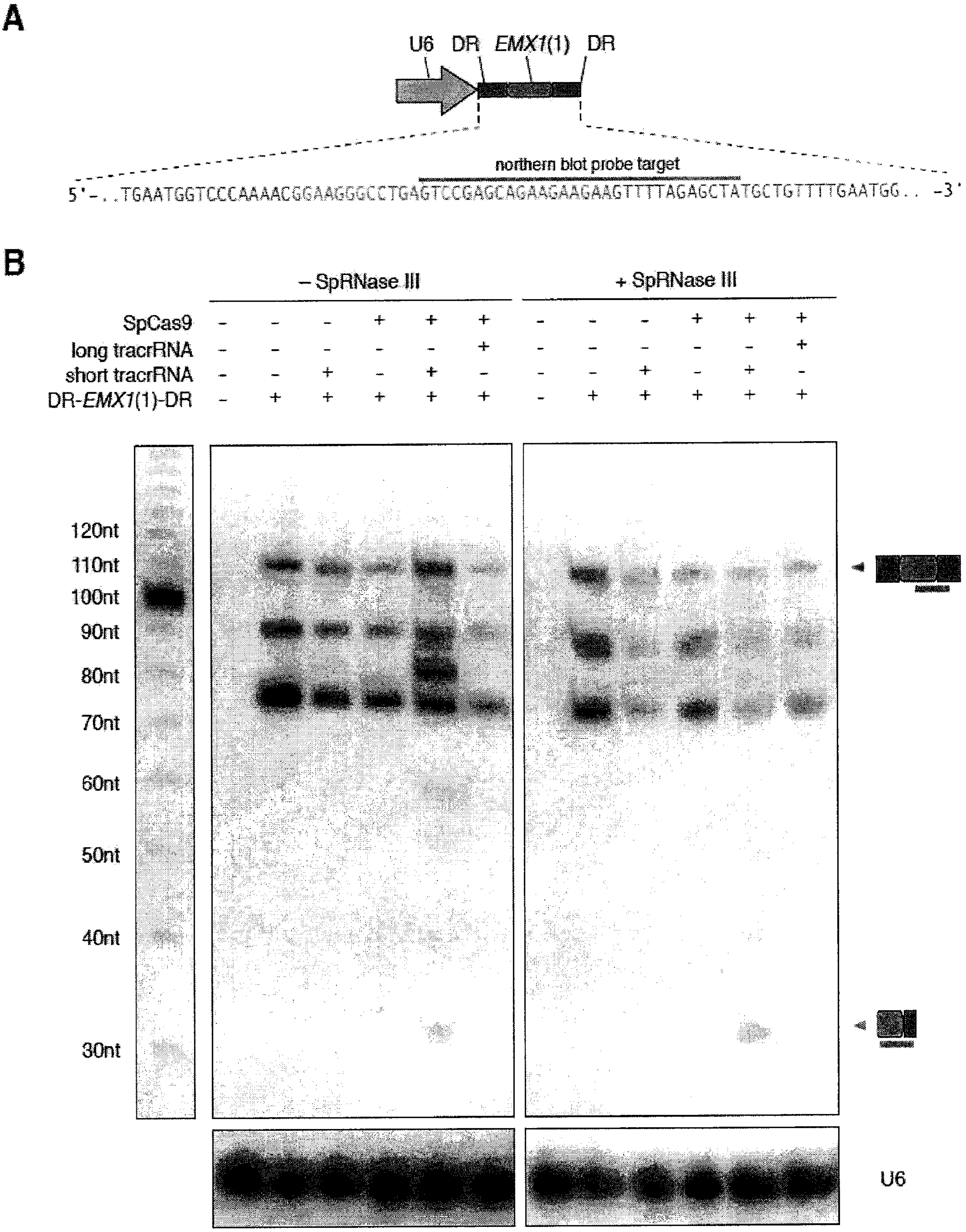

A
U6
DR
EMX1(1)
DR
northern blot probe target
5'-..TGAATGGTCCCAAAACGGAAGGGCCTGAGTCCGAGCAGAAGAAGAAGTTTTAGAGCTATGCTGTTTTGAATGG.. -3'
B
– SpRNase III
+ SpRNase III
SpCas9 - - - + + + - - - + + +
long tracrRNA - - - - - + - - - - - +
short tracrRNA - - + - + - - - + - + -
DR-*EMX1*(1)-DR - + + + + + - + + + + +
120nt
110nt
100nt
90nt
80nt
70nt
60nt
50nt
40nt
30nt
U6

FIG. 12A-B

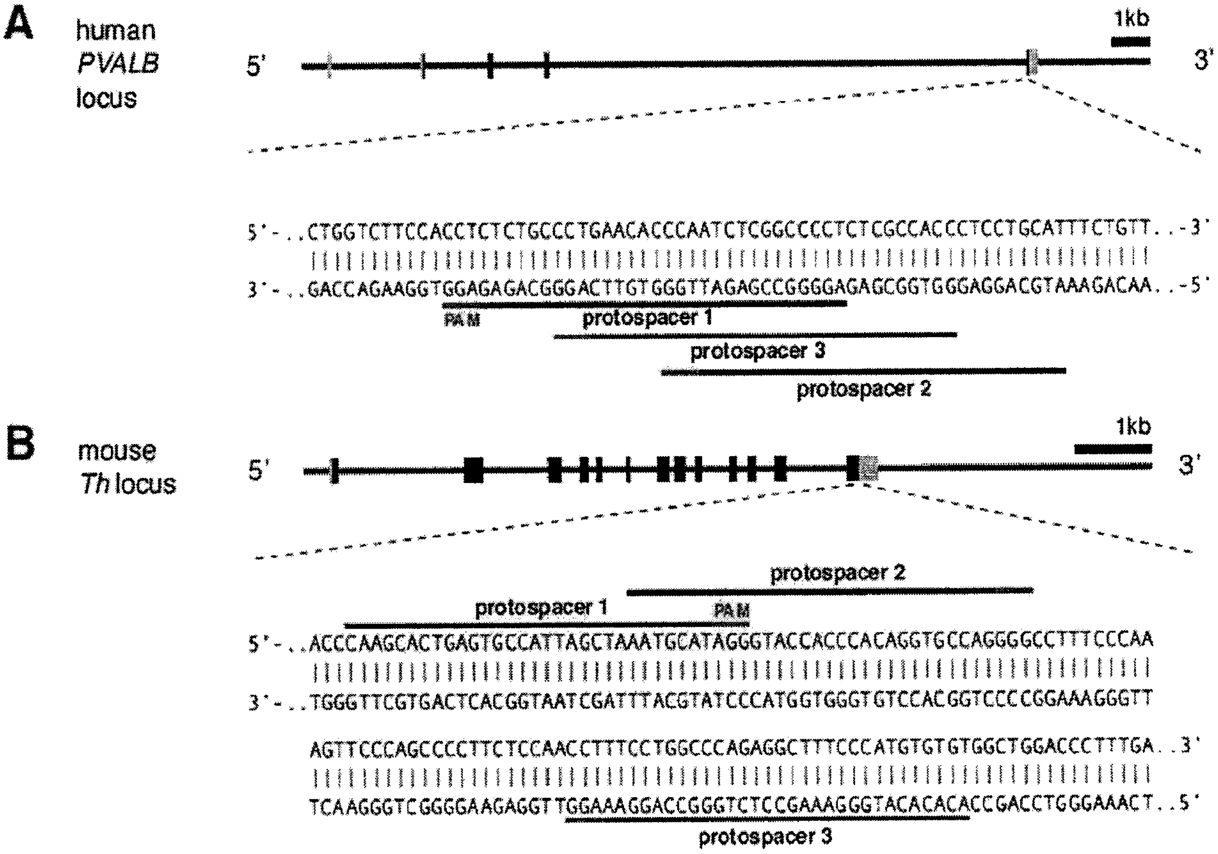

A
human
PVALB
locus
1kb
5'
3'
5'-..CTGGTCTTCCACCTCTCTGCCCTGAACACCCAATCTCGGCCCCTCTCGCCACCCTCCTGCATTTCTGTT..-3'
3'-..GACCAGAAGGTGGAGAGACGGGACTTGTGGGTTAGAGCCGGGGAGAGCGGTGGGAGGACGTAAAGACAA..-5'
PAM
protospacer 1
protospacer 3
protospacer 2
B
mouse
Th locus
1kb
5'
3'
protospacer 2
protospacer 1
PAM
5'-..ACCCAAGCACTGAGTGCCATTAGCTAAATGCATAGGGTACCACCCACAGGTGCCAGGGGCCTTTCCCAA
3'-..TGGGTTCGTGACTCACGGTAATCGATTTACGTATCCCATGGTGGGTGTCCACGGTCCCCGGAAAGGGTT
AGTTCCCAGCCCCTTCTCCAACCTTTCCTGGCCCAGAGGCTTTCCCATGTGTGTGGCTGGACCCTTTGA..3'
TCAAGGGTCGGGGAAGAGGTTGGAAAGGACCGGGTCTCCGAAAGGGTACACACACCGACCTGGGAAACT..5'
protospacer 3

FIG. 13A-B

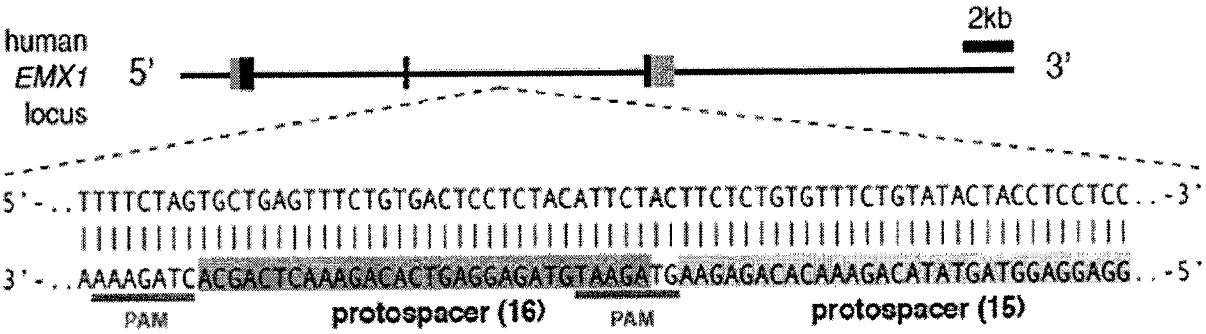

human
EMX1
locus
5'
2kb
3'
5'-..TTTTCTAGTGCTGAGTTTCTGTGACTCCTCTACATTCTACTTCTCTGTGTTTCTGTATACTACCTCCTCC..-3'
3'-..AAAAGATCACGACTCAAAGACACTGAGGAGATGTAAGATGAAGAGACACAAAGACATATGATGGAGGAGG..-5'
PAM
protospacer (16)
PAM
protospacer (15)

FIG. 14

Primer name	Assay	Genomic Target	Primer sequence
Sp-EMX1-F	SURVEYOR assay, sequencing	*EMX1*	AAAACCACCCTTCTCTCTGGC
Sp-EMX1-R	SURVEYOR assay, sequencing	*EMX1*	GGAGATTGGAGACACGGAGAG
Sp-PVALB-F	SURVEYOR assay, sequencing	*PVALB*	CTGGAAAGCCAATGCCTGAC
Sp-PVALB-R	SURVEYOR assay, sequencing	*PVALB*	GGCAGCAAACTCCTTGTCCT
Sp-Th-F	SURVEYOR assay, sequencing	*Th*	GTGCTTTGCAGAGGCCTACC
Sp-Th-R	SURVEYOR assay, sequencing	*Th*	CCTGGAGCGCATGCAGTAGT
St-EMX1-F	SURVEYOR assay, sequencing	*EMX1*	ACCTTCTGTGTTTCCACCATTC
St-EMX1-R	SURVEYOR assay, sequencing	*EMX1*	TTGGGGAGTGCACAGACTTC
Sp-EMX1-RFLP-F	RFLP, sequencing	*EMX1*	GGCTCCCTGGGTTCAAAGTA
Sp-EMX1-RFLP-R	RFLP, sequencing	*EMX1*	AGAGGGGTCTGGATGTCGTAA
Pb_EMX1_sp1	Northern Blot Probe	Not applicable	TAGCTCTAAAACTTCTTCTTCTGCTCGGAC
Pb_tracrRNA	Northern Blot Probe	Not applicable	CTAGCCTTATTTTAACTTGCTATGCTGTTT

FIG. 15

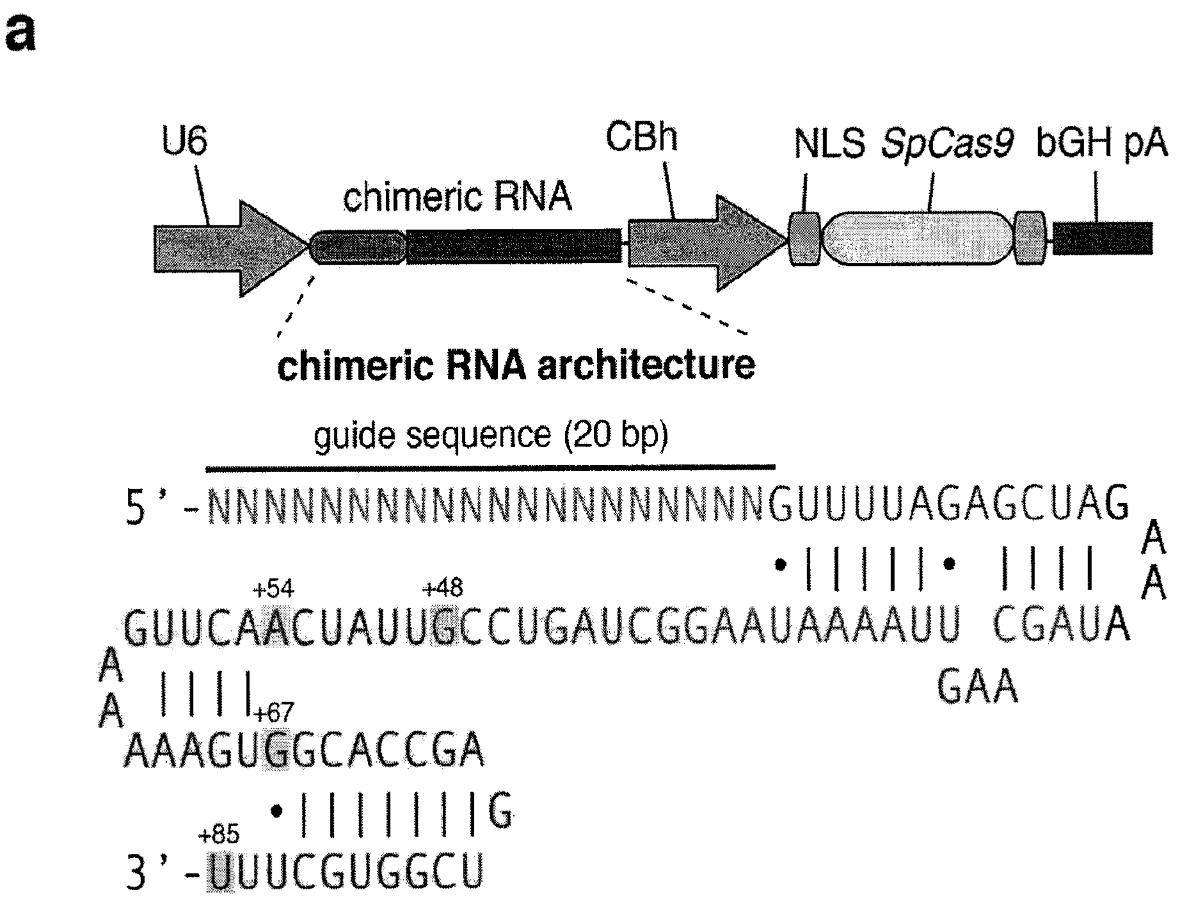

a
U6
chimeric RNA
CBh
NLS
SpCas9
bGH pA
chimeric RNA architecture
guide sequence (20 bp)
5'-NNNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAG
A
A
+54
+48
GUUCAACUAUUGCCUGAUCGGAAUAAAAUU CGAUA
A
A
GAA
+67
AAAGUGGCACCGA
G
+85
3'-UUUCGUGGCU

FIG. 16A

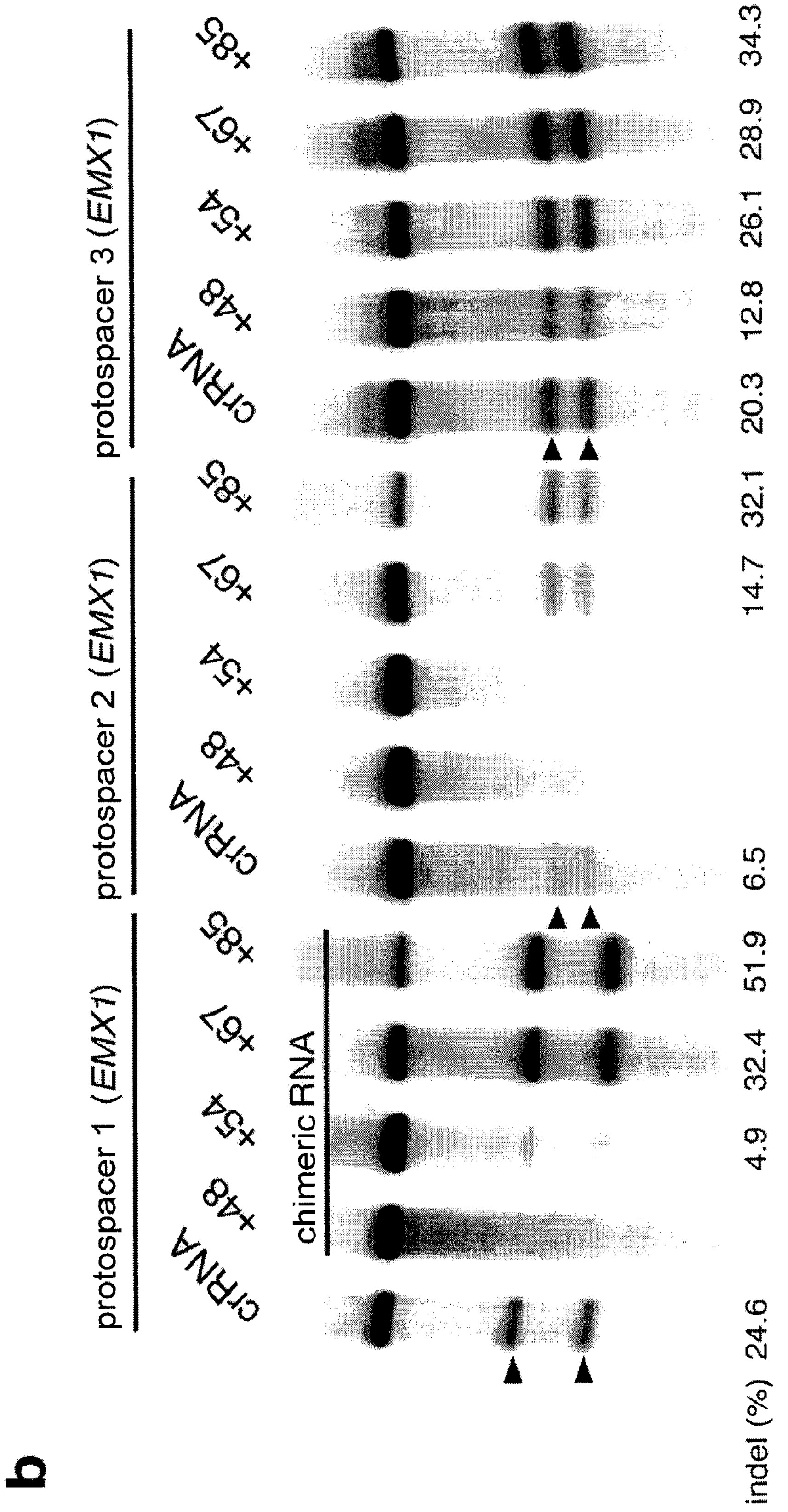

b
protospacer 1 (*EMX1*)
protospacer 2 (*EMX1*)
protospacer 3 (*EMX1*)
crRNA
+48
+54
+67
+85
crRNA
+48
+54
+67
+85
crRNA
+48
+54
+67
+85
chimeric RNA
indel (%)
24.6
4.9
32.4
51.9
6.5
14.7
32.1
20.3
12.8
26.1
28.9
34.3

FIG. 16B

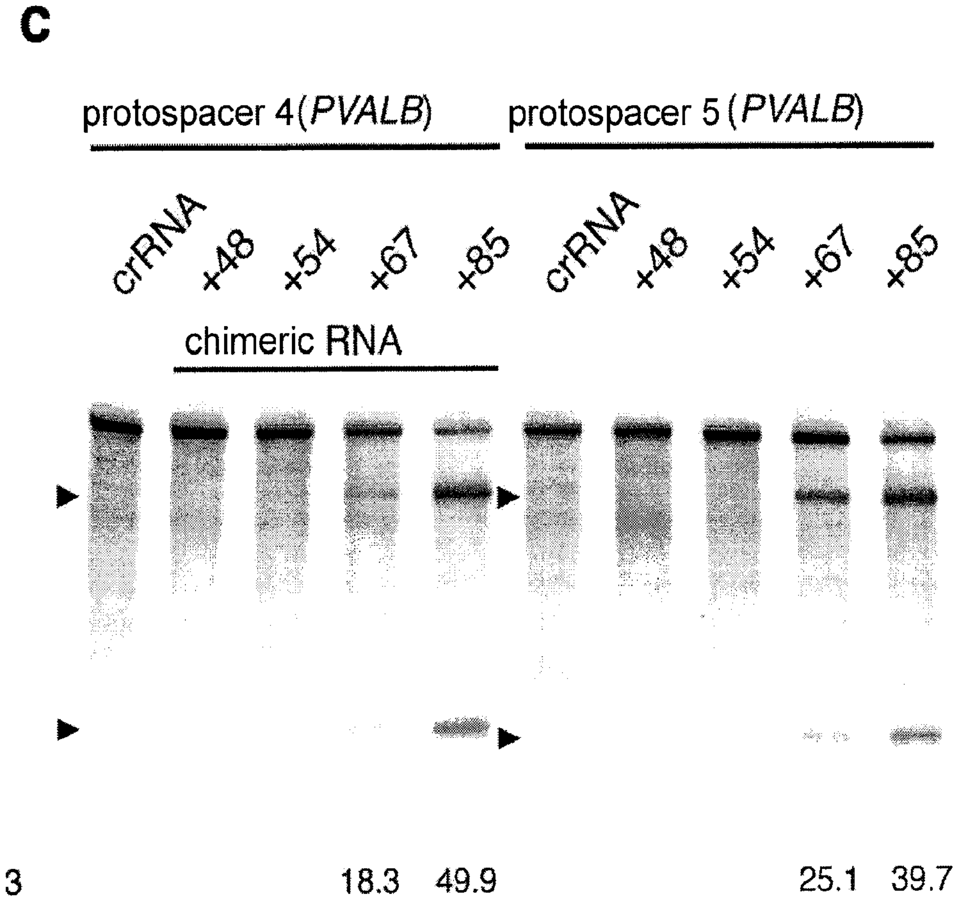

C
protospacer 4 (*PVALB*)
protospacer 5 (*PVALB*)
crRNA
+48
+54
+67
+85
crRNA
+48
+54
+67
+85
chimeric RNA
3
18.3
49.9
25.1
39.7

FIG. 16C

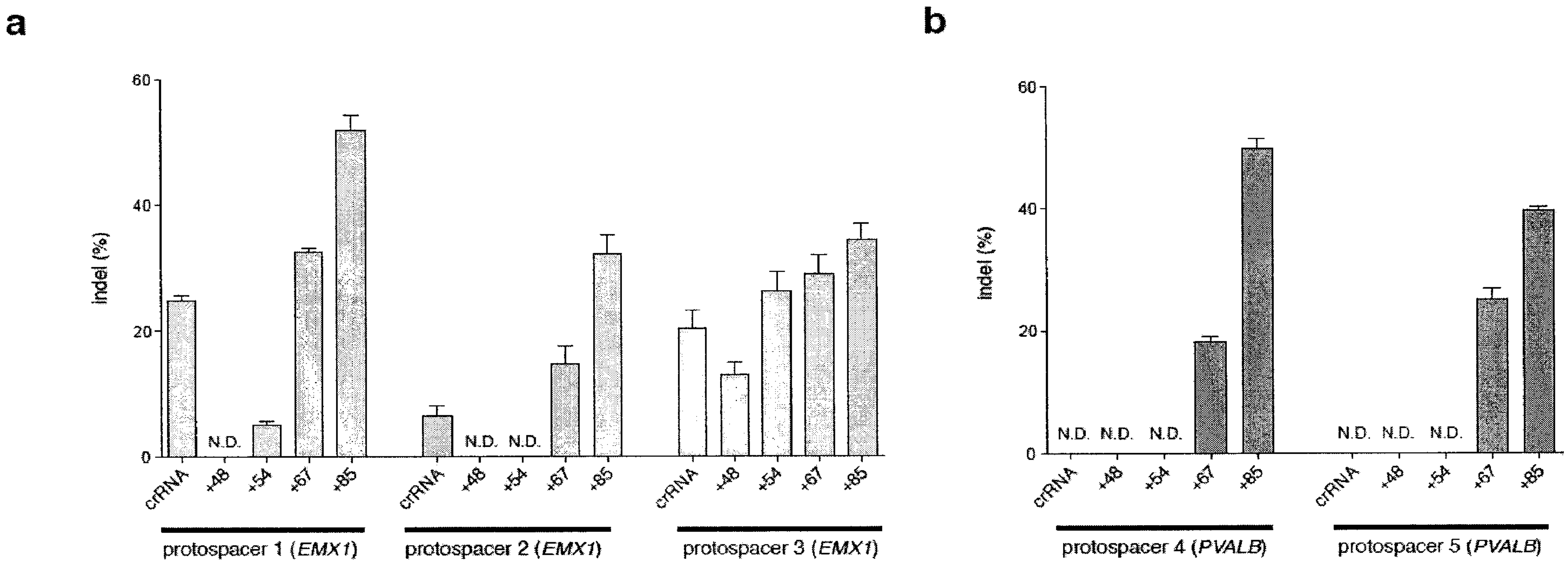

a
60
40
20
0
indel (%)
N.D.
N.D. N.D.
crRNA
+48
+54
+67
+85
protospacer 1 (*EMX1*)
protospacer 2 (*EMX1*)
protospacer 3 (*EMX1*)
b
60
40
20
0
indel (%)
N.D. N.D. N.D.
N.D. N.D. N.D.
crRNA
+48
+54
+67
+85
protospacer 4 (*PVALB*)
protospacer 5 (*PVALB*)

FIG. 17A-B

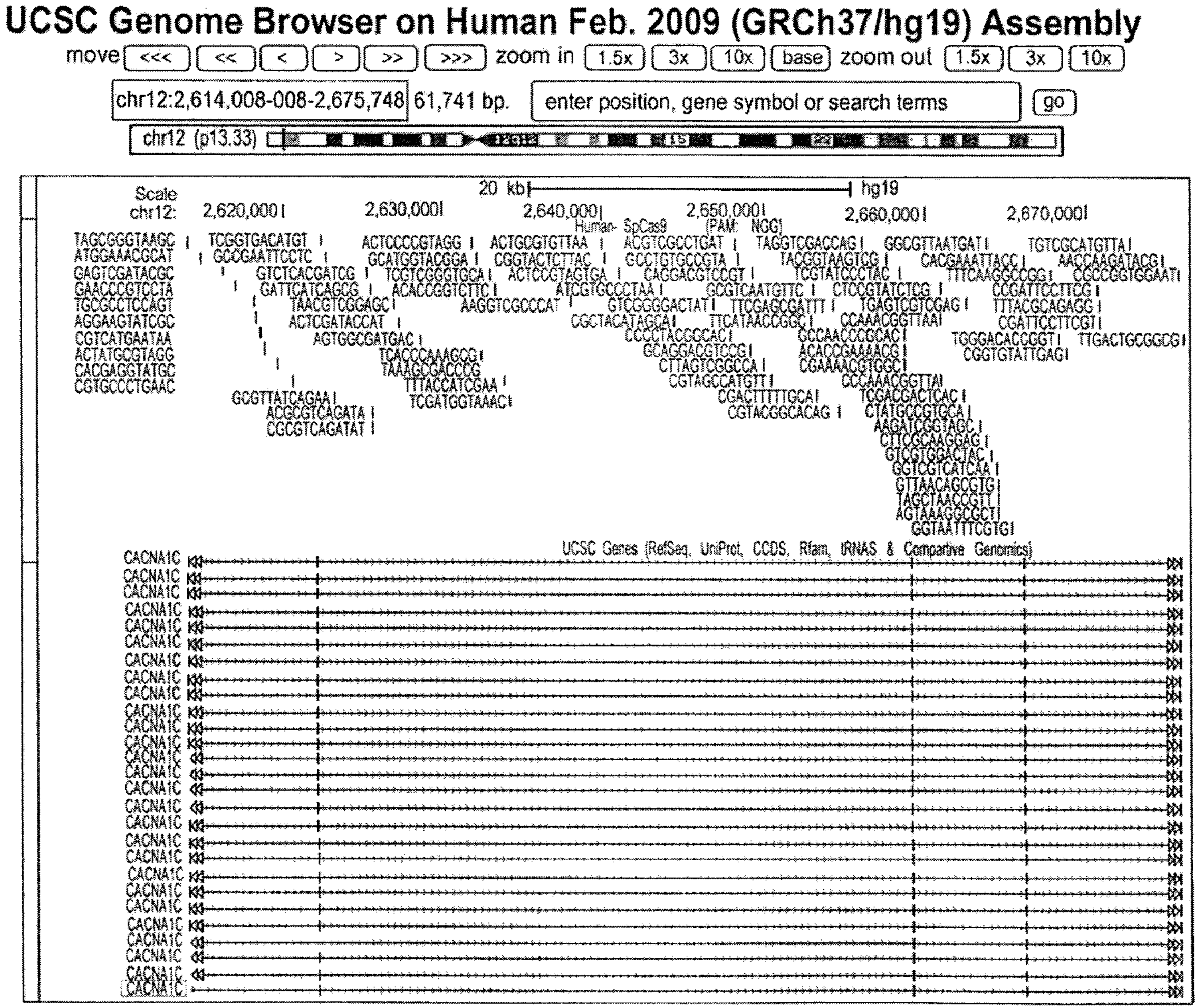

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x
chr12:2,614,008-008-2,675,748 61,741 bp.
enter position, gene symbol or search terms
go
chr12 (p13.33)
Scale
20 kb
hg19
chr12:
2,620,000
2,630,000
2,640,000
2,650,000
2,660,000
2,670,000
Human- SpCas9 (PAM: NGG)
UCSC Genes (RefSeq, UniProt, CCDS, Rfam, tRNAS & Comparative Genomics)
CACNA1C

FIG. 18


hypothetical protein BBta_3952 [Bradyrhizobium sp. BTAi1]
CRISPR-associated protein, Csn1 family [Candidatus Puniceispirillum marinum IMCC1322]
CRISPR-associated endonuclease Csn1 family protein [Elusimicrobium minutum Pei191]
Csn1-like CRISPR-associated protein [uncultured Termite group 1 bacterium phylotype Rs-D17]
CRISPR-associated protein, Csn1 family [Sphaerochaeta globus str. Buddy]
CRISPR-associated endonuclease Csn1 family protein [Rhodospirillum rubrum ATCC 11170]
CRISPR-associated endonuclease Csn1 family protein [Parvibaculum lavamentivorans DS-1]
conserved hypothetical protein [Bacteroides sp. 20_3]
hypothetical protein BACDOR_03889 [Bacteroides dorei DSM 17855]
hypothetical protein BACCOPRO_03113 [Bacteroides coprophilus DSM 18228]
CRISPR-associated protein, Csn1 family [Fibrobacter succinogenes subsp. succinogenes S85]
csn1 family CRISPR-associated protein [Prevotella buccae ATCC 33574]
conserved hypothetical protein [Prevotella melaninogenica D18]
CRISPR-associated protein, Csn1 family [Prevotella veroralis F0319]
CRISPR-associated protein, Csn1 family [Prevotella bivia JCVIHMP010]
CRISPR-associated protein, Csn1 family [Fluvilcola taffensis DSM 16823]
CRISPR-associated protein [Sphingobacterium spiritivorum ATCC 33861]
CRISPR-associated protein, Csn1 family [Weeksella virosa DSM 16922]
CRISPR-associated protein, Csn1 family [Mucilaginibacter paludis DSM 18603]
csn1 family CRISPR-associated protein [Flavobacterium columnare ATCC 49512]
CRISPR-associated protein, Csn1 family [Capnocytophaga gingivalis ATCC 33624]
CRISPR-associated protein, Csn1 family [Bacteroidetes oral taxon 274 str. F0058]
hypothetical protein Ccan_14650 [Capnocytophaga canimorsus Cc5]
hypothetical protein, Csn1 family [Capnocytophaga ochracea DSM 7271]
crispr-associated protein, Csn1 family [Capnocytophaga sputigena Capno]
hypothetical protein KAOT1_02362 [Kordia algicida OT-1]
hypothetical protein ZPR_4422 [Zunongwangia profunda SM-A87]
CRISPR-associated endonuclease Csn1 family protein [Flavobacterium psychrophilum JIP02/86]
hypothetical protein BACCELL_00696 [Bacteroides cellulosilyticus DSM 14838]
CRISPR-associated protein [Parabacteroides sp. D13]
hypothetical protein PRABACTJOHN_00621 [Parabacteroides johnsonii DSM 18315]
hypothetical protein BF3954 [Bacteroides fragilis NCTC 9343]
csn1 family CRISPR-associated protein [Prevotella oralis ATCC 33269]
CRISPR-associated protein, Csn1 family [Prevotella timonensis CRIS 5C-B1]
CRISPR-associated protein, Csn1 family [Prevotella buccalis ATCC 35310]
Csn1 family CRISPR-associated protein [Prevotella tannerae ATCC 51259]
CRISPR-associated protein [Prevotella ruminicola 23]
putative CRISPR-associated (Cas) protein [Flavobacterium columnare ATCC 49512]
putative CRISPR-associated (Cas) protein [Flavobacterium branchiophilum FL-15]
hypothetical protein HMPREF9140_01667 [Prevotella micans F0438]
conserved hypothetical protein [Corynebacterium accolens ATCC 49726]
hypothetical protein DIP0036 [Corynebacterium diphtheriae NCTC 13129]
CRISPR-associated protein, Csn1 family [Corynebacterium matruchotii ATCC 14266]
conserved hypothetical protein [Actinomyces coleocanis DSM 15436]
exopolyphosphatase [Mobiluncus curtisii subsp. holmesii ATCC 35242]
crispr-associated protein, Csn1 family [Mobiluncus mulieris 28-1]
restriction endonuclease [Bifidobacterium longum DJO10A]
CRISPR-associated endonuclease Csn1 [Bifidobacterium dentium Bd1]
putative HNH endonuclease domain protein [Scardovia inopinata F0304]
McrA/HNH-like CRISPR-associated nuclease Csn1 [Gardnerella vaginalis 5-1]
HNH endonuclease [Acidothermus cellulolyticus 11B]
hypothetical protein Amuc_2010 [Akkermansia muciniphila ATCC BAA-835]

FIG. 19A

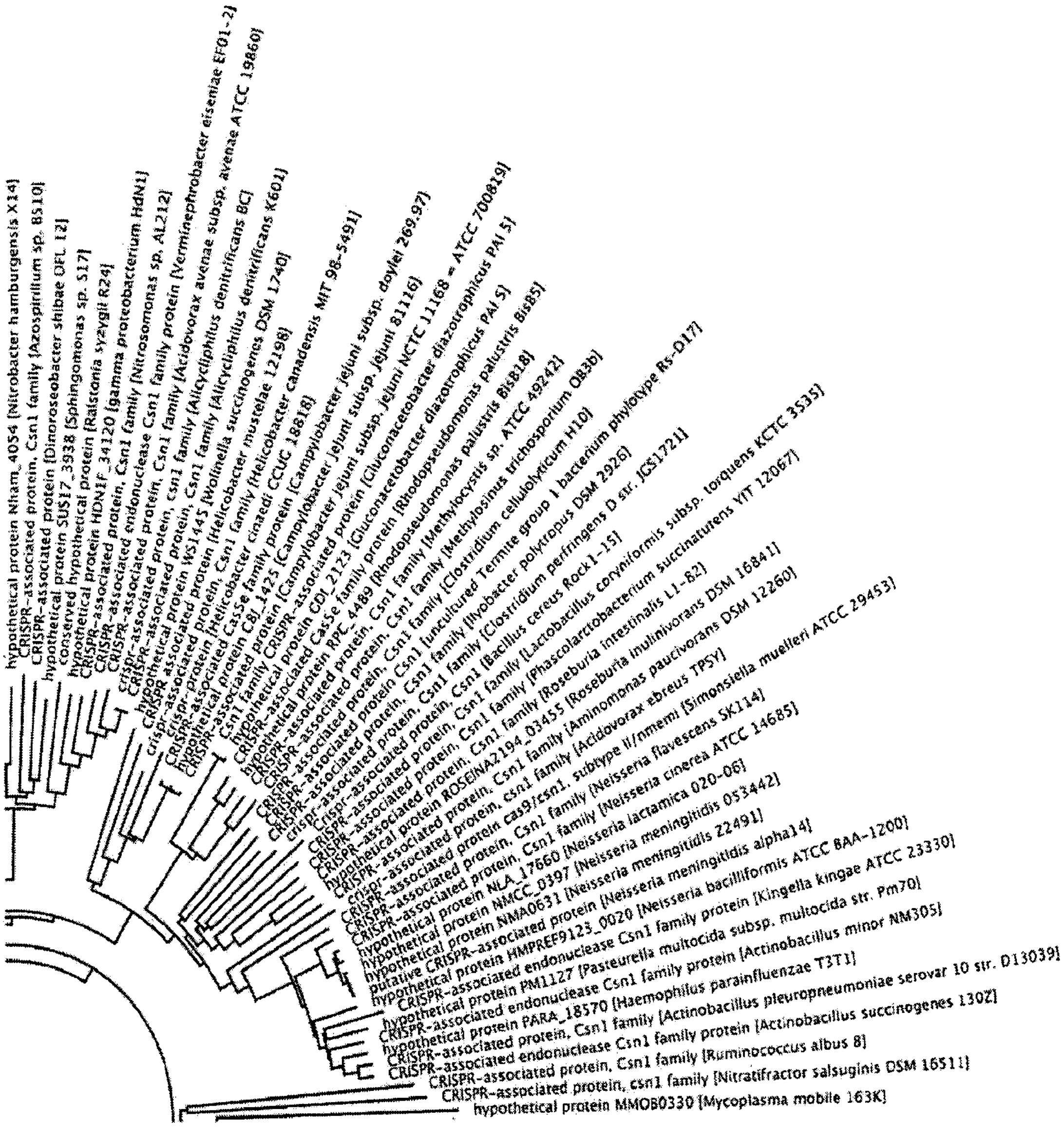

hypothetical protein Nham_4054 [Nitrobacter hamburgensis X14]
CRISPR-associated protein, Csn1 family [Azospirillum sp. B510]
CRISPR-associated protein [Dinoroseobacter shibae DFL 12]
hypothetical protein SUS17_3938 [Sphingomonas sp. S17]
conserved hypothetical protein [Ralstonia syzygii R24]
hypothetical protein HDN1F_34120 [gamma proteobacterium HdN1]
CRISPR-associated protein, Csn1 family [Nitrosomonas sp. AL212]
CRISPR-associated endonuclease Csn1 family protein [Verminephrobacter eiseniae EF01-2]
crispr-associated protein, Csn1 family [Acidovorax avenae subsp. avenae ATCC 19860]
CRISPR-associated protein, Csn1 family [Alicycliphilus denitrificans BC]
CRISPR-associated protein, Csn1 family [Alicycliphilus denitrificans K601]
hypothetical protein WS1445 [Wolinella succinogenes DSM 1740]
CRISPR associated protein [Helicobacter mustelae 12198]
crispr-associated protein, Csn1 family [Helicobacter cinaedi CCUG 18818]
crispr-protein [Helicobacter canadensis MIT 98-5491]
CRISPR-associated Cas5e family protein [Campylobacter jejuni subsp. doylei 269.97]
hypothetical protein CBJ_1425 [Campylobacter jejuni subsp. jejuni 81116]
CRISPR-associated protein [Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819]
Csn1 family CRISPR-associated protein [Gluconacetobacter diazotrophicus PAl 5]
hypothetical protein CDI_2123 [Gluconacetobacter diazotrophicus PAl 5]
CRISPR-associated Cas5e family protein [Rhodopseudomonas palustris BisB5]
hypothetical protein RPC_4489 [Rhodopseudomonas palustris BisB18]
CRISPR-associated protein, Csn1 family [Methylocystis sp. ATCC 49242]
CRISPR-associated protein, Csn1 family [Methylosinus trichosporium OB3b]
CRISPR-associated protein, Csn1 family [Clostridium cellulolyticum H10]
CRISPR-associated protein Csn1 [uncultured Termite group 1 bacterium phylotype Rs-D17]
CRISPR-associated protein, Csn1 family [Ilyobacter polytropus DSM 2926]
crispr-associated protein, Csn1 family [Clostridium perfringens D str. JGS1721]
Crispr-associated protein, Csn1 [Bacillus cereus Rock1-15]
CRISPR-associated protein, Csn1 family [Lactobacillus coryniformis subsp. torquens KCTC 3535]
CRISPR-associated protein, Csn1 family [Phascolarctobacterium succinatutens YIT 12067]
crispr-associated protein, Csn1 family [Roseburia intestinalis L1-82]
CRISPR-associated protein ROSEINA2194_03455 [Roseburia inulinivorans DSM 16841]
CRISPR-associated protein, Csn1 family [Aminomonas paucivorans DSM 12260]
hypothetical protein, csn1 family [Acidovorax ebreus TPSY]
CRISPR-associated protein cas9/csn1, subtype II/nmemi [Simonsiella muelleri ATCC 29453]
crispr-associated protein, Csn1 family [Neisseria flavescens SK114]
CRISPR-associated protein, Csn1 family [Neisseria cinerea ATCC 14685]
CRISPR-associated protein NLA_17660 [Neisseria lactamica 020-06]
hypothetical protein NMCC_0397 [Neisseria meningitidis 053442]
hypothetical protein NMA0631 [Neisseria meningitidis Z2491]
hypothetical CRISPR-associated protein [Neisseria meningitidis alpha14]
putative CRISPR-associated protein HMPREF9123_0020 [Neisseria bacilliformis ATCC BAA-1200]
hypothetical protein endonuclease Csn1 family protein [Kingella kingae ATCC 23330]
CRISPR-associated protein PM1127 [Pasteurella multocida subsp. multocida str. Pm70]
hypothetical protein endonuclease Csn1 family protein [Actinobacillus minor NM305]
CRISPR-associated protein PARA_18570 [Haemophilus parainfluenzae T3T1]
hypothetical protein, Csn1 family [Actinobacillus pleuropneumoniae serovar 10 str. D13039]
CRISPR-associated endonuclease Csn1 family protein [Actinobacillus succinogenes 130Z]
CRISPR-associated protein, Csn1 family [Ruminococcus albus 8]
CRISPR-associated protein, csn1 family [Nitratifractor salsuginis DSM 16511]
hypothetical protein MMOB0330 [Mycoplasma mobile 163K]

FIG. 19B

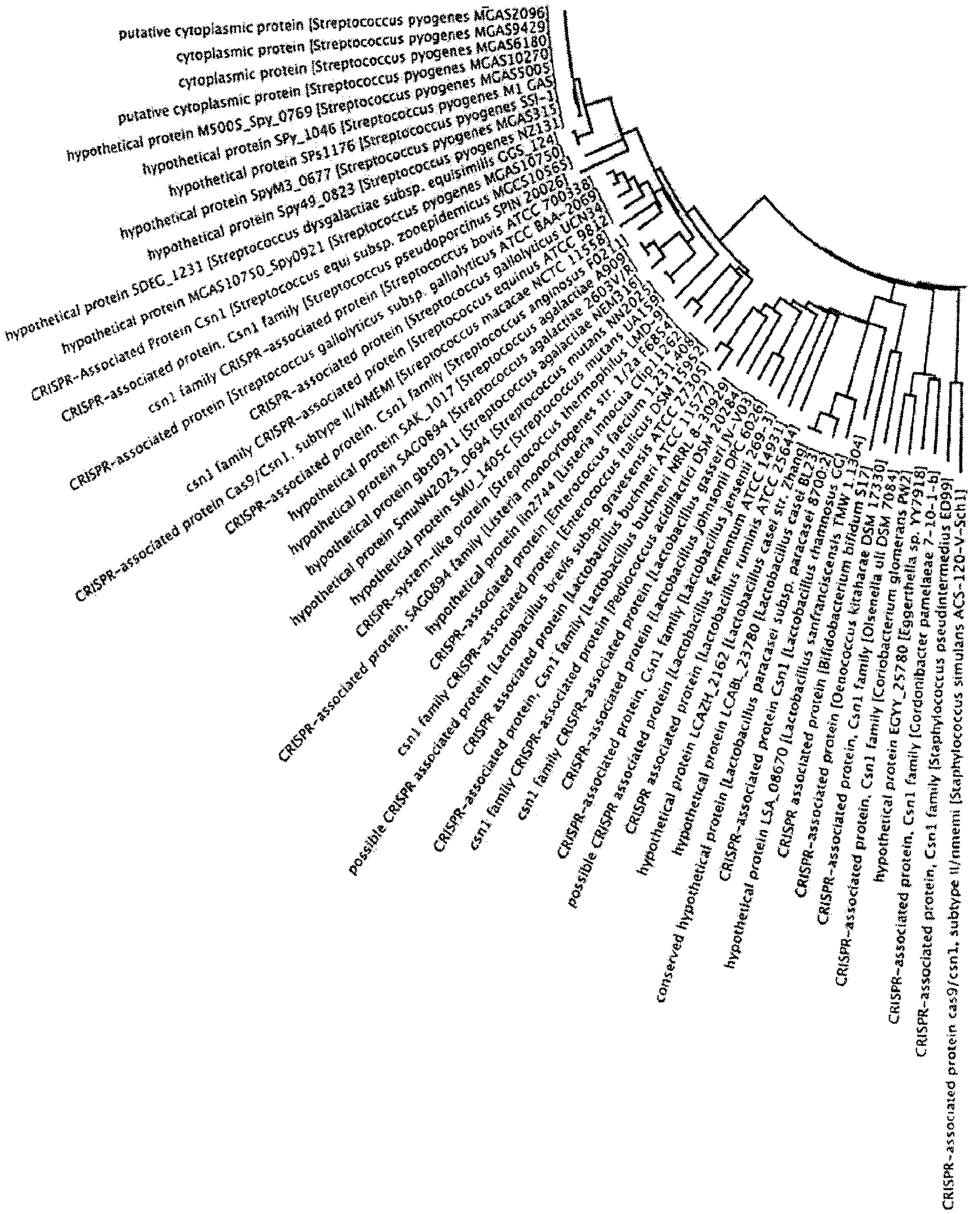

putative cytoplasmic protein [Streptococcus pyogenes MGAS2096]
cytoplasmic protein [Streptococcus pyogenes MGAS9429]
cytoplasmic protein [Streptococcus pyogenes MGAS6180]
putative cytoplasmic protein [Streptococcus pyogenes MGAS10270]
hypothetical protein M5005_Spy_0769 [Streptococcus pyogenes MGAS5005]
hypothetical protein SPy_1046 [Streptococcus pyogenes M1 GAS]
hypothetical protein SPs1176 [Streptococcus pyogenes SSI-1]
hypothetical protein SpyM3_0677 [Streptococcus pyogenes MGAS315]
hypothetical protein Spy49_0823 [Streptococcus pyogenes NZ131]
hypothetical protein SDEG_1231 [Streptococcus dysgalactiae subsp. equisimilis GGS_124]
hypothetical protein MGAS10750_Spy0921 [Streptococcus pyogenes MGAS10750]
CRISPR-Associated Protein Csn1 [Streptococcus equi subsp. zooepidemicus MGCS10565]
CRISPR-associated protein, Csn1 family [Streptococcus pseudoporcinus SPIN 20026]
csn1 family CRISPR-associated protein [Streptococcus bovis ATCC 700338]
CRISPR-associated protein [Streptococcus gallolyticus subsp. gallolyticus ATCC BAA-2069]
CRISPR-associated protein [Streptococcus gallolyticus UCN34]
csn1 family CRISPR-associated protein [Streptococcus equinus ATCC 9812]
CRISPR-associated protein Cas9/Csn1, subtype II/NMEMI [Streptococcus macacae NCTC 11558]
CRISPR-associated protein, Csn1 family [Streptococcus anginosus F0211]
hypothetical protein SAK_1017 [Streptococcus agalactiae A909]
hypothetical protein SAG0894 [Streptococcus agalactiae 2603V/R]
hypothetical protein gbs0911 [Streptococcus agalactiae NEM316]
hypothetical protein SmuNN2025_0694 [Streptococcus mutans NN2025]
hypothetical protein SMU_1405c [Streptococcus mutans UA159]
CRISPR-system-like protein [Streptococcus thermophilus LMD-9]
CRISPR-associated protein, SAG0894 family [Listeria monocytogenes str. 1/2a F6854]
hypothetical protein lin2744 [Listeria innocua Clip11262]
CRISPR-associated protein [Enterococcus faecium 1,231,408]
Csn1 family CRISPR-associated protein [Enterococcus italicus DSM 15952]
possible CRISPR associated protein [Lactobacillus brevis subsp. gravesensis ATCC 27305]
CRISPR associated protein [Lactobacillus buchneri ATCC 11577]
CRISPR-associated protein, Csn1 family [Lactobacillus buchneri NRRL B-30929]
csn1 family CRISPR-associated protein [Pediococcus acidilactici DSM 20284]
csn1 family CRISPR-associated protein [Lactobacillus gasseri JV-V03]
CRISPR-associated protein [Lactobacillus johnsonii DPC 6026]
CRISPR-associated protein, Csn1 family [Lactobacillus jensenii 269-3]
possible CRISPR associated protein [Lactobacillus fermentum ATCC 14931]
CRISPR associated protein [Lactobacillus ruminis ATCC 25644]
hypothetical protein LCAZH_2162 [Lactobacillus casei str. Zhang]
hypothetical protein LCABL_23780 [Lactobacillus casei BL23]
conserved hypothetical protein [Lactobacillus paracasei subsp. paracasei 8700:2]
CRISPR-associated protein Csn1 [Lactobacillus rhamnosus GG]
hypothetical protein LSA_08670 [Lactobacillus sanfranciscensis TMW 1.1304]
CRISPR associated protein [Bifidobacterium bifidum S17]
CRISPR-associated protein [Oenococcus kitaharae DSM 17330]
CRISPR-associated protein, Csn1 family [Olsenella uli DSM 7084]
CRISPR-associated protein, Csn1 family [Coriobacterium glomerans PW2]
hypothetical protein EGYY_25780 [Eggerthella sp. YY7918]
CRISPR-associated protein, Csn1 family [Gordonibacter pamelaeae 7-10-1-b]
CRISPR-associated protein, Csn1 family [Staphylococcus pseudintermedius ED99]
CRISPR-associated protein cas9/csn1, subtype II/nmemi [Staphylococcus simulans ACS-120-V-Sch1]

FIG. 19C

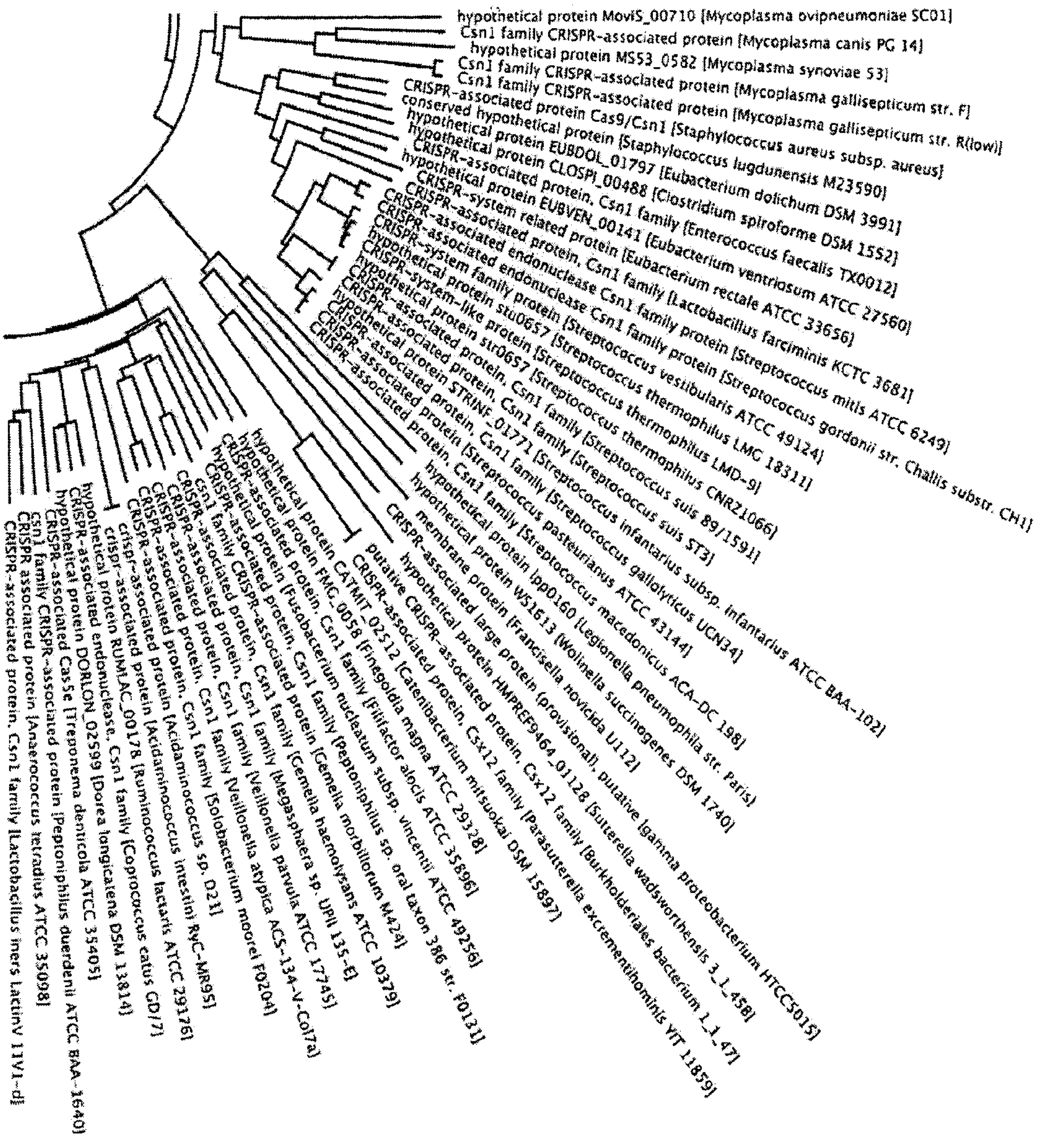

hypothetical protein MoviS_00710 [Mycoplasma ovipneumoniae SC01]
Csn1 family CRISPR-associated protein [Mycoplasma canis PG 14]
hypothetical protein MS53_0582 [Mycoplasma synoviae 53]
Csn1 family CRISPR-associated protein [Mycoplasma gallisepticum str. F]
Csn1 family CRISPR-associated protein [Mycoplasma gallisepticum str. R(low)]
CRISPR-associated protein Cas9/Csn1 [Staphylococcus aureus subsp. aureus]
conserved hypothetical protein [Staphylococcus lugdunensis M23590]
hypothetical protein EUBDOL_01797 [Eubacterium dolichum DSM 3991]
hypothetical protein CLOSPI_00488 [Clostridium spiroforme DSM 1552]
CRISPR-associated protein, Csn1 family [Enterococcus faecalis TX0012]
hypothetical protein EUBVEN_00141 [Eubacterium ventriosum ATCC 27560]
CRISPR-system related protein [Eubacterium rectale ATCC 33656]
CRISPR-associated protein, Csn1 family [Lactobacillus farciminis KCTC 3681]
CRISPR-associated endonuclease Csn1 family protein [Streptococcus mitis ATCC 6249]
CRISPR-associated endonuclease Csn1 family protein [Streptococcus gordonii str. Challis substr. CH1]
CRISPR-system family protein [Streptococcus vestibularis ATCC 49124]
hypothetical protein stu0657 [Streptococcus thermophilus LMG 18311]
CRISPR-system-like protein [Streptococcus thermophilus LMD-9]
hypothetical protein str0657 [Streptococcus thermophilus CNRZ1066]
CRISPR-associated protein, Csn1 family [Streptococcus suis 89/1591]
hypothetical protein STRINF_01771 [Streptococcus infantarius subsp. infantarius ATCC BAA-102]
CRISPR-associated protein [Streptococcus suis ST3]
CRISPR-associated protein, Csn1 family [Streptococcus gallolyticus UCN34]
CRISPR-associated protein, Csn1 family [Streptococcus pasteurianus ATCC 43144]
CRISPR-associated protein, Csn1 family [Streptococcus macedonicus ACA-DC 198]
hypothetical protein lpp0160 [Legionella pneumophila str. Paris]
hypothetical protein WS1613 [Wolinella succinogenes DSM 1740]
membrane protein [Francisella novicida U112]
CRISPR-associated large protein (provisional), putative [gamma proteobacterium HTCC5015]
hypothetical protein HMPREF9464_01128 [Sutterella wadsworthensis 3_1_45B]
putative CRISPR-associated protein, Csx12 family [Burkholderiales bacterium 1_1_47]
CRISPR-associated protein, Csx12 family [Parasutterella excrementihominis YIT 11859]
hypothetical protein CATMIT_02512 [Catenibacterium mitsuokai DSM 15897]
hypothetical protein FMG_0058 [Finegoldia magna ATCC 29328]
CRISPR-associated protein, Csn1 family [Filifactor alocis ATCC 35896]
hypothetical protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
CRISPR-associated protein, Csn1 family [Peptoniphilus sp. oral taxon 386 str. F0131]
Csn1 family CRISPR-associated protein [Gemella morbillorum M424]
CRISPR-associated protein, Csn1 family [Gemella haemolysans ATCC 10379]
CRISPR-associated protein, Csn1 family [Megasphaera sp. UPII 135-E]
CRISPR-associated protein, Csn1 family [Veillonella parvula ATCC 17745]
CRISPR-associated protein, Csn1 family [Veillonella atypica ACS-134-V-Col7a]
CRISPR-associated protein, Csn1 family [Solobacterium moorei F0204]
CRISPR-associated protein, Csn1 family [Acidaminococcus sp. D21]
CRISPR-associated protein [Acidaminococcus intestini RyC-MR95]
crispr-associated protein RUMLAC_00178 [Ruminococcus lactaris ATCC 29176]
crispr-associated endonuclease, Csn1 family [Coprococcus catus GD/7]
hypothetical protein DORLON_02599 [Dorea longicatena DSM 13814]
CRISPR-associated Cas5e [Treponema denticola ATCC 35405]
hypothetical protein [Peptoniphilus duerdenii ATCC BAA-1640]
Csn1 family CRISPR-associated protein
CRISPR associated protein [Anaerococcus tetradius ATCC 35098]
CRISPR-associated protein, Csn1 family [Lactobacillus iners LactinV 11V1-d]

FIG. 19D

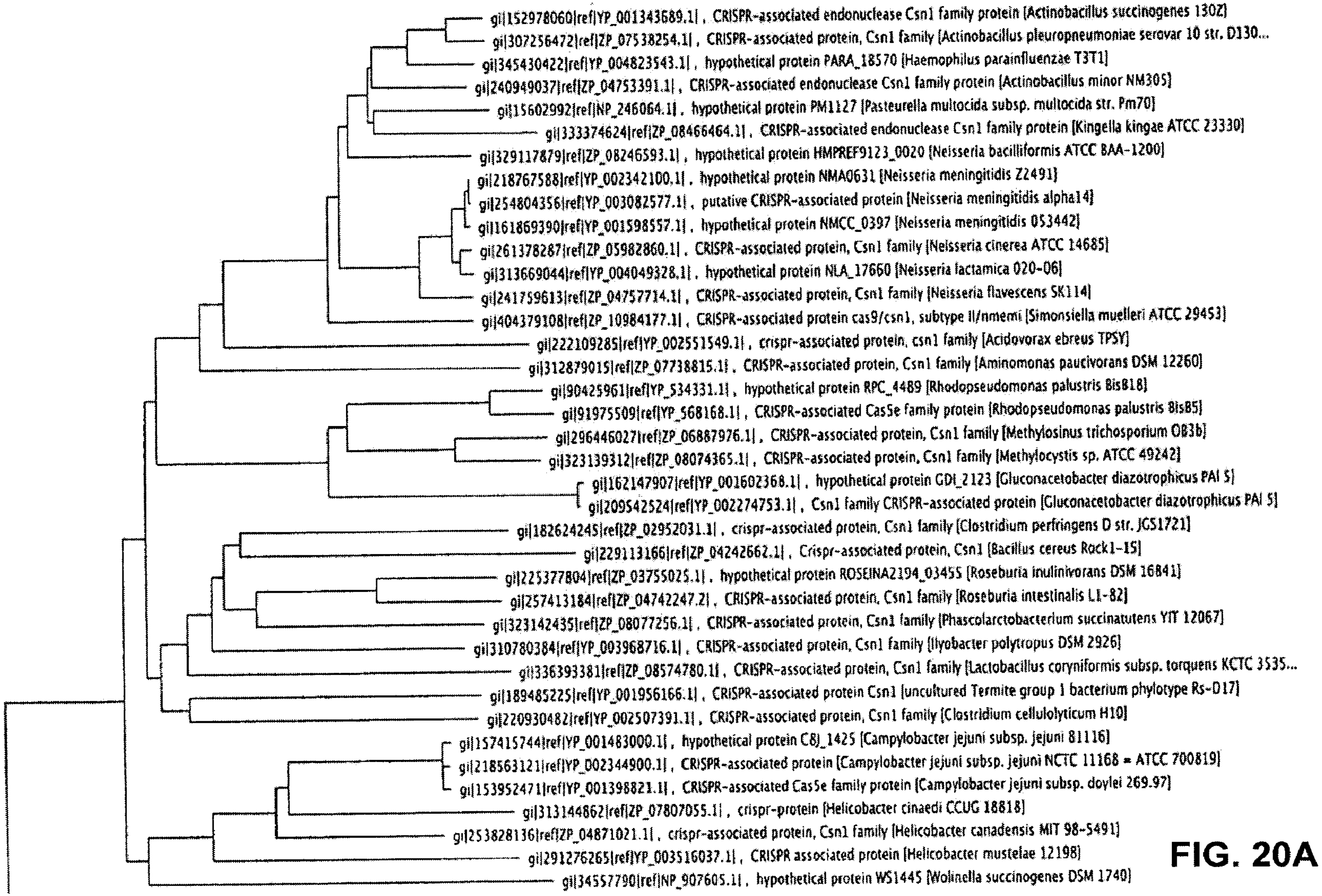
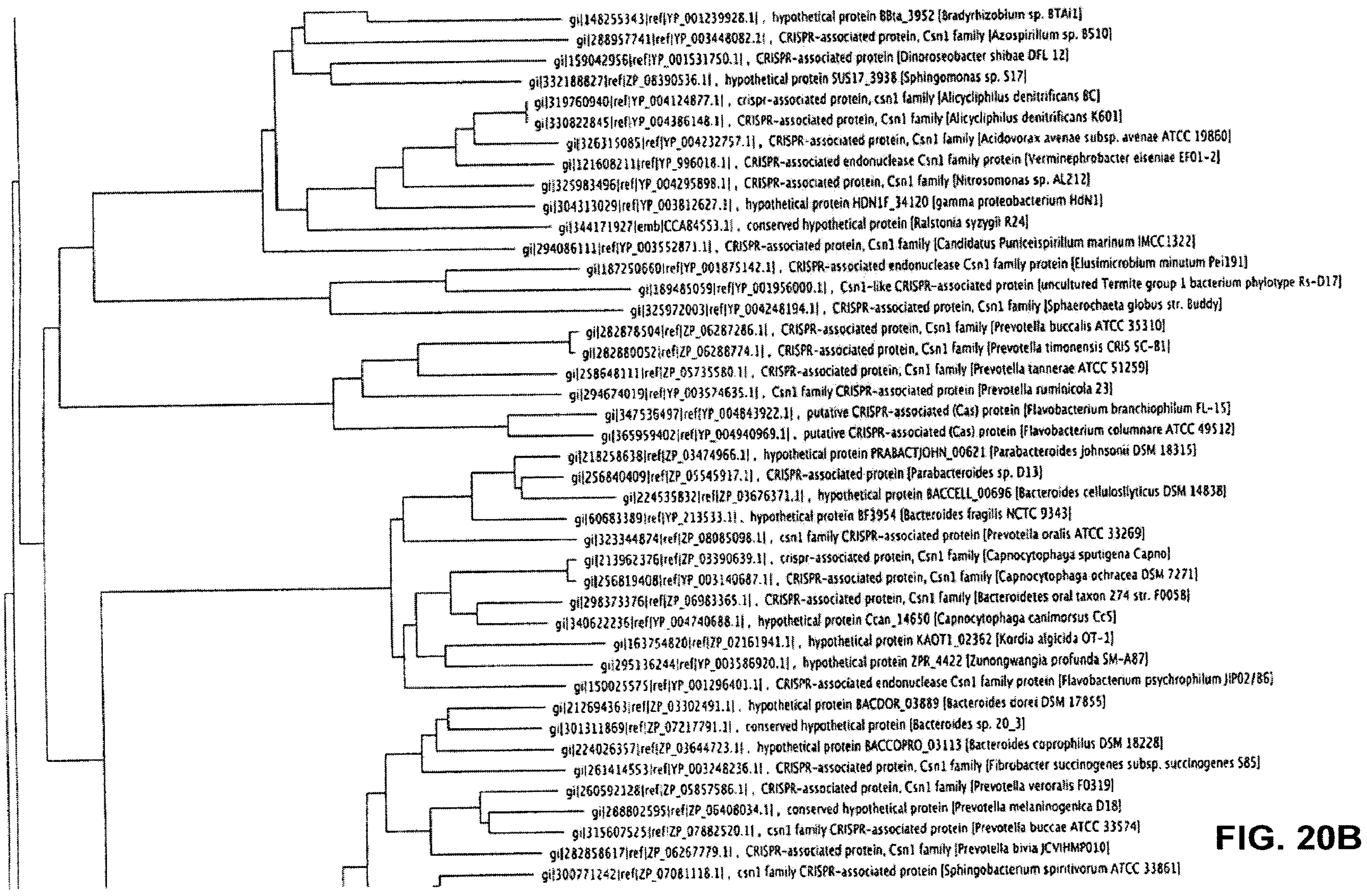

gi|152978060|ref|YP_001343689.1| , CRISPR-associated endonuclease Csn1 family protein [Actinobacillus succinogenes 130Z]
gi|307256472|ref|ZP_07538254.1| , CRISPR-associated protein, Csn1 family [Actinobacillus pleuropneumoniae serovar 10 str. D130...
gi|345430422|ref|YP_004823543.1| , hypothetical protein PARA_18570 [Haemophilus parainfluenzae T3T1]
gi|240949037|ref|ZP_04753391.1| , CRISPR-associated endonuclease Csn1 family protein [Actinobacillus minor NM305]
gi|15602992|ref|NP_246064.1| , hypothetical protein PM1127 [Pasteurella multocida subsp. multocida str. Pm70]
gi|333374624|ref|ZP_08466464.1| , CRISPR-associated endonuclease Csn1 family protein [Kingella kingae ATCC 23330]
gi|329117879|ref|ZP_08246593.1| , hypothetical protein HMPREF9123_0020 [Neisseria bacilliformis ATCC BAA-1200]
gi|218767588|ref|YP_002342100.1| , hypothetical protein NMA0631 [Neisseria meningitidis Z2491]
gi|254804356|ref|YP_003082577.1| , putative CRISPR-associated protein [Neisseria meningitidis alpha14]
gi|161869390|ref|YP_001598557.1| , hypothetical protein NMCC_0397 [Neisseria meningitidis 053442]
gi|261378287|ref|ZP_05982860.1| , CRISPR-associated protein, Csn1 family [Neisseria cinerea ATCC 14685]
gi|313669044|ref|YP_004049328.1| , hypothetical protein NLA_17660 [Neisseria lactamica 020-06]
gi|241759613|ref|ZP_04757714.1| , CRISPR-associated protein, Csn1 family [Neisseria flavescens SK114]
gi|404379108|ref|ZP_10984177.1| , CRISPR-associated protein cas9/csn1, subtype II/nmemi [Simonsiella muelleri ATCC 29453]
gi|222109285|ref|YP_002551549.1| , crispr-associated protein, csn1 family [Acidovorax ebreus TPSY]
gi|312879015|ref|ZP_07738815.1| , CRISPR-associated protein, Csn1 family [Aminomonas paucivorans DSM 12260]
gi|90425961|ref|YP_534331.1| , hypothetical protein RPC_4489 [Rhodopseudomonas palustris BisB18]
gi|91975509|ref|YP_568168.1| , CRISPR-associated Cas5e family protein [Rhodopseudomonas palustris BisB5]
gi|296446027|ref|ZP_06887976.1| , CRISPR-associated protein, Csn1 family [Methylosinus trichosporium OB3b]
gi|323139312|ref|ZP_08074365.1| , CRISPR-associated protein, Csn1 family [Methylocystis sp. ATCC 49242]
gi|162147907|ref|YP_001602368.1| , hypothetical protein GDI_2123 [Gluconacetobacter diazotrophicus PAl 5]
gi|209542524|ref|YP_002274753.1| , Csn1 family CRISPR-associated protein [Gluconacetobacter diazotrophicus PAl 5]
gi|182624245|ref|ZP_02952031.1| , crispr-associated protein, Csn1 family [Clostridium perfringens D str. JGS1721]
gi|229113166|ref|ZP_04242662.1| , Crispr-associated protein, Csn1 [Bacillus cereus Rock1-15]
gi|225377804|ref|ZP_03755025.1| , hypothetical protein ROSEINA2194_03455 [Roseburia inulinivorans DSM 16841]
gi|257413184|ref|ZP_04742247.2| , CRISPR-associated protein, Csn1 family [Roseburia intestinalis L1-82]
gi|323142435|ref|ZP_08077256.1| , CRISPR-associated protein, Csn1 family [Phascolarctobacterium succinatutens YIT 12067]
gi|310780384|ref|YP_003968716.1| , CRISPR-associated protein, Csn1 family [Ilyobacter polytropus DSM 2926]
gi|336393381|ref|ZP_08574780.1| , CRISPR-associated protein, Csn1 family [Lactobacillus coryniformis subsp. torquens KCTC 3535...
gi|189485225|ref|YP_001956166.1| , CRISPR-associated protein Csn1 [uncultured Termite group 1 bacterium phylotype Rs-D17]
gi|220930482|ref|YP_002507391.1| , CRISPR-associated protein, Csn1 family [Clostridium cellulolyticum H10]
gi|157415744|ref|YP_001483000.1| , hypothetical protein C8J_1425 [Campylobacter jejuni subsp. jejuni 81116]
gi|218563121|ref|YP_002344900.1| , CRISPR-associated protein [Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819]
gi|153952471|ref|YP_001398821.1| , CRISPR-associated Cas5e family protein [Campylobacter jejuni subsp. doylei 269.97]
gi|313144862|ref|ZP_07807055.1| , crispr-protein [Helicobacter cinaedi CCUG 18818]
gi|253828136|ref|ZP_04871021.1| , crispr-associated protein, Csn1 family [Helicobacter canadensis MIT 98-5491]
gi|291276265|ref|YP_003516037.1| , CRISPR associated protein [Helicobacter mustelae 12198]
gi|34557790|ref|NP_907605.1| , hypothetical protein WS1445 [Wolinella succinogenes DSM 1740]

FIG. 20A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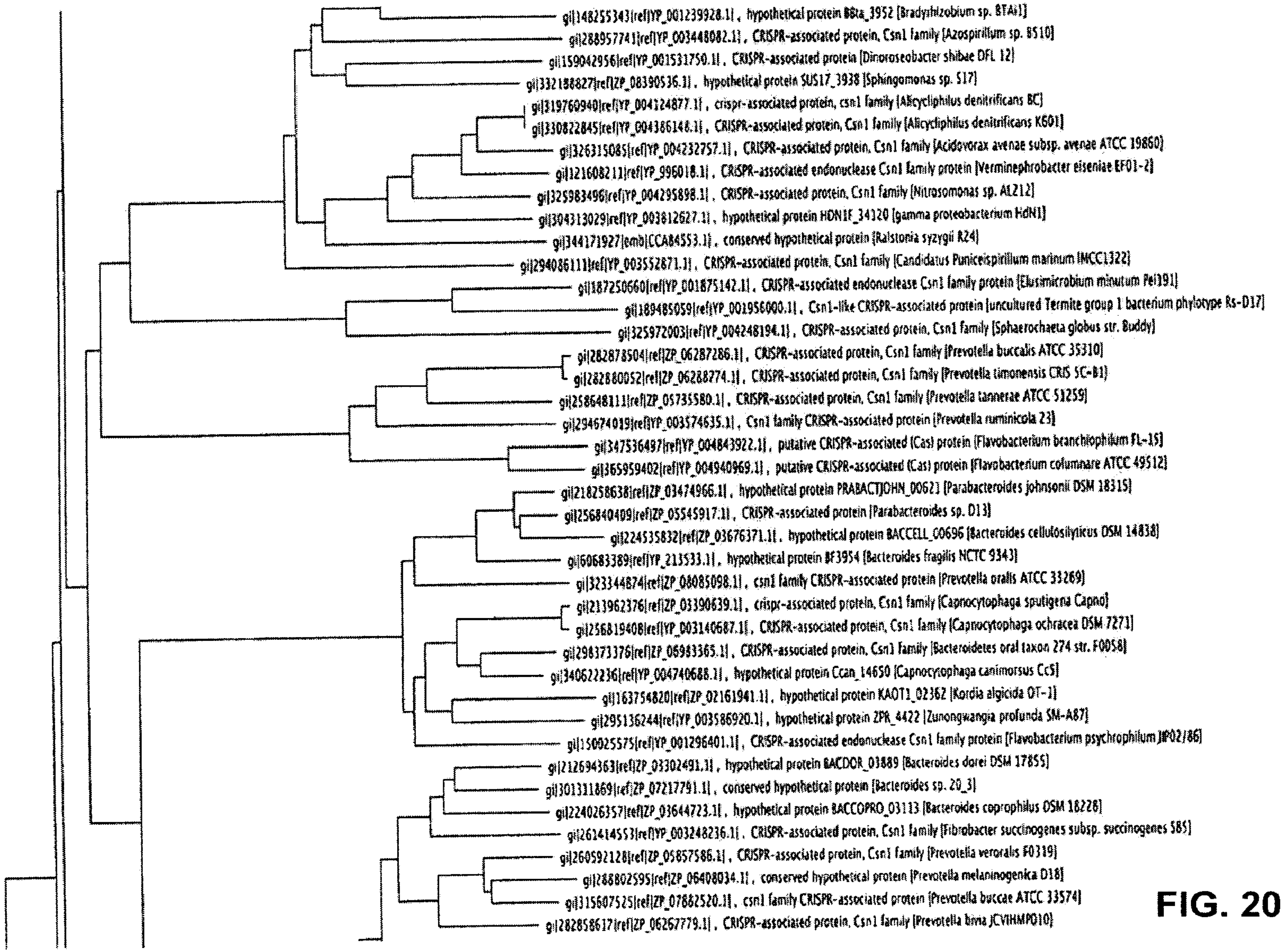
gi|288957741|ref|YP_003448082.1| , CRISPR-associated protein, Csn1 family [Azospirillum sp. B510]
gi|159042956|ref|YP_001531750.1| , CRISPR-associated protein [Dinoroseobacter shibae DFL 12]
gi|332188827|ref|ZP_08390536.1| , hypothetical protein SUS17_3938 [Sphingomonas sp. S17]
gi|319760940|ref|YP_004124877.1| , crispr-associated protein, csn1 family [Alicycliphilus denitrificans BC]
gi|330822845|ref|YP_004386148.1| , CRISPR-associated protein, Csn1 family [Alicycliphilus denitrificans K601]
gi|326315085|ref|YP_004232757.1| , CRISPR-associated protein, Csn1 family [Acidovorax avenae subsp. avenae ATCC 19860]
gi|121608211|ref|YP_996018.1| , CRISPR-associated endonuclease Csn1 family protein [Verminephrobacter eiseniae EF01-2]
gi|325983496|ref|YP_004295898.1| , CRISPR-associated protein, Csn1 family [Nitrosomonas sp. AL212]
gi|304313029|ref|YP_003812627.1| , hypothetical protein HDN1F_34120 [gamma proteobacterium HdN1]
gi|344171927|emb|CCA84553.1| , conserved hypothetical protein [Ralstonia syzygii R24]
gi|294086111|ref|YP_003552871.1| , CRISPR-associated protein, Csn1 family [Candidatus Puniceispirillum marinum IMCC1322]
gi|187250660|ref|YP_001875142.1| , CRISPR-associated endonuclease Csn1 family protein [Elusimicrobium minutum Pei191]
gi|189485059|ref|YP_001956000.1| , Csn1-like CRISPR-associated protein [uncultured Termite group 1 bacterium phylotype Rs-D17]
gi|325972003|ref|YP_004248194.1| , CRISPR-associated protein, Csn1 family [Sphaerochaeta globus str. Buddy]
gi|282878504|ref|ZP_06287286.1| , CRISPR-associated protein, Csn1 family [Prevotella buccalis ATCC 35310]
gi|282880052|ref|ZP_06288774.1| , CRISPR-associated protein, Csn1 family [Prevotella timonensis CRIS 5C-B1]
gi|258648111|ref|ZP_05735580.1| , CRISPR-associated protein, Csn1 family [Prevotella tannerae ATCC 51259]
gi|294674019|ref|YP_003574635.1| , Csn1 family CRISPR-associated protein [Prevotella ruminicola 23]
gi|347536497|ref|YP_004843922.1| , putative CRISPR-associated (Cas) protein [Flavobacterium branchiophilum FL-15]
gi|365959402|ref|YP_004940969.1| , putative CRISPR-associated (Cas) protein [Flavobacterium columnare ATCC 49512]
gi|218258638|ref|ZP_03474966.1| , hypothetical protein PRABACTJOHN_00621 [Parabacteroides johnsonii DSM 18315]
gi|256840409|ref|ZP_05545917.1| , CRISPR-associated protein [Parabacteroides sp. D13]
gi|224535832|ref|ZP_03676371.1| , hypothetical protein BACCELL_00696 [Bacteroides cellulosilyticus DSM 14838]
gi|60683389|ref|YP_213533.1| , hypothetical protein BF3954 [Bacteroides fragilis NCTC 9343]
gi|323344874|ref|ZP_08085098.1| , csn1 family CRISPR-associated protein [Prevotella oralis ATCC 33269]
gi|213962376|ref|ZP_03390639.1| , crispr-associated protein, Csn1 family [Capnocytophaga sputigena Capno]
gi|256819408|ref|YP_003140687.1| , CRISPR-associated protein, Csn1 family [Capnocytophaga ochracea DSM 7271]
gi|298373376|ref|ZP_06983365.1| , CRISPR-associated protein, Csn1 family [Bacteroidetes oral taxon 274 str. F0058]
gi|340622236|ref|YP_004740688.1| , hypothetical protein Ccan_14650 [Capnocytophaga canimorsus Cc5]
gi|163754820|ref|ZP_02161941.1| , hypothetical protein KAOT1_02362 [Kordia algicida OT-1]
gi|295136244|ref|YP_003586920.1| , hypothetical protein ZPR_4422 [Zunongwangia profunda SM-A87]
gi|150025575|ref|YP_001296401.1| , CRISPR-associated endonuclease Csn1 family protein [Flavobacterium psychrophilum JIP02/86]
gi|212694363|ref|ZP_03302491.1| , hypothetical protein BACDOR_03889 [Bacteroides dorei DSM 17855]
gi|301311869|ref|ZP_07217791.1| , conserved hypothetical protein [Bacteroides sp. 20_3]
gi|224026357|ref|ZP_03644723.1| , hypothetical protein BACCOPRO_03113 [Bacteroides coprophilus DSM 18228]
gi|261414553|ref|YP_003248236.1| , CRISPR-associated protein, Csn1 family [Fibrobacter succinogenes subsp. succinogenes S85]
gi|260592128|ref|ZP_05857586.1| , CRISPR-associated protein, Csn1 family [Prevotella veroralis F0319]
gi|288802595|ref|ZP_06408034.1| , conserved hypothetical protein [Prevotella melaninogenica D18]
gi|315607525|ref|ZP_07882520.1| , csn1 family CRISPR-associated protein [Prevotella buccae ATCC 33574]
gi|282858617|ref|ZP_06267779.1| , CRISPR-associated protein, Csn1 family [Prevotella bivia JCVIHMP010]
gi|300771242|ref|ZP_07081118.1| , csn1 family CRISPR-associated protein [Sphingobacterium spiritivorum ATCC 33861]

FIG. 20B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gi|288957741|ref|YP_003448082.1| , CRISPR-associated protein, Csn1 family [Azospirillum sp. B510]
gi|159042956|ref|YP_001531750.1| , CRISPR-associated protein [Dinoroseobacter shibae DFL 12]
gi|332188827|ref|ZP_08390536.1| , hypothetical protein SUS17_3938 [Sphingomonas sp. S17]
gi|319760940|ref|YP_004124877.1| , crispr-associated protein, csn1 family [Alicycliphilus denitrificans BC]
gi|330822845|ref|YP_004386148.1| , CRISPR-associated protein, Csn1 family [Alicycliphilus denitrificans K601]
gi|326315085|ref|YP_004232757.1| , CRISPR-associated protein, Csn1 family [Acidovorax avenae subsp. avenae ATCC 19860]
gi|121608211|ref|YP_996018.1| , CRISPR-associated endonuclease Csn1 family protein [Verminephrobacter eiseniae EF01-2]
gi|325983496|ref|YP_004295898.1| , CRISPR-associated protein, Csn1 family [Nitrosomonas sp. AL212]
gi|304313029|ref|YP_003812627.1| , hypothetical protein HDN1F_34120 [gamma proteobacterium HdN1]
gi|344171927|emb|CCA84553.1| , conserved hypothetical protein [Ralstonia syzygii R24]
gi|294086111|ref|YP_003552871.1| , CRISPR-associated protein, Csn1 family [Candidatus Puniceispirillum marinum IMCC1322]
gi|187250660|ref|YP_001875142.1| , CRISPR-associated endonuclease Csn1 family protein [Elusimicrobium minutum Pei191]
gi|189485059|ref|YP_001956000.1| , Csn1-like CRISPR-associated protein [uncultured Termite group 1 bacterium phylotype Rs-D17]
gi|325972003|ref|YP_004248194.1| , CRISPR-associated protein, Csn1 family [Sphaerochaeta globus str. Buddy]
gi|282878504|ref|ZP_06287286.1| , CRISPR-associated protein, Csn1 family [Prevotella buccalis ATCC 35310]
gi|282880052|ref|ZP_06288774.1| , CRISPR-associated protein, Csn1 family [Prevotella timonensis CRIS 5C-B1]
gi|258648111|ref|ZP_05735580.1| , CRISPR-associated protein, Csn1 family [Prevotella tannerae ATCC 51259]
gi|294674019|ref|YP_003574635.1| , Csn1 family CRISPR-associated protein [Prevotella ruminicola 23]
gi|347536497|ref|YP_004843922.1| , putative CRISPR-associated (Cas) protein [Flavobacterium branchiophilum FL-15]
gi|365959402|ref|YP_004940969.1| , putative CRISPR-associated (Cas) protein [Flavobacterium columnare ATCC 49512]
gi|218258638|ref|ZP_03474966.1| , hypothetical protein PRABACTJOHN_00621 [Parabacteroides johnsonii DSM 18315]
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gi|224535832|ref|ZP_03676371.1| , hypothetical protein BACCELL_00696 [Bacteroides cellulosilyticus DSM 14838]
gi|60683389|ref|YP_213533.1| , hypothetical protein BF3954 [Bacteroides fragilis NCTC 9343]
gi|323344874|ref|ZP_08085098.1| , csn1 family CRISPR-associated protein [Prevotella oralis ATCC 33269]
gi|213962376|ref|ZP_03390639.1| , crispr-associated protein, Csn1 family [Capnocytophaga sputigena Capno]
gi|256819408|ref|YP_003140687.1| , CRISPR-associated protein, Csn1 family [Capnocytophaga ochracea DSM 7271]
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gi|340622236|ref|YP_004740688.1| , hypothetical protein Ccan_14650 [Capnocytophaga canimorsus Cc5]
gi|163754820|ref|ZP_02161941.1| , hypothetical protein KAOT1_02362 [Kordia algicida OT-1]
gi|295136244|ref|YP_003586920.1| , hypothetical protein ZPR_4422 [Zunongwangia profunda SM-A87]
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gi|224026357|ref|ZP_03644723.1| , hypothetical protein BACCOPRO_03113 [Bacteroides coprophilus DSM 18228]
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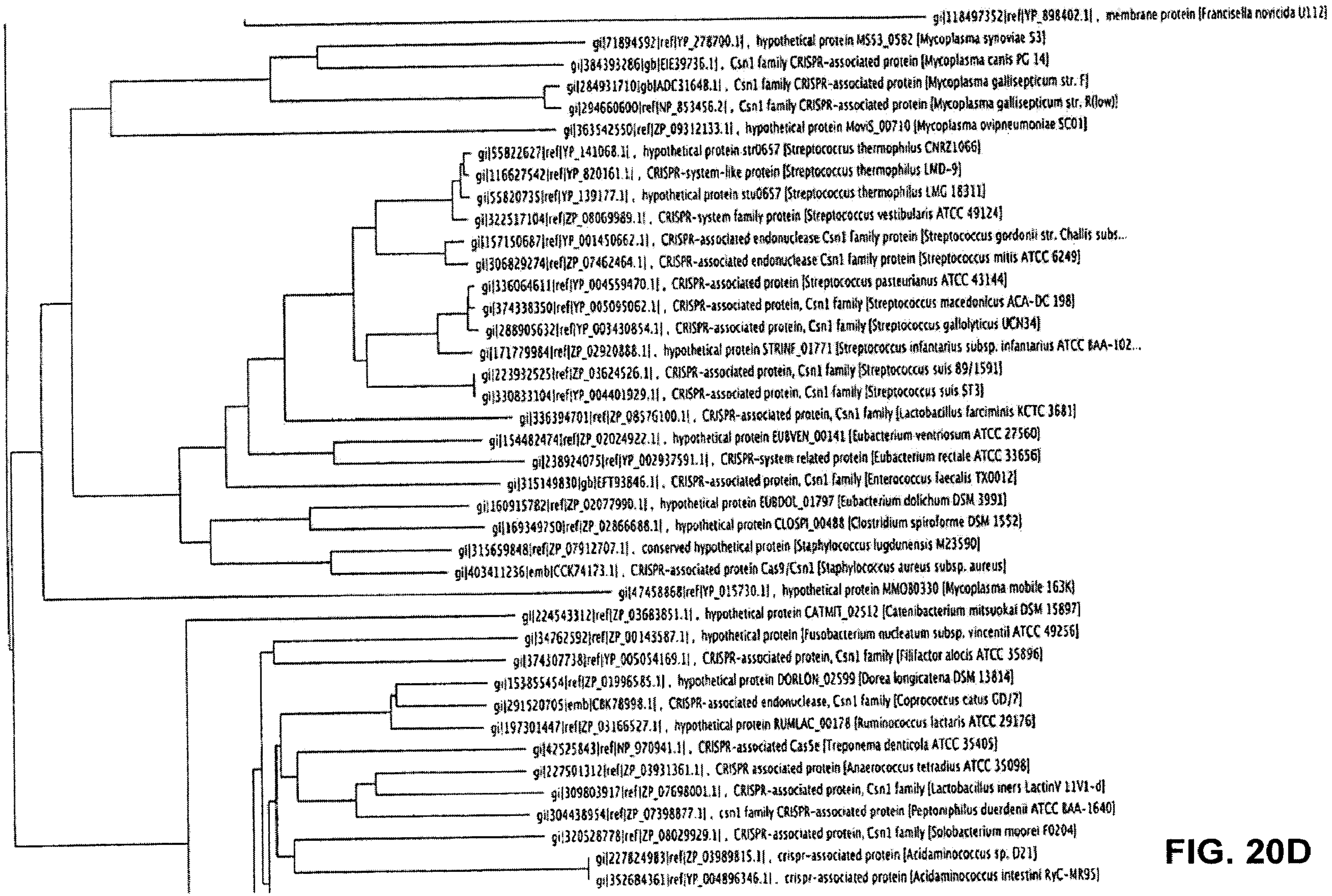
gi|260592128|ref|ZP_05857586.1| , CRISPR-associated protein, Csn1 family [Prevotella veroralis F0319]
gi|288802595|ref|ZP_06408034.1| , conserved hypothetical protein [Prevotella melaninogenica D18]
gi|315607525|ref|ZP_07882520.1| , csn1 family CRISPR-associated protein [Prevotella buccae ATCC 33574]
gi|282858617|ref|ZP_06267779.1| , CRISPR-associated protein, Csn1 family [Prevotella bivia JCVIHMP010]

FIG. 20C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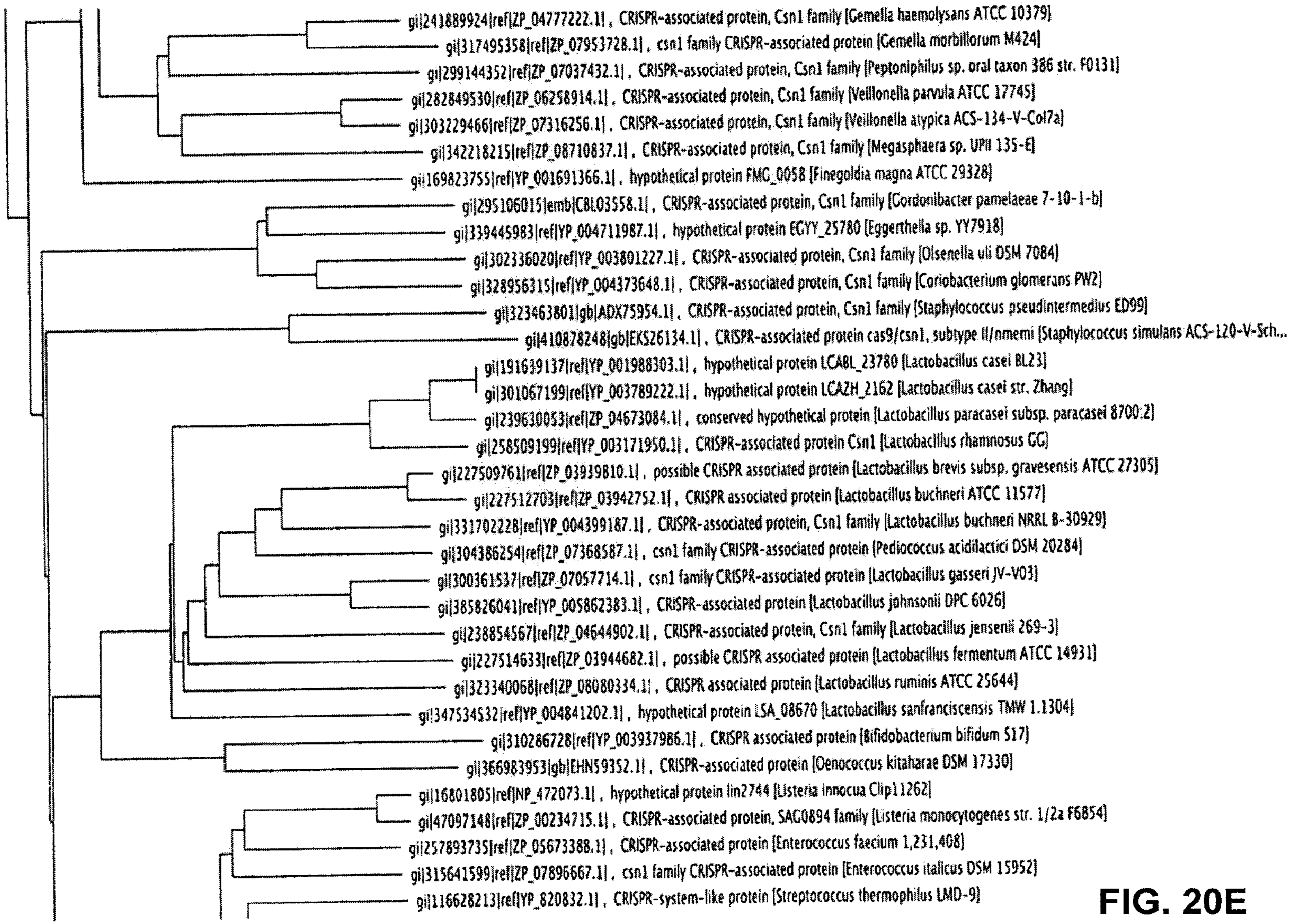
gi|71894592|ref|YP_278700.1| , hypothetical protein MS53_0582 [Mycoplasma synoviae 53]
gi|384393286|gb|EIE39736.1| , Csn1 family CRISPR-associated protein [Mycoplasma canis PG 14]
gi|284931710|gb|ADC31648.1| , Csn1 family CRISPR-associated protein [Mycoplasma gallisepticum str. F]
gi|294660600|ref|NP_853456.2| , Csn1 family CRISPR-associated protein [Mycoplasma gallisepticum str. R(low)]
gi|363542550|ref|ZP_09312133.1| , hypothetical protein MoviS_00710 [Mycoplasma ovipneumoniae SC01]
gi|55822627|ref|YP_141068.1| , hypothetical protein str0657 [Streptococcus thermophilus CNRZ1066]
gi|116627542|ref|YP_820161.1| , CRISPR-system-like protein [Streptococcus thermophilus LMD-9]
gi|55820735|ref|YP_139177.1| , hypothetical protein stu0657 [Streptococcus thermophilus LMG 18311]
gi|322517104|ref|ZP_08069989.1| , CRISPR-system family protein [Streptococcus vestibularis ATCC 49124]
gi|157150687|ref|YP_001450662.1| , CRISPR-associated endonuclease Csn1 family protein [Streptococcus gordonii str. Challis subs...
gi|306829274|ref|ZP_07462464.1| , CRISPR-associated endonuclease Csn1 family protein [Streptococcus mitis ATCC 6249]
gi|336064611|ref|YP_004559470.1| , CRISPR-associated protein [Streptococcus pasteurianus ATCC 43144]
gi|374338350|ref|YP_005095062.1| , CRISPR-associated protein, Csn1 family [Streptococcus macedonicus ACA-DC 198]
gi|288905632|ref|YP_003430854.1| , CRISPR-associated protein, Csn1 family [Streptococcus gallolyticus UCN34]
gi|171779984|ref|ZP_02920888.1| , hypothetical protein STRINF_01771 [Streptococcus infantarius subsp. infantarius ATCC BAA-102...
gi|223932525|ref|ZP_03624526.1| , CRISPR-associated protein, Csn1 family [Streptococcus suis 89/1591]
gi|330833104|ref|YP_004401929.1| , CRISPR-associated protein, Csn1 family [Streptococcus suis ST3]
gi|336394701|ref|ZP_08576100.1| , CRISPR-associated protein, Csn1 family [Lactobacillus farciminis KCTC 3681]
gi|154482474|ref|ZP_02024922.1| , hypothetical protein EUBVEN_00141 [Eubacterium ventriosum ATCC 27560]
gi|238924075|ref|YP_002937591.1| , CRISPR-system related protein [Eubacterium rectale ATCC 33656]
gi|315149830|gb|EFT93846.1| , CRISPR-associated protein, Csn1 family [Enterococcus faecalis TX0012]
gi|160915782|ref|ZP_02077990.1| , hypothetical protein EUBDOL_01797 [Eubacterium dolichum DSM 3991]
gi|169349750|ref|ZP_02866688.1| , hypothetical protein CLOSPI_00488 [Clostridium spiroforme DSM 1552]
gi|315659848|ref|ZP_07912707.1| , conserved hypothetical protein [Staphylococcus lugdunensis M23590]
gi|403411236|emb|CCK74173.1| , CRISPR-associated protein Cas9/Csn1 [Staphylococcus aureus subsp. aureus]
gi|47458868|ref|YP_015730.1| , hypothetical protein MMOB0330 [Mycoplasma mobile 163K]
gi|224543312|ref|ZP_03683851.1| , hypothetical protein CATMIT_02512 [Catenibacterium mitsuokai DSM 15897]
gi|34762592|ref|ZP_00143587.1| , hypothetical protein]Fusobacterium nucleatum subsp. vincentii ATCC 49256]
gi|374307738|ref|YP_005054169.1| , CRISPR-associated protein, Csn1 family [Filifactor alocis ATCC 35896]
gi|153855454|ref|ZP_01996585.1| , hypothetical protein DORLON_02599 [Dorea longicatena DSM 13814]
gi|291520705|emb|CBK78998.1| , CRISPR-associated endonuclease, Csn1 family [Coprococcus catus GD/7]
gi|197301447|ref|ZP_03166527.1| , hypothetical protein RUMLAC_00178 [Ruminococcus lactaris ATCC 29176]
gi|42525843|ref|NP_970941.1| , CRISPR-associated Cas5e [Treponema denticola ATCC 35405]
gi|227501312|ref|ZP_03931361.1| , CRISPR associated protein [Anaerococcus tetradius ATCC 35098]
gi|309803917|ref|ZP_07698001.1| , CRISPR-associated protein, Csn1 family [Lactobacillus iners LactinV 11V1-d]
gi|304438954|ref|ZP_07398877.1| , csn1 family CRISPR-associated protein [Peptoniphilus duerdenii ATCC BAA-1640]
gi|320528778|ref|ZP_08029929.1| , CRISPR-associated protein, Csn1 family [Solobacterium moorei F0204]
gi|227824983|ref|ZP_03989815.1| , crispr-associated protein [Acidaminococcus sp. D21]
gi|352684361|ref|YP_004896346.1| , crispr-associated protein [Acidaminococcus intestini RyC-MR95]

FIG. 20D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gi|299144352|ref|ZP_07037432.1| , CRISPR-associated protein, Csn1 family [Peptoniphilus sp. oral taxon 386 str. F0131]
gi|282849530|ref|ZP_06258914.1| , CRISPR-associated protein, Csn1 family [Veillonella parvula ATCC 17745]
gi|303229466|ref|ZP_07316256.1| , CRISPR-associated protein, Csn1 family [Veillonella atypica ACS-134-V-Col7a]
gi|342218215|ref|ZP_08710837.1| , CRISPR-associated protein, Csn1 family [Megasphaera sp. UPII 135-E]
gi|169823755|ref|YP_001691366.1| , hypothetical protein FMG_0058 [Finegoldia magna ATCC 29328]
gi|295106015|emb|CBL03558.1| , CRISPR-associated protein, Csn1 family [Gordonibacter pamelaeae 7-10-1-b]
gi|339445983|ref|YP_004711987.1| , hypothetical protein EGYY_25780 [Eggerthella sp. YY7918]
gi|302336020|ref|YP_003801227.1| , CRISPR-associated protein, Csn1 family [Olsenella uli DSM 7084]
gi|328956315|ref|YP_004373648.1| , CRISPR-associated protein, Csn1 family [Coriobacterium glomerans PW2]
gi|323463801|gb|ADX75954.1| , CRISPR-associated protein, Csn1 family [Staphylococcus pseudintermedius ED99]
gi|410878248|gb|EKS26134.1| , CRISPR-associated protein cas9/csn1, subtype II/nmemi [Staphylococcus simulans ACS-120-V-Sch...
gi|191639137|ref|YP_001988303.1| , hypothetical protein LCABL_23780 [Lactobacillus casei BL23]
gi|301067199|ref|YP_003789222.1| , hypothetical protein LCAZH_2162 [Lactobacillus casei str. Zhang]
gi|239630053|ref|ZP_04673084.1| , conserved hypothetical protein [Lactobacillus paracasei subsp. paracasei 8700:2]
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gi|227509761|ref|ZP_03939810.1| , possible CRISPR associated protein [Lactobacillus brevis subsp. gravesensis ATCC 27305]
gi|227512703|ref|ZP_03942752.1| , CRISPR associated protein [Lactobacillus buchneri ATCC 11577]
gi|331702228|ref|YP_004399187.1| , CRISPR-associated protein, Csn1 family [Lactobacillus buchneri NRRL B-30929]
gi|304386254|ref|ZP_07368587.1| , csn1 family CRISPR-associated protein [Pediococcus acidilactici DSM 20284]
gi|300361537|ref|ZP_07057714.1| , csn1 family CRISPR-associated protein [Lactobacillus gasseri JV-V03]
gi|385826041|ref|YP_005862383.1| , CRISPR-associated protein [Lactobacillus johnsonii DPC 6026]
gi|238854567|ref|ZP_04644902.1| , CRISPR-associated protein, Csn1 family [Lactobacillus jensenii 269-3]
gi|227514633|ref|ZP_03944682.1| , possible CRISPR associated protein [Lactobacillus fermentum ATCC 14931]
gi|323340068|ref|ZP_08080334.1| , CRISPR associated protein [Lactobacillus ruminis ATCC 25644]
gi|347534532|ref|YP_004841202.1| , hypothetical protein LSA_08670 [Lactobacillus sanfranciscensis TMW 1.1304]
gi|310286728|ref|YP_003937986.1| , CRISPR associated protein [Bifidobacterium bifidum S17]
gi|366983953|gb|EHN59352.1| , CRISPR-associated protein [Oenococcus kitaharae DSM 17330]
gi|16801805|ref|NP_472073.1| , hypothetical protein lin2744 [Listeria innocua Clip11262]
gi|47097148|ref|ZP_00234715.1| , CRISPR-associated protein, SAG0894 family [Listeria monocytogenes str. 1/2a F6854]
gi|257893735|ref|ZP_05673388.1| , CRISPR-associated protein [Enterococcus faecium 1,231,408]
gi|315641599|ref|ZP_07896667.1| , csn1 family CRISPR-associated protein [Enterococcus italicus DSM 15952]
gi|116628213|ref|YP_820832.1| , CRISPR-system-like protein [Streptococcus thermophilus LMD-9]

FIG. 20E

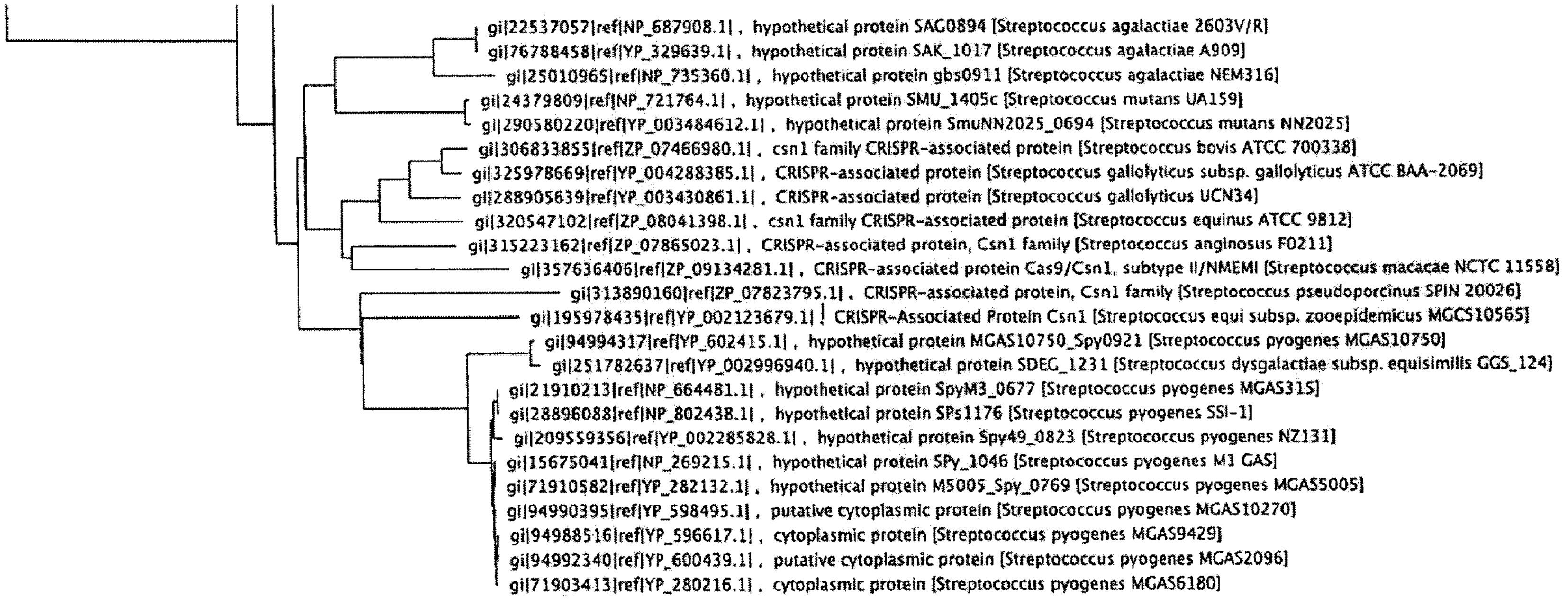

gi|22537057|ref|NP_687908.1| , hypothetical protein SAG0894 [Streptococcus agalactiae 2603V/R]
gi|76788458|ref|YP_329639.1| , hypothetical protein SAK_1017 [Streptococcus agalactiae A909]
gi|25010965|ref|NP_735360.1| , hypothetical protein gbs0911 [Streptococcus agalactiae NEM316]
gi|24379809|ref|NP_721764.1| , hypothetical protein SMU_1405c [Streptococcus mutans UA159]
gi|290580220|ref|YP_003484612.1| , hypothetical protein SmuNN2025_0694 [Streptococcus mutans NN2025]
gi|306833855|ref|ZP_07466980.1| , csn1 family CRISPR-associated protein [Streptococcus bovis ATCC 700338]
gi|325978669|ref|YP_004288385.1| , CRISPR-associated protein [Streptococcus gallolyticus subsp. gallolyticus ATCC BAA-2069]
gi|288905639|ref|YP_003430861.1| , CRISPR-associated protein [Streptococcus gallolyticus UCN34]
gi|320547102|ref|ZP_08041398.1| , csn1 family CRISPR-associated protein [Streptococcus equinus ATCC 9812]
gi|315223162|ref|ZP_07865023.1| , CRISPR-associated protein, Csn1 family [Streptococcus anginosus F0211]
gi|357636406|ref|ZP_09134281.1| , CRISPR-associated protein Cas9/Csn1, subtype II/NMEMI [Streptococcus macacae NCTC 11558]
gi|313890160|ref|ZP_07823795.1| , CRISPR-associated protein, Csn1 family [Streptococcus pseudoporcinus SPIN 20026]
gi|195978435|ref|YP_002123679.1| , CRISPR-Associated Protein Csn1 [Streptococcus equi subsp. zooepidemicus MGCS10565]
gi|94994317|ref|YP_602415.1| , hypothetical protein MGAS10750_Spy0921 [Streptococcus pyogenes MGAS10750]
gi|251782637|ref|YP_002996940.1| , hypothetical protein SDEG_1231 [Streptococcus dysgalactiae subsp. equisimilis GGS_124]
gi|21910213|ref|NP_664481.1| , hypothetical protein SpyM3_0677 [Streptococcus pyogenes MGAS315]
gi|28896088|ref|NP_802438.1| , hypothetical protein SPs1176 [Streptococcus pyogenes SSI-1]
gi|209559356|ref|YP_002285828.1| , hypothetical protein Spy49_0823 [Streptococcus pyogenes NZ131]
gi|15675041|ref|NP_269215.1| , hypothetical protein SPy_1046 [Streptococcus pyogenes M1 GAS]
gi|71910582|ref|YP_282132.1| , hypothetical protein M5005_Spy_0769 [Streptococcus pyogenes MGAS5005]
gi|94990395|ref|YP_598495.1| , putative cytoplasmic protein [Streptococcus pyogenes MGAS10270]
gi|94988516|ref|YP_596617.1| , cytoplasmic protein [Streptococcus pyogenes MGAS9429]
gi|94992340|ref|YP_600439.1| , putative cytoplasmic protein [Streptococcus pyogenes MGAS2096]
gi|71903413|ref|YP_280216.1| , cytoplasmic protein [Streptococcus pyogenes MGAS6180]

FIG. 20F

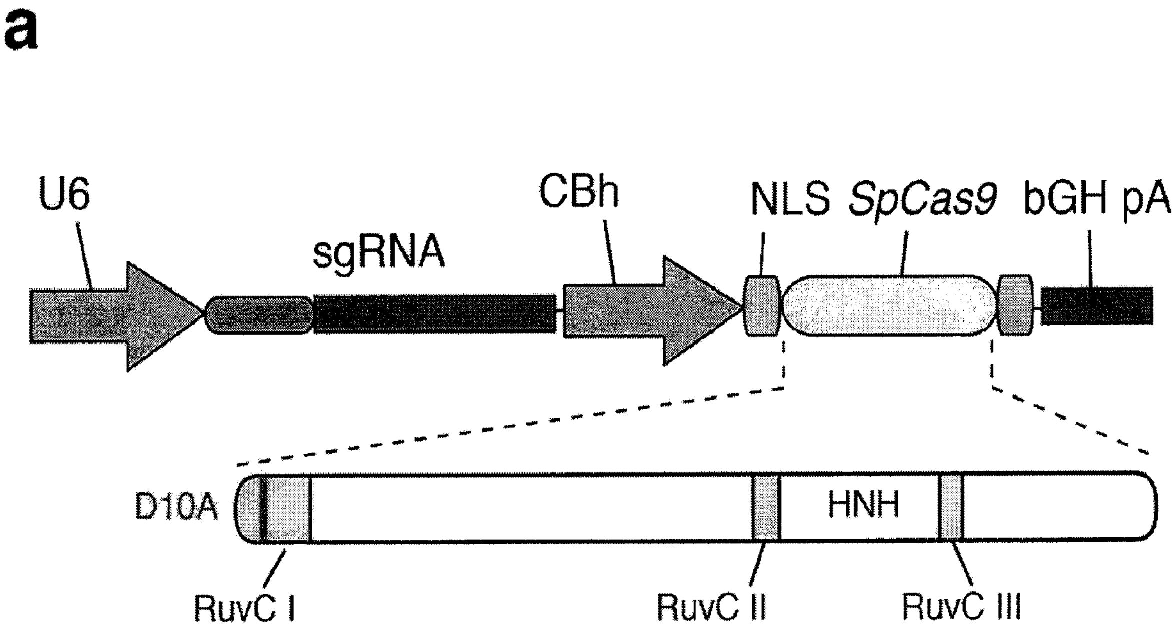

a
U6
sgRNA
CBh
NLS *SpCas9* bGH pA
D10A
HNH
RuvC I
RuvC II
RuvC III

FIG. 21A

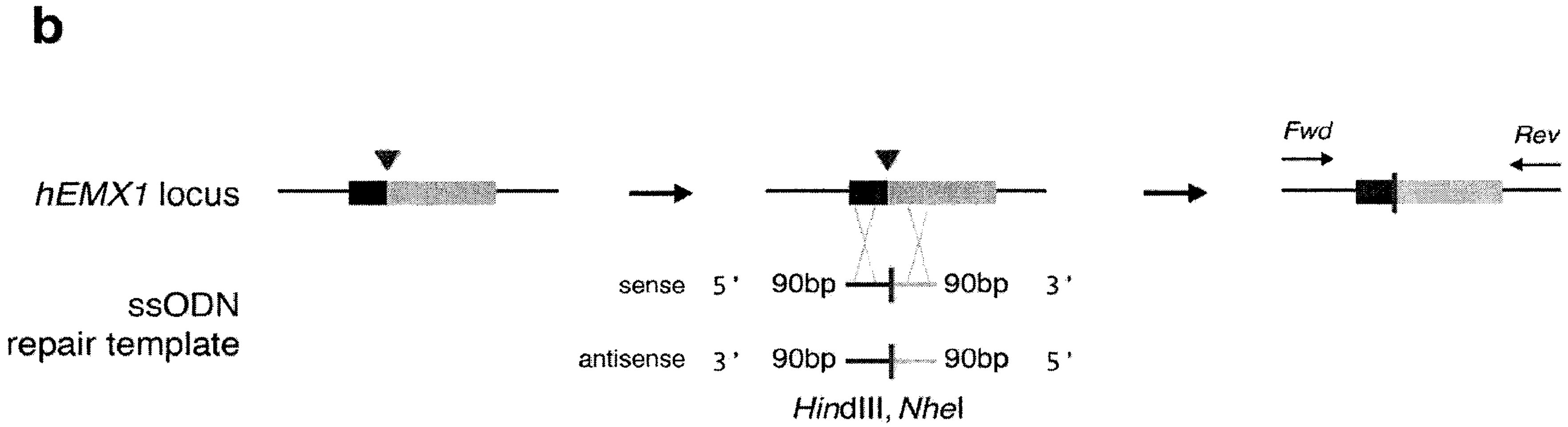

b
hEMX1 locus
ssODN repair template
sense
5'
90bp
90bp
3'
antisense
3'
90bp
90bp
5'
HindIII, NheI
Fwd
Rev

FIG. 21B

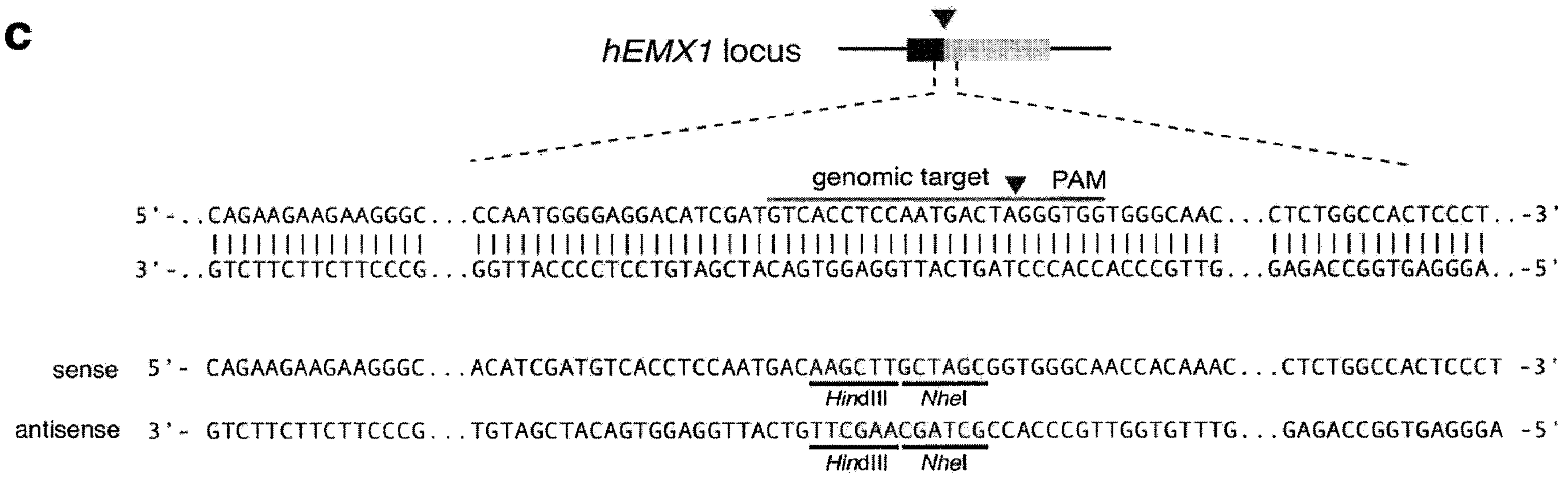

c
hEMX1 locus
genomic target
PAM
5'-..CAGAAGAAGAAGGGC...CCAATGGGGAGGACATCGATGTCACCTCCAATGACTAGGGTGGTGGGCAAC...CTCTGGCCACTCCCT..-3'
3'-..GTCTTCTTCTTCCCG...GGTTACCCCTCCTGTAGCTACAGTGGAGGTTACTGATCCCACCACCCGTTG...GAGACCGGTGAGGGA..-5'
sense 5'- CAGAAGAAGAAGGGC...ACATCGATGTCACCTCCAATGACAAGCTTGCTAGCGGTGGGCAACCACAAAC...CTCTGGCCACTCCCT -3'
HindIII
NheI
antisense 3'- GTCTTCTTCTTCCCG...TGTAGCTACAGTGGAGGTTACTGTTCGAACGATCGCCACCCGTTGGTGTTTG...GAGACCGGTGAGGGA -5'
HindIII
NheI

FIG. 21C

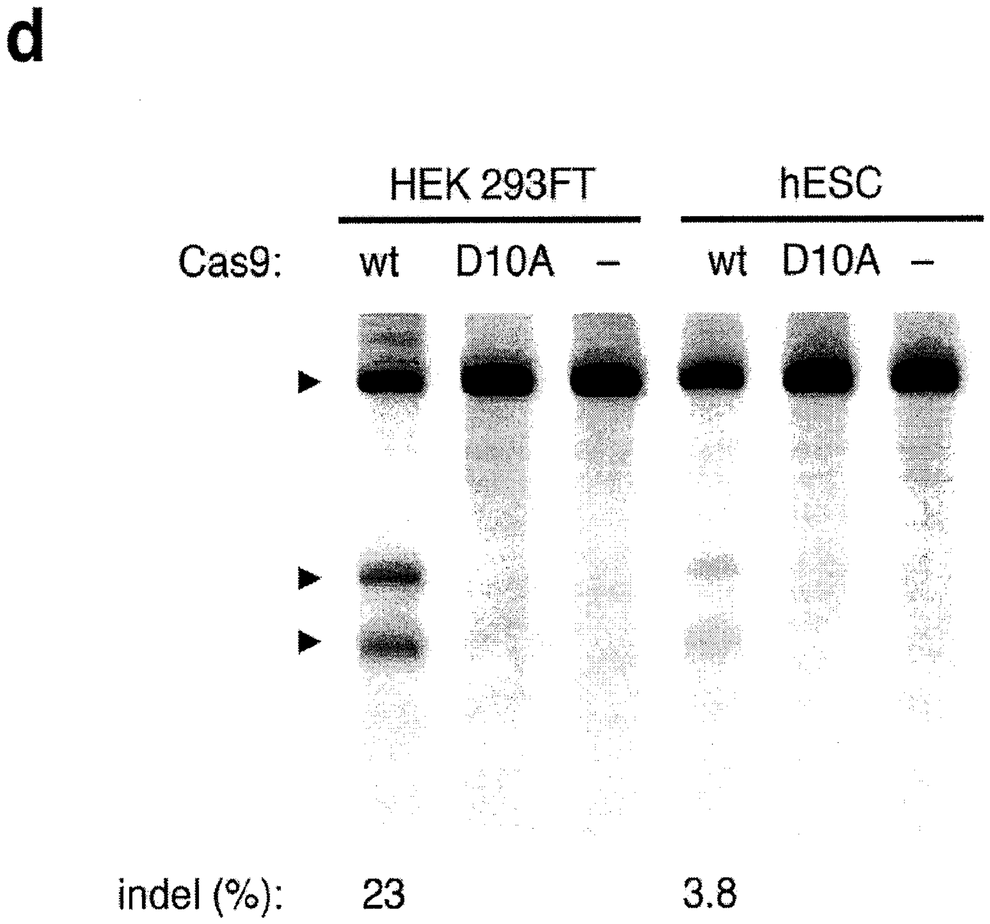


FIG. 21D

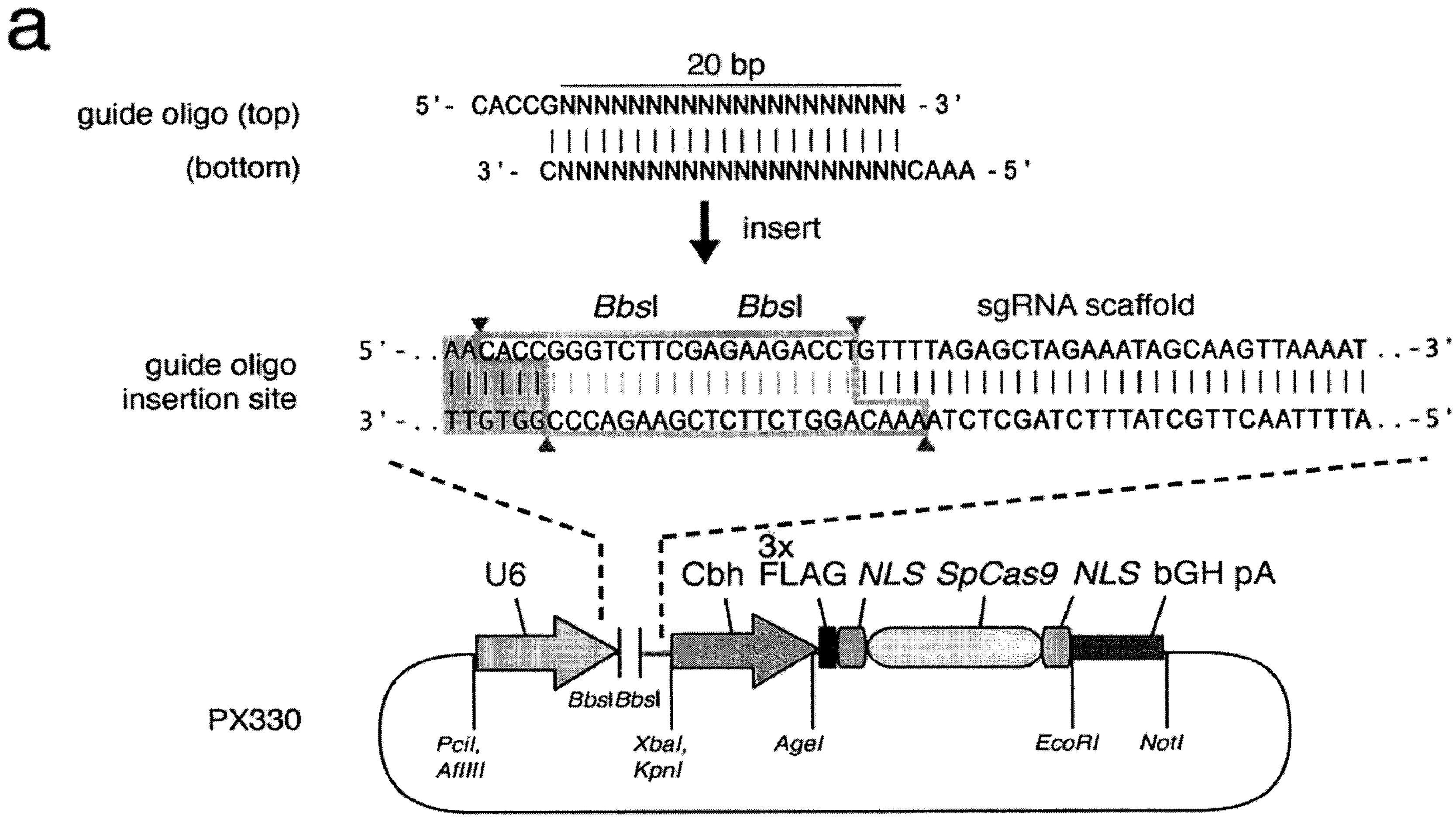

a
20 bp
guide oligo (top)
5'- CACCGNNNNNNNNNNNNNNNNNNNN - 3'
(bottom)
3'- CNNNNNNNNNNNNNNNNNNNNCAAA - 5'
insert
BbsI
BbsI
sgRNA scaffold
guide oligo insertion site
5'-..AACACCGGGTCTTCGAGAAGACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAT..-3'
3'-..TTGTGGCCCAGAAGCTCTTCTGGACAAAATCTCGATCTTTATCGTTCAATTTTA..-5'
U6
Cbh
3x FLAG
NLS
SpCas9
NLS
bGH pA
PX330
BbsI BbsI
PciI, AflIII
XbaI, KpnI
AgeI
EcoRI
NotI

FIG. 22A

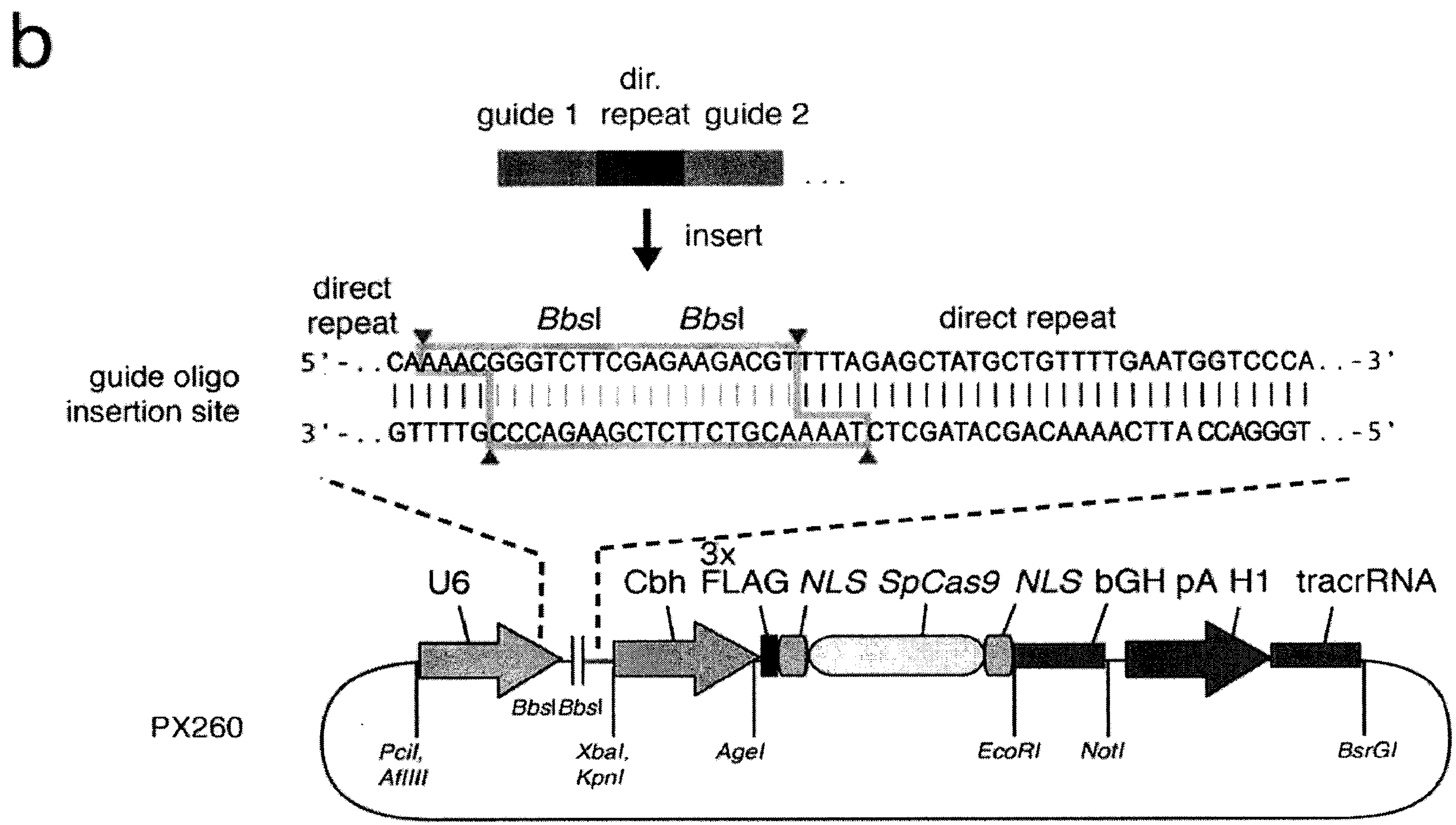

b
dir.
guide 1 repeat guide 2
...
insert
guide oligo
insertion site
direct
repeat
BbsI
BbsI
direct repeat
5'-..CAAAACGGGTCTTCGAGAAGACGTTTTAGAGCTATGCTGTTTTGAATGGTCCCA..-3'
3'-..GTTTTGCCCAGAAGCTCTTCTGCAAAATCTCGATACGACAAAACTTACCAGGGT..-5'
PX260
U6
Cbh
3x
FLAG
NLS
SpCas9
NLS
bGH pA
H1
tracrRNA
BbsI BbsI
PciI,
AflIII
XbaI,
KpnI
AgeI
EcoRI
NotI
BsrGI

FIG. 22B

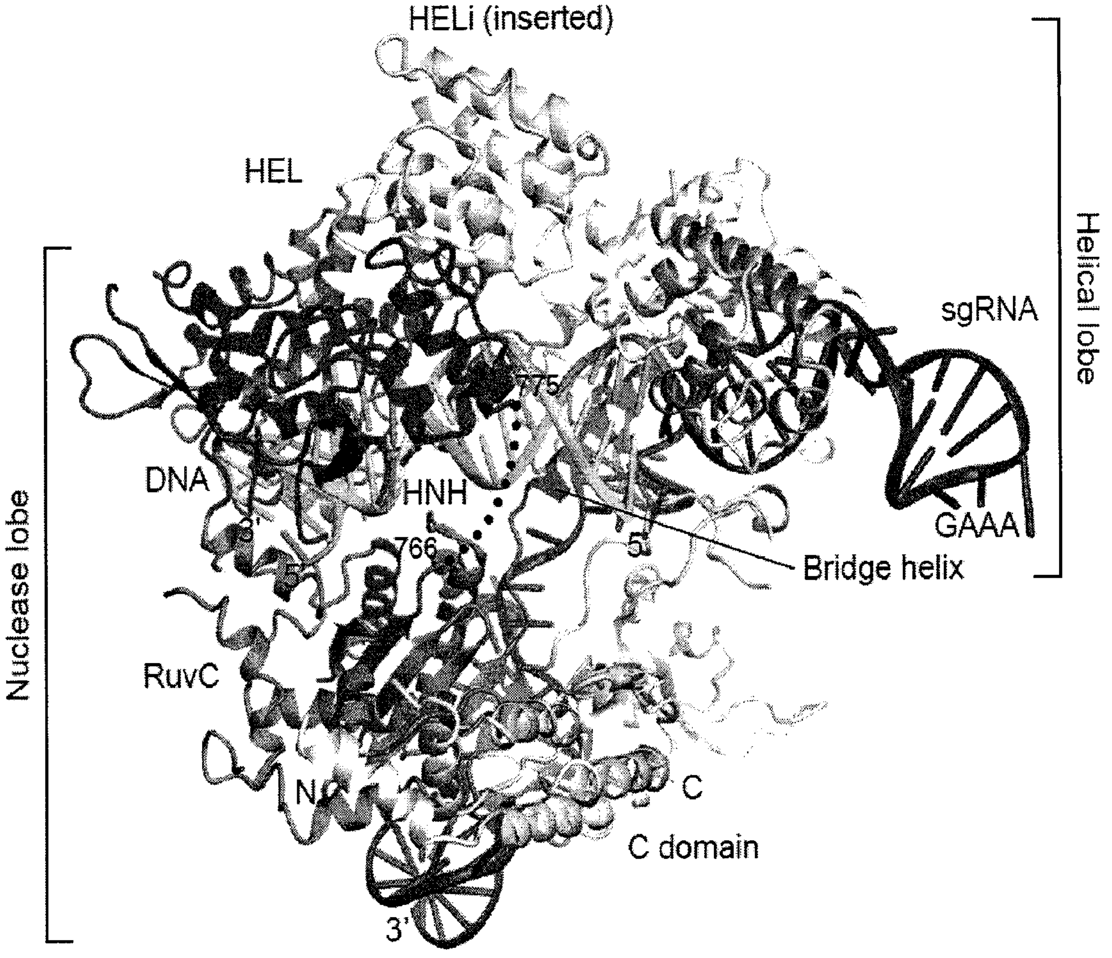

HELi (inserted)
HEL
Helical lobe
sgRNA
775
DNA
HNH
3'
5'
766
5'
GAAA
Bridge helix
Nuclease lobe
RuvC
N
C
C domain
3'

FIG. 23A

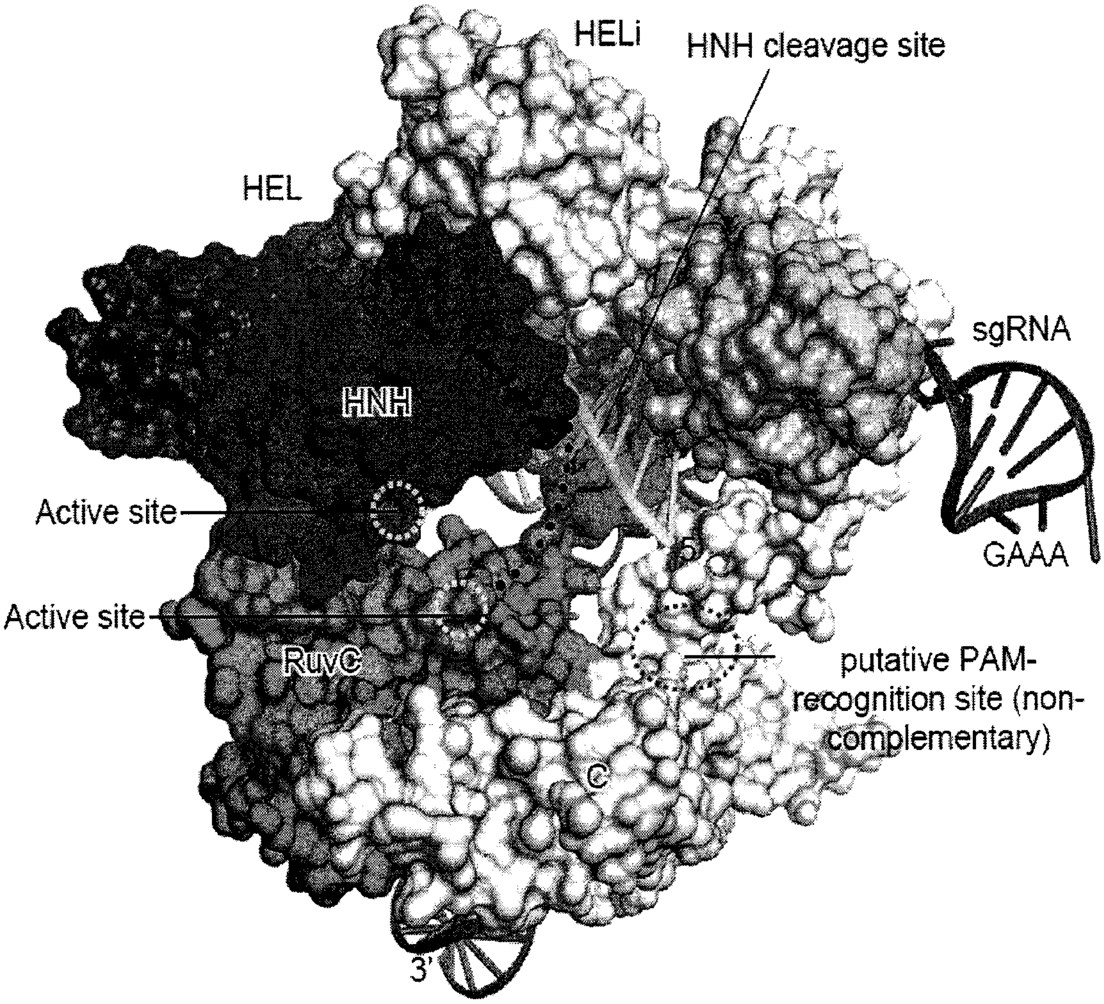

HELi
HNH cleavage site
HEL
sgRNA
HNH
Active site
5'
GAAA
Active site
RuvC
putative PAM-recognition site (non-complementary)
C
3'

FIG. 23B

FIG. 23C

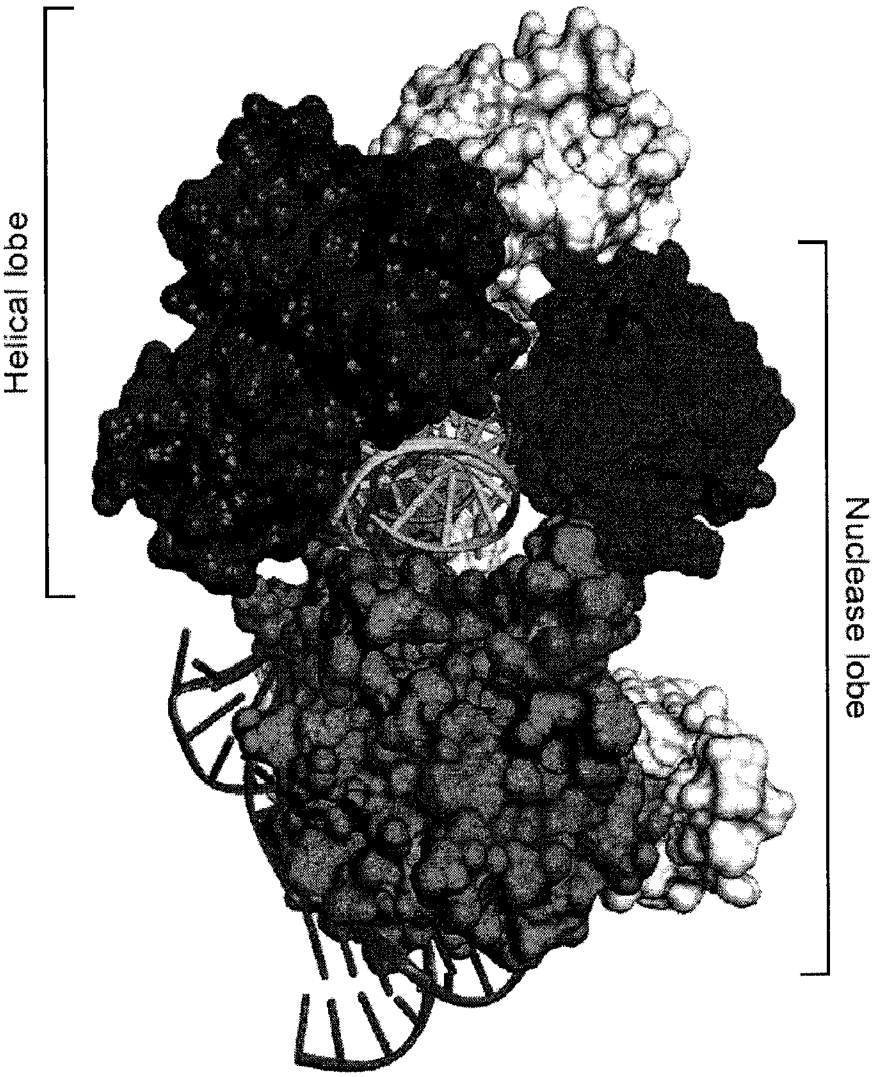


FIG. 23D

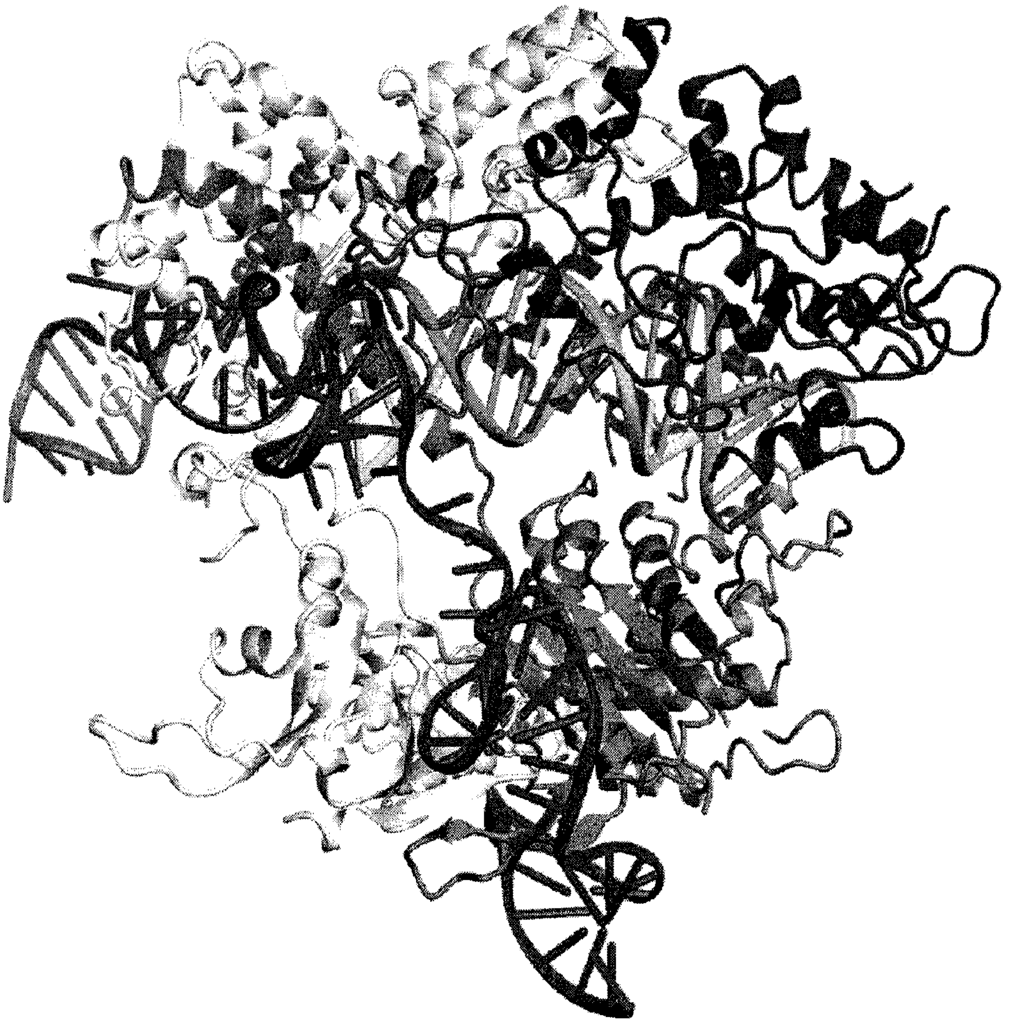


FIG. 23E

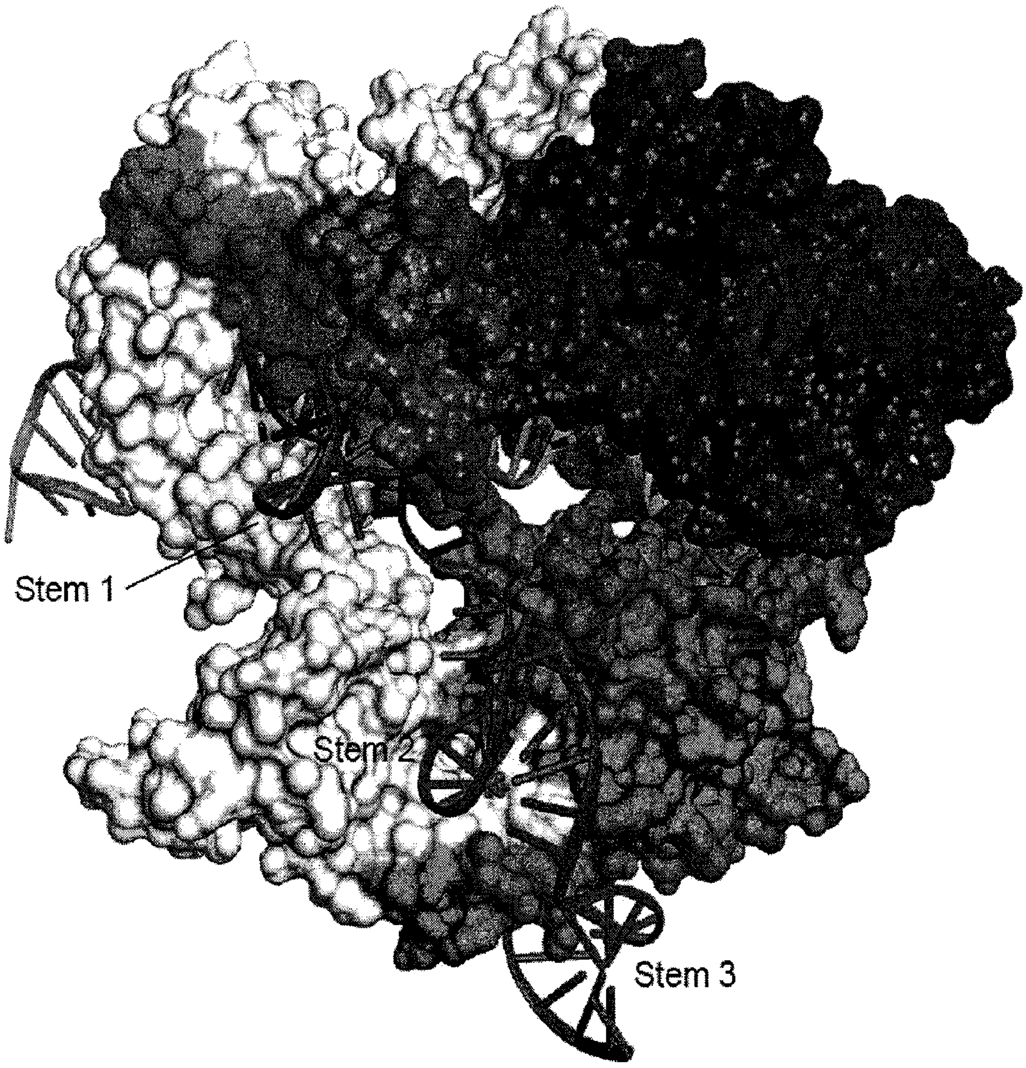
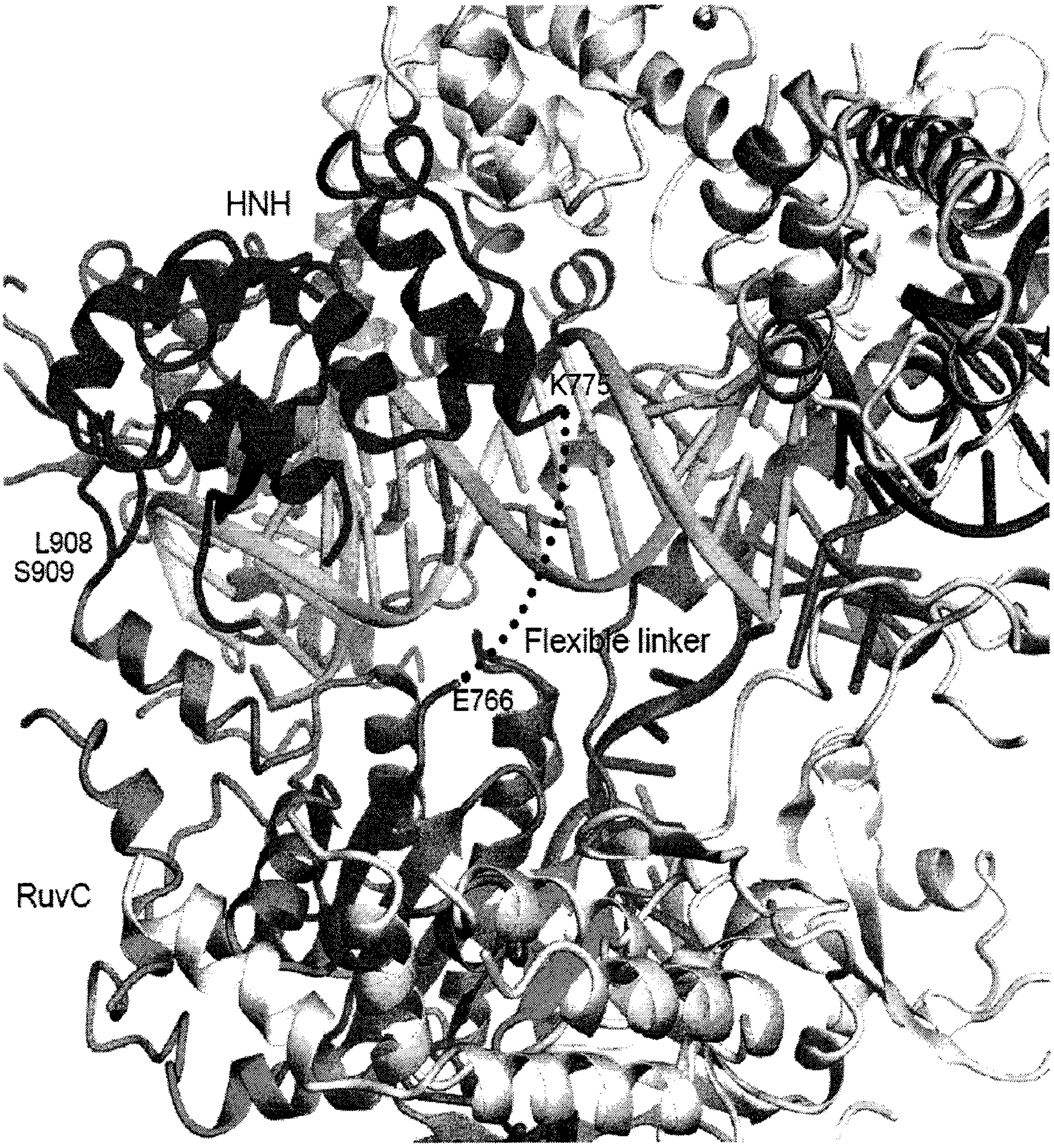
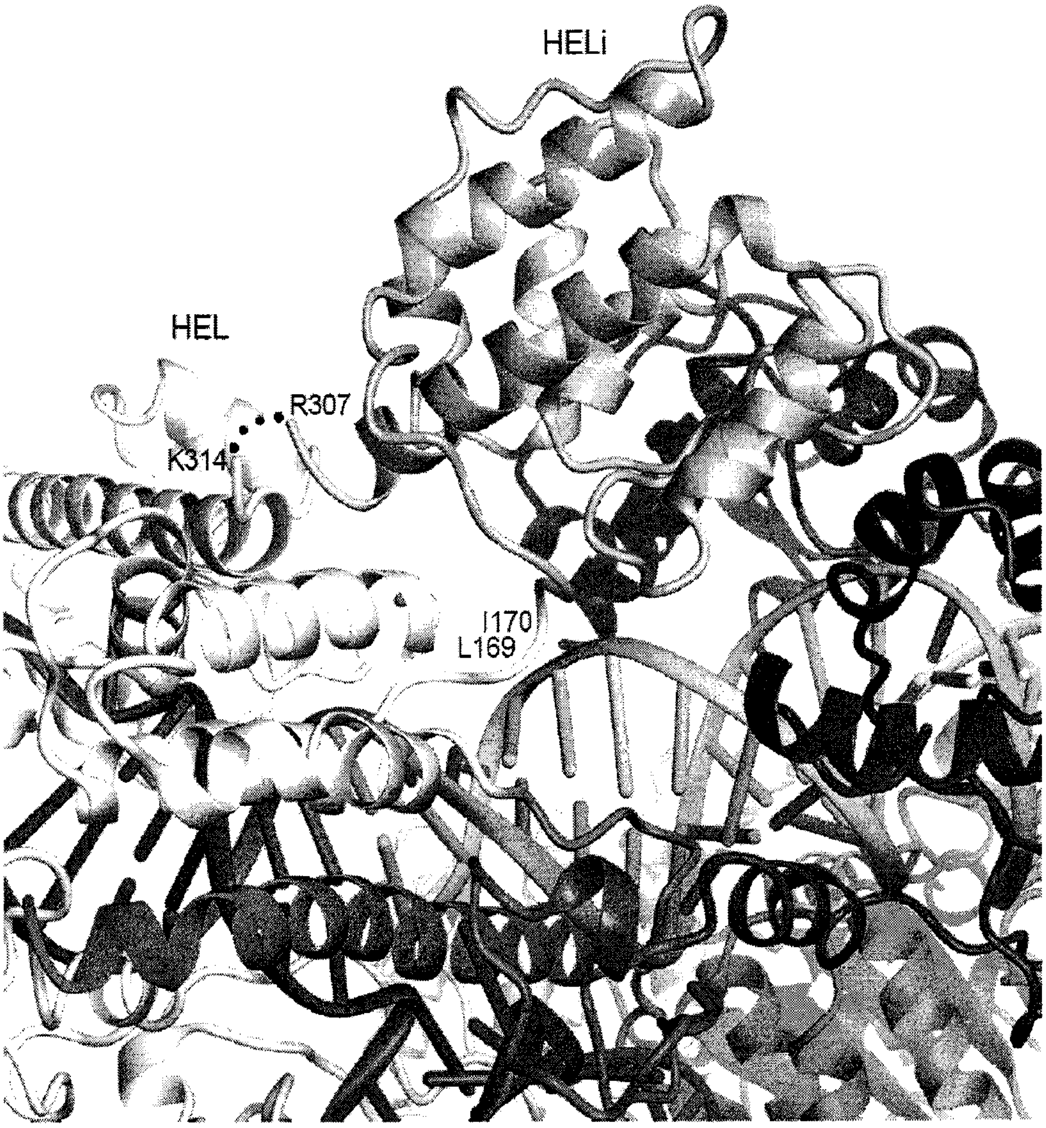


FIG. 23F



RuvC (E766)-linker-Effector-linker-RuvC (S909)

FIG. 23G



HEL (L169)-linker-Effector-linker-HEL (K314)

FIG. 23H

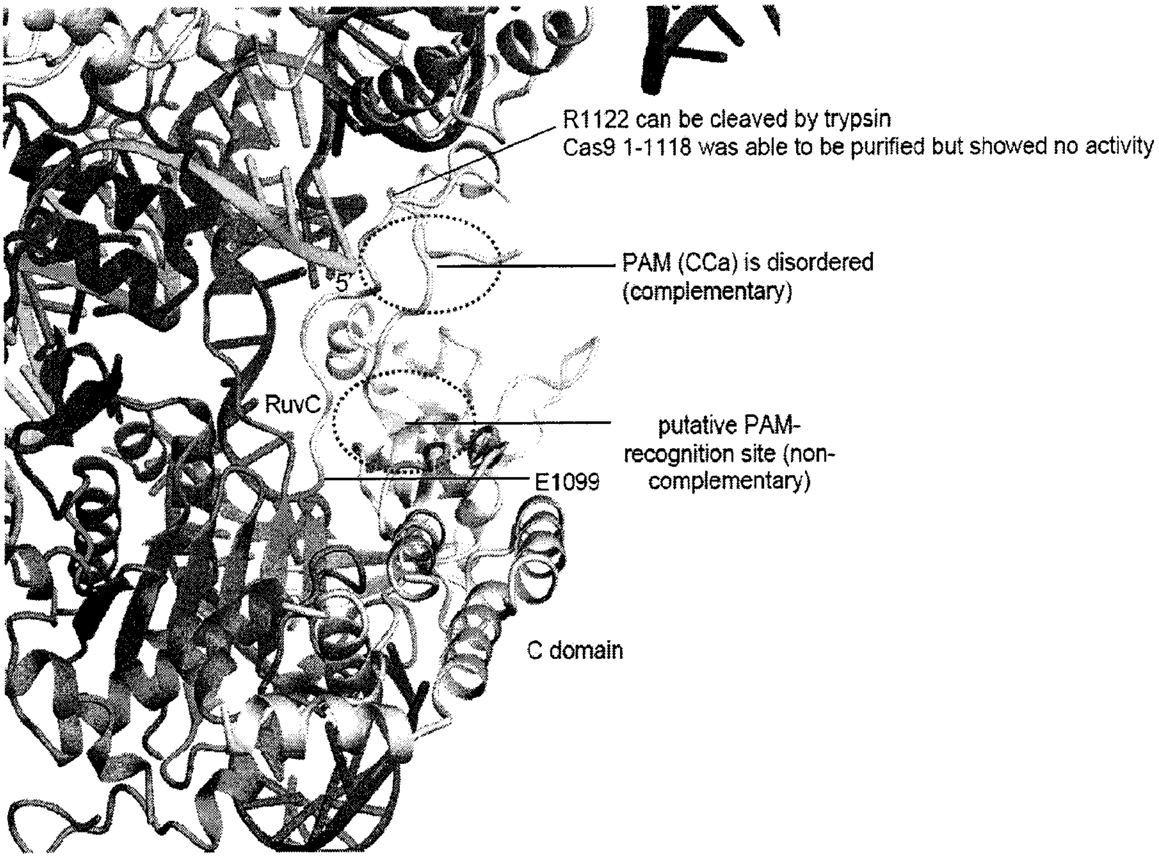
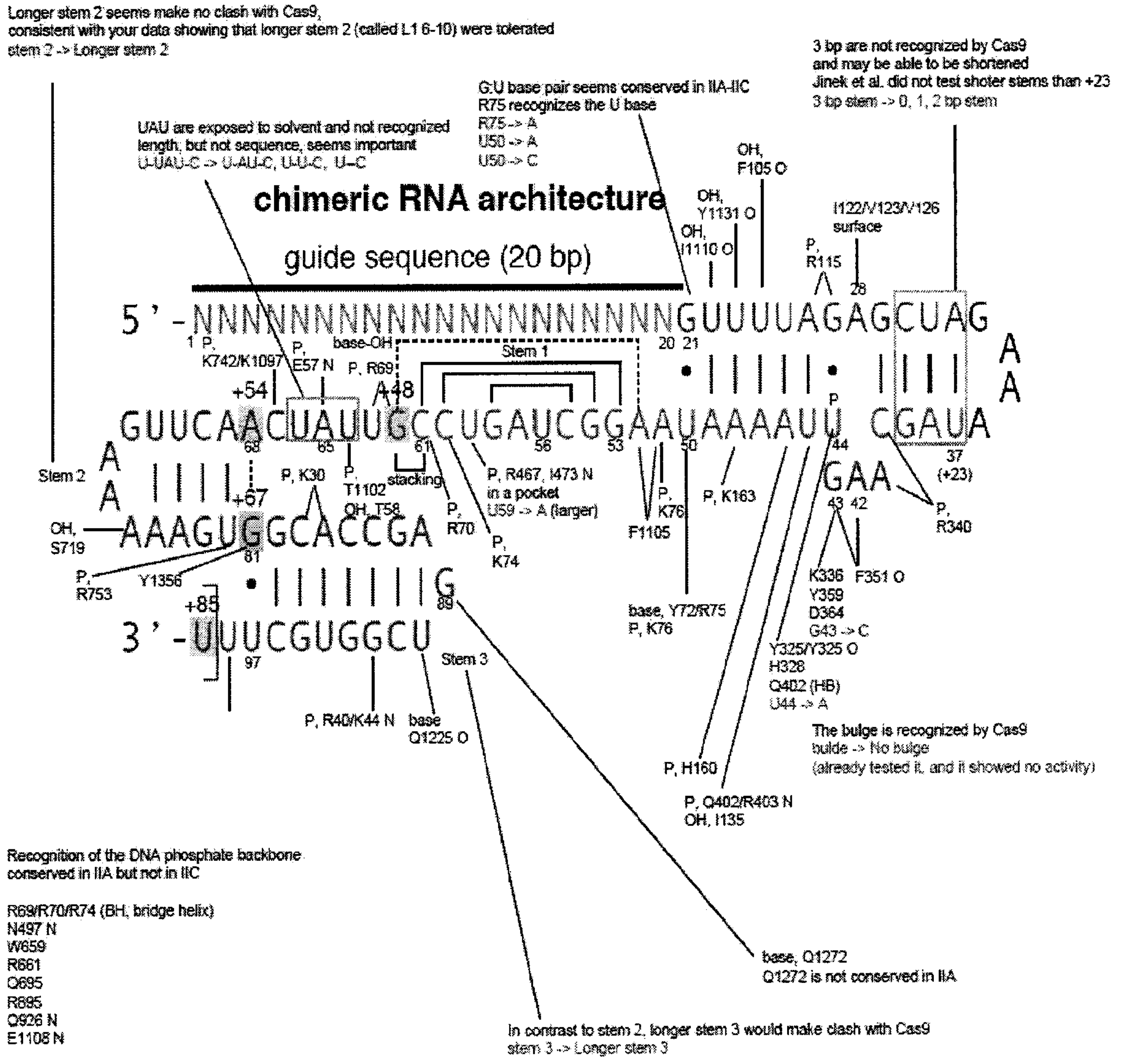

R1122 can be cleaved by trypsin
Cas9 1-1118 was able to be purified but showed no activity
5'
PAM (CCa) is disordered (complementary)
RuvC
putative PAM-recognition site (non-complementary)
E1099
C domain

FIG. 23I



Longer stem 2 seems make no clash with Cas9,
consistent with your data showing that longer stem 2 (called L1 6-10) were tolerated
stem 2 -> Longer stem 2

3 bp are not recognized by Cas9
and may be able to be shortened
Jinek et al. did not test shoter stems than +23
3 bp stem -> 0, 1, 2 bp stem

G:U base pair seems conserved in IIA-IIC
R75 recognizes the U base
R75 -> A
U50 -> A
U50 -> C

UAU are exposed to solvent and not recognized
length, but not sequence, seems important
U-UAU-C -> U-AU-C, U-U-C, U–C

The bulge is recognized by Cas9
bulde -> No bulge
(already tested it, and it showed no activity)

In contrast to stem 2, longer stem 3 would make clash with Cas9
stem 3 -> Longer stem 3

Recognition of the DNA phosphate backbone
conserved in IIA but not in IIC

R69/R70/R74 (BH, bridge helix)
N497 N
W659
R661
Q695
R695
Q926 N
E1108 N

Recognition of the RNA phosphate backbone (guide sequence)

R63/R66/R69/R70/R74/R78 (BH)
R165
N407
K510
R661
V1009 O
W1010 O

Y1013 (stacking with 5' G1)

Arg residues on BH are conserved in IIA and IIC; R63, R66, R69, R70, R74, R78 -> A
R165, K510 is conserved in IIA and IIC; R165, K510 -> A
R661 is conserved in IIA but not in IIC, but recognizes both DNA and RNA: R661 -> A

FIG. 23J

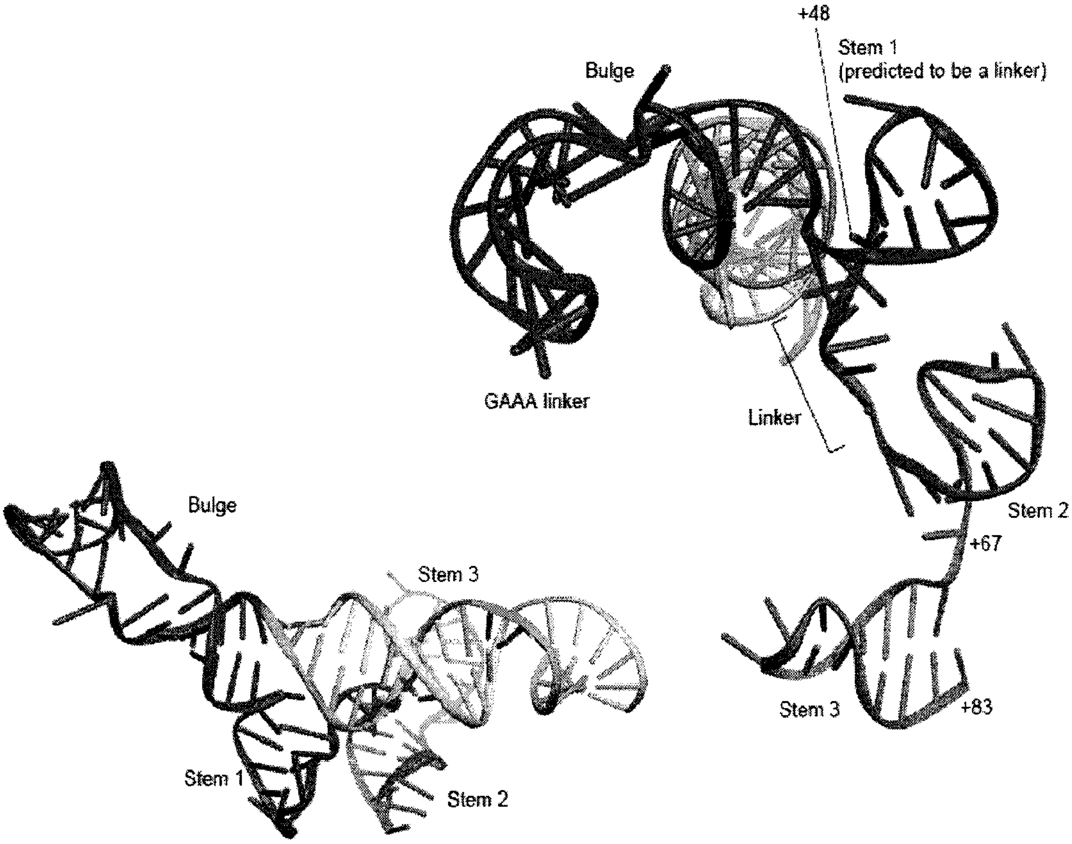

+48
Stem 1
(predicted to be a linker)
Bulge
GAAA linker
Linker
Stem 2
+67
Stem 3
+83
Bulge
Stem 3
Stem 1
Stem 2

FIG. 23K

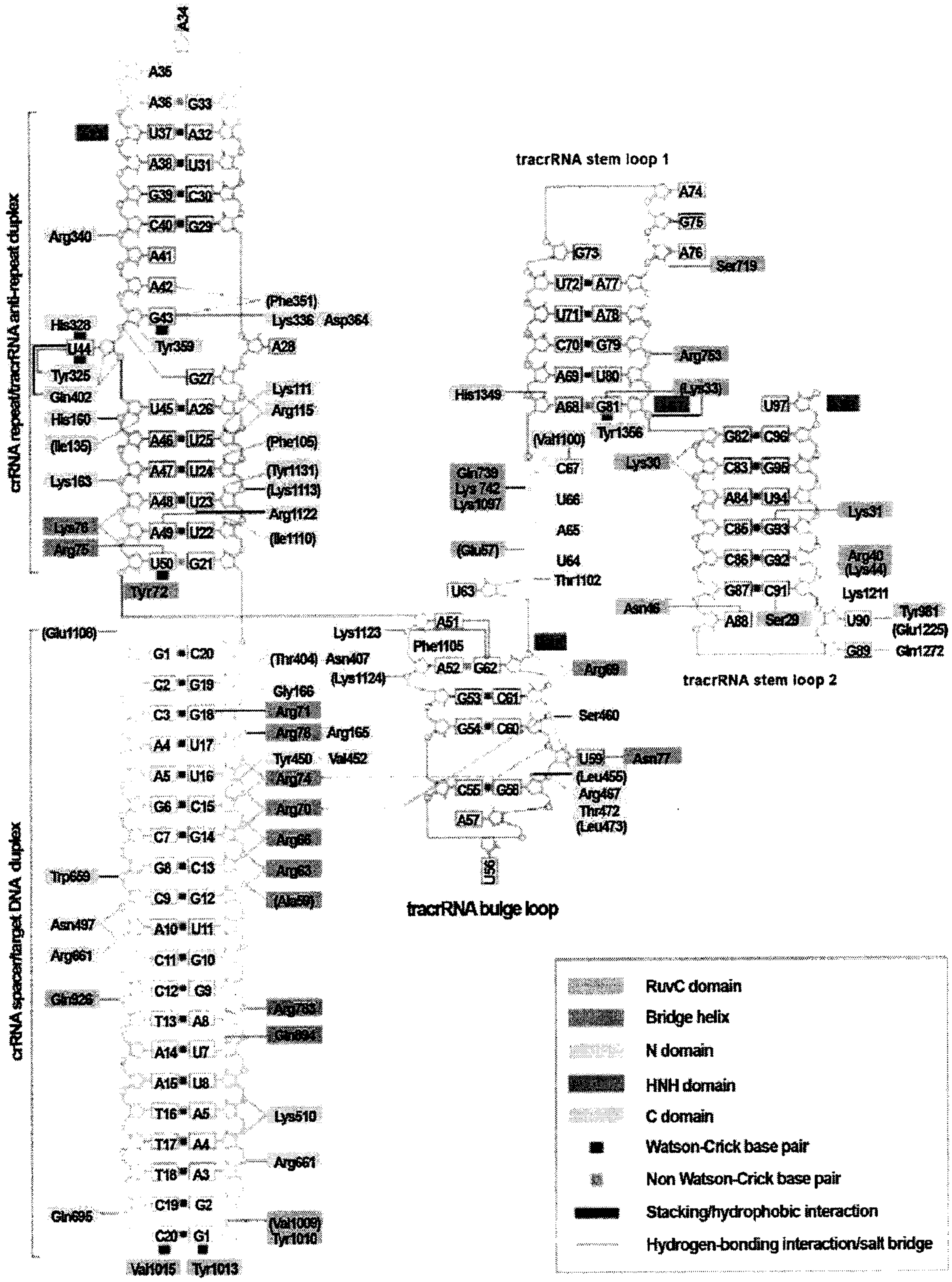

A34
A35
A36 G33
U37 A32
A38 U31
G39 C30
C40 G29
A41
A42
G43
U44
U45 A26
A46 U25
A47 U24
A48 U23
A49 U22
U50 G21
G27
A28
Arg340
His328
Tyr325
Gln402
His160
(Ile135)
Lys163
Lys78
Arg75
Tyr72
(Phe351)
Lys336 Asp364
Tyr359
Lys111
Arg115
(Phe105)
(Tyr1131)
(Lys1113)
Arg1122
(Ile1110)
crRNA repeat/tracrRNA anti-repeat duplex
(Glu1108)
G1 C20
C2 G19
C3 G18
A4 U17
A5 U16
G6 C15
C7 G14
G8 C13
C9 G12
A10 U11
C11 G10
C12 G9
T13 A8
A14 U7
A15 U6
T16 A5
T17 A4
T18 A3
C19 G2
C20 G1
Val1015 Tyr1013
Trp659
Asn497
Arg661
Gln926
Gln695
(Thr404) Asn407
(Lys1124)
Gly166
Arg71
Arg78 Arg165
Tyr450 Val452
Arg74
Arg70
Arg66
Arg63
(Ala59)
Arg753
Gln894
Lys510
Arg661
(Val1009)
Tyr1010
crRNA spacer/target DNA duplex
tracrRNA stem loop 1
A74
G75
A76
G73
Ser719
U72 A77
U71 A78
C70 G79
A69 U80
A68 G81
Arg753
(Lys33)
His1349
Tyr1356
(Val1100)
C67
U66
A65
U64
U63
Thr1102
Gln739
Lys 742
Lys1097
(Glu57)
Lys1123
A51
Phe1105
A52 G62
Arg69
G53 C61
G54 C60
Ser460
U59 Asn77
(Leu455)
C55 G58
Arg467
Thr472
(Leu473)
A57
U56
tracrRNA bulge loop
U97
G82 C96
C83 G95
A84 U94
C85 G93
C86 G92
G87 C91
A88
G89
U90
Lys30
Lys31
Arg40
(Lys44)
Lys1211
Asn46
Ser29
Tyr981
(Glu1225)
Gln1272
tracrRNA stem loop 2
RuvC domain
Bridge helix
N domain
HNH domain
C domain
Watson-Crick base pair
Non Watson-Crick base pair
Stacking/hydrophobic interaction
Hydrogen-bonding interaction/salt bridge

FIG. 23L

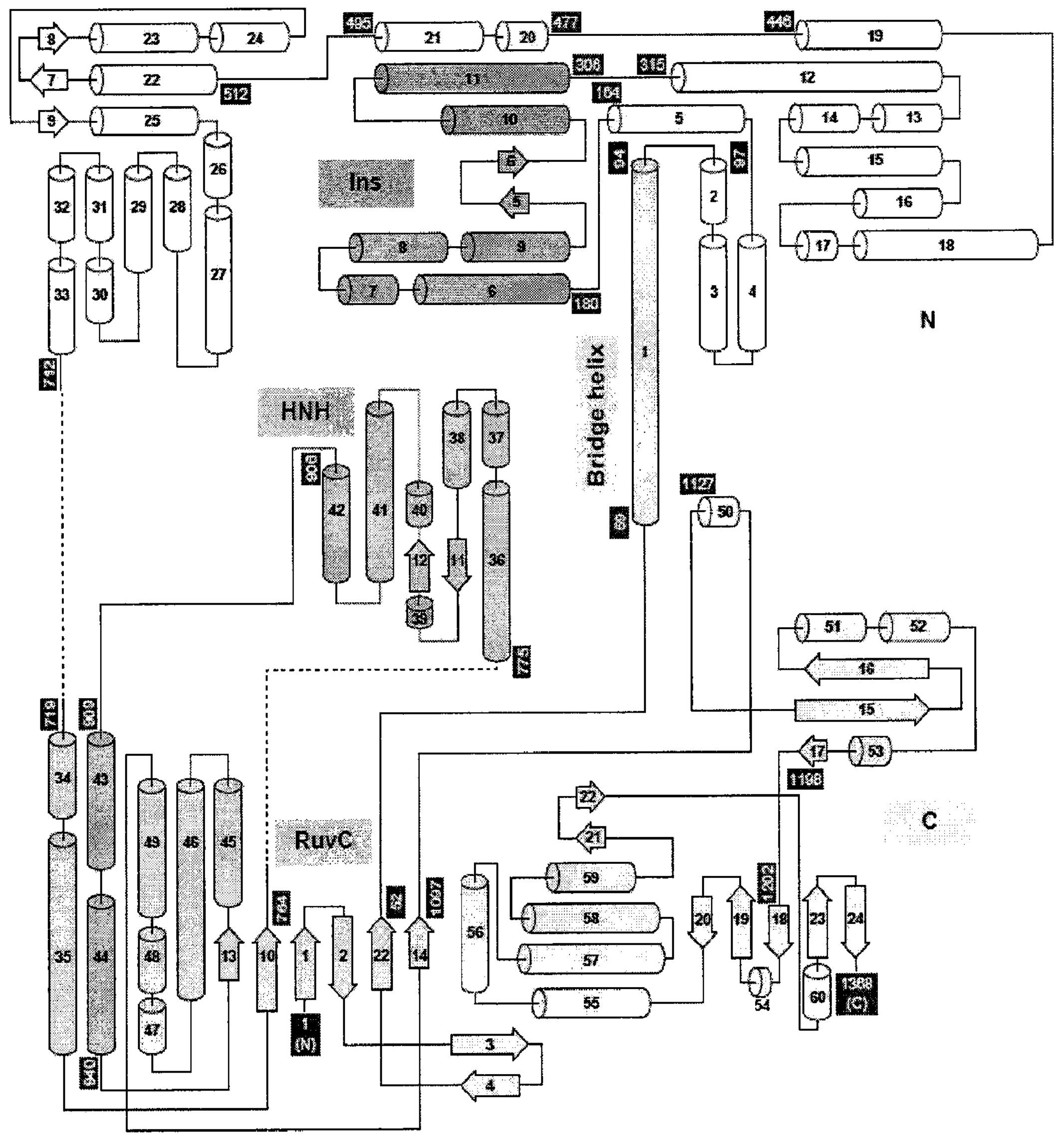

495
477
448
308
315
512
164
94
97
180
Ins
N
712
HNH
Bridge helix
906
60
1127
775
718
909
1198
C
RuvC
764
62
1097
1202
840
1
(N)
1368
(C)

FIG. 23M

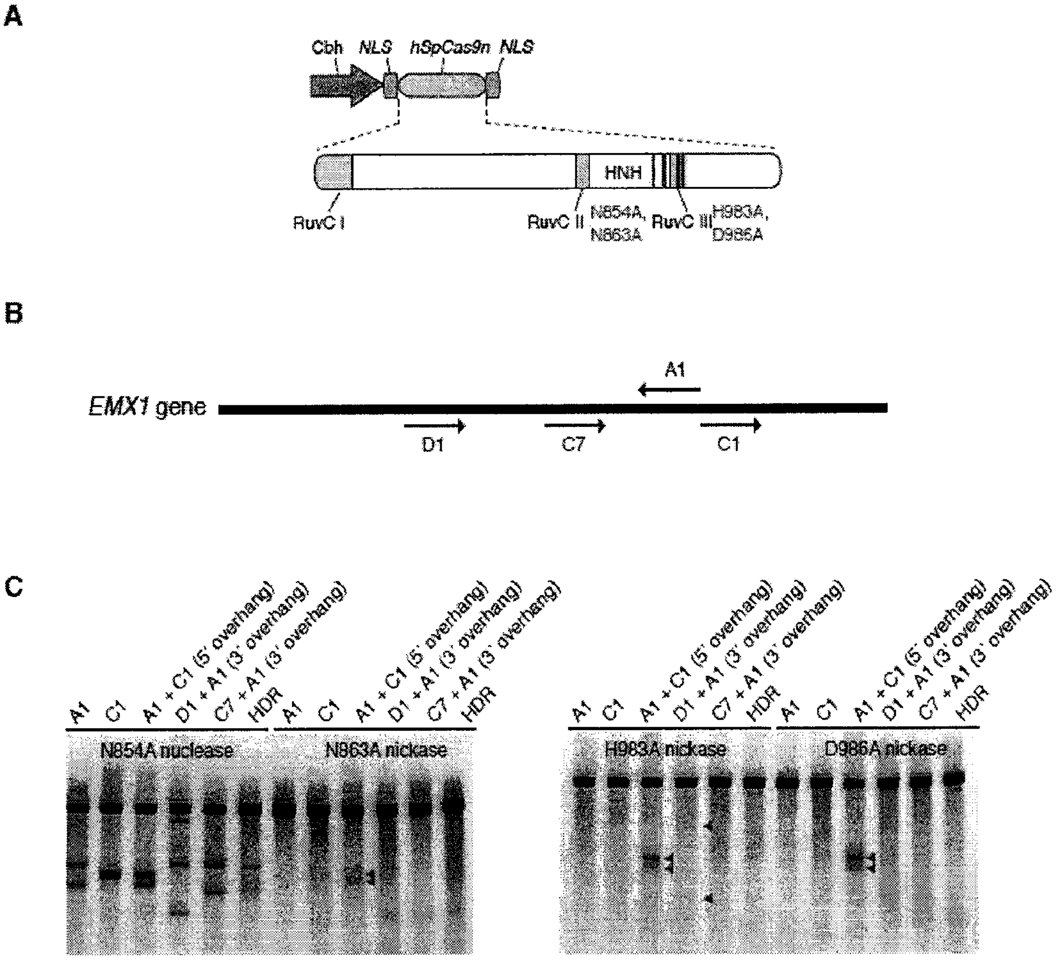
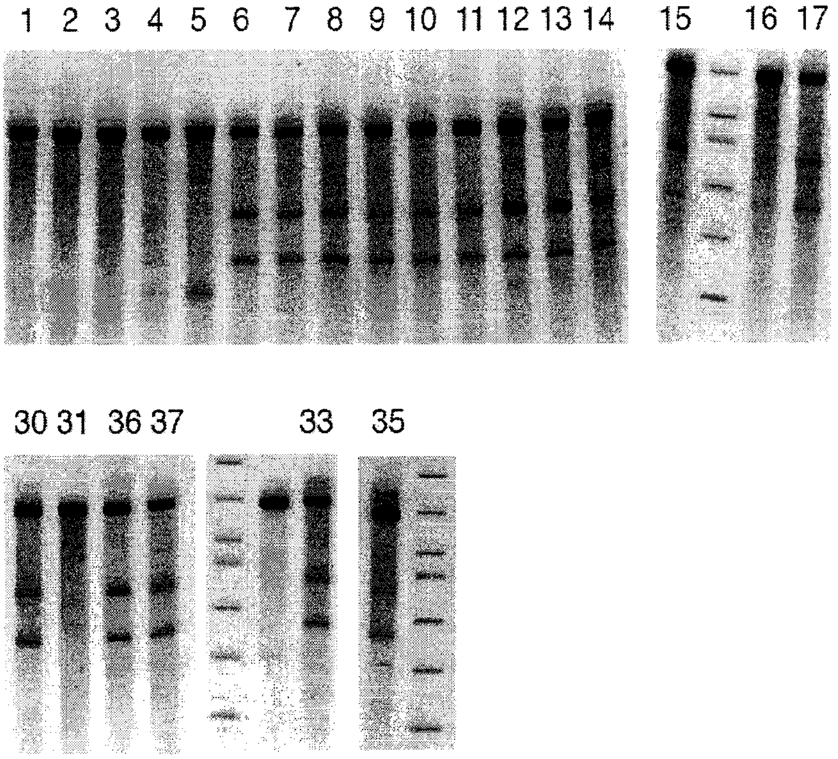

A
Cbh
NLS
hSpCas9n
NLS
HNH
RuvC I
RuvC II
N854A,
N863A
RuvC III
H983A,
D986A
B
A1
EMX1 gene
D1
C7
C1
C
A1
C1
A1 + C1 (5' overhang)
D1 + A1 (3' overhang)
C7 + A1 (3' overhang)
HDR
N854A nuclease
N863A nickase
H983A nickase
D986A nickase

FIG. 24A-C

A



B

1	Sp_Δ_hel 1(87-173)
2	Sp_Δ_hel 1(87-102)
3	Sp_Δ_hel 1(103-121)
4	Sp_Δ_hel 1(122-134)
5	Sp_Δ_hel 1(135-173)
6	Sp_Δ_hel 2(174-311)
7	Sp_Δ_hel 2-(GGGGS)3
8	Sp_Δ_hel 2-(GGGGS)6
9	Sp_Δ_hel 2-(GGGGS)9
11	Sp_Δ_hel 2-A(EAAAK)3A
12	Sp_Δ_hel 2-A(EAAAK)6A
13	Sp_Δ_hel 2-A(EAAAK)9A
14	Sp_Δ_hel 2-A(EAAAK)12A
15	Sp_Δ_hel 2(174-182)
16	Sp_Δ_hel 2(183-190)
17	Sp_Δ_hel 2(191-219)

30	Sp_Δ (175-307)
31	Sp_Δ (1098-1368)
36	Sp_Δ(175-307)-A(EAAAK)3A
37	Sp_Δ(175-307)-A(EAAAK)6A

33	Sp_Δ (175-307)-(GGGGS)6
35	Sp_Δ (175-307)-(GGGGS)12

FIG. 25A-B

sgRNA mutations

Region of mutation	Activity (indel %)	Specific description of mutation	Complete Sequence	Length
Stem 1	14.33	Proximal poly U tract switch to C	gCCCCagagctaGAAAtagcaagttGGGGtaaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Stem 1	14.74	Distal CUA to CCC	gttttagagcCCGAAAGGgcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Stem 1	15.16	Truncate distal UA	gttttagagcGAAAgcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	77
Stem 1	16.05	Truncate distal CUA	gttttagagGAAAcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	75
Stem 1	18.19	Truncate distal CUA and Loop 1	gttttagagAcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	72
Bulge	NONE	Replace Bulge with A-U pair	gttttagagctaGAAAtagcTttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	79
Bulge	1.30	Replace Bulge with C-G pair (keep G43)	gttttagCgctaGAAAtagcGttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	79
Bulge	21.55	Replace Bulge with C-AAG pair	gttttagCgctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Bulge	17.56	Replace Bulge with T-AAG pair	gttttagTgctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Bulge	19.64	Replace Bulge with G-AAG pair	gttttagGgctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Bulge	12.11	Replace Bulge with A-TTG (keep G43)	gttttagagctaGAAAtagcTTGttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Bulge	5.44	Replace Bulge with A-AAC (remove G43)	gttttagagctaGAAAtagcAACttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Bulge	14.74	Replace Bulge with A-AAA (remove G43)	gttttagagctaGAAAtagcAAAttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Bulge	10.63	Replace Bulge with A-AAT (remove G43)	gttttagagctaGAAAtagcAATttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Linker 1	14.66	Shorten Linker 1 (del UAUC)	gttttagagctaGAAAtagcaagttaaaataaggctagtccgtaacttGAAAaagtggcaccgAGTcggtgcTTTTT	77
Linker 1	14.99	Change Linker 1 (UAUC to AUAG)	gttttagagctaGAAAtagcaagttaaaataaggctagtccgtATAGaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Stem 2	20.35	Replace Stem 2 with G-C track	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaCGCCGAAAGGCGggcaccgAGTcggtgcTTTTT	82
Stem 2	16.87	Replace and lengthen Stem 2 with G-C track	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaCGCCggccGAAAggccGGCGggcaccgAGTcggtgcTTTTT	82
Loop 2	17.57	Change Loop 2 sequence	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttAAAGaagtggcaccgAGTcggtgcTTTTT	81
Stem 3	13.07	Replace Stem 3 with G-C track	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcCccgCGGcggGgcTTTTT	81
Stem 3	20.05	Add 1 bp to Stem 3	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAAGTTcggtgcTTTTT	83
Stem 3	12.86	Add 2 bp to Stem 3	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAAAGTTTcggtgcTTTTT	85
Cas9 contact (S1)	16.35	mutate G•U44 to C44 (basepairing)	gttttagagctaGAAAtagcaagCtaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Cas9 contact		mutate G•U44 to U•G44	gttttagaTctaGAAAtagcaagGtaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81

FIG. 26A

(S1) NONE		(wobble pairing)		
Cas9 contact (S1)	3.42	mutate G-U44 to A44 (non-basepairing)	gttttagagctaGAAAtagcaagAtaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Cas9 contact (S1)	14.31	mutate G-U50 to C50 (basepairing)	gttttagagctaGAAAtagcaagttaaaaCaaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Cas9 contact (S1)	8.88	mutate G-U50 to U-G50 (wobble pairing)	TttttagagctaGAAAtagcaagttaaaaGaaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Cas9 contact (S1)	15.47	mutate G-U50 to A50 (non-basepairing)	gttttagagctaGAAAtagcaagttaaaaAaaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Cas9 contact (L1)	6.72	mutate U59 to A (larger)	gttttagagctaGAAAtagcaagttaaaataaggctagAccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Cas9 contact (L1)	15.34	mutate U59 to C (transition)	gttttagagctaGAAAtagcaagttaaaataaggctagCccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
Cas9 contact (L3)	14.95	Change Loop 3 from G89 to A	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAATcggtgcTTTTT	81
Cas9 contact (L3)	17.45	Change Loop 3 from G89 to C	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgACTcggtgcTTTTT	81
Cas9 contact (L3)	19.73	Change Loop 3 from G89 to T	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgATTcggtgcTTTTT	81
Cas9 contact (S3)	16.24	mutate U-90 to A (larger)	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGAcggtgcTTTTT	81
Cas9 contact (S3)	19.95	mutate U90 to C (transition)	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGCcggtgcTTTTT	81
WT	16.33	WT	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttGAAAaagtggcaccgAGTcggtgcTTTTT	81
MS2 addition		MS2 in loop 1	gttttagagctaggccAACATGAGGATCACCCATGTCTGCAGggcctagcaagttaaaataaggctagtccgttatcaCGCCGAAAGGCGggcaccgAGTcggtgcTTTTT	111
MS2 addition		MS2 in loop 2	gttttagagctaGAAAtagcaagttaaaataaggctagtccgttatcaacttggccAACATGAGGATCACCCATGTCTGCAGggccaagtggcaccgAGTcggtgcTTTTT	111
MS2 addition		MS2 in loop 1 +2	gttttagagctaggccAACATGAGGATCACCCATGTCTGCAGggcctagcaagttaaaataaggctagtccgttatcaacttggccAACATGAGGATCACCCATGTCTGCAG ggccaagtggcaccgAGTcggtgcTTTTT	141

FIG. 26B

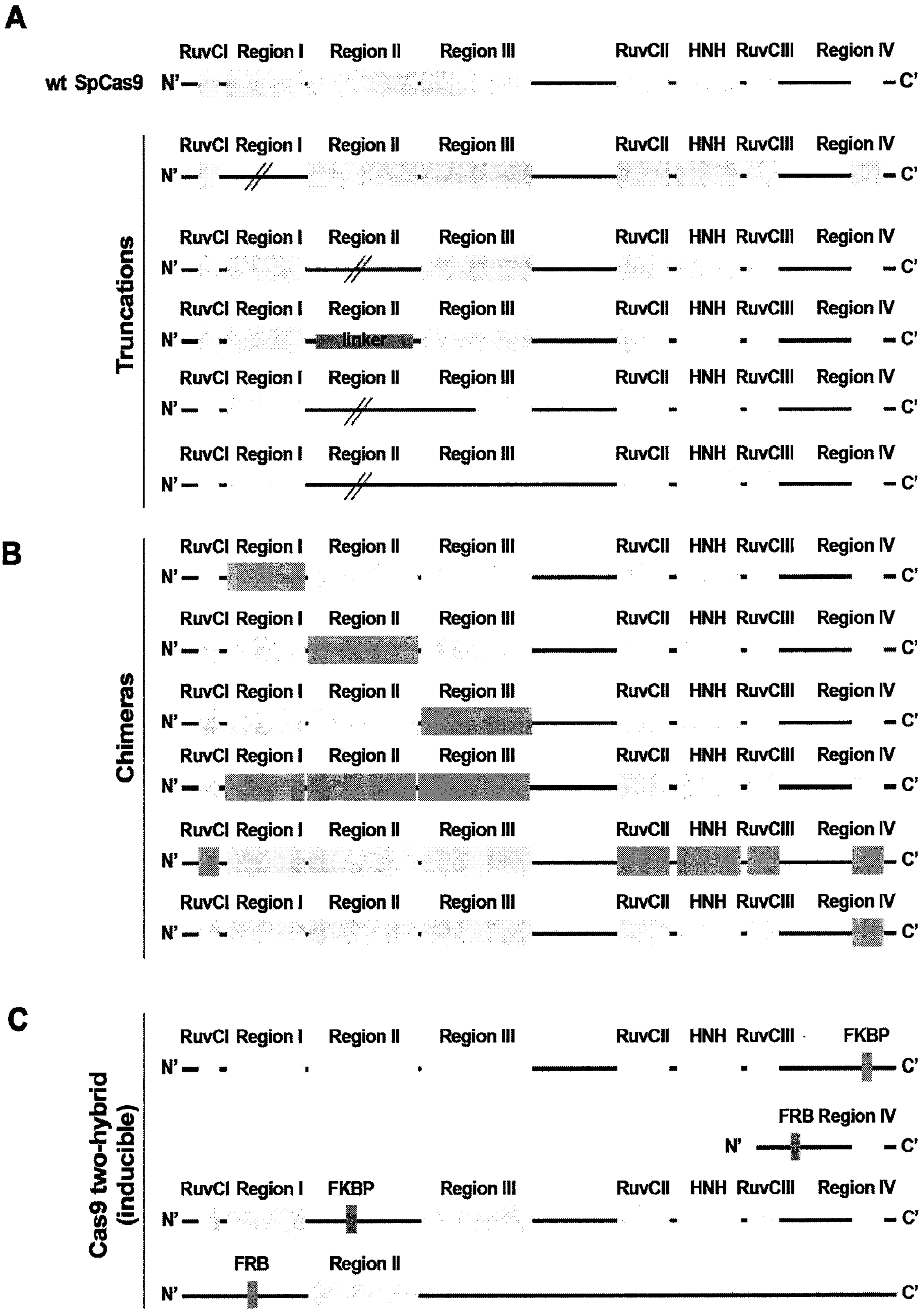

A
RuvCI
Region I
Region II
Region III
RuvCII
HNH
RuvCIII
Region IV
wt SpCas9
N'
C'
Truncations
linker
B
Chimeras
C
Cas9 two-hybrid (inducible)
FKBP
FRB

FIG. 27A-C

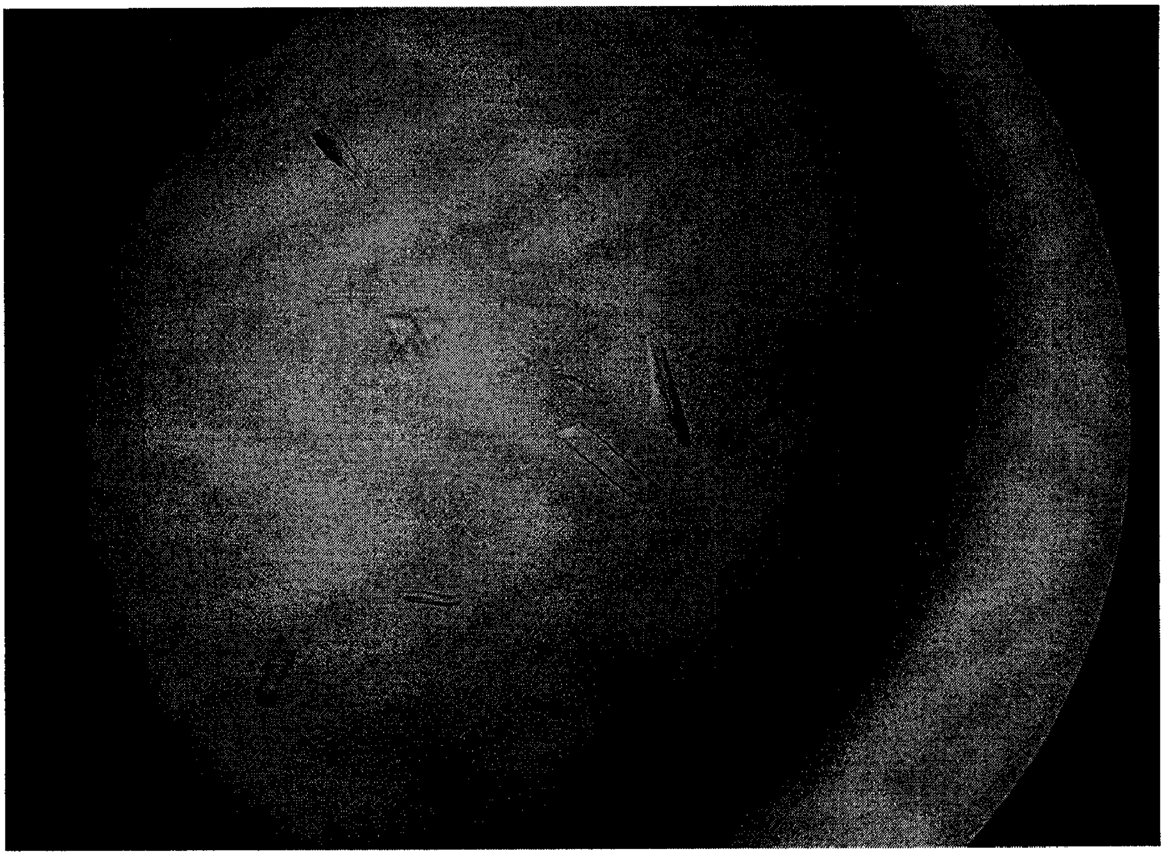


FIG. 28

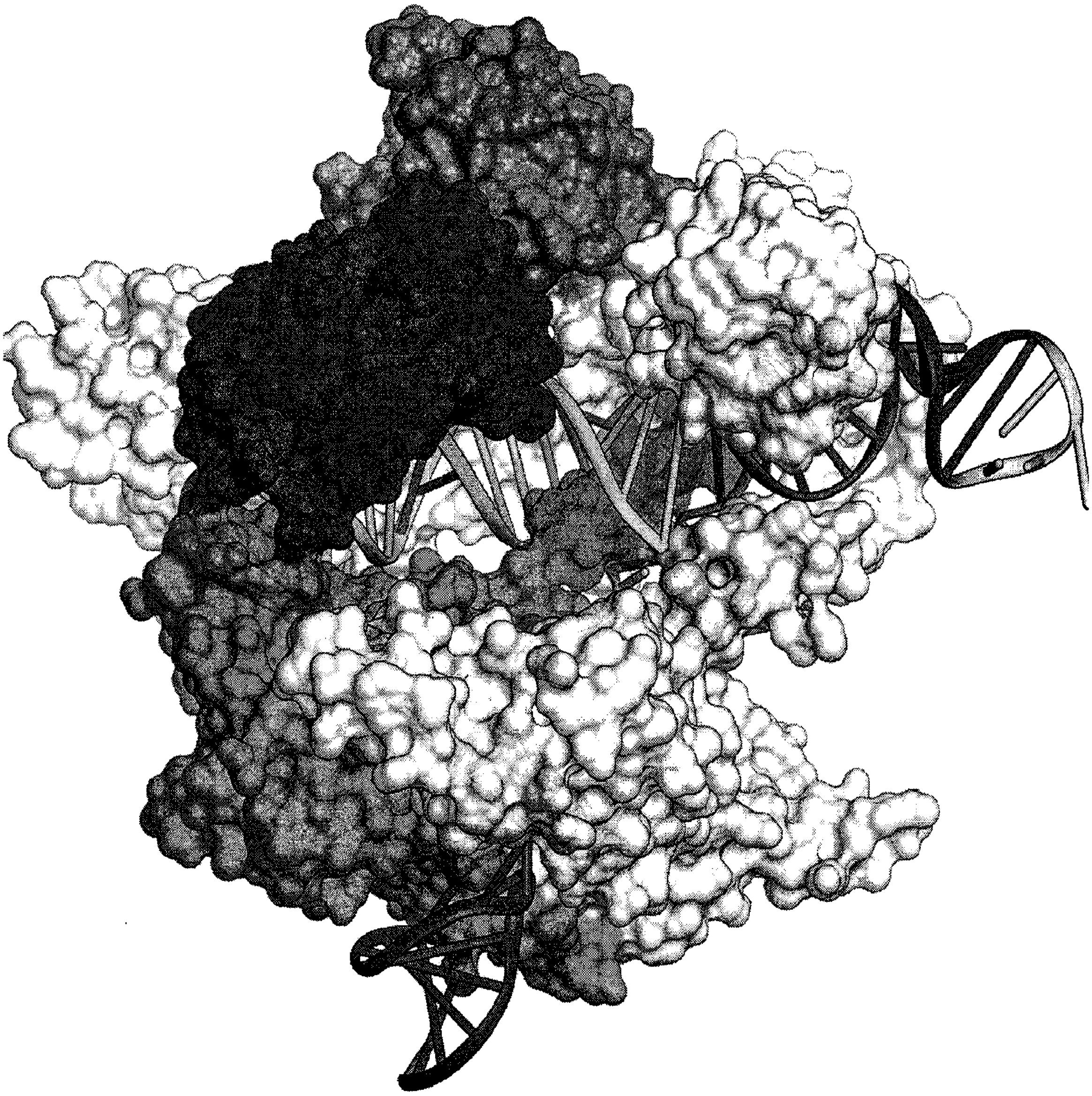


FIG. 29

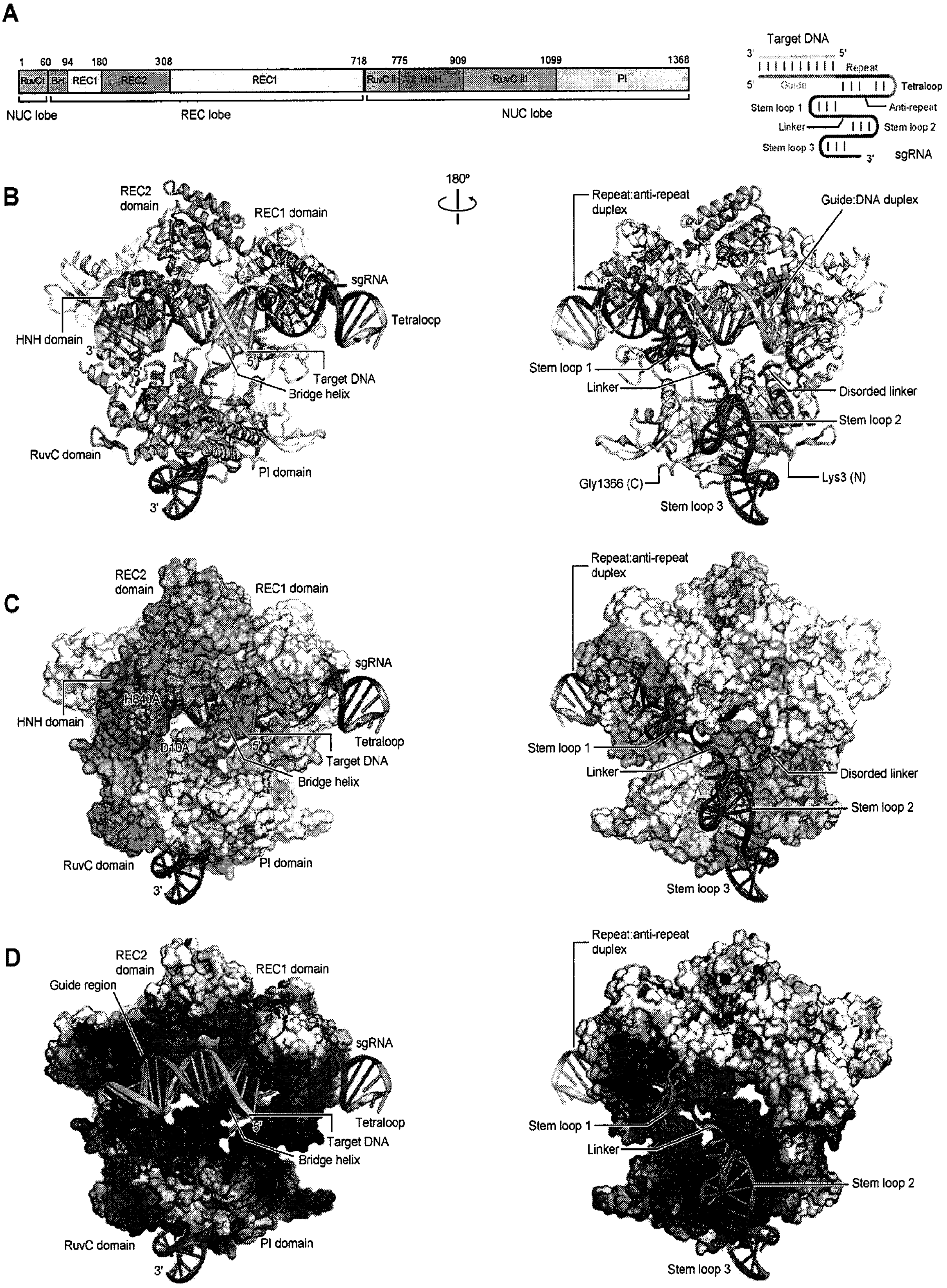

A
1
60
94
180
308
718
775
909
1099
1368
RuvC I
BH
REC1
REC2
REC1
RuvC II
HNH
RuvC III
PI
NUC lobe
REC lobe
NUC lobe
Target DNA
3'
5'
Repeat
5'
Guide
Tetraloop
Stem loop 1
Anti-repeat
Linker
Stem loop 2
Stem loop 3
3'
sgRNA
B
REC2 domain
REC1 domain
sgRNA
Tetraloop
HNH domain
3'
5'
5'
Target DNA
Bridge helix
RuvC domain
PI domain
3'
180°
Repeat:anti-repeat duplex
Guide:DNA duplex
Stem loop 1
Linker
Disorded linker
Stem loop 2
Gly1366 (C)
Lys3 (N)
Stem loop 3
C
REC2 domain
REC1 domain
sgRNA
HNH domain
H840A
D10A
5'
Tetraloop
Target DNA
Bridge helix
RuvC domain
PI domain
3'
Repeat:anti-repeat duplex
Stem loop 1
Linker
Disorded linker
Stem loop 2
Stem loop 3
D
REC2 domain
REC1 domain
Guide region
sgRNA
5'
Tetraloop
Target DNA
Bridge helix
RuvC domain
PI domain
3'
Repeat:anti-repeat duplex
Stem loop 1
Linker
Stem loop 2
Stem loop 3

FIG. 30A-D

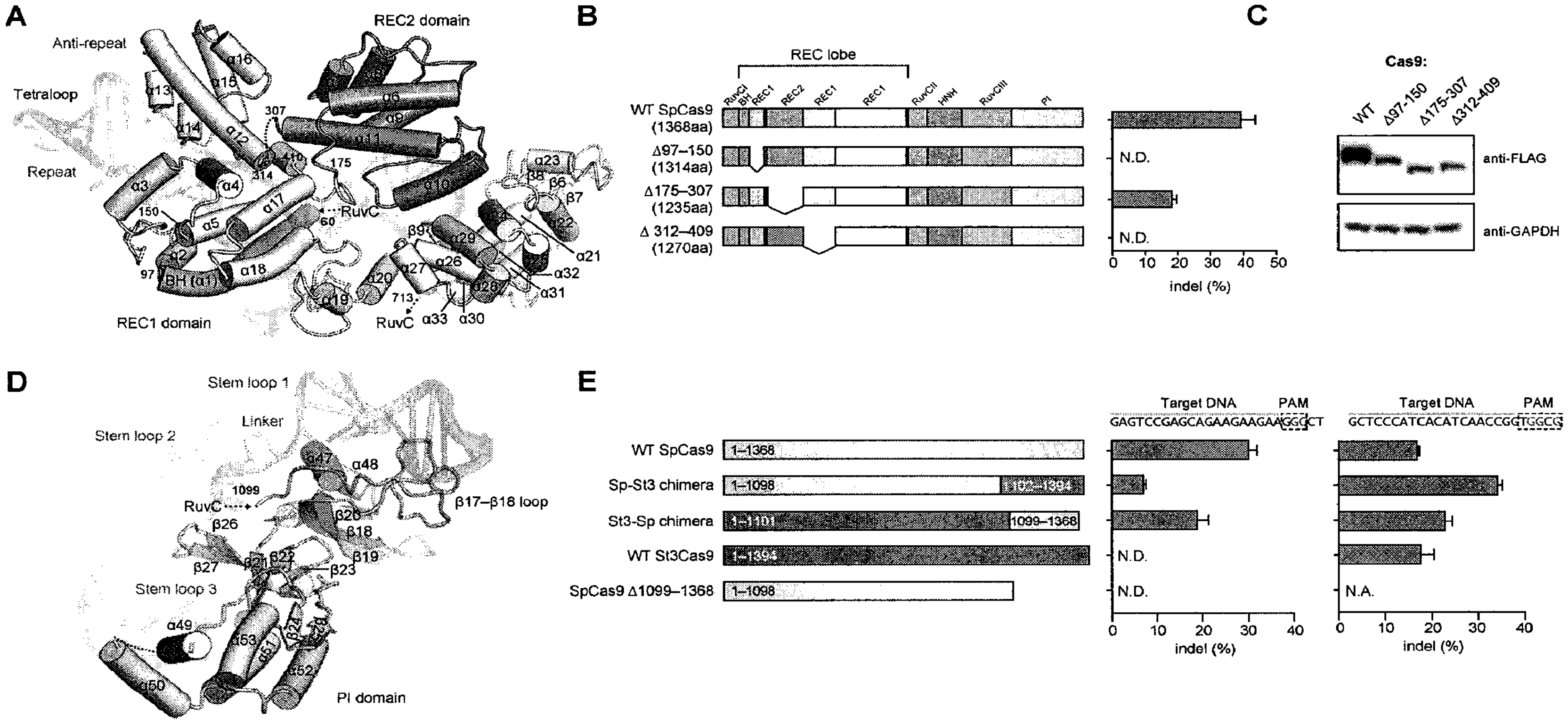

A
Anti-repeat
Tetraloop
Repeat
REC2 domain
REC1 domain
α3
α4
α5
α2
BH (α1)
α12
α13
α14
α15
α16
α17
α18
α19
α20
α10
α11
α9
α6
α21
α22
α23
α26
α27
α28
α29
α30
α31
α32
α33
β6
β7
β8
β9
97
150
307
314
175
60
713
RuvC
RuvC
B
REC lobe
RuvCI
BH
REC1
REC2
REC1
REC1
RuvCII
HNH
RuvCIII
PI
WT SpCas9 (1368aa)
Δ97–150 (1314aa)
Δ175–307 (1235aa)
Δ 312–409 (1270aa)
N.D.
N.D.
0
10
20
30
40
50
indel (%)
C
Cas9:
WT
Δ97-150
Δ175-307
Δ312-409
anti-FLAG
anti-GAPDH
D
Stem loop 1
Stem loop 2
Stem loop 3
Linker
1099
RuvC
β17–β18 loop
α47
α48
α49
α50
α51
α52
α53
β18
β19
β20
β21
β22
β23
β24
β26
β27
PI domain
E
WT SpCas9
Sp-St3 chimera
St3-Sp chimera
WT St3Cas9
SpCas9 Δ1099–1368
1–1368
1–1098
1102–1394
1–1101
1099–1368
1–1394
1–1098
Target DNA
PAM
GAGTCCGAGCAGAAGAAGAAGGGCT
N.D.
N.D.
0
10
20
30
40
indel (%)
Target DNA
PAM
GCTCCCATCACATCAACCGGTGGCG
N.A.
0
10
20
30
40
indel (%)

FIG. 31A-E

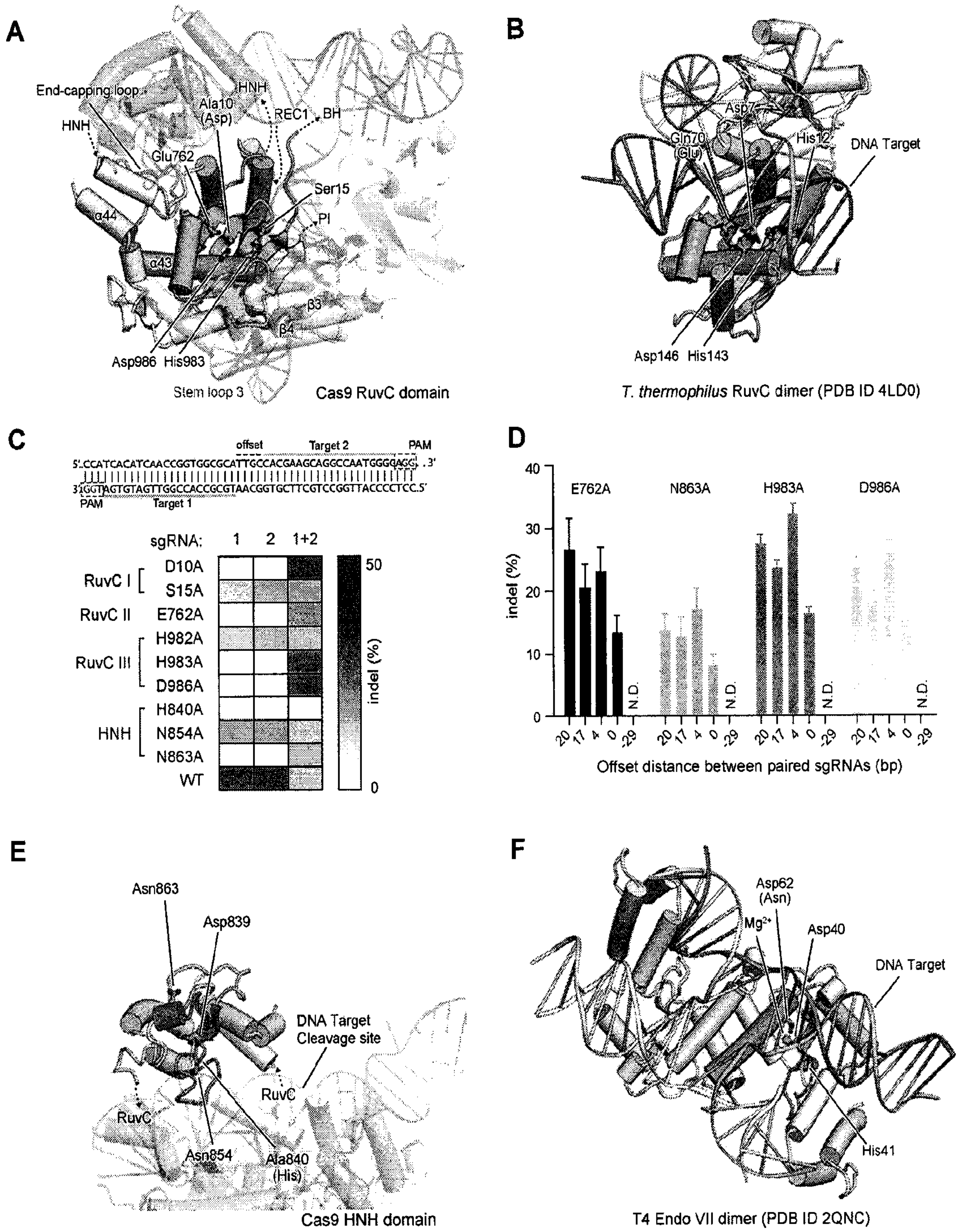

A
End-capping loop
HNH
HNH
Ala10
(Asp)
REC1
BH
Glu762
Ser15
PI
α44
α43
β3
β4
Asp986 His983
Stem loop 3
Cas9 RuvC domain
B
Asp7
Gln70
(Glu)
His12
DNA Target
Asp146 His143
T. thermophilus RuvC dimer (PDB ID 4LD0)
C
offset
Target 2
PAM
5'..CCATCACATCAACCGGTGGCGCATTGCCACGAAGCAGGCCAATGGGGAGG. .3'
3'GGTAGTGTAGTTGGCCACCGCGTAACGGTGCTTCGTCCGGTTACCCCTCC.5'
PAM
Target 1
sgRNA:
1
2
1+2
RuvC I
D10A
S15A
RuvC II
E762A
RuvC III
H982A
H983A
D986A
HNH
H840A
N854A
N863A
WT
50
indel (%)
0
D
E762A
N863A
H983A
D986A
indel (%)
40
30
20
10
0
N.D.
N.D.
N.D.
N.D.
20 17 4 0 -29
20 17 4 0 -29
20 17 4 0 -29
20 17 4 0 -29
Offset distance between paired sgRNAs (bp)
E
Asn863
Asp839
DNA Target
Cleavage site
RuvC
RuvC
Asn854
Ala840
(His)
Cas9 HNH domain
F
Asp62
(Asn)
Mg2+
Asp40
DNA Target
His41
T4 Endo VII dimer (PDB ID 2QNC)

FIG. 32A-F

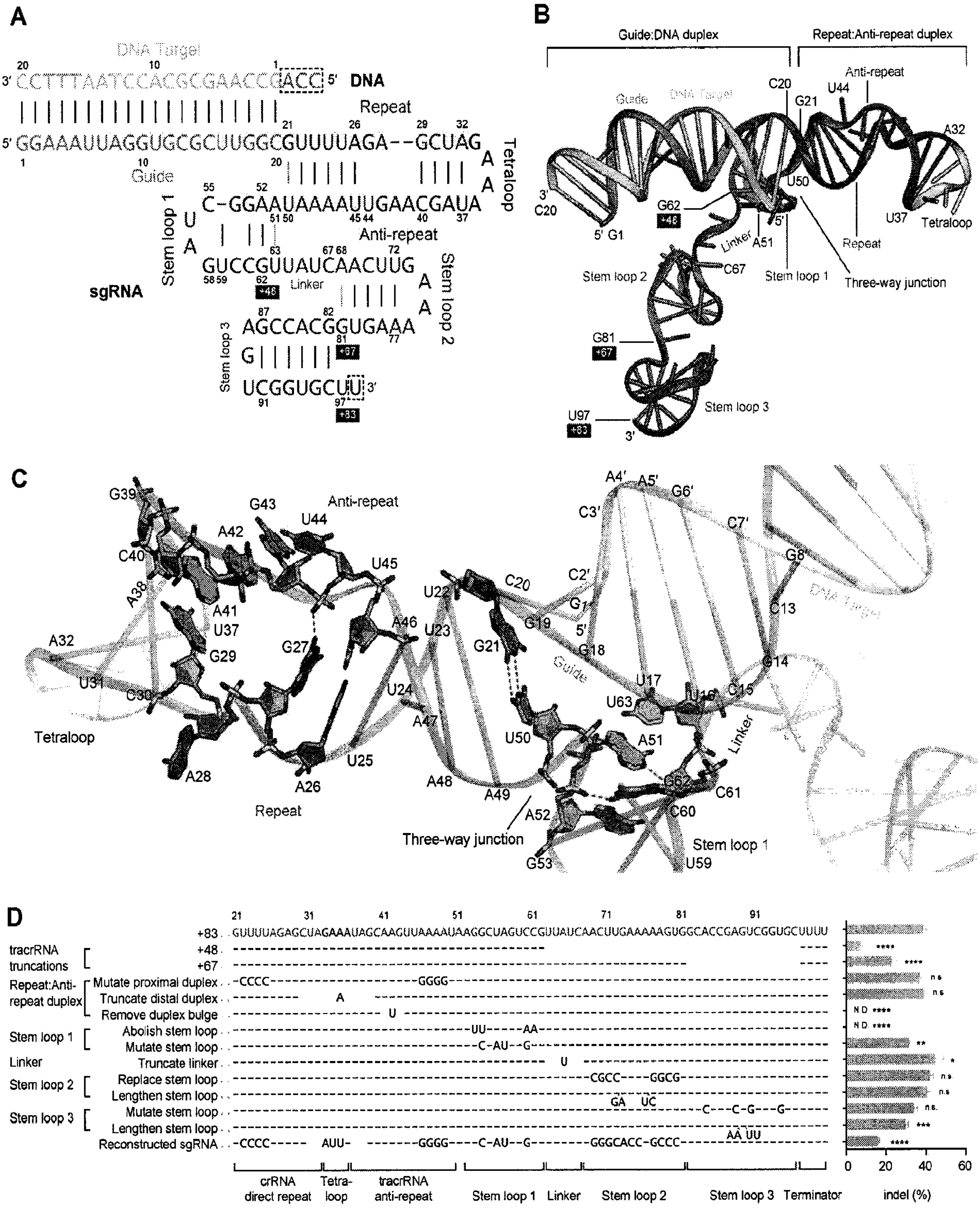

A
DNA Target
3' CCTTTTAATCCACGCGAACCGACC 5' DNA
Repeat
5' GGAAAUUAGGUGCGCUUGGCGUUUUAGA--GCUAG
Guide
Tetraloop
C-GGAAUAAAAUUGAACGAUA
Stem loop 1
Anti-repeat
GUCCGUUAUCAACUUG
Linker
Stem loop 2
AGCCACGGUGAAA
Stem loop 3
UCGGUGCUU 3'
sgRNA
+48
+67
+83
B
Guide:DNA duplex
Repeat:Anti-repeat duplex
Guide
DNA Target
Anti-repeat
C20
G21
U44
A32
U50
3' C20
5' G1
G62
Linker
A51
C67
U37
Tetraloop
Repeat
Stem loop 2
Stem loop 1
Three-way junction
G81
U97
3'
Stem loop 3
C
G39
G43
Anti-repeat
U44
A42
C40
U45
A38
A41
U37
A32
G29
G27
A46
U22
C20
U23
G21
G19
G1
G18
5'
Guide
U31
C30
U24
A47
U50
U17
U63
U16
C15
A51
Linker
Tetraloop
A28
U25
A26
Repeat
A48
A49
A52
G62
C61
C60
Three-way junction
G53
Stem loop 1
U59
A4'
A5'
G6'
C3'
C7'
C2'
G8'
C13
G14
DNA Target
D
21 31 41 51 61 71 81 91
+83 GUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU
tracrRNA truncations
+48
+67
Repeat:Anti-repeat duplex
Mutate proximal duplex -CCCC GGGG
Truncate distal duplex A
Remove duplex bulge U
Stem loop 1
Abolish stem loop UU AA
Mutate stem loop C-AU--G
Linker
Truncate linker U
Stem loop 2
Replace stem loop CGCC GGCG
Lengthen stem loop GA UC
Stem loop 3
Mutate stem loop C---C-G---G
Lengthen stem loop AA UU
Reconstructed sgRNA -CCCC AUU- GGGG C-AU--G GGGCACC-GCCC
crRNA direct repeat
Tetra-loop
tracrRNA anti-repeat
Stem loop 1
Linker
Stem loop 2
Stem loop 3
Terminator
****
n.s
N.D ****
**
*
***
0 20 40 60
indel (%)

FIG. 33A-D

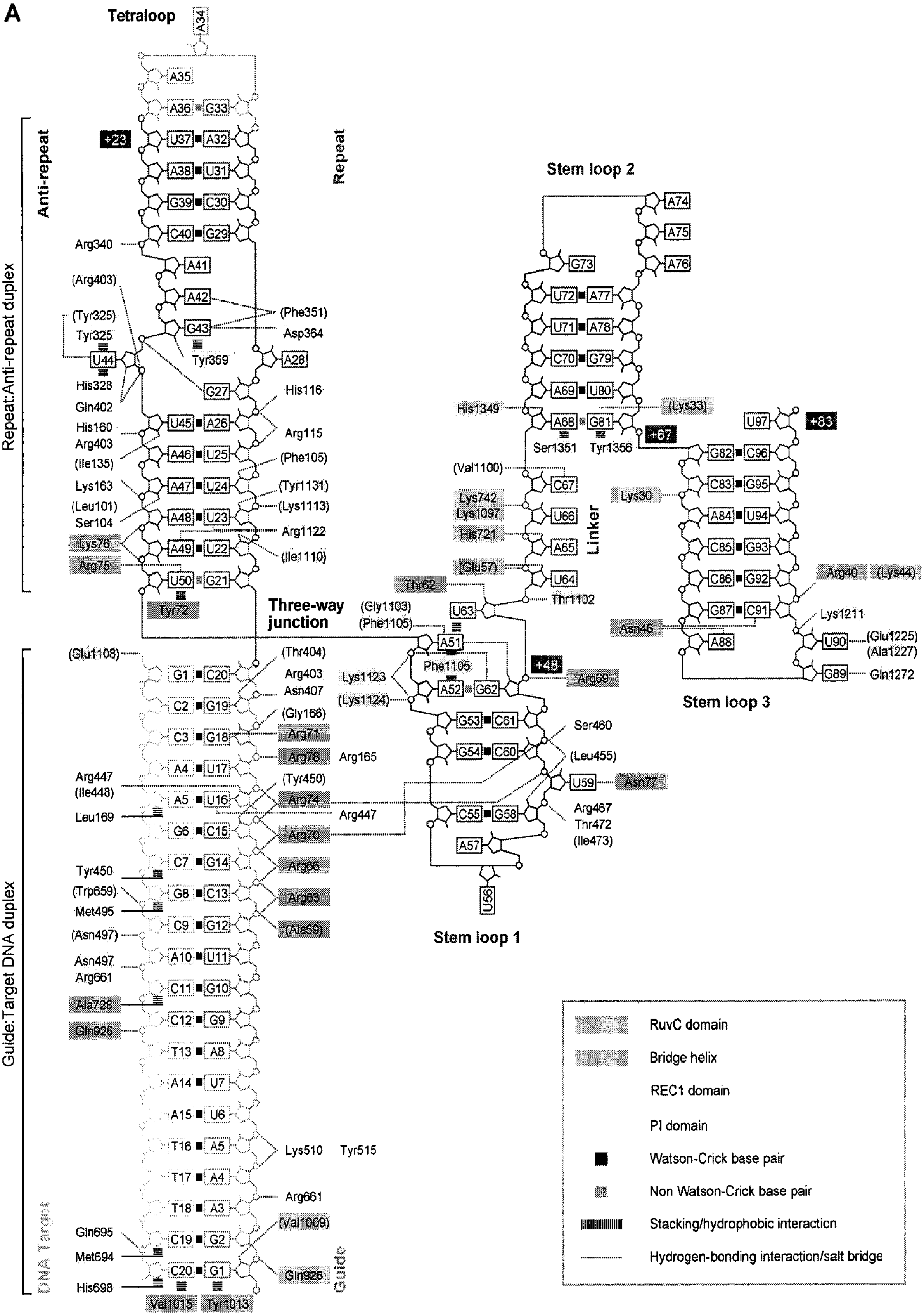

A
Tetraloop
A34
A35
A36 G33
+23
U37 A32
A38 U31
G39 C30
C40 G29
Anti-repeat
Repeat
Repeat:Anti-repeat duplex
Arg340
A41
(Arg403)
A42
G43
(Phe351)
Asp364
(Tyr325)
Tyr325
U44
Tyr359
A28
His328
G27
His116
Gln402
His160
U45 A26
Arg115
Arg403
A46 U25
(Ile135)
(Phe105)
Lys163
A47 U24
(Tyr1131)
(Leu101)
(Lys1113)
Ser104
A48 U23
Arg1122
Lys76
A49 U22
(Ile1110)
Arg75
U50 G21
Tyr72
Three-way junction
(Gly1103)
(Phe1105)
Stem loop 2
A74
A75
A76
G73
U72 A77
U71 A78
C70 G79
A69 U80
His1349
(Lys33)
A68 G81
U97
+83
Ser1351
Tyr1356
+67
G82 C96
(Val1100)
C67
C83 G95
Lys742
Lys1097
Lys30
U66
A84 U94
His721
Linker
A65
C85 G93
(Glu57)
U64
C86 G92
Arg40
(Lys44)
Thr62
Thr1102
U63
G87 C91
Lys1211
Asn46
A51
A88
U90
(Glu1225)
(Ala1227)
+48
Phe1105
Arg69
Lys1123
A52 G62
G89
Gln1272
(Lys1124)
Stem loop 3
(Glu1108)
(Thr404)
G1 C20
Arg403
Asn407
C2 G19
(Gly166)
G53 C61
Ser460
C3 G18
Arg71
Arg78
Arg165
G54 C60
(Leu455)
A4 U17
Arg447
(Ile448)
(Tyr450)
U59
Asn77
A5 U16
Arg74
Leu169
Arg447
C55 G58
Arg467
G6 C15
Arg70
Thr472
(Ile473)
A57
C7 G14
Tyr450
Arg66
(Trp659)
G8 C13
Arg63
Met495
U56
C9 G12
(Ala59)
(Asn497)
Stem loop 1
A10 U11
Asn497
Arg661
C11 G10
Ala728
C12 G9
Gln926
T13 A8
A14 U7
A15 U6
T16 A5
Lys510
Tyr515
T17 A4
Arg661
T18 A3
(Val1009)
Gln695
C19 G2
Met694
C20 G1
Gln926
His698
Val1015
Tyr1013
Guide:Target DNA duplex
DNA Target
Guide
RuvC domain
Bridge helix
REC1 domain
PI domain
■ Watson-Crick base pair
■ Non Watson-Crick base pair
Stacking/hydrophobic interaction
Hydrogen-bonding interaction/salt bridge

FIG. 34A

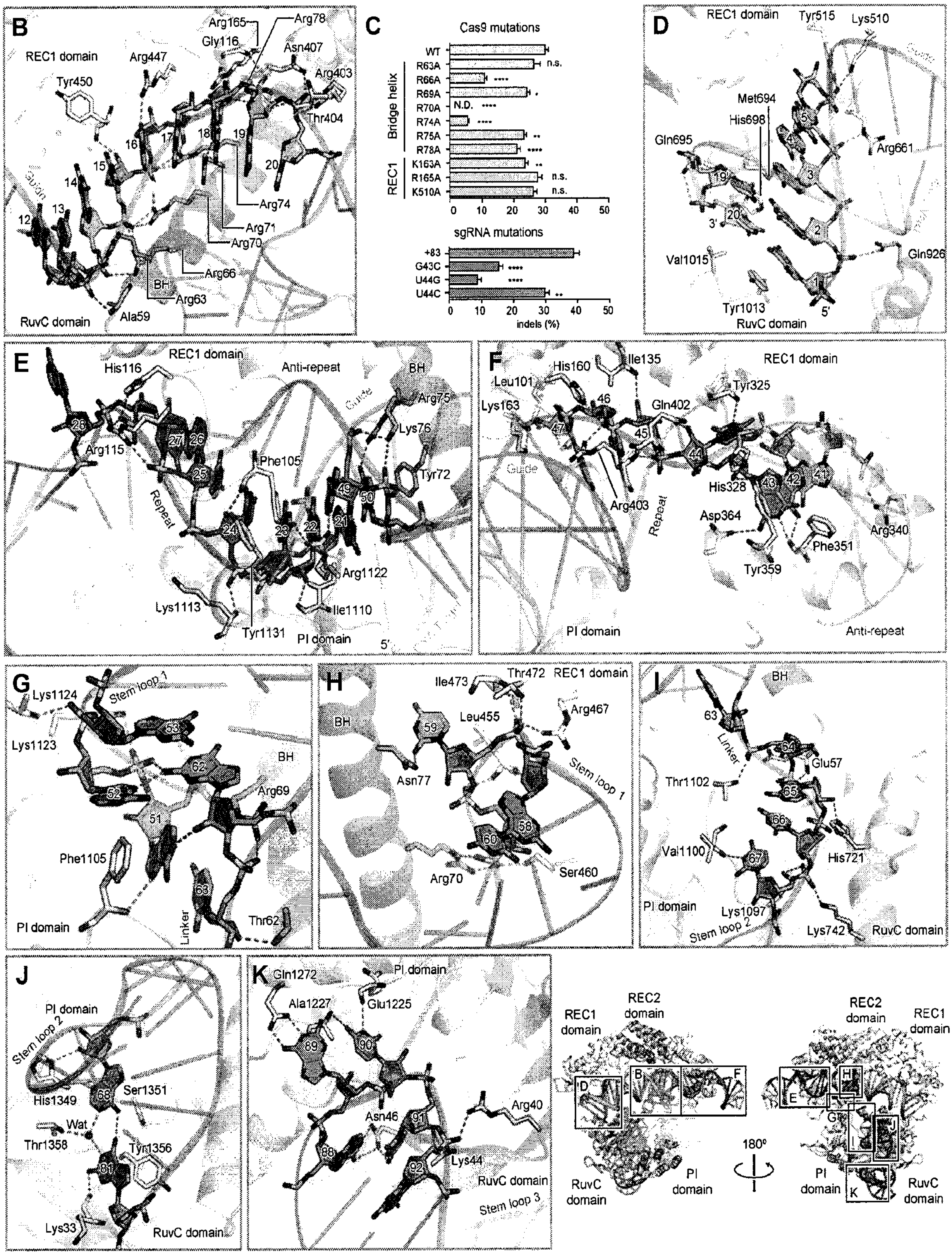

B
REC1 domain
Arg165
Gly116
Arg78
Asn407
Arg403
Thr404
Arg447
Tyr450
16
17
18
19
20
15
14
13
12
Arg74
Arg71
Arg70
Arg66
BH
Arg63
RuvC domain
Ala59
C
Cas9 mutations
WT
R63A n.s.
R66A ****
R69A *
R70A N.D. ****
R74A ****
R75A **
R78A ****
K163A **
R165A n.s.
K510A n.s.
Bridge helix
REC1
0 10 20 30 40 50
sgRNA mutations
+83
G43C ****
U44G ****
U44C **
0 10 20 30 40 50
indels (%)
D
REC1 domain
Tyr515
Lys510
Met694
His698
Gln695
Arg661
5
4
3
19
20
3'
2
Val1015
Gln926
1
Tyr1013
5'
RuvC domain
E
His116
REC1 domain
Anti-repeat
BH
Guide
Arg75
Lys76
28
27
26
Arg115
25
Phe105
Tyr72
49
50
Repeat
24
23
22
21
Arg1122
Lys1113
Ile1110
Tyr1131
PI domain
5'
F
Ile135
REC1 domain
His160
Leu101
Lys163
46
47
45
Gln402
Tyr325
44
Guide
Arg403
Repeat
His328
43
42
41
Asp364
Arg340
Phe351
Tyr359
PI domain
Anti-repeat
G
Lys1124
Stem loop 1
53
Lys1123
62
BH
52
Arg69
51
Phe1105
PI domain
63
Linker
Thr62
H
Ile473
Thr472
REC1 domain
BH
59
Leu455
Arg467
Asn77
Stem loop 1
60
58
Arg70
Ser460
I
BH
63
Linker
64
Glu57
Thr1102
65
66
Val1100
67
His721
PI domain
Lys1097
Stem loop 2
Lys742
RuvC domain
J
PI domain
Stem loop 2
68
Ser1351
His1349
Wat
Thr1358
Tyr1356
81
Lys33
RuvC domain
K
Gln1272
PI domain
Ala1227
Glu1225
69
90
Arg40
Asn46
91
88
Lys44
92
RuvC domain
Stem loop 3
REC1 domain
REC2 domain
D
B
F
RuvC domain
PI domain
180°
REC2 domain
REC1 domain
E
H
G
I
J
PI domain
K
RuvC domain

FIG. 34B-K

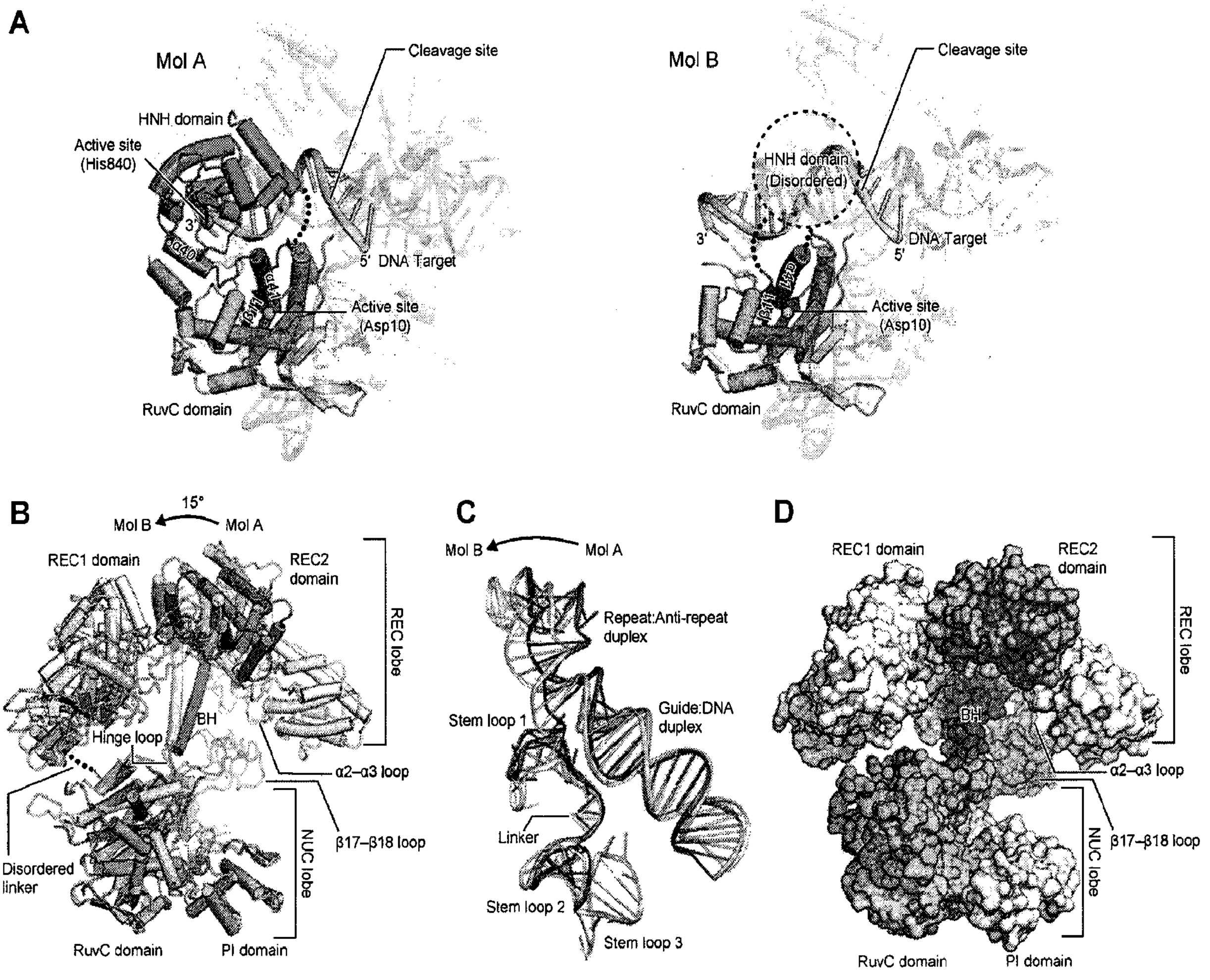

A
Mol A
Cleavage site
HNH domain
Active site
(His840)
3'
5' DNA Target
Active site
(Asp10)
RuvC domain
Mol B
Cleavage site
HNH domain
(Disordered)
3'
DNA Target
5'
Active site
(Asp10)
RuvC domain
B
15°
Mol B
Mol A
REC1 domain
REC2
domain
REC lobe
BH
Hinge loop
α2–α3 loop
β17–β18 loop
Disordered
linker
NUC lobe
RuvC domain
PI domain
C
Mol B
Mol A
Repeat:Anti-repeat
duplex
Guide:DNA
duplex
Stem loop 1
Linker
Stem loop 2
Stem loop 3
D
REC1 domain
REC2
domain
REC lobe
BH
α2–α3 loop
β17–β18 loop
NUC lobe
RuvC domain
PI domain

FIG. 35A-D

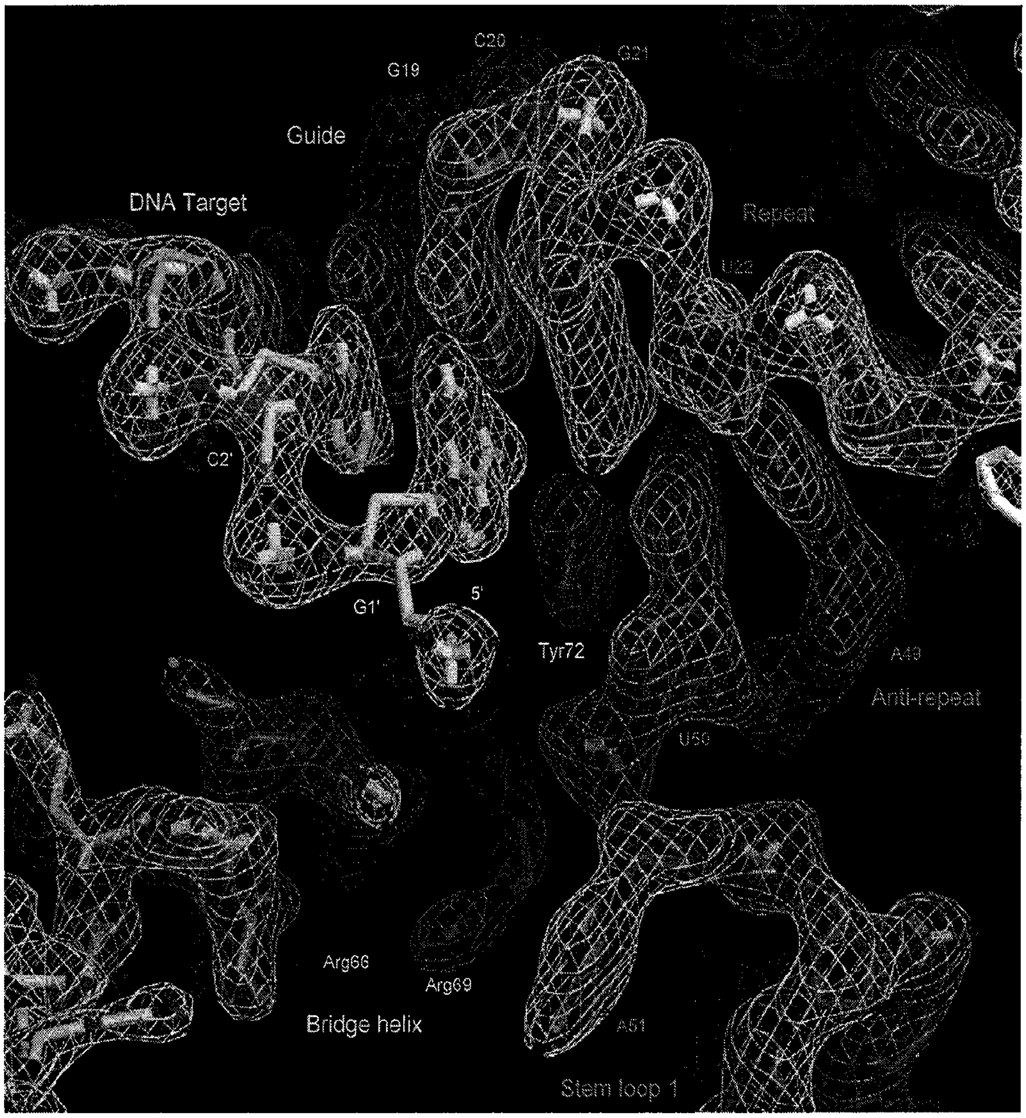

C20
G21
G19
Guide
DNA Target
Repeat
U22
C2'
G1'
5'
Tyr72
A49
Anti-repeat
U50
Arg66
Arg69
Bridge helix
A51
Stem loop 1

FIG. 37

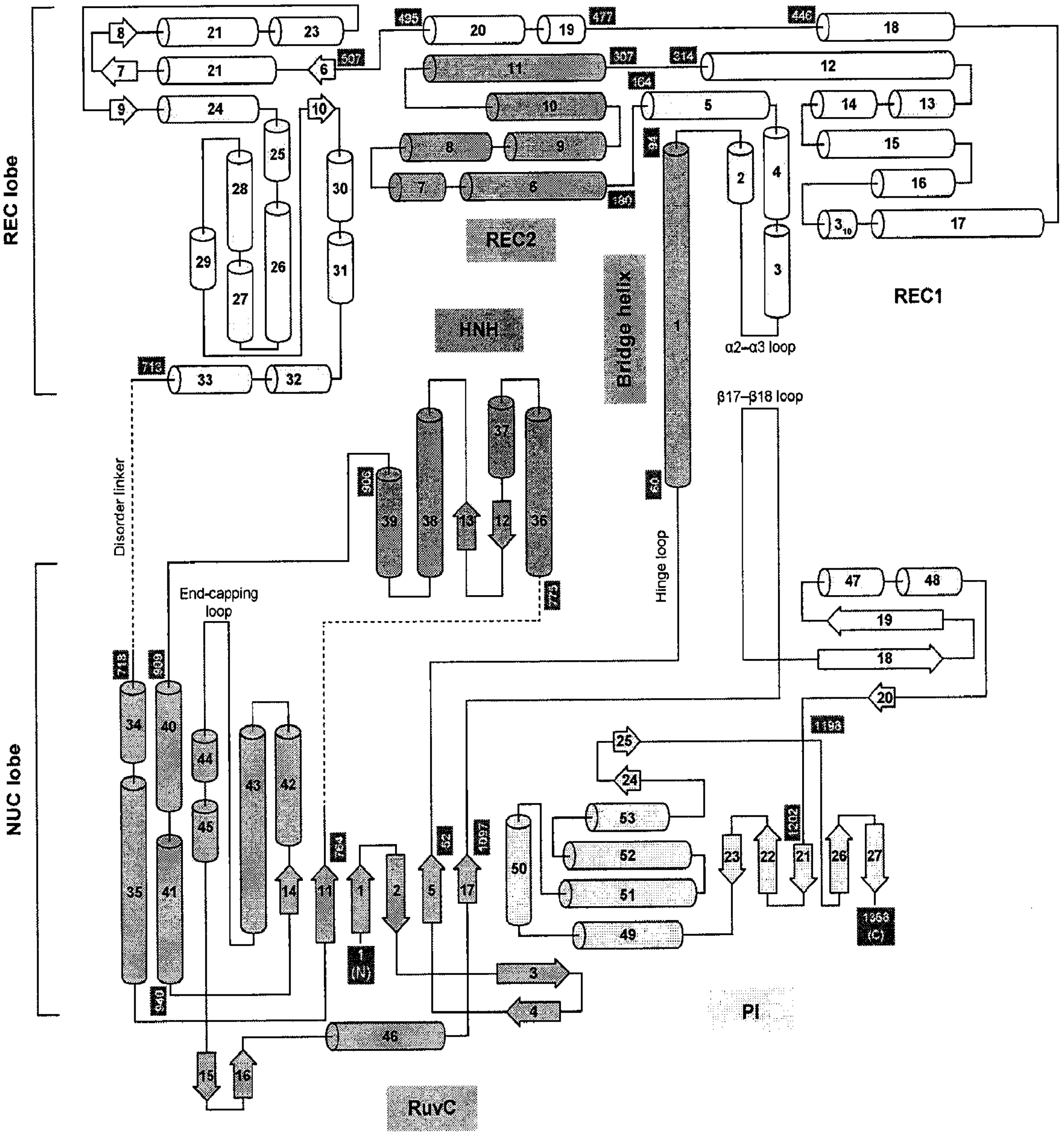

REC lobe
NUC lobe
REC2
HNH
Bridge helix
REC1
α2–α3 loop
β17–β18 loop
Disorder linker
End-capping loop
Hinge loop
RuvC
PI
495
477
446
507
307
314
164
94
180
713
906
60
775
718
909
940
754
52
1097
1198
1202
1
(N)
1368
(C)

FIG. 39

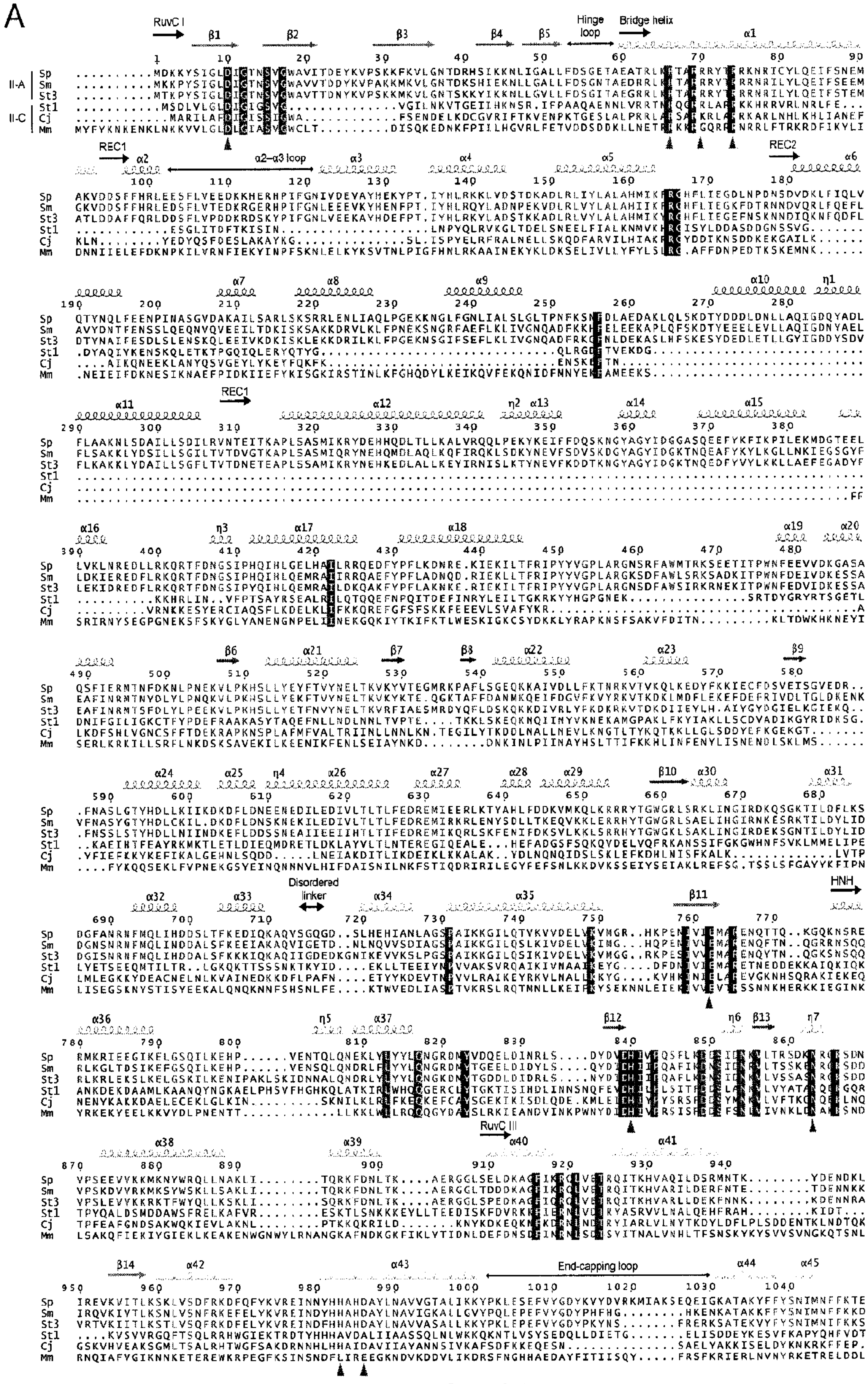
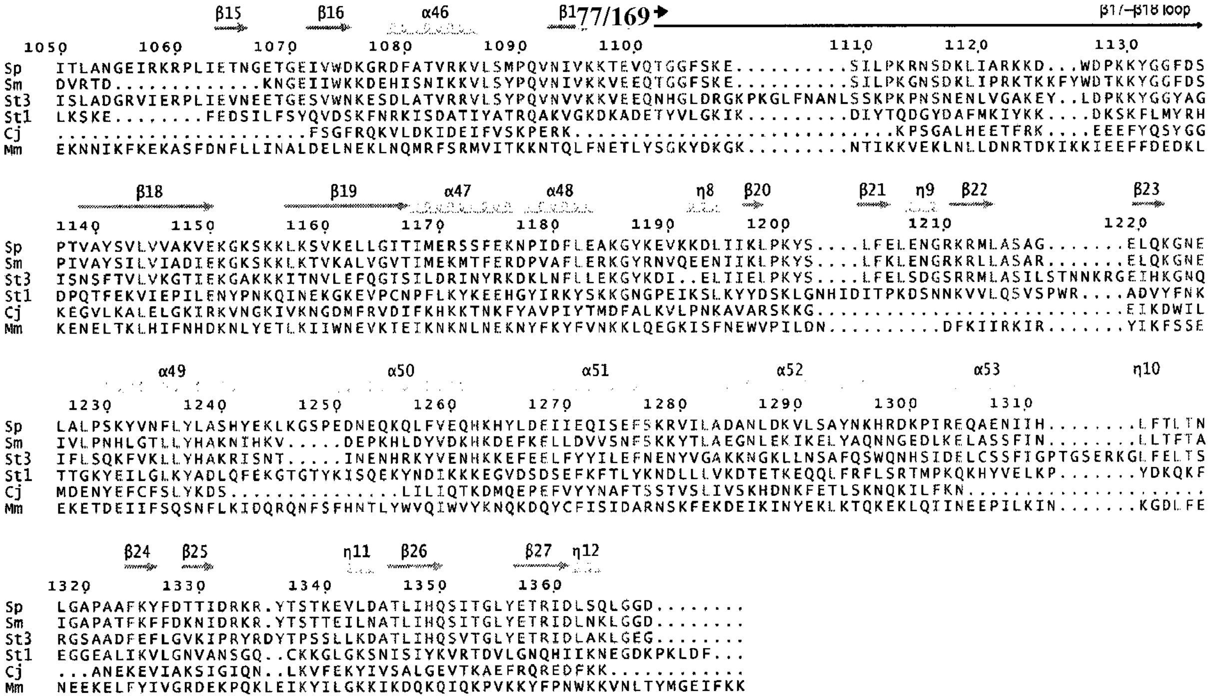

A
RuvC I
β1
β2
β3
β4
β5
Hinge loop
Bridge helix
α1
II-A
II-C
Sp
Sm
St3
St1
Cj
Mm
REC1
α2
α2–α3 loop
α3
α4
α5
REC2
α6
α7
α8
α9
α10
η1
α11
REC1
α12
η2
α13
α14
α15
α16
η3
α17
α18
α19
α20
β6
α21
β7
β8
α22
α23
β9
α24
α25
η4
α26
α27
α28
α29
β10
α30
α31
α32
α33
Disordered linker
α34
α35
β11
HNH
α36
η5
α37
β12
η6
β13
η7
α38
α39
RuvC III
α40
α41
β14
α42
α43
End-capping loop
α44
α45

FIG. 40A



```
                 β15       β16       α46          β177/169➔                                   β17–β18 loop
1050       1060       1070       1080       1090       1100                  1110       1120       1130
Sp   ITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKE..........SILPKRNSDKLIARKKD...WDPKKYGGFDS
Sm   DVRTD.............KNGEIIWKKDEHISNIKKVLSYPQVNIVKKVEEQTGGFSKE..........SILPKGNSDKLIPRKTKKFYWDTKKYGGFDS
St3  ISLADGRVIERPLIEVNEETGESVWNKESDLATVRRVLSYPQVNVVKKVEEQNHGLDRGKPKGLFNANLSSKPKPNSNENLVGAKEY..LDPKKYGGYAG
St1  LKSKE........FEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADETYVLGKIK.........DIYTQDGYDAFMKIYKK....DKSKFLMYRH
Cj   ......................FSGFRQKVLDKIDEIFVSKPERK............................KPSGALHEETFRK....EEEFYQSYGG
Mm   EKNNIKFKEKASFDNFLLINALDELNEKLNQMRFSRMVITKKNTQLFNETLYSGKYDKGK.........NTIKKVEKLNLLDNRTDKIKKIEEFFDEDKL

          β18               β19       α47      α48          η8   β20        β21  η9  β22            β23
1140       1150       1160       1170       1180       1190       1200            1210             1220
Sp   PTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYS....LFELENGRKRMLASAG.......ELQKGNE
Sm   PIVAYSILVIADIEKGKSKKLKTVKALVGVTIMEKMTFERDPVAFLERKGYRNVQEENIIKLPKYS....LFKLENGRKRLLASAR.......ELQKGNE
St3  ISNSFTVLVKGTIEKGAKKKITNVLEFQGTSILDRINYRKDKLNFLLEKGYKDI..ELIIELPKYS....LFELSDGSRRMLASILSTNNKRGEIHKGNQ
St1  DPQTFEKVIEPILENYPNKQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYDSKLGNHIDITPKDSNNKVVLQSVSPWR....ADVYFNK
Cj   KEGVLKALELGKIRKVNGKIVKNGDMFRVDIFKHKKTNKFYAVPIYTMDFALKVLPNKAVARSKKG...........................EIKDWIL
Mm   KENELTKLHIFNHDKNLYETLKIIWNEVKIEIKNKNLNEKNYFKYFVNKKLQEGKISFNEWVPILDN.........DFKIIRKIR........YIKFSSE

          α49                 α50                 α51                 α52                 α53           η10
 1230       1240       1250       1260       1270       1280       1290       1300       1310
Sp   LALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIH........LFTLTN
Sm   IVLPNHLGTLLYHAKNIHKV.....DEPKHLDYVDKHKDEFKELLDVVSNFSKKYTLAEGNLEKIKELYAQNNGEDLKELASSFIN........LLTFTA
St3  IFLSQKFVKLLYHAKRISNT.....INENHRKYVENHKKEFEELFYYILEFNENYVGAKKNGKLLNSAFQSWQNHSIDELCSSFIGPTGSERKGLFELTS
St1  TTGKYEILGLKYADLQFEKGTGTYKISQEKYNDIKKKEGVDSDSEFKFTLYKNDLLLVKDTETKEQQLFRFLSRTMPKQKHYVELKP.......YDKQKF
Cj   MDENYEFCFSLYKDS...............LILIQTKDMQEPEFVYYNAFTSSTVSLIVSKHDNKFETLSKNQKILFKN.....................
Mm   EKETDEIIFSQSNFLKIDQRQNFSFHNTLYWVQIWVYKNQKDQYCFISIDARNSKFEKDEIKINYEKLKTQKEKLQIINEEPILKIN.......KGDLFE

          β24   β25             η11  β26          β27  η12
1320       1330       1340       1350       1360
Sp   LGAPAAFKYFDTTIDRKR.YTSTKEVLDATLIHQSITGLYETRIDLSQLGGD........
Sm   IGAPATFKFFDKNIDRKR.YTSTTEILNATLIHQSITGLYETRIDLNKLGGD........
St3  RGSAADFEFLGVKIPRYRDYTPSSLLKDATLIHQSVTGLYETRIDLAKLGEG........
St1  EGGEALIKVLGNVANSGQ..CKKGLGKSNISIYKVRTDVLGNQHIIKNEGDKPKLDF...
Cj   ...ANEKEVIAKSIGIQN..LKVFEKYIVSALGEVTKAEFRQREDFKK............
Mm   NEEKELFYIVGRDEKPQKLEIKYILGKKIKDQKQIQKPVKKYFPNWKKVNLTYMGEIFKK
```

FIG. 40B

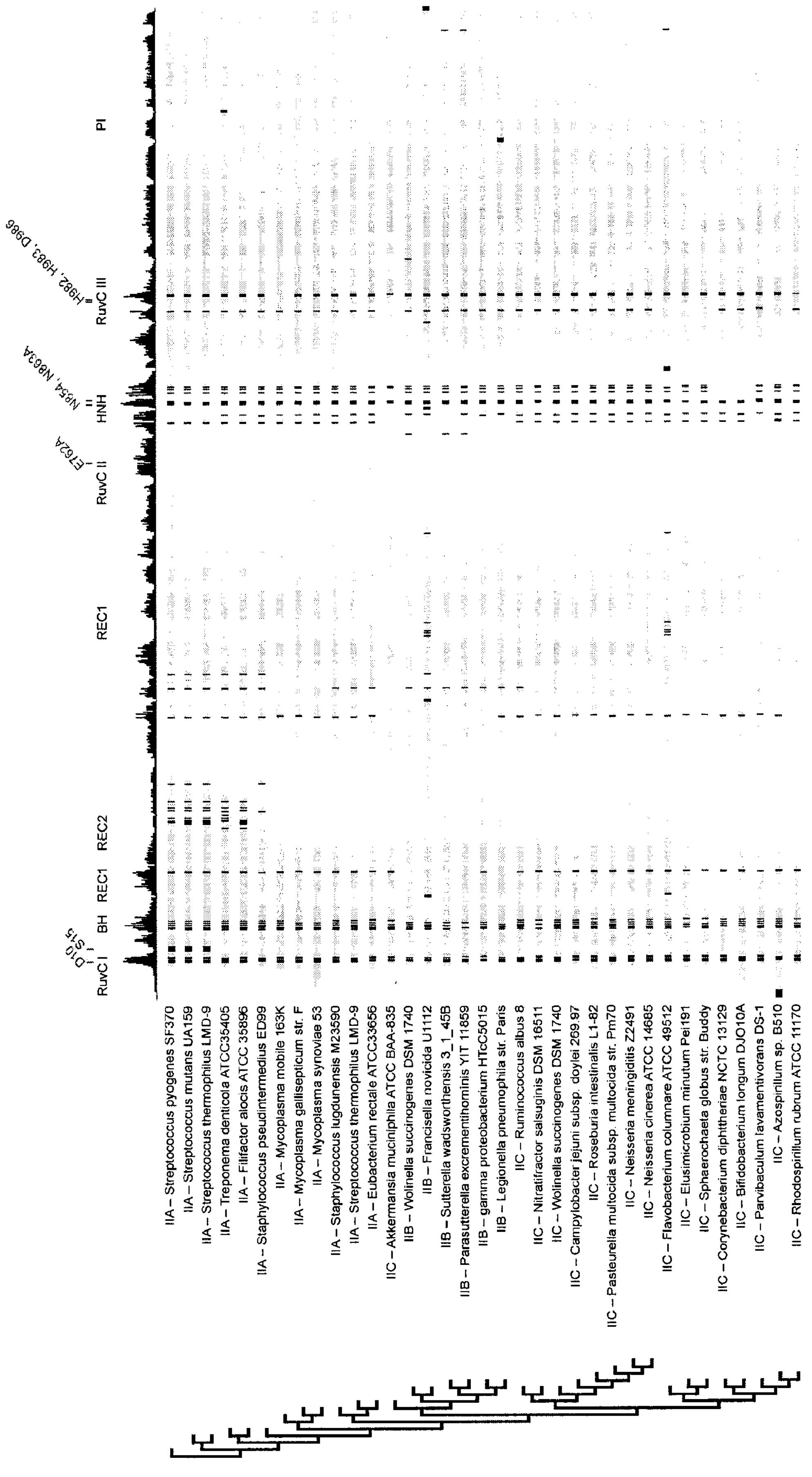

D10
S15
RuvC I
BH
REC1
REC2
REC1
RuvC II
E762A
HNH
N854, N863A
RuvC III
H982, H983, D986
PI
IIA – Streptococcus pyogenes SF370
IIA – Streptococcus mutans UA159
IIA – Streptococcus thermophilus LMD-9
IIA – Treponema denticola ATCC35405
IIA – Filifactor alocis ATCC 35896
IIA – Staphylococcus pseudintermedius ED99
IIA – Mycoplasma mobile 163K
IIA – Mycoplasma gallisepticum str. F
IIA – Mycoplasma synoviae 53
IIA – Staphylococcus lugdunensis M23590
IIA – Streptococcus thermophilus LMD-9
IIA – Eubacterium rectale ATCC33656
IIC – Akkermansia muciniphila ATCC BAA-835
IIB – Wolinella succinogenes DSM 1740
IIB – Francisella novicida U1112
IIB – Sutterella wadsworthensis 3_1_45B
IIB – Parasutterella excrementihominis YIT 11859
IIB – gamma proteobacterium HTcC5015
IIB – Legionella pneumophila str. Paris
IIC – Ruminococcus albus 8
IIC – Nitratifractor salsuginis DSM 16511
IIC – Wolinella succinogenes DSM 1740
IIC – Campylobacter jejuni subsp. doylei 269.97
IIC – Roseburia intestinalis L1-82
IIC – Pasteurella multocida subsp. multocida str. Pm70
IIC – Neisseria meningitidis Z2491
IIC – Neisseria cinerea ATCC 14685
IIC – Flavobacterium columnare ATCC 49512
IIC – Elusimicrobium minutum Pei191
IIC – Sphaerochaeta globus str. Buddy
IIC – Corynebacterium diphtheriae NCTC 13129
IIC – Bifidobacterium longum DJO10A
IIC – Parvibaculum lavamentivorans DS-1
IIC – Azospirillum sp. B510
IIC – Rhodospirillum rubrum ATCC 11170

FIG. 41

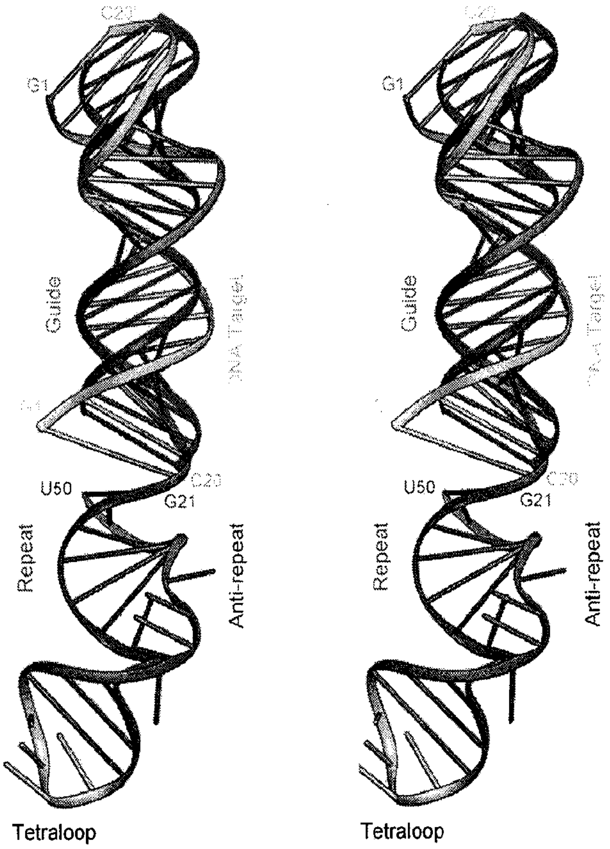

C20'
G1
Guide
DNA Target
U50
C20
G21
Repeat
Anti-repeat
Tetraloop
C20'
G1
Guide
DNA Target
U50
C20
G21
Repeat
Anti-repeat
Tetraloop

FIG. 42

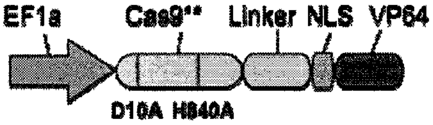


FIG. 43

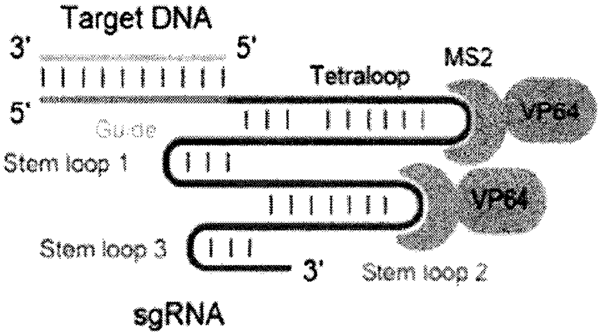

Target DNA
3'
5'
5'
Guide
Tetraloop
MS2
VP64
Stem loop 1
VP64
Stem loop 3
3'
Stem loop 2
sgRNA

FIG. 44

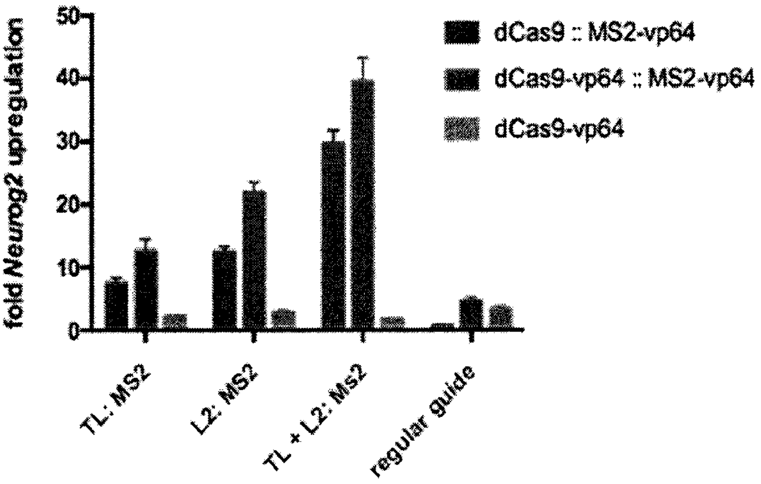

fold *Neurog2* upregulation
50
40
30
20
10
0
dCas9 :: MS2-vp64
dCas9-vp64 :: MS2-vp64
dCas9-vp64
TL: MS2
L2: MS2
TL + L2: Ms2
regular guide

FIG. 45

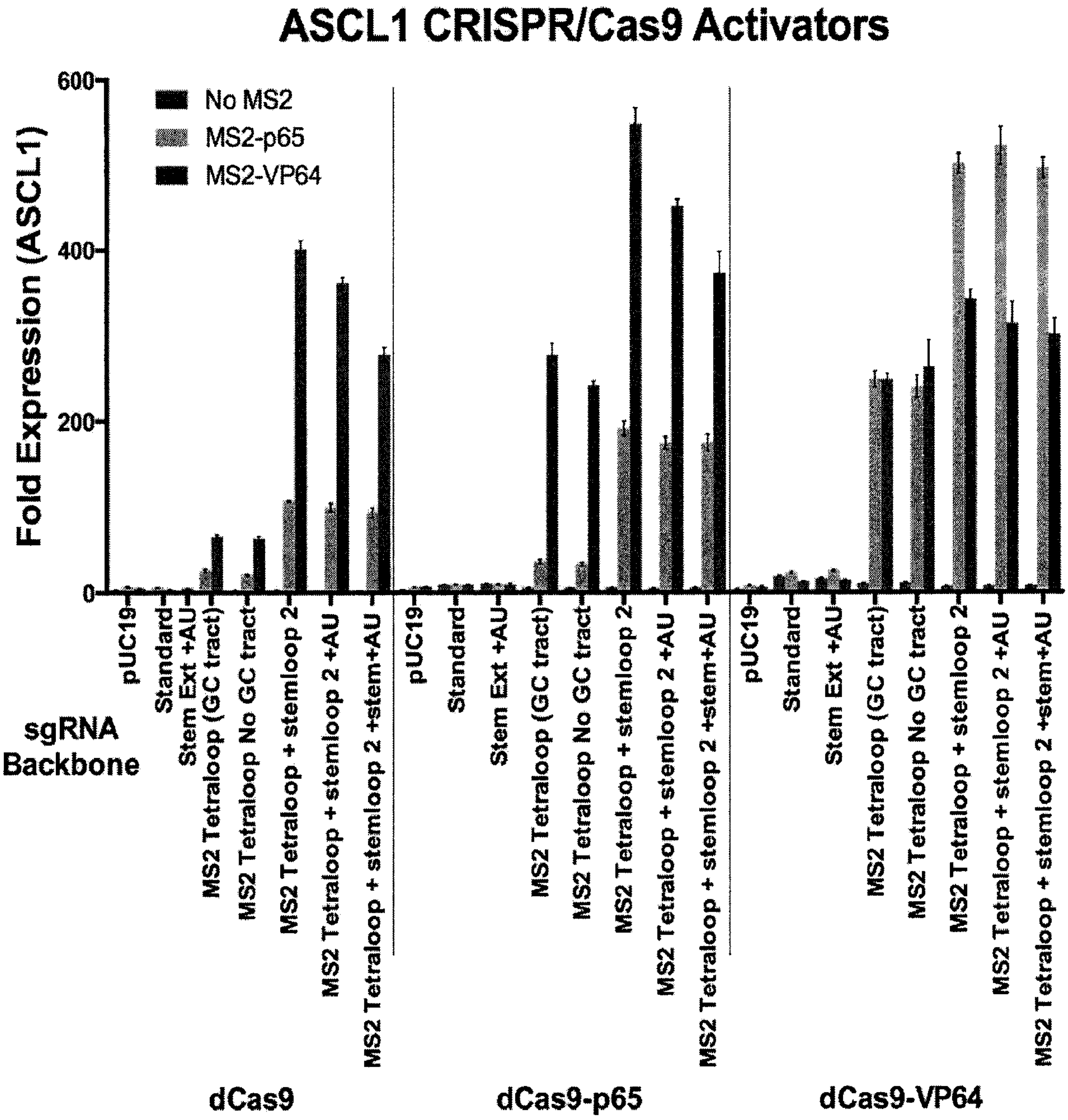

ASCL1 CRISPR/Cas9 Activators
Fold Expression (ASCL1)
600
400
200
0
No MS2
MS2-p65
MS2-VP64
sgRNA Backbone
pUC19
Standard
Stem Ext +AU
MS2 Tetraloop (GC tract)
MS2 Tetraloop No GC tract
MS2 Tetraloop + stemloop 2
MS2 Tetraloop + stemloop 2 +AU
MS2 Tetraloop + stemloop 2 +stem+AU
dCas9
dCas9-p65
dCas9-VP64

FIG. 46

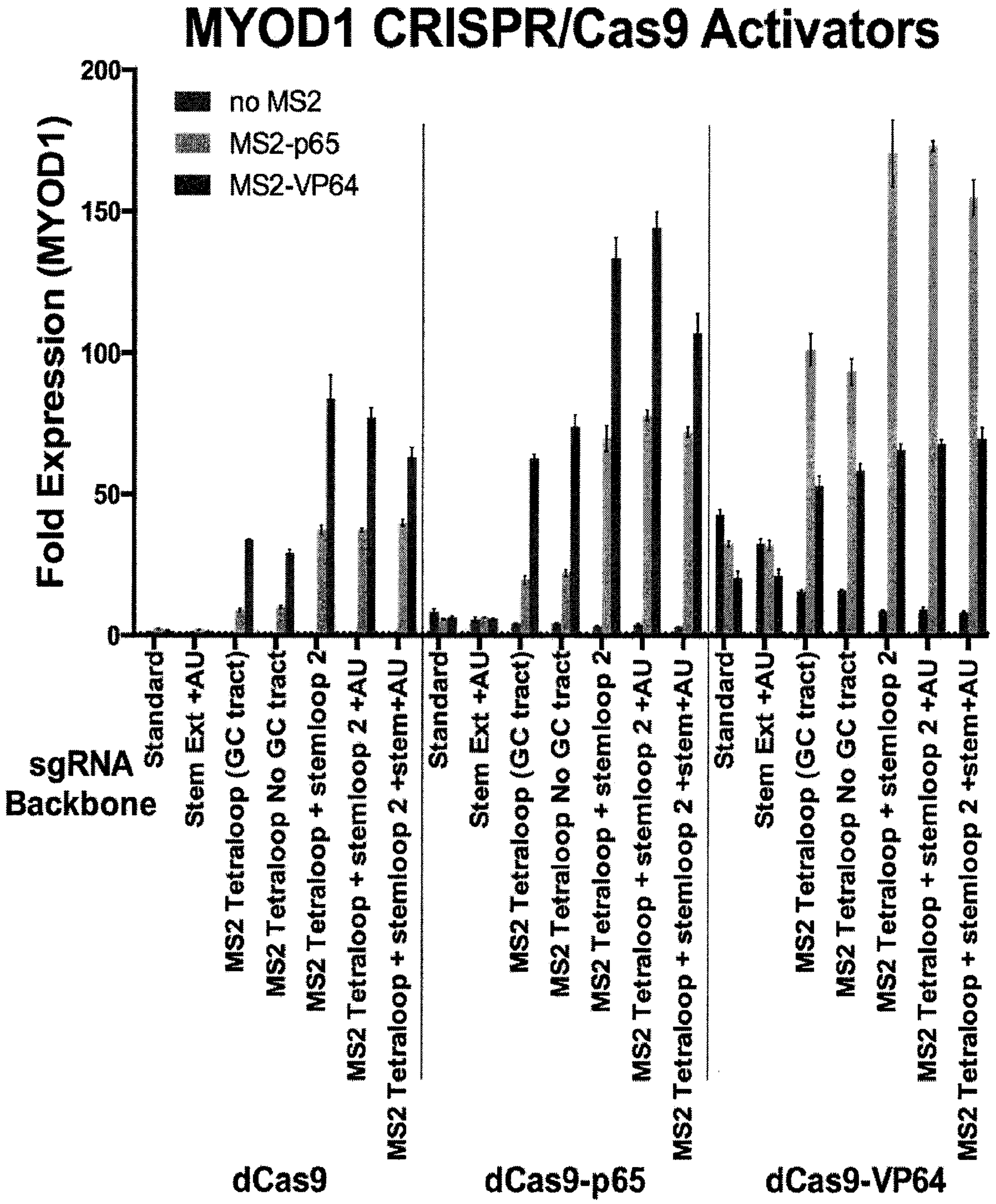

MYOD1 CRISPR/Cas9 Activators
Fold Expression (MYOD1)
200
150
100
50
0
no MS2
MS2-p65
MS2-VP64
sgRNA Backbone
Standard
Stem Ext +AU
MS2 Tetraloop (GC tract)
MS2 Tetraloop No GC tract
MS2 Tetraloop + stemloop 2
MS2 Tetraloop + stemloop 2 +AU
MS2 Tetraloop + stemloop 2 +stem+AU
dCas9
dCas9-p65
dCas9-VP64

FIG. 47

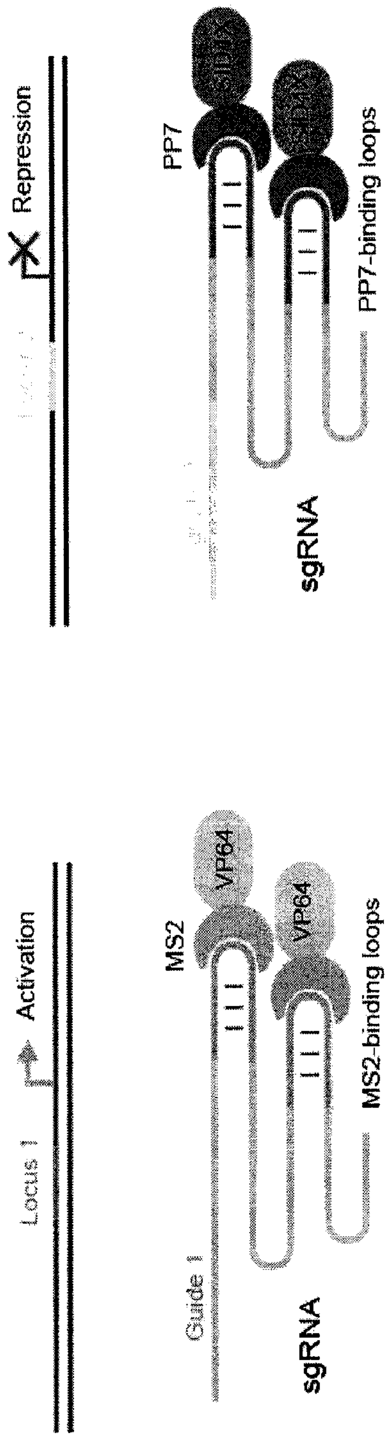

Repression
PP7
SID4X
SID4X
PP7-binding loops
sgRNA
Activation
MS2
VP64
VP64
MS2-binding loops
Locus 1
Guide 1
sgRNA

FIG. 48

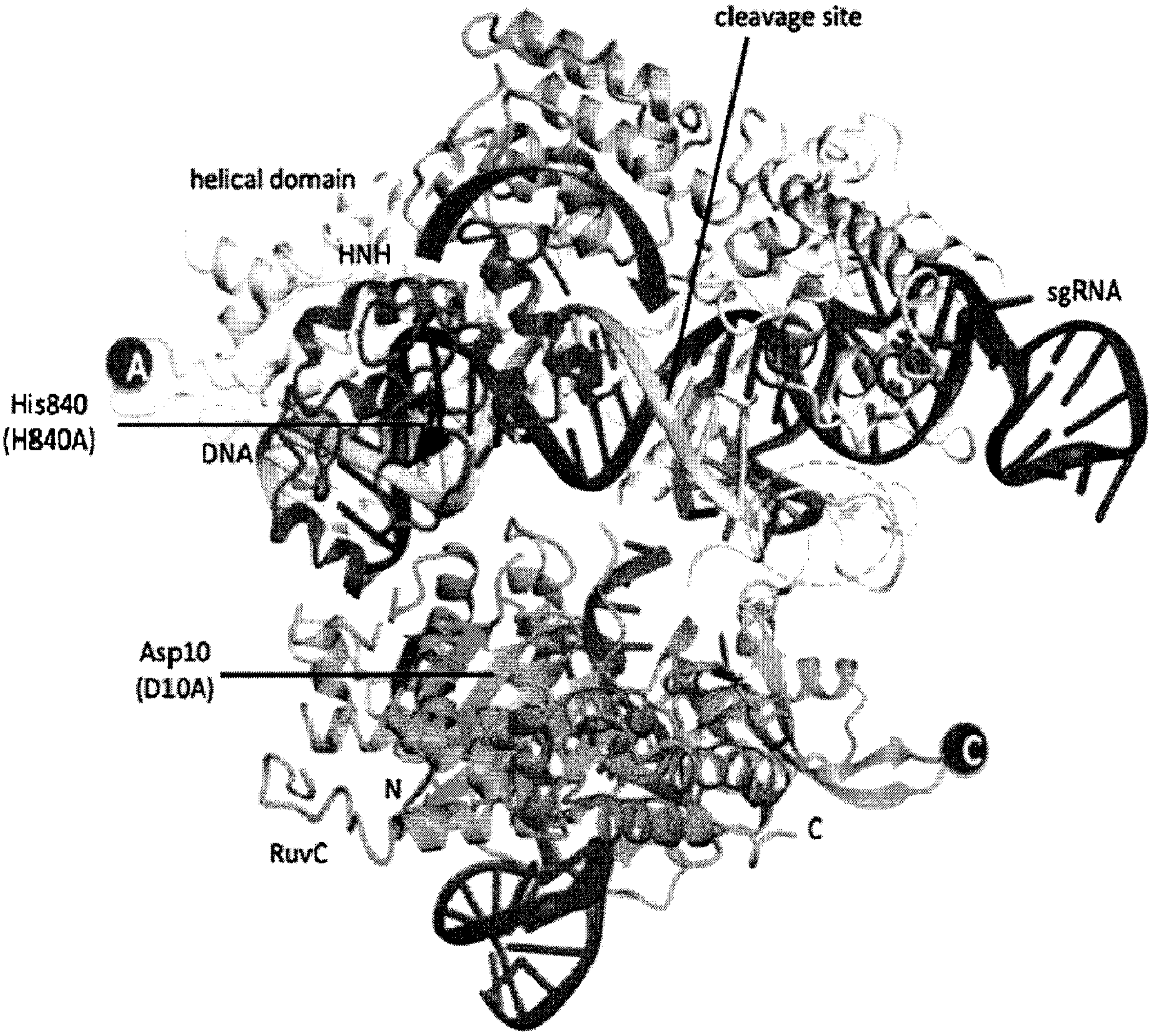

cleavage site
helical domain
HNH
sgRNA
A
His840
(H840A)
DNA
Asp10
(D10A)
C
N
RuvC
C

FIG. 49

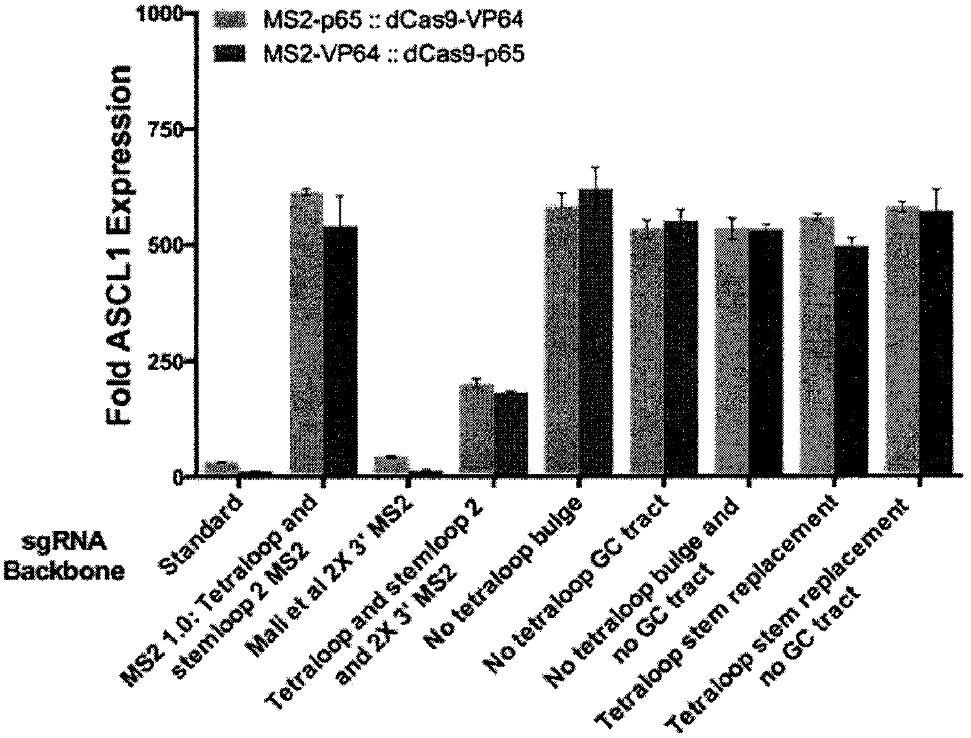

MS2-p65 :: dCas9-VP64
MS2-VP64 :: dCas9-p65
Fold ASCL1 Expression
1000
750
500
250
0
sgRNA Backbone
Standard
MS2 1.0: Tetraloop and stemloop 2 MS2
Mali et al 2X 3' MS2
Tetraloop and stemloop 2 and 2X 3' MS2
No tetraloop bulge
No tetraloop GC tract
No tetraloop bulge and no GC tract
Tetraloop stem replacement
Tetraloop stem replacement no GC tract

FIG. 50

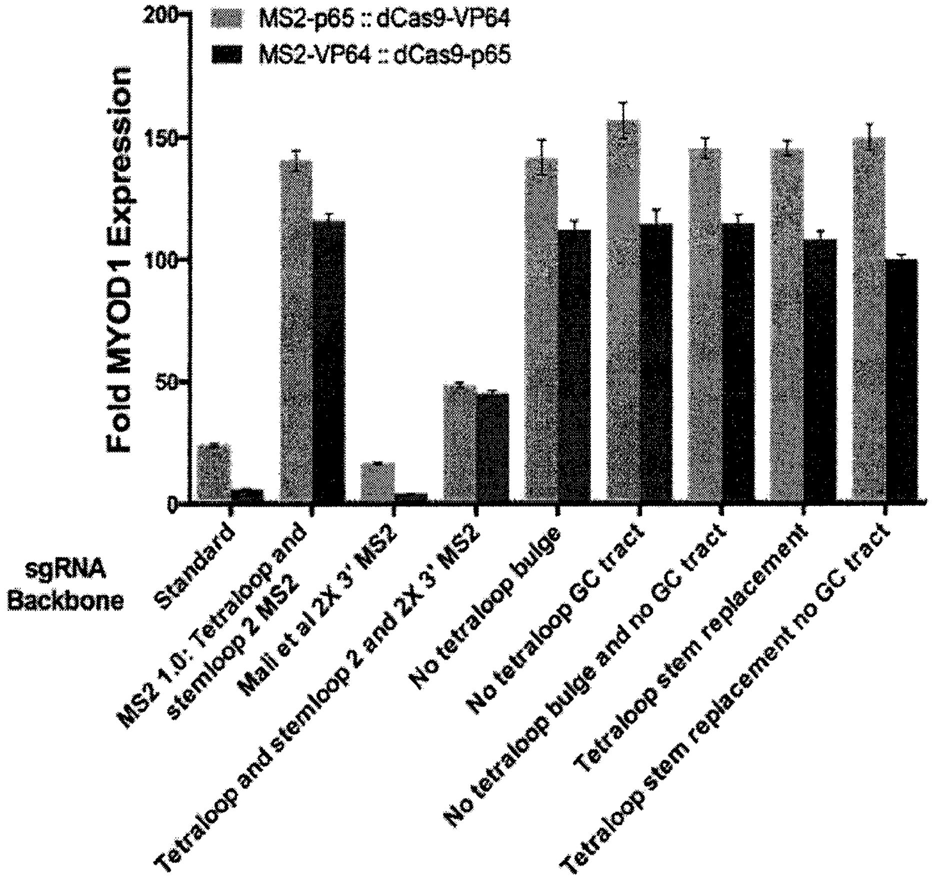

200
150
100
50
0
Fold MYOD1 Expression
MS2-p65 :: dCas9-VP64
MS2-VP64 :: dCas9-p65
sgRNA Backbone
Standard
MS2 1.0: Tetraloop and stemloop 2 MS2
Mali et al 2X 3' MS2
Tetraloop and stemloop 2 and 2X 3' MS2
No tetraloop bulge
No tetraloop GC tract
No tetraloop bulge and no GC tract
Tetraloop stem replacement
Tetraloop stem replacement no GC tract

FIG. 51

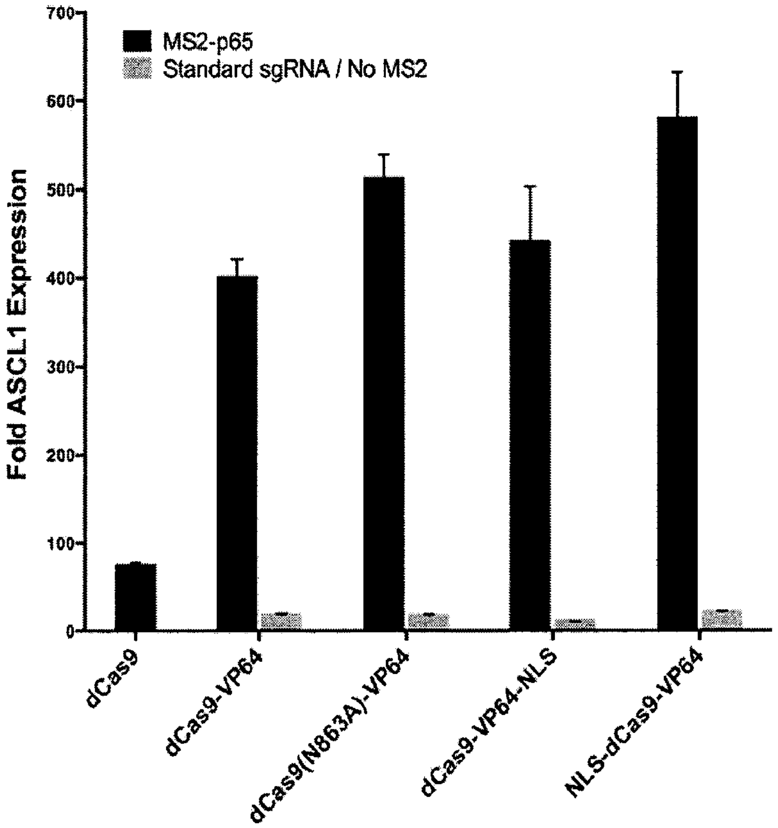

700
600
500
400
300
200
100
0
Fold ASCL1 Expression
MS2-p65
Standard sgRNA / No MS2
dCas9
dCas9-VP64
dCas9(N863A)-VP64
dCas9-VP64-NLS
NLS-dCas9-VP64

FIG. 52

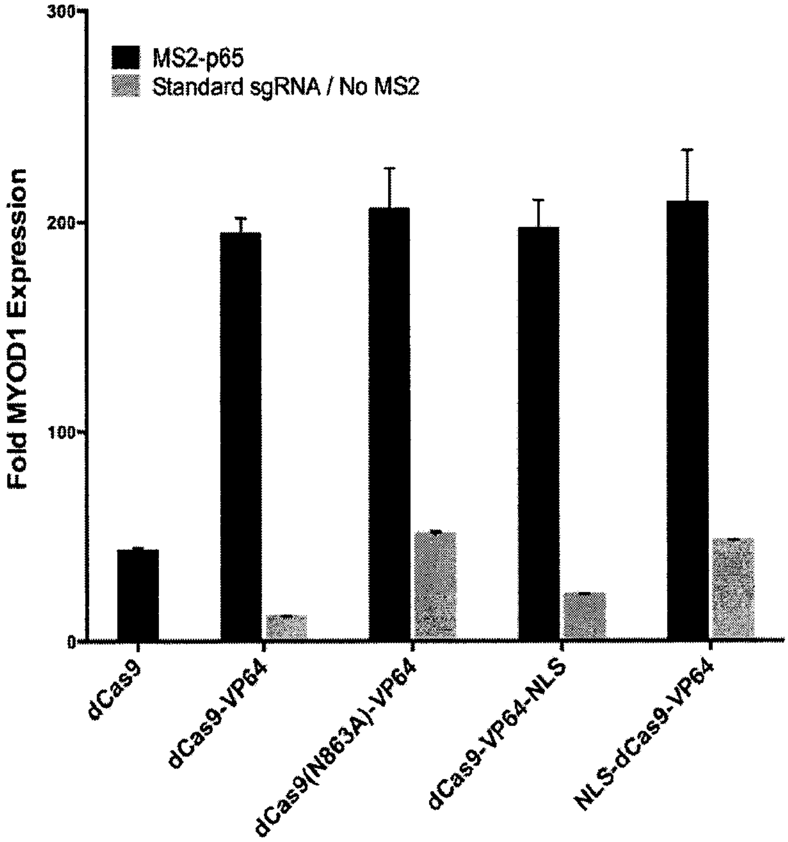

300
200
100
0
Fold MYOD1 Expression
MS2-p65
Standard sgRNA / No MS2
dCas9
dCas9-VP64
dCas9(N863A)-VP64
dCas9-VP64-NLS
NLS-dCas9-VP64

FIG. 53

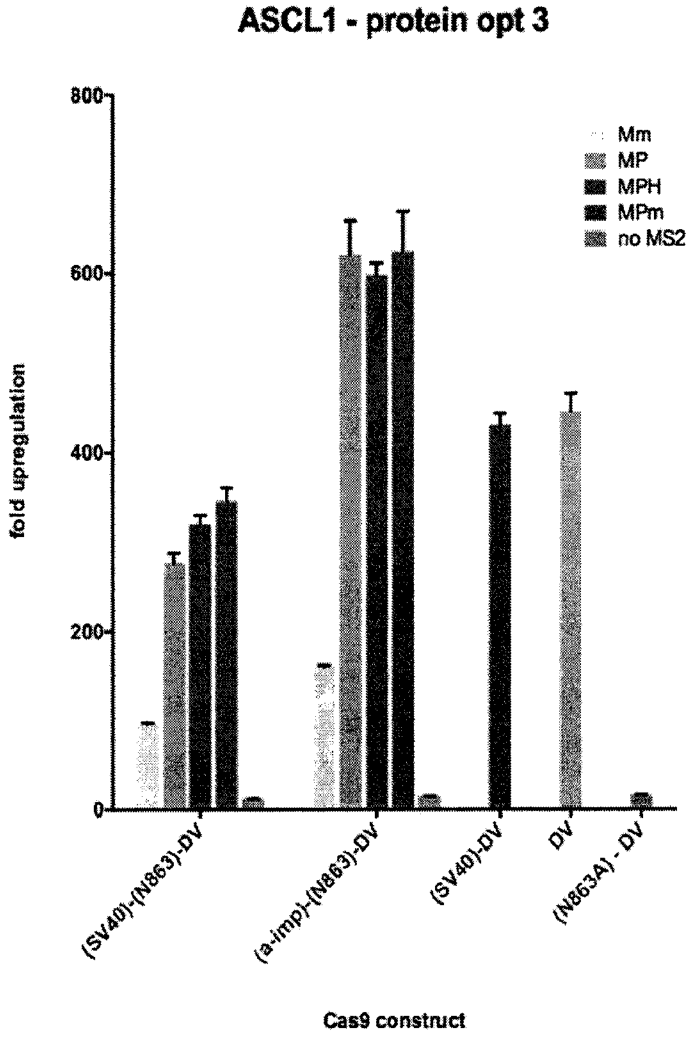

ASCL1 - protein opt 3
800
600
400
200
0
fold upregulation
Mm
MP
MPH
MPm
no MS2
(SV40)-(N863)-DV
(a-imp)-(N863)-DV
(SV40)-DV
DV
(N863A) - DV
Cas9 construct

FIG. 54

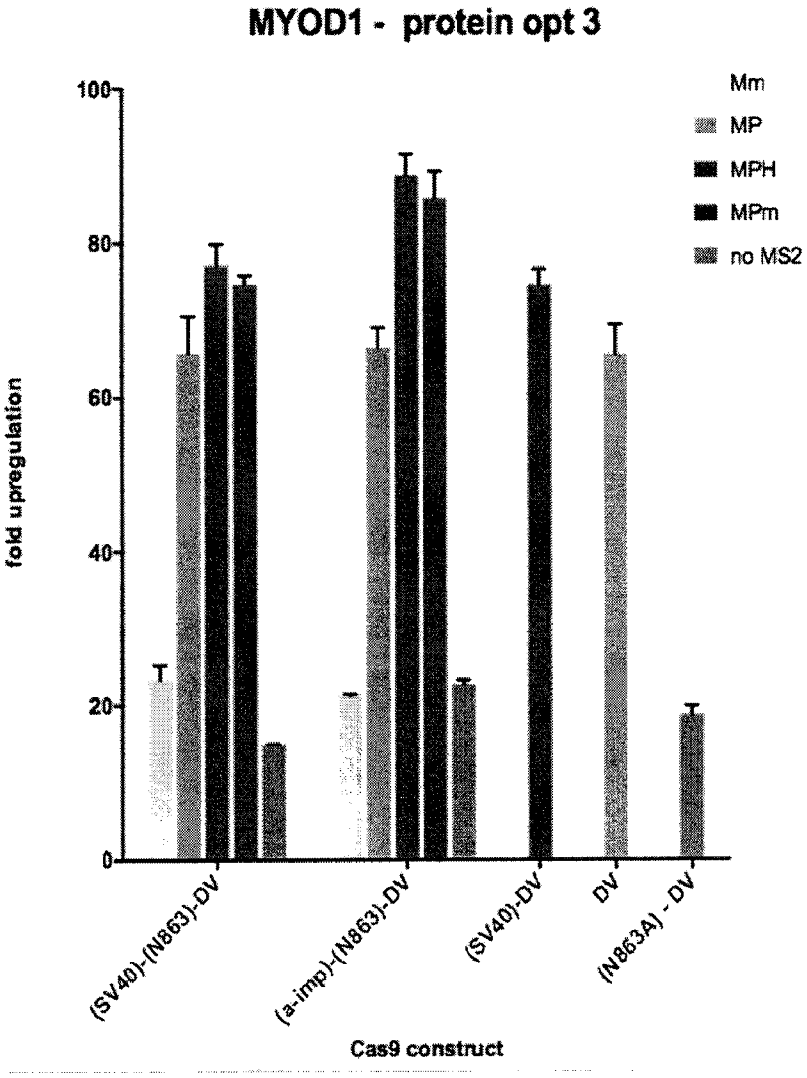

MYOD1 - protein opt 3
fold upregulation
100
80
60
40
20
0
Mm
MP
MPH
MPm
no MS2
(SV40)-(N863)-DV
(a-imp)-(N863)-DV
(SV40)-DV
DV
(N863A) - DV
Cas9 construct

FIG. 55

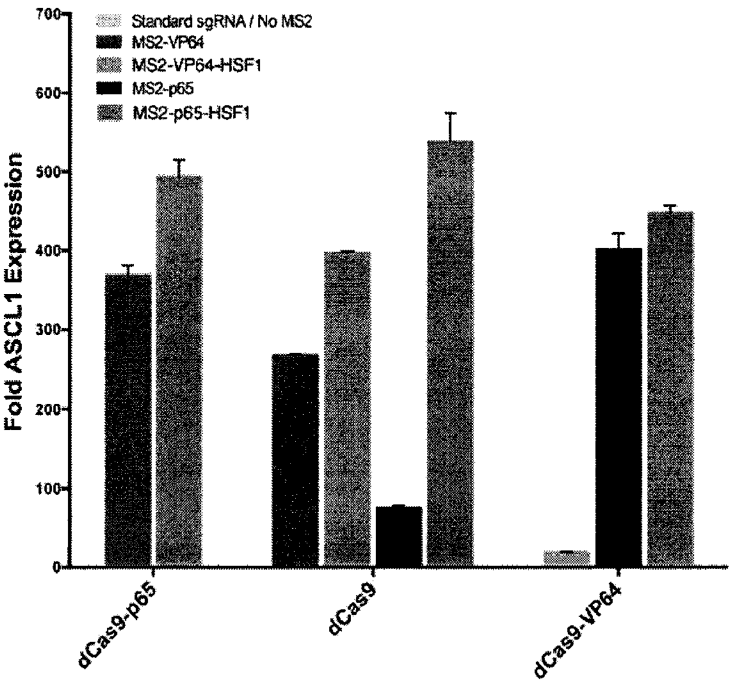

Standard sgRNA / No MS2
MS2-VP64
MS2-VP64-HSF1
MS2-p65
MS2-p65-HSF1
Fold ASCL1 Expression
700
600
500
400
300
200
100
0
dCas9-p65
dCas9
dCas9-VP64

FIG. 56

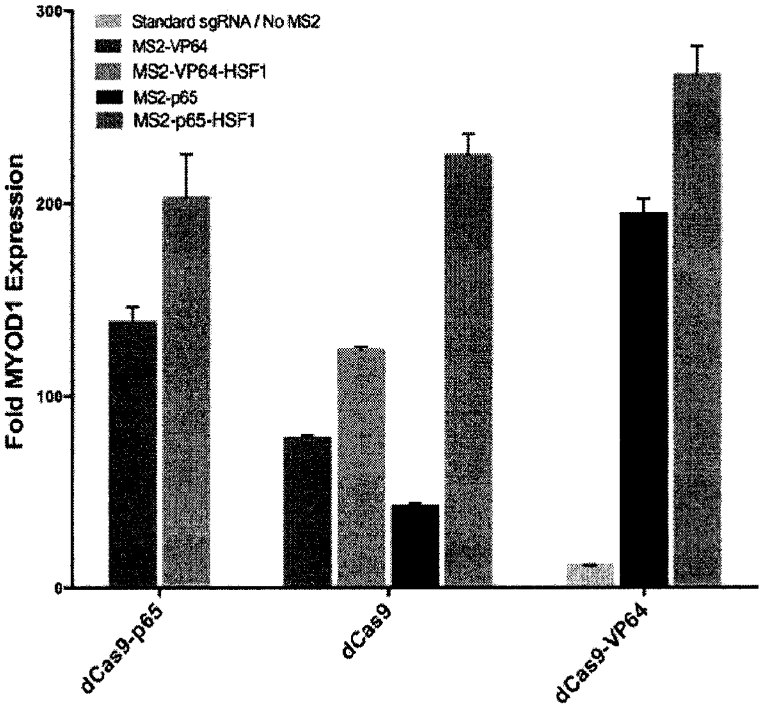

Standard sgRNA / No MS2
MS2-VP64
MS2-VP64-HSF1
MS2-p65
MS2-p65-HSF1
Fold MYOD1 Expression
300
200
100
0
dCas9-p65
dCas9
dCas9-VP64

FIG. 57

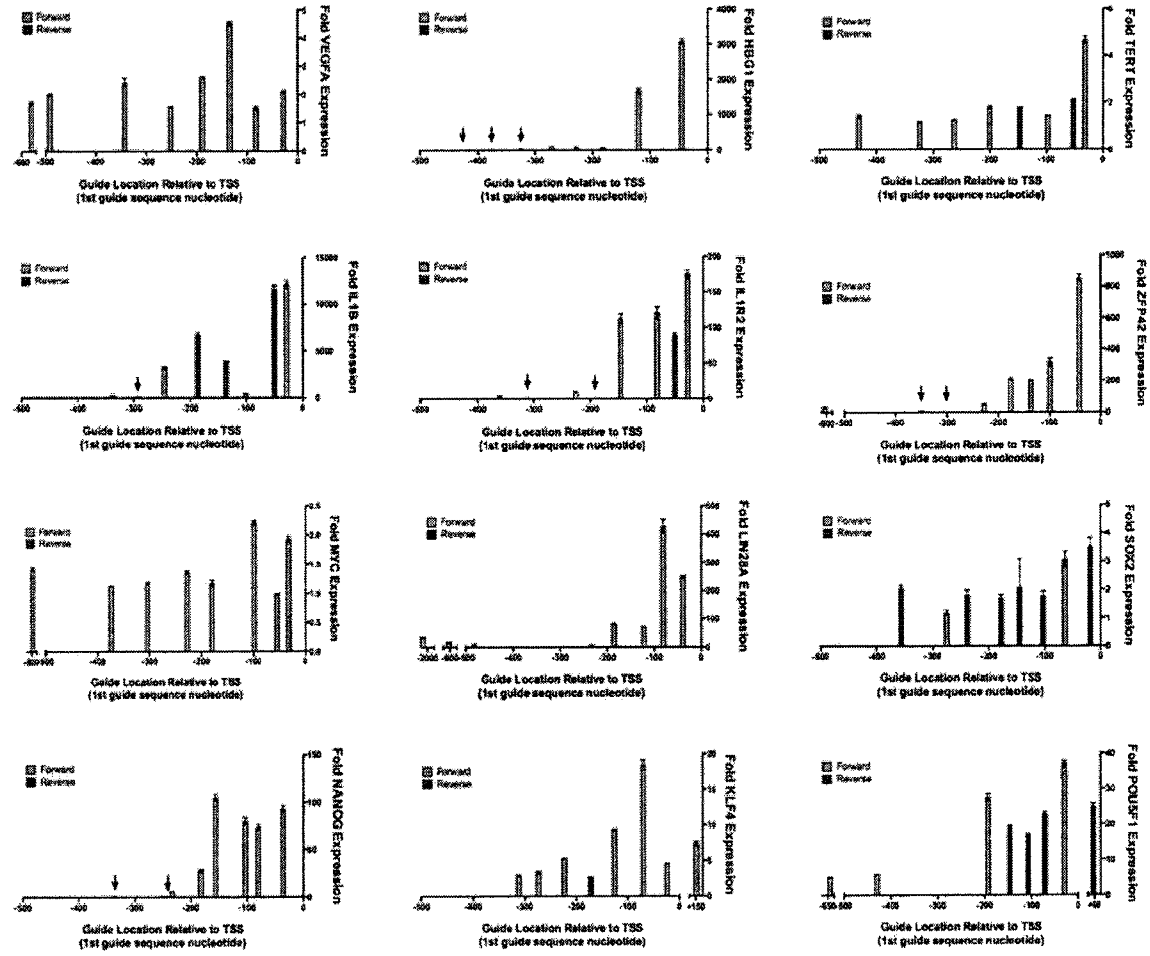

Forward
Reverse
Fold VEGFA Expression
Fold HBG1 Expression
Fold TERT Expression
Fold IL1B Expression
Fold IL1R2 Expression
Fold ZFP42 Expression
Fold MYC Expression
Fold LIN28A Expression
Fold SOX2 Expression
Fold NANOG Expression
Fold KLF4 Expression
Fold POU5F1 Expression
Guide Location Relative to TSS
(1st guide sequence nucleotide)

FIG. 58

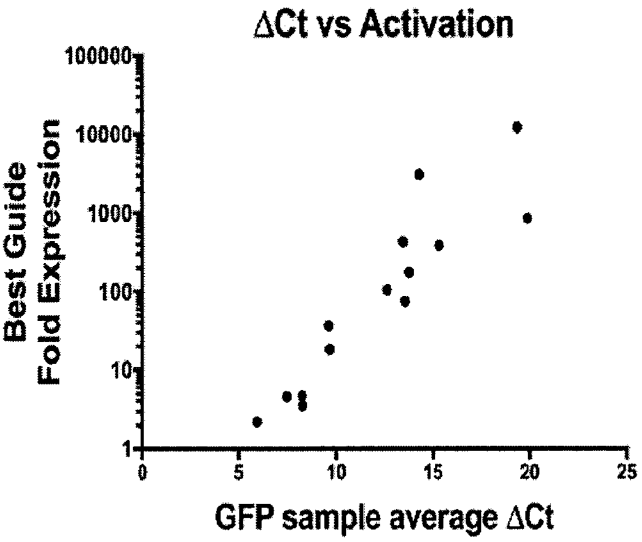

ΔCt vs Activation
Best Guide
Fold Expression
100000
10000
1000
100
10
1
0
5
10
15
20
25
GFP sample average ΔCt

FIG. 59

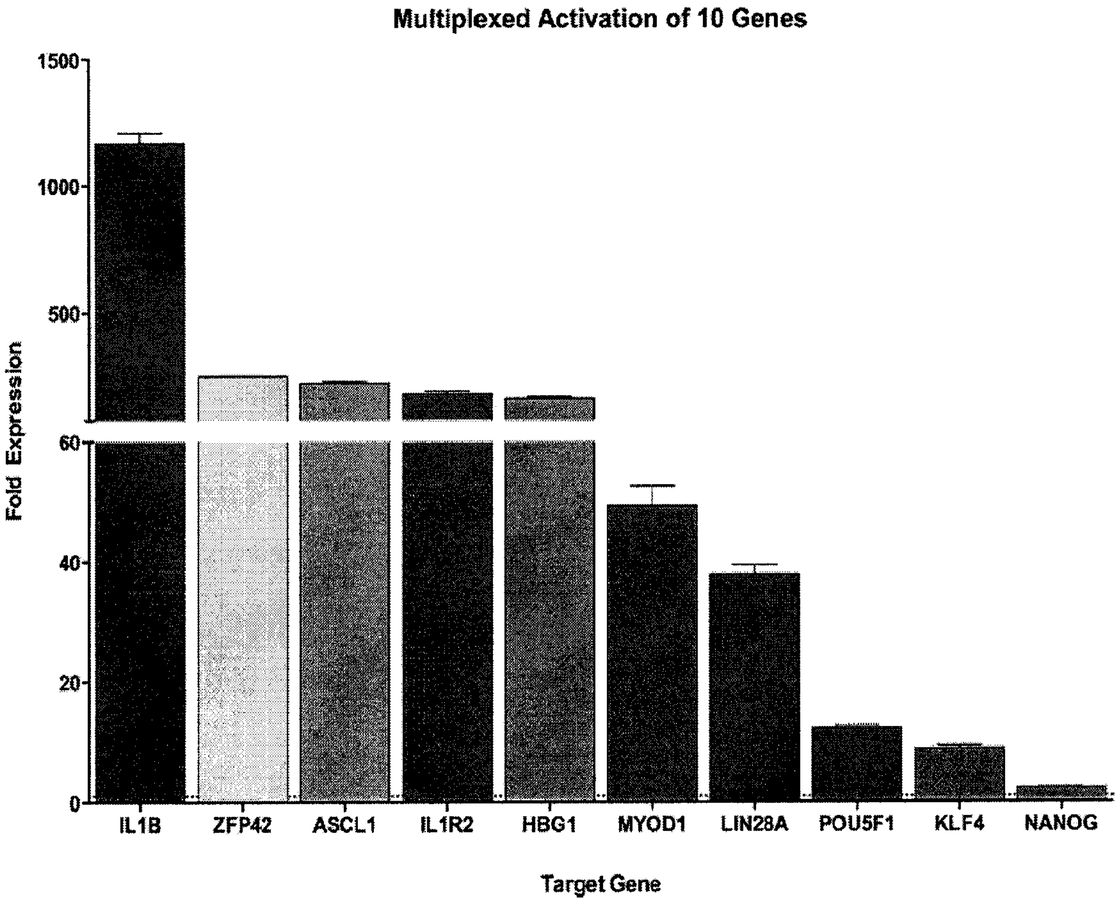

Multiplexed Activation of 10 Genes
1500
1000
500
60
40
20
0
Fold Expression
IL1B
ZFP42
ASCL1
IL1R2
HBG1
MYOD1
LIN28A
POU5F1
KLF4
NANOG
Target Gene

FIG. 60

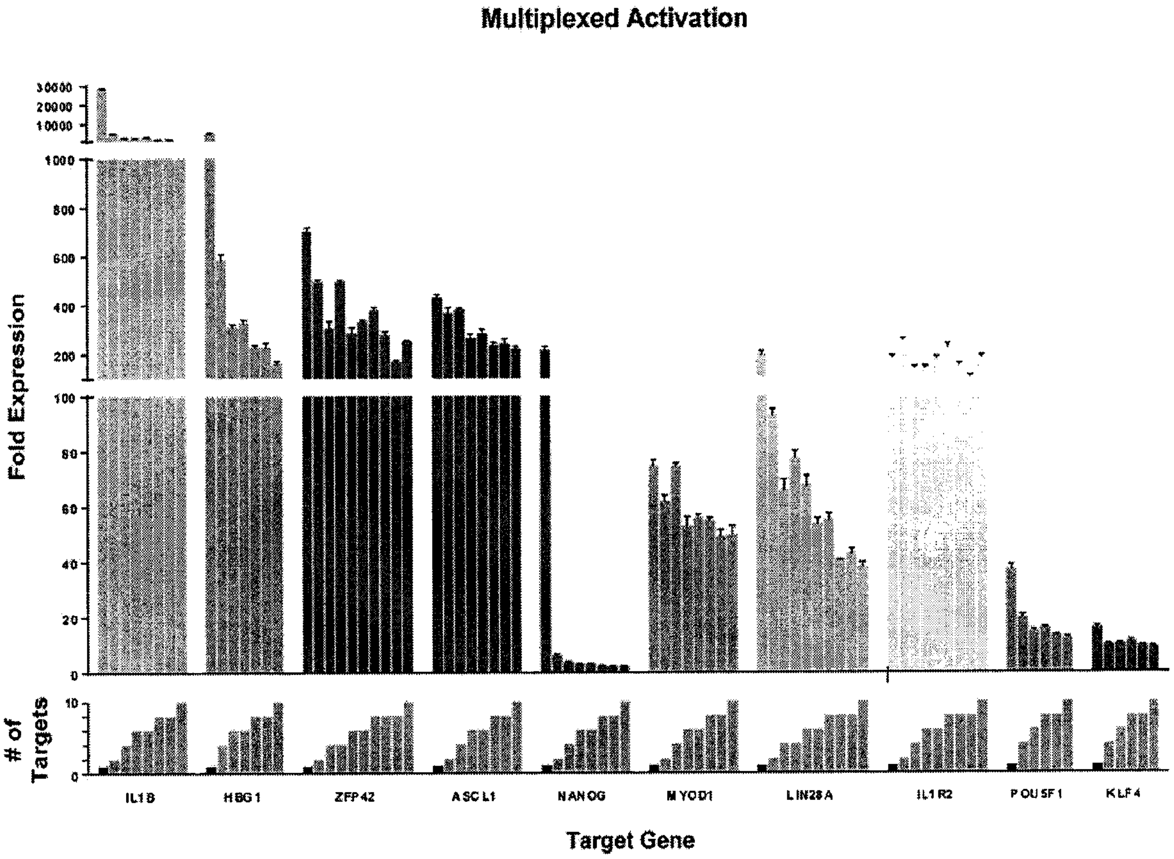

Multiplexed Activation
Fold Expression
30000
20000
10000
1000
800
600
400
200
100
80
60
40
20
0
# of Targets
10
0
IL1B
HBG1
ZFP42
ASCL1
NANOG
MYOD1
LIN28A
IL1R2
POU5F1
KLF4
Target Gene

FIG. 61

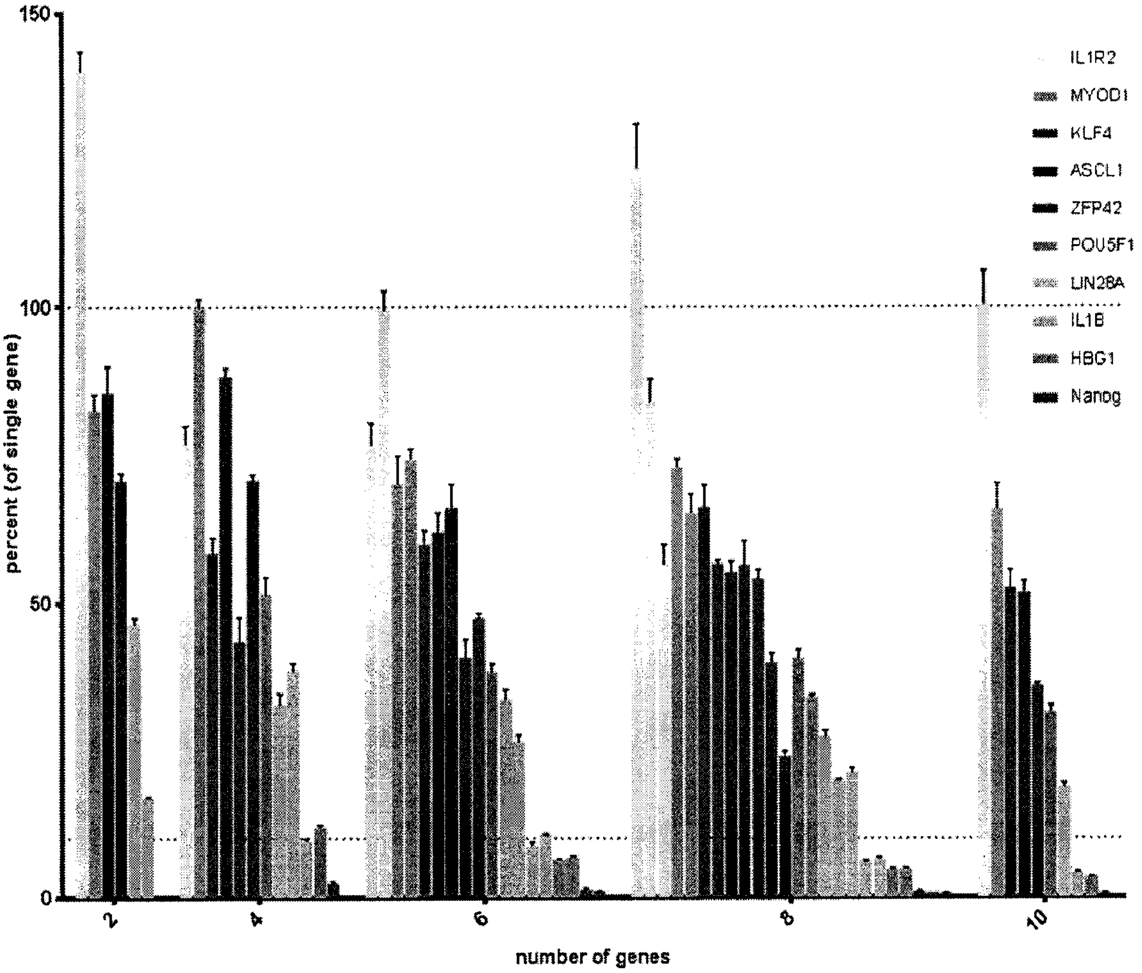
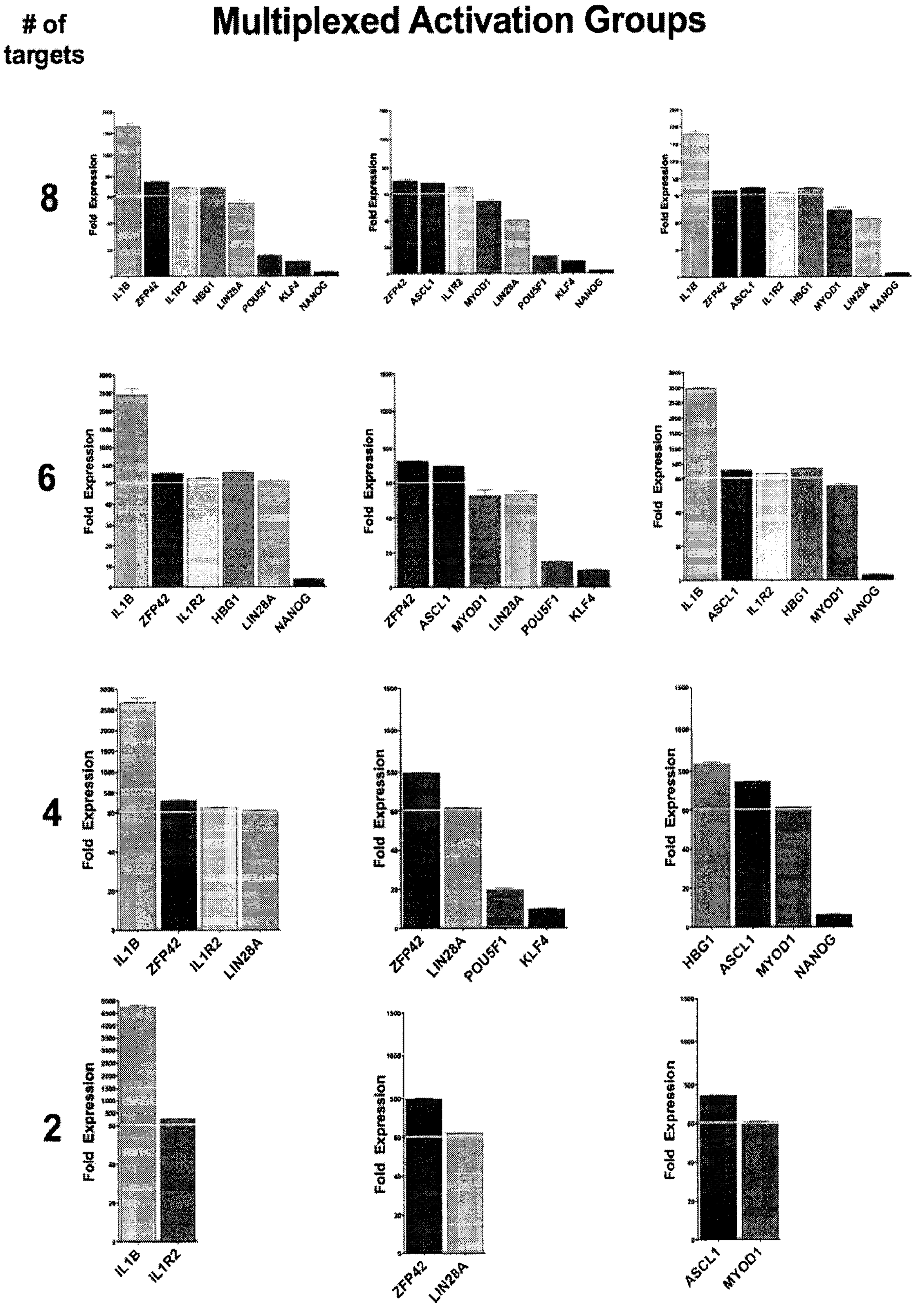

150
100
50
0
percent (of single gene)
2
4
6
8
10
number of genes
IL1R2
MYOD1
KLF4
ASCL1
ZFP42
POU5F1
LIN28A
IL1B
HBG1
Nanog

FIG. 62



# of targets
Multiplexed Activation Groups
8
Fold Expression
IL1B
ZFP42
IL1R2
HBG1
LIN28A
POU5F1
KLF4
NANOG
Fold Expression
ZFP42
ASCL1
IL1R2
MYOD1
LIN28A
POU5F1
KLF4
NANOG
Fold Expression
IL1B
ZFP42
ASCL1
IL1R2
HBG1
MYOD1
LIN28A
NANOG
6
Fold Expression
IL1B
ZFP42
IL1R2
HBG1
LIN28A
NANOG
Fold Expression
ZFP42
ASCL1
MYOD1
LIN28A
POU5F1
KLF4
Fold Expression
IL1B
ASCL1
IL1R2
HBG1
MYOD1
NANOG
4
Fold Expression
IL1B
ZFP42
IL1R2
LIN28A
Fold Expression
ZFP42
LIN28A
POU5F1
KLF4
Fold Expression
HBG1
ASCL1
MYOD1
NANOG
2
Fold Expression
IL1B
IL1R2
Fold Expression
ZFP42
LIN28A
Fold Expression
ASCL1
MYOD1

FIG. 63

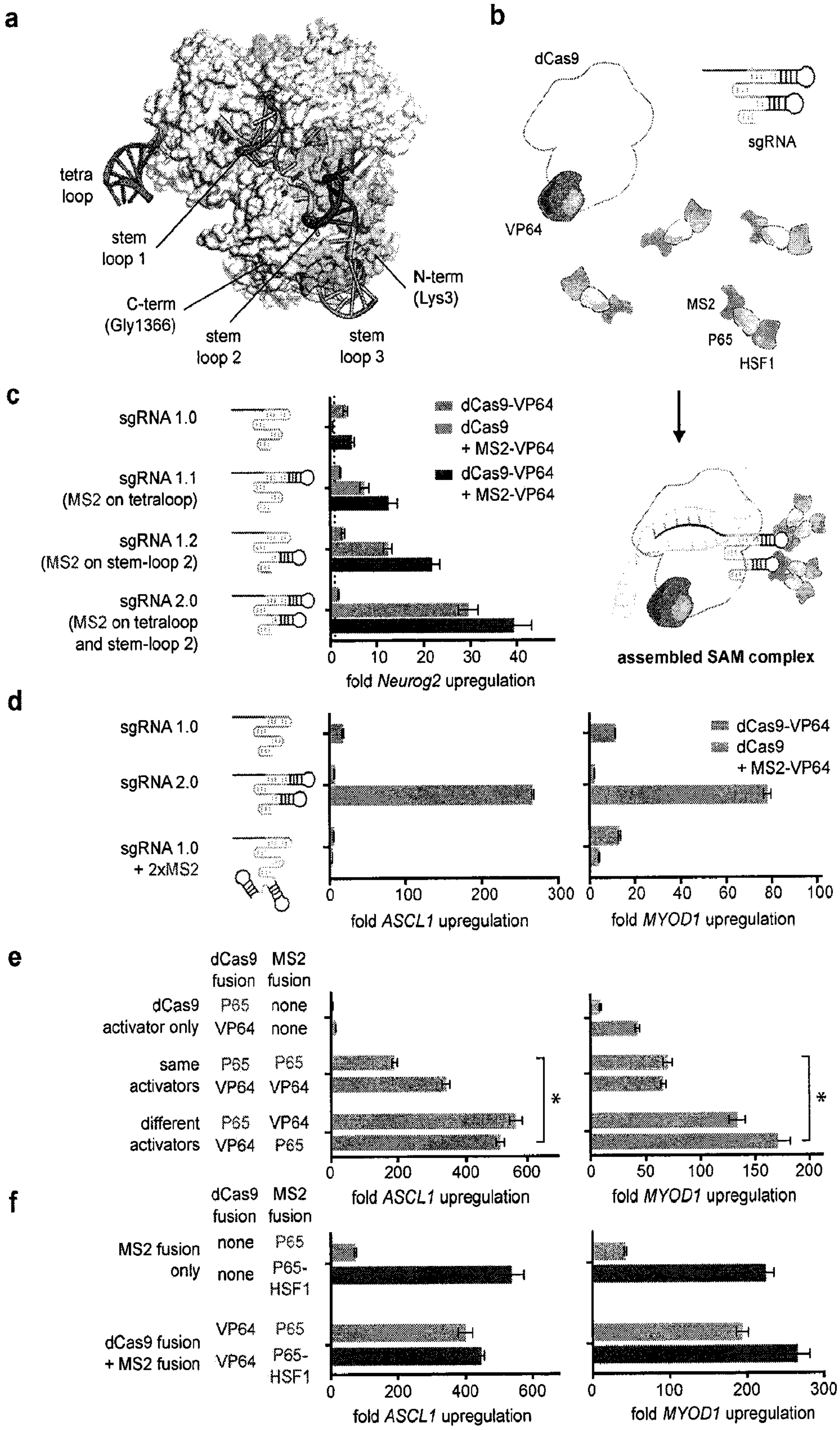

a
tetra loop
stem loop 1
C-term (Gly1366)
stem loop 2
stem loop 3
N-term (Lys3)
b
dCas9
sgRNA
VP64
MS2
P65
HSF1
assembled SAM complex
c
sgRNA 1.0
sgRNA 1.1 (MS2 on tetraloop)
sgRNA 1.2 (MS2 on stem-loop 2)
sgRNA 2.0 (MS2 on tetraloop and stem-loop 2)
dCas9-VP64
dCas9 + MS2-VP64
dCas9-VP64 + MS2-VP64
0
10
20
30
40
fold Neurog2 upregulation
d
sgRNA 1.0
sgRNA 2.0
sgRNA 1.0 + 2xMS2
dCas9-VP64
dCas9 + MS2-VP64
0
100
200
300
fold ASCL1 upregulation
0
20
40
60
80
100
fold MYOD1 upregulation
e
dCas9 fusion
MS2 fusion
dCas9 activator only
P65 none
VP64 none
same activators
P65 P65
VP64 VP64
different activators
P65 VP64
VP64 P65
*
0
200
400
600
fold ASCL1 upregulation
*
0
50
100
150
200
fold MYOD1 upregulation
f
dCas9 fusion
MS2 fusion
MS2 fusion only
none P65
none P65-HSF1
dCas9 fusion + MS2 fusion
VP64 P65
VP64 P65-HSF1
0
200
400
600
fold ASCL1 upregulation
0
100
200
300
fold MYOD1 upregulation

FIG. 64A-F

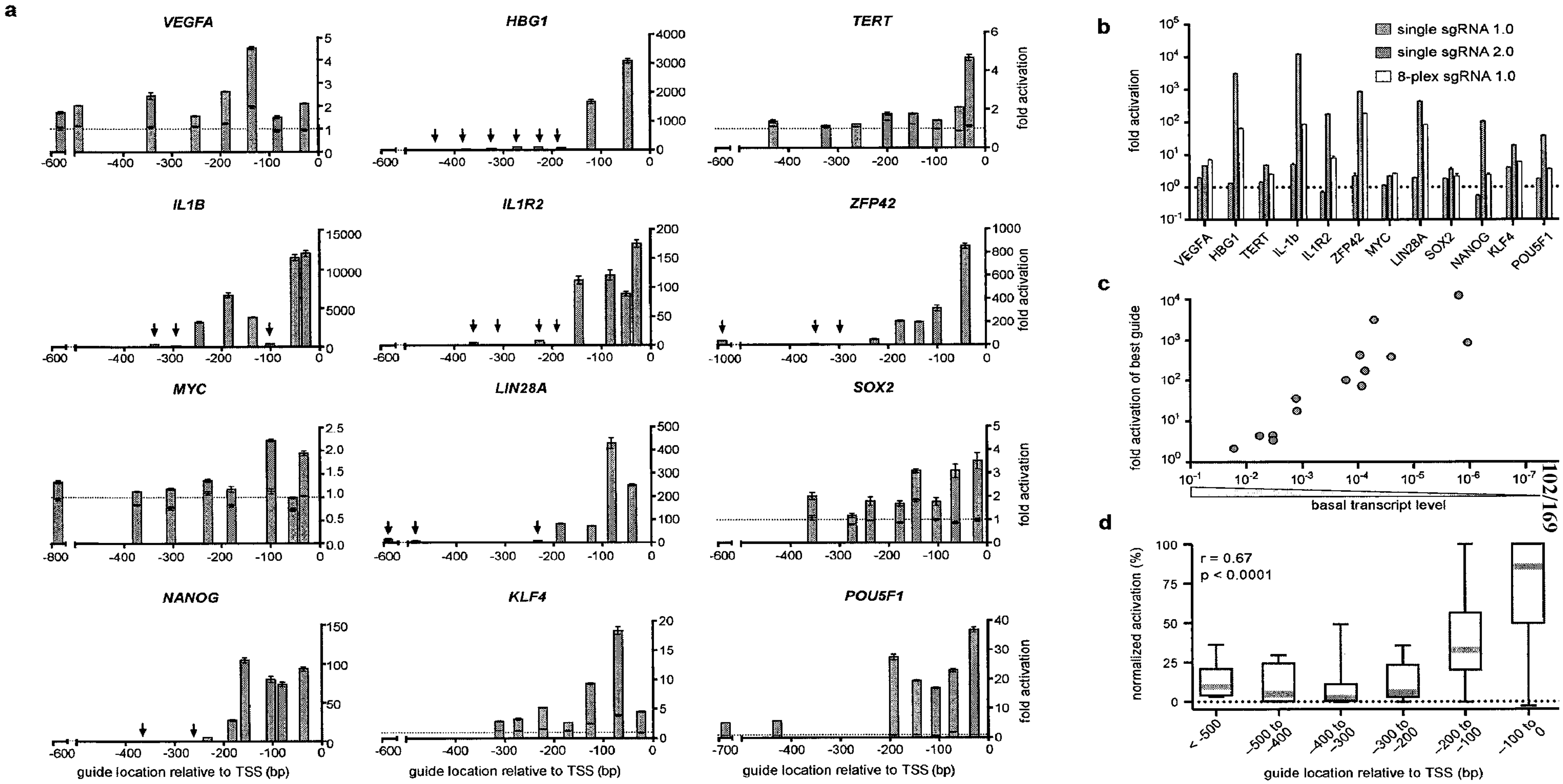

a
VEGFA
HBG1
TERT
IL1B
IL1R2
ZFP42
MYC
LIN28A
SOX2
NANOG
KLF4
POU5F1
fold activation
guide location relative to TSS (bp)
b
single sgRNA 1.0
single sgRNA 2.0
8-plex sgRNA 1.0
fold activation
VEGFA
HBG1
TERT
IL-1b
IL1R2
ZFP42
MYC
LIN28A
SOX2
NANOG
KLF4
POU5F1
c
fold activation of best guide
basal transcript level
d
normalized activation (%)
r = 0.67
p < 0.0001
< -500
-500 to -400
-400 to -300
-300 to -200
-200 to -100
-100 to 0
guide location relative to TSS (bp)

FIG. 65A-D

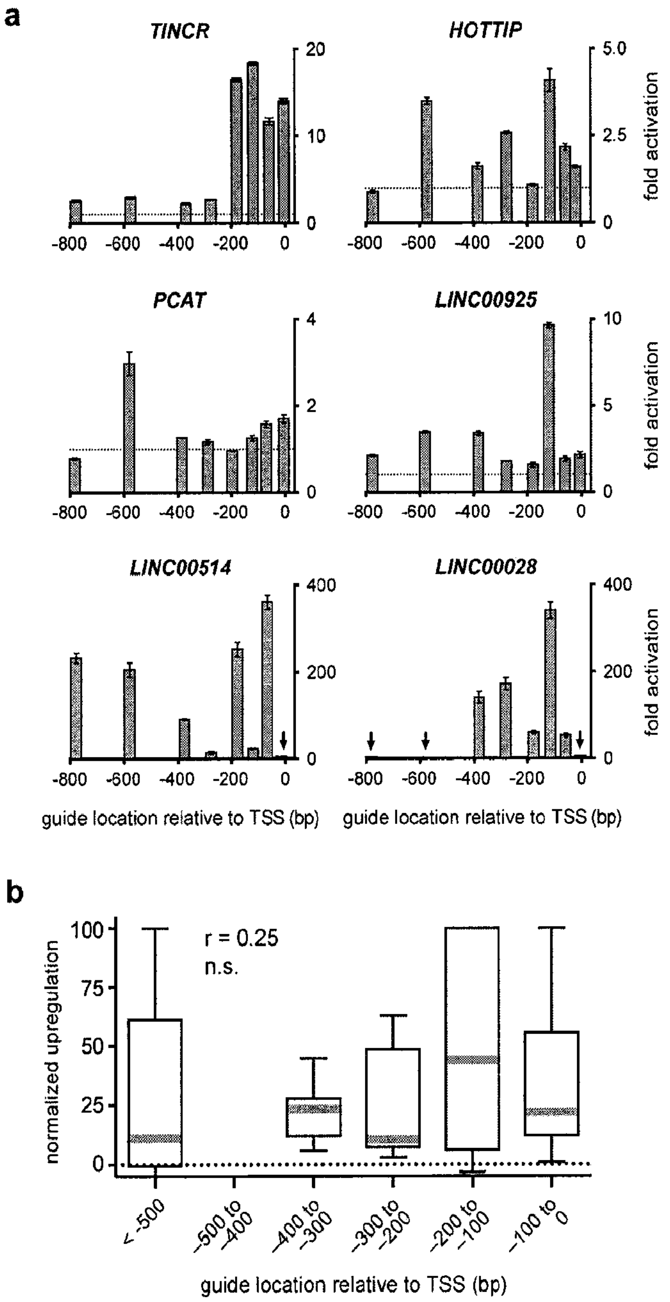

a
TINCR
HOTTIP
PCAT
LINC00925
LINC00514
LINC00028
20
10
0
5.0
2.5
0
4
2
0
10
5
0
400
200
0
400
200
0
fold activation
fold activation
fold activation
-800 -600 -400 -200 0
guide location relative to TSS (bp)
guide location relative to TSS (bp)
b
normalized upregulation
100
75
50
25
0
r = 0.25
n.s.
< -500
-500 to -400
-400 to -300
-300 to -200
-200 to -100
-100 to 0
guide location relative to TSS (bp)

FIG. 66A-B

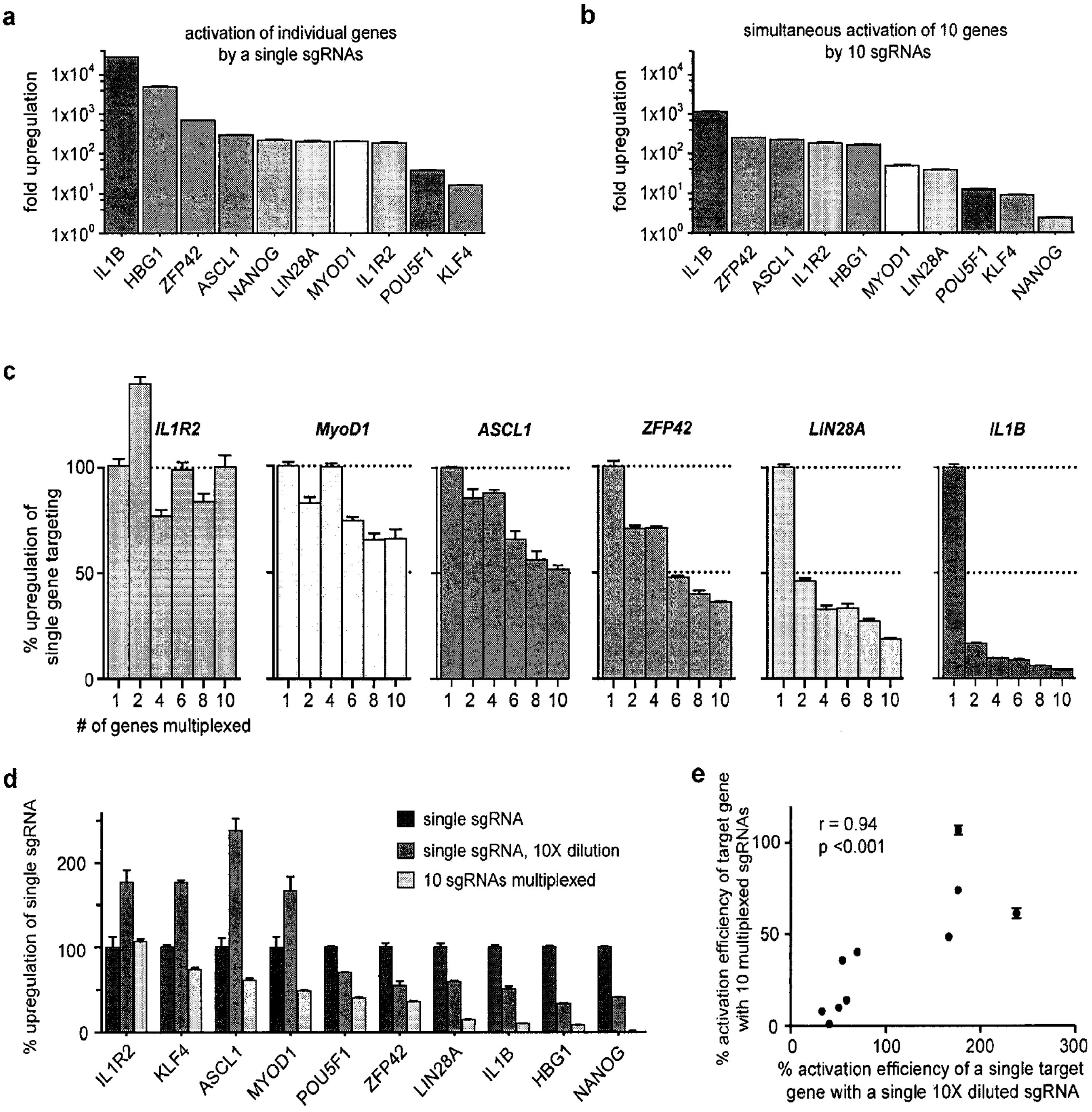
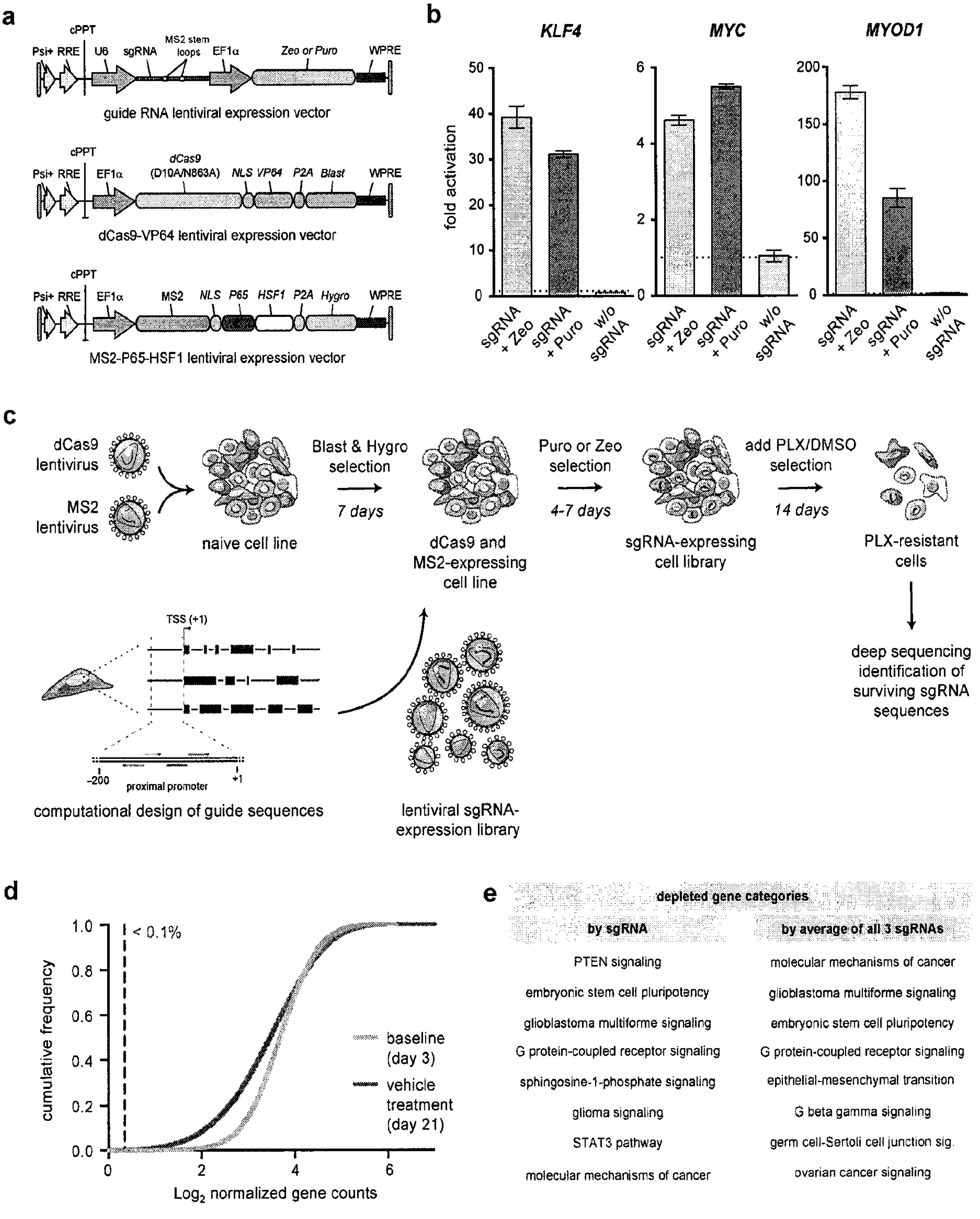

a
activation of individual genes
by a single sgRNAs
fold upregulation
1x10⁴
1x10³
1x10²
1x10¹
1x10⁰
IL1B
HBG1
ZFP42
ASCL1
NANOG
LIN28A
MYOD1
IL1R2
POU5F1
KLF4
b
simultaneous activation of 10 genes
by 10 sgRNAs
fold upregulation
1x10⁴
1x10³
1x10²
1x10¹
1x10⁰
IL1B
ZFP42
ASCL1
IL1R2
HBG1
MYOD1
LIN28A
POU5F1
KLF4
NANOG
c
IL1R2
MyoD1
ASCL1
ZFP42
LIN28A
IL1B
% upregulation of
single gene targeting
100
50
0
1 2 4 6 8 10
# of genes multiplexed
d
% upregulation of single sgRNA
200
100
0
single sgRNA
single sgRNA, 10X dilution
10 sgRNAs multiplexed
IL1R2
KLF4
ASCL1
MYOD1
POU5F1
ZFP42
LIN28A
IL1B
HBG1
NANOG
e
% activation efficiency of target gene
with 10 multiplexed sgRNAs
r = 0.94
p <0.001
100
50
0
0
100
200
300
% activation efficiency of a single target
gene with a single 10X diluted sgRNA

FIG. 67A-E



depleted gene categories	
by sgRNA	by average of all 3 sgRNAs
PTEN signaling	molecular mechanisms of cancer
embryonic stem cell pluripotency	glioblastoma multiforme signaling
glioblastoma multiforme signaling	embryonic stem cell pluripotency
G protein-coupled receptor signaling	G protein-coupled receptor signaling
sphingosine-1-phosphate signaling	epithelial-mesenchymal transition
glioma signaling	G beta gamma signaling
STAT3 pathway	germ cell-Sertoli cell junction sig.
molecular mechanisms of cancer	ovarian cancer signaling

FIG. 68A-E

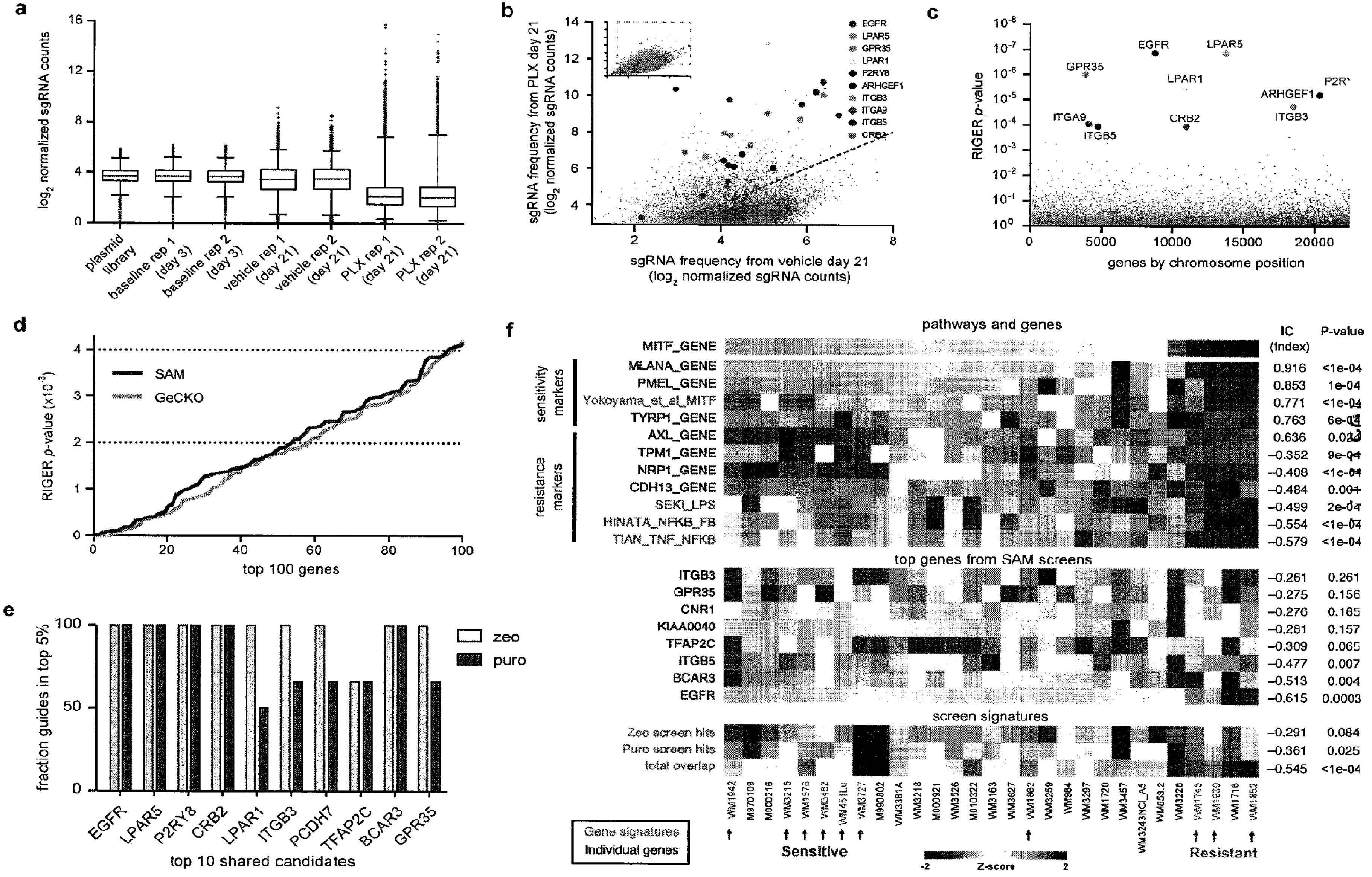

a
log2 normalized sgRNA counts
16
12
8
4
0
plasmid library
baseline rep 1 (day 3)
baseline rep 2 (day 3)
vehicle rep 1 (day 21)
vehicle rep 2 (day 21)
PLX rep 1 (day 21)
PLX rep 2 (day 21)
b
sgRNA frequency from PLX day 21 (log2 normalized sgRNA counts)
14
12
10
8
6
4
2
sgRNA frequency from vehicle day 21 (log2 normalized sgRNA counts)
EGFR
LPAR5
GPR35
LPAR1
P2RY8
ARHGEF1
ITGB3
ITGA9
ITGB5
CRB2
c
RIGER p-value
10-8
10-7
10-6
10-5
10-4
10-3
10-2
10-1
100
0
5000
10000
15000
20000
genes by chromosome position
GPR35
EGFR
LPAR5
LPAR1
P2R
ARHGEF1
ITGA9
ITGB5
CRB2
ITGB3
d
RIGER p-value (x10-3)
SAM
GeCKO
top 100 genes
e
fraction guides in top 5%
100
50
0
zeo
puro
EGFR
LPAR5
P2RY8
CRB2
LPAR1
ITGB3
PCDH7
TFAP2C
BCAR3
GPR35
top 10 shared candidates
f
pathways and genes
IC (Index)
P-value
MITF_GENE
sensitivity markers
MLANA_GENE 0.916 <1e-04
PMEL_GENE 0.853 1e-04
Yokoyama_et_al_MITF 0.771 <1e-04
TYRP1_GENE 0.763 6e-03
resistance markers
AXL_GENE 0.636 0.023
TPM1_GENE −0.352 9e-04
NRP1_GENE −0.408 <1e-04
CDH13_GENE −0.484 0.004
SEKI_LPS −0.499 2e-04
HINATA_NFKB_FB −0.554 <1e-04
TIAN_TNF_NFKB −0.579 <1e-04
top genes from SAM screens
ITGB3 −0.261 0.261
GPR35 −0.275 0.156
CNR1 −0.276 0.185
KIAA0040 −0.281 0.157
TFAP2C −0.309 0.065
ITGB5 −0.477 0.007
BCAR3 −0.513 0.004
EGFR −0.615 0.0003
screen signatures
Zeo screen hits −0.291 0.084
Puro screen hits −0.361 0.025
total overlap −0.545 <1e-04
WM1942
M970109
M000216
WM3215
WM1975
WM3482
WM451Lu
WM3727
M990802
WM3381A
WM3218
M000921
WM3526
M010322
WM3163
WM3627
WM1862
WM3259
WM984
WM3297
WM1720
WM3457
WM3243NCI_A5
WM653.2
WM3226
WM1745
WM1930
WM1716
WM1852
Sensitive
Resistant
-2
Z-score
2
Gene signatures
Individual genes

FIG. 69A-F

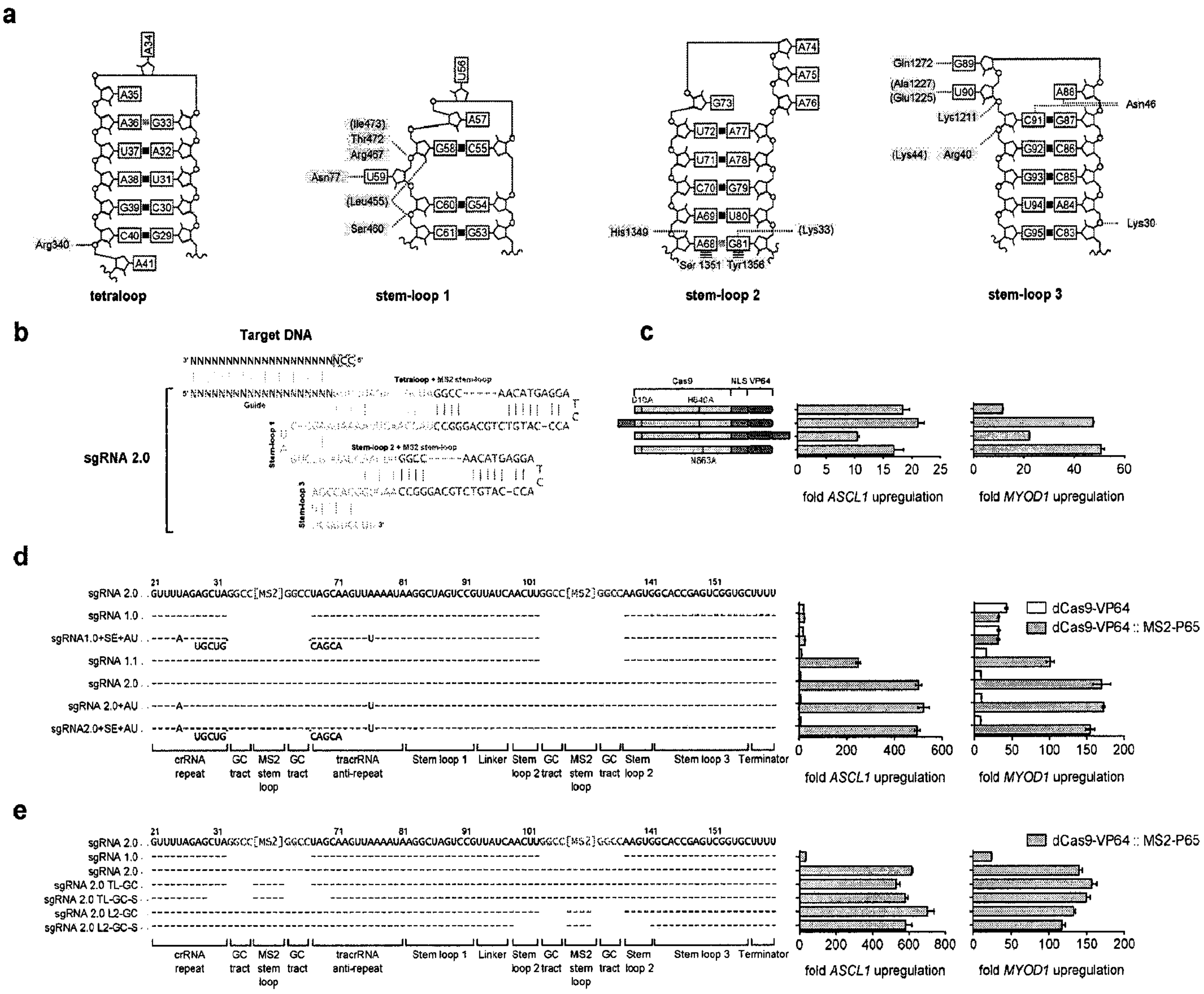

a
A34
A35
A36 G33
U37 A32
A38 U31
G39 C30
C40 G29
Arg340
A41
tetraloop
U56
A57
(Ile473)
Thr472
Arg467
G58 C55
Asn77
U59
(Leu455)
C60 G54
Ser460
C61 G53
stem-loop 1
A74
A75
A76
G73
U72 A77
U71 A78
C70 G79
A69 U80
His1349
(Lys33)
A68 G81
Ser 1351 Tyr1356
stem-loop 2
Gln1272
G89
(Ala1227)
(Glu1225)
U90
A88
Asn46
Lys1211
C91 G87
(Lys44) Arg40
G92 C86
G93 C85
U94 A84
Lys30
G95 C83
stem-loop 3
b
Target DNA
3' NNNNNNNNNNNNNNNNNNNNNCC 5'
Tetraloop + MS2 stem-loop
5' NNNNNNNNNNNNNNNNNNNN GGCC AACATGAGGA
Guide
CGGGACGTCTGTAC-CCA
Stem-loop 1
Stem-loop 2 + MS2 stem-loop
GGCC AACATGAGGA
CCGGGACGTCTGTAC-CCA
Stem-loop 3
sgRNA 2.0
c
Cas9
NLS VP64
D10A
H840A
N863A
0 5 10 15 20 25
fold ASCL1 upregulation
0 20 40 60
fold MYOD1 upregulation
d
21 31 71 81 91 101 141 151
sgRNA 2.0 GUUUUAGAGCUAGGCC[MS2]GGCCUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGGCC[MS2]GGCCAAGUGGCACCGAGUCGGUGCUUUU
sgRNA 1.0
sgRNA1.0+SE+AU
UGCUG
CAGCA
sgRNA 1.1
sgRNA 2.0
sgRNA 2.0+AU
sgRNA2.0+SE+AU
UGCUG
CAGCA
crRNA repeat
GC tract
MS2 stem loop
GC tract
tracrRNA anti-repeat
Stem loop 1
Linker
Stem loop 2
GC tract
MS2 stem loop
GC tract
Stem loop 2
Stem loop 3
Terminator
☐ dCas9-VP64
▨ dCas9-VP64 :: MS2-P65
0 200 400 600
fold ASCL1 upregulation
0 50 100 150 200
fold MYOD1 upregulation
e
21 31 71 81 91 101 141 151
sgRNA 2.0 GUUUUAGAGCUAGGCC[MS2]GGCCUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGGCC[MS2]GGCCAAGUGGCACCGAGUCGGUGCUUUU
sgRNA 1.0
sgRNA 2.0
sgRNA 2.0 TL-GC
sgRNA 2.0 TL-GC-S
sgRNA 2.0 L2-GC
sgRNA 2.0 L2-GC-S
crRNA repeat
GC tract
MS2 stem loop
GC tract
tracrRNA anti-repeat
Stem loop 1
Linker
Stem loop 2
GC tract
MS2 stem loop
GC tract
Stem loop 2
Stem loop 3
Terminator
▨ dCas9-VP64 :: MS2-P65
0 200 400 600 800
fold ASCL1 upregulation
0 50 100 150 200
fold MYOD1 upregulation

FIG. 70A-E

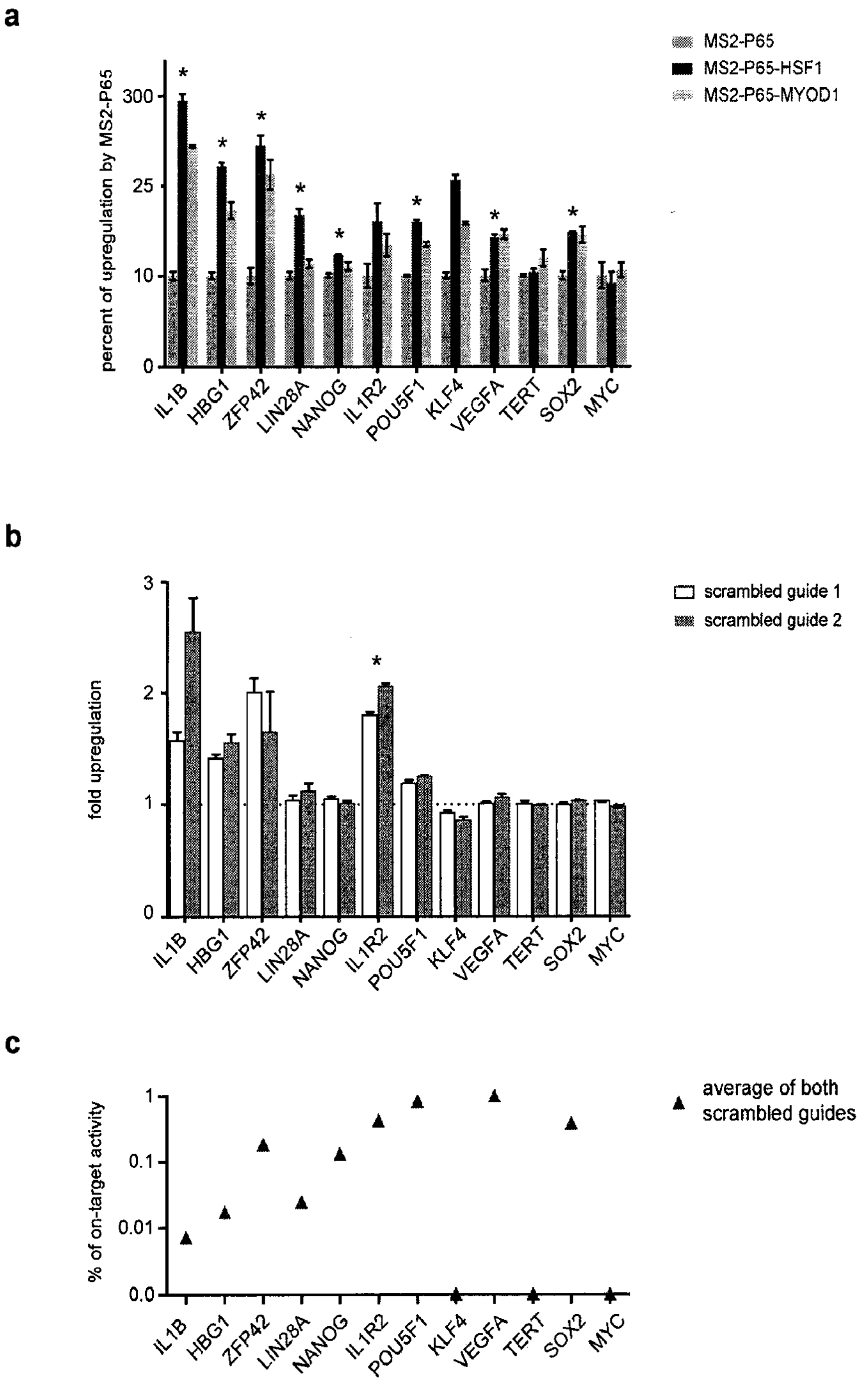

a
MS2-P65
MS2-P65-HSF1
MS2-P65-MYOD1
percent of upregulation by MS2-P65
300
25
10
0
*
IL1B
HBG1
ZFP42
LIN28A
NANOG
IL1R2
POU5F1
KLF4
VEGFA
TERT
SOX2
MYC
b
scrambled guide 1
scrambled guide 2
fold upregulation
3
2
1
0
*
IL1B
HBG1
ZFP42
LIN28A
NANOG
IL1R2
POU5F1
KLF4
VEGFA
TERT
SOX2
MYC
c
average of both scrambled guides
% of on-target activity
1
0.1
0.01
0.0
IL1B
HBG1
ZFP42
LIN28A
NANOG
IL1R2
POU5F1
KLF4
VEGFA
TERT
SOX2
MYC

FIG. 71A-C

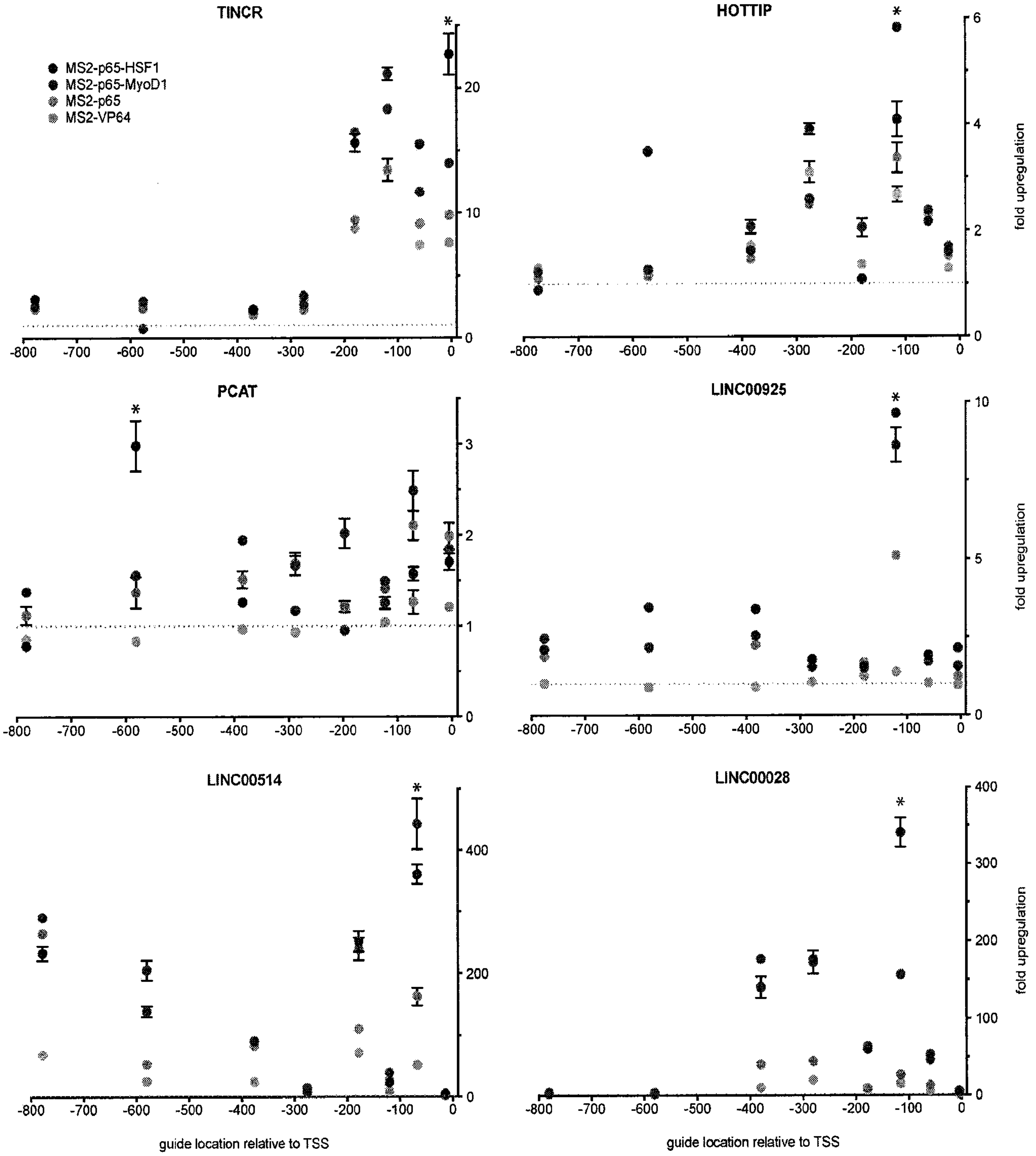

TINCR
● MS2-p65-HSF1
● MS2-p65-MyoD1
● MS2-p65
● MS2-VP64
*
0
10
20
HOTTIP
*
0
2
4
6
fold upregulation
PCAT
*
0
1
2
3
LINC00925
*
0
5
10
fold upregulation
LINC00514
*
0
200
400
LINC00028
*
0
100
200
300
400
fold upregulation
-800 -700 -600 -500 -400 -300 -200 -100 0
guide location relative to TSS
guide location relative to TSS

Figure 72

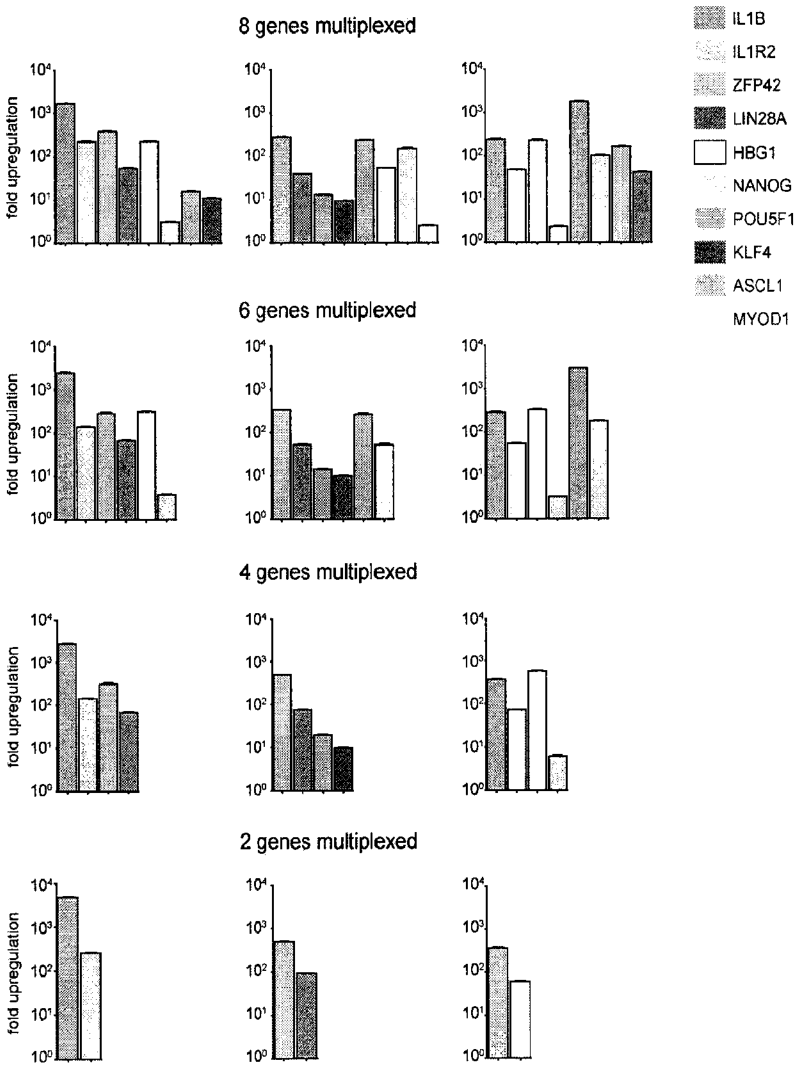

8 genes multiplexed
6 genes multiplexed
4 genes multiplexed
2 genes multiplexed
fold upregulation
10⁰
10¹
10²
10³
10⁴
IL1B
IL1R2
ZFP42
LIN28A
HBG1
NANOG
POU5F1
KLF4
ASCL1
MYOD1

Figure 73

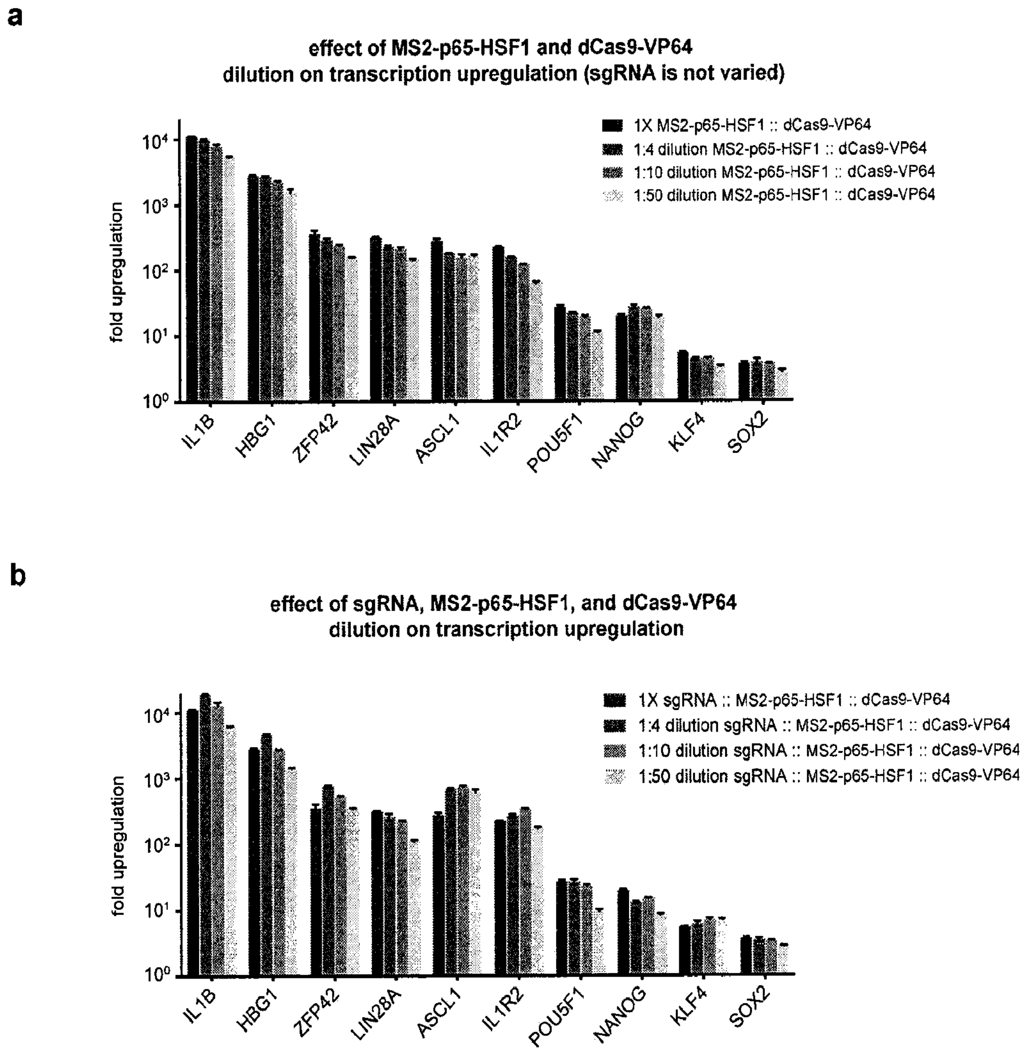
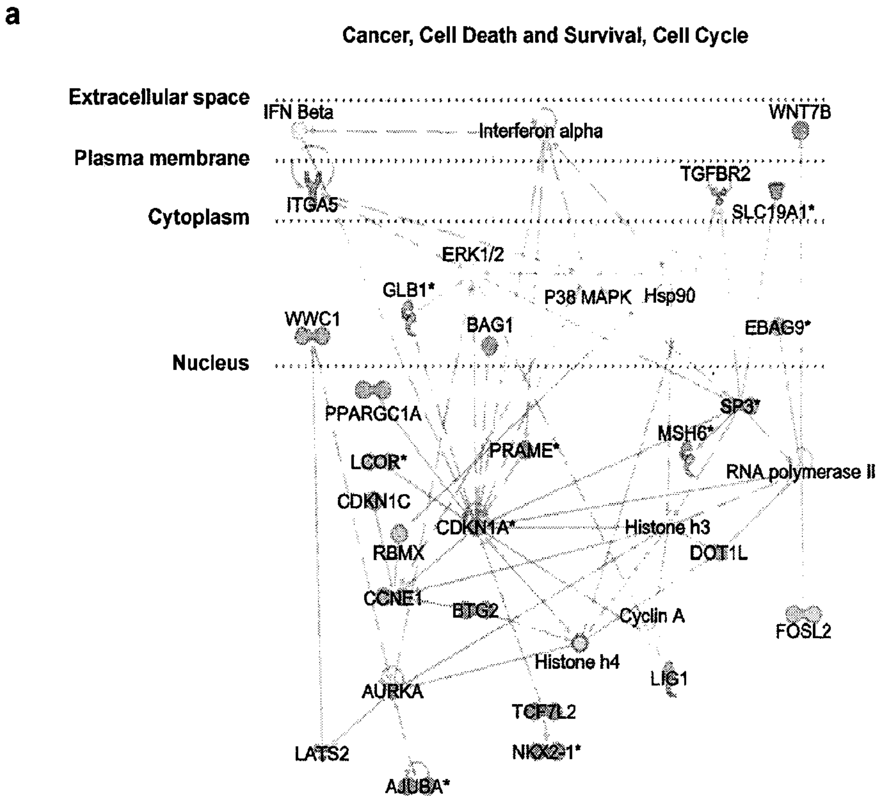

a
effect of MS2-p65-HSF1 and dCas9-VP64
dilution on transcription upregulation (sgRNA is not varied)
fold upregulation
10⁴
10³
10²
10¹
10⁰
1X MS2-p65-HSF1 :: dCas9-VP64
1:4 dilution MS2-p65-HSF1 :: dCas9-VP64
1:10 dilution MS2-p65-HSF1 :: dCas9-VP64
1:50 dilution MS2-p65-HSF1 :: dCas9-VP64
IL1B
HBG1
ZFP42
LIN28A
ASCL1
IL1R2
POU5F1
NANOG
KLF4
SOX2
b
effect of sgRNA, MS2-p65-HSF1, and dCas9-VP64
dilution on transcription upregulation
fold upregulation
10⁴
10³
10²
10¹
10⁰
1X sgRNA :: MS2-p65-HSF1 :: dCas9-VP64
1:4 dilution sgRNA :: MS2-p65-HSF1 :: dCas9-VP64
1:10 dilution sgRNA :: MS2-p65-HSF1 :: dCas9-VP64
1:50 dilution sgRNA :: MS2-p65-HSF1 :: dCas9-VP64
IL1B
HBG1
ZFP42
LIN28A
ASCL1
IL1R2
POU5F1
NANOG
KLF4
SOX2

FIG. 74A-B


a
Cancer, Cell Death and Survival, Cell Cycle
Extracellular space
IFN Beta
Interferon alpha
WNT7B
Plasma membrane
TGFBR2
ITGA5
SLC19A1*
Cytoplasm
ERK1/2
GLB1*
P38 MAPK
Hsp90
WWC1
BAG1
EBAG9*
Nucleus
PPARGC1A
SP3*
MSH6*
PRAME*
LCOR*
RNA polymerase II
CDKN1C
CDKN1A*
Histone h3
RBMX
DOT1L
CCNE1
BTG2
Cyclin A
FOSL2
Histone h4
AURKA
LIG1
TCF7L2
LATS2
NKX2-1*
AJUBA*

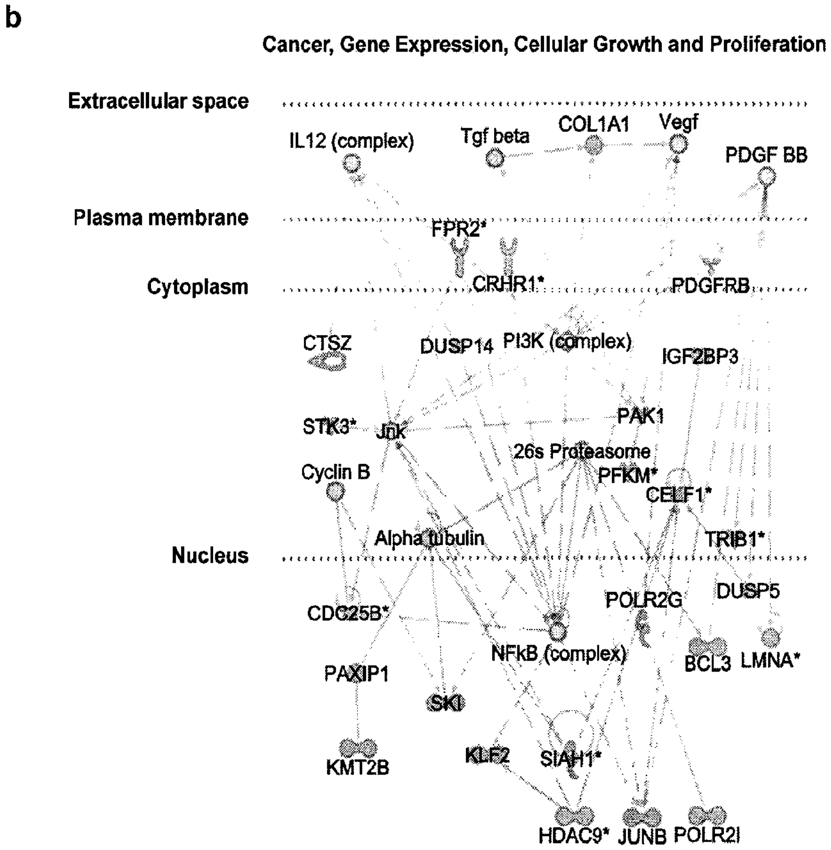

b
Cancer, Gene Expression, Cellular Growth and Proliferation
Extracellular space
IL12 (complex)
Tgf beta
COL1A1
Vegf
PDGF BB
Plasma membrane
FPR2*
CRHR1*
Cytoplasm
PDGFRB
CTSZ
DUSP14
PI3K (complex)
IGF2BP3
STK3*
Jnk
PAK1
26s Proteasome
Cyclin B
PFKM*
CELF1*
Alpha tubulin
TRIB1*
Nucleus
POLR2G
DUSP5
CDC25B*
NFkB (complex)
BCL3
LMNA*
PAXIP1
SKI
KMT2B
KLF2
SIAH1*
HDAC9*
JUNB
POLR2I

FIG. 75A-B

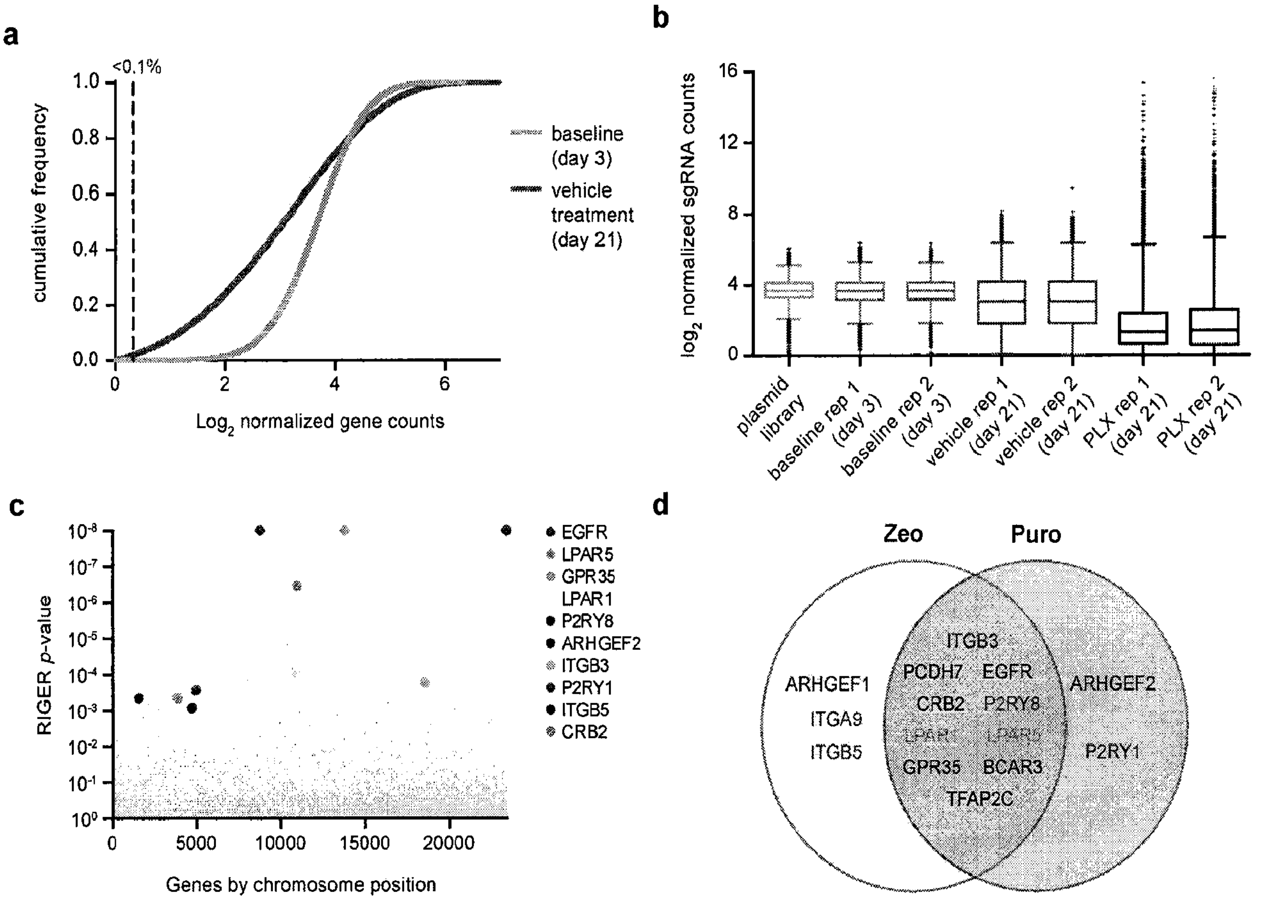

a
<0.1%
1.0
0.8
0.6
0.4
0.2
0.0
cumulative frequency
0
2
4
6
Log$_2$ normalized gene counts
baseline (day 3)
vehicle treatment (day 21)
b
16
12
8
4
0
log$_2$ normalized sgRNA counts
plasmid library
baseline rep 1 (day 3)
baseline rep 2 (day 3)
vehicle rep 1 (day 21)
vehicle rep 2 (day 21)
PLX rep 1 (day 21)
PLX rep 2 (day 21)
c
10^{-8}
10^{-7}
10^{-6}
10^{-5}
10^{-4}
10^{-3}
10^{-2}
10^{-1}
10^{0}
RIGER p-value
0
5000
10000
15000
20000
Genes by chromosome position
EGFR
LPAR5
GPR35
LPAR1
P2RY8
ARHGEF2
ITGB3
P2RY1
ITGB5
CRB2
d
Zeo
Puro
ARHGEF1
ITGA9
ITGB5
ITGB3
PCDH7
EGFR
CRB2
P2RY8
LPAR1
LPAR5
GPR35
BCAR3
TFAP2C
ARHGEF2
P2RY1

FIG. 76A-D

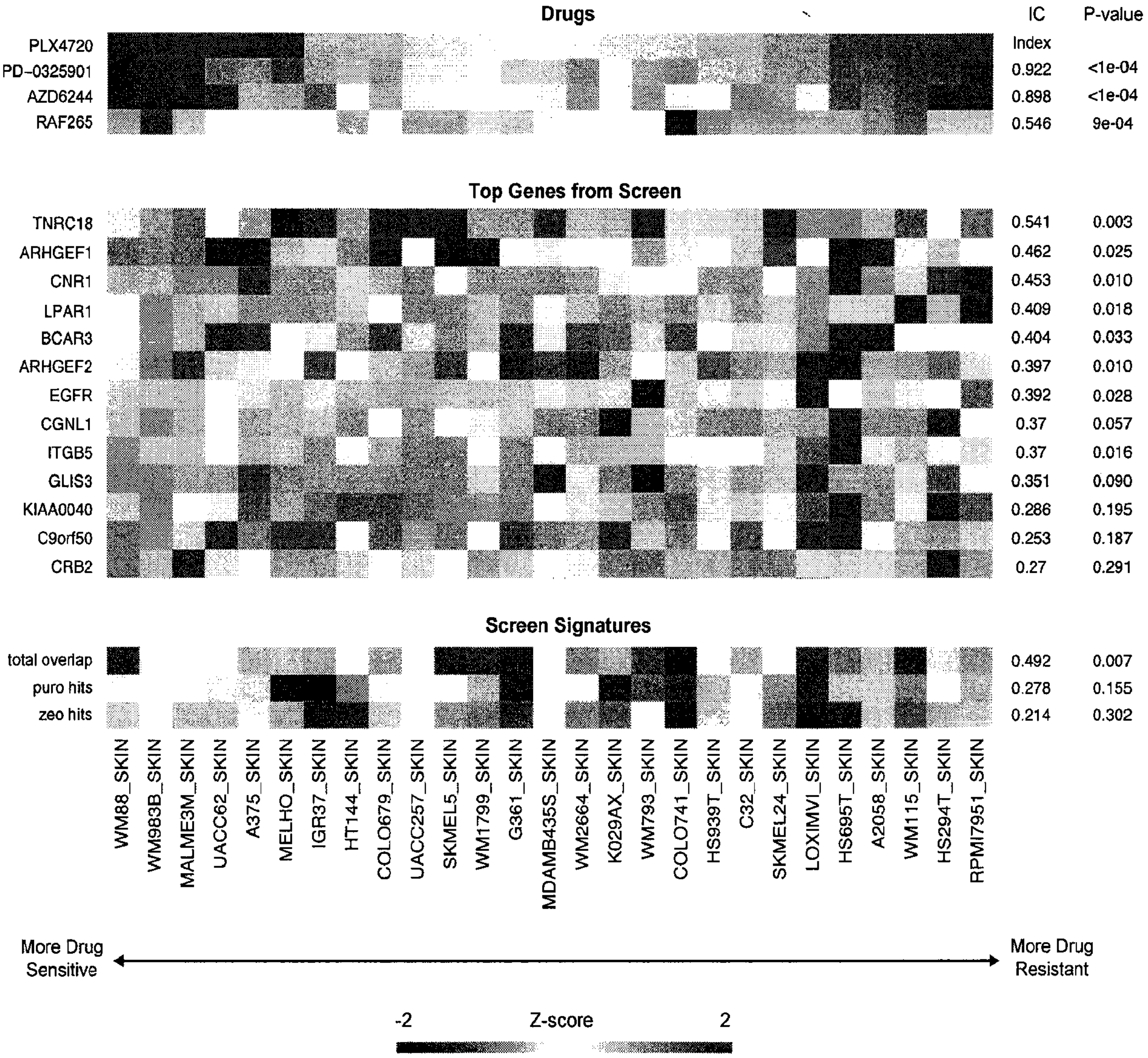

Drugs
IC Index
P-value
PLX4720
PD-0325901 0.922 <1e-04
AZD6244 0.898 <1e-04
RAF265 0.546 9e-04
Top Genes from Screen
TNRC18 0.541 0.003
ARHGEF1 0.462 0.025
CNR1 0.453 0.010
LPAR1 0.409 0.018
BCAR3 0.404 0.033
ARHGEF2 0.397 0.010
EGFR 0.392 0.028
CGNL1 0.37 0.057
ITGB5 0.37 0.016
GLIS3 0.351 0.090
KIAA0040 0.286 0.195
C9orf50 0.253 0.187
CRB2 0.27 0.291
Screen Signatures
total overlap 0.492 0.007
puro hits 0.278 0.155
zeo hits 0.214 0.302
WM88_SKIN
WM983B_SKIN
MALME3M_SKIN
UACC62_SKIN
A375_SKIN
MELHO_SKIN
IGR37_SKIN
HT144_SKIN
COLO679_SKIN
UACC257_SKIN
SKMEL5_SKIN
WM1799_SKIN
G361_SKIN
MDAMB435S_SKIN
WM2664_SKIN
K029AX_SKIN
WM793_SKIN
COLO741_SKIN
HS939T_SKIN
C32_SKIN
SKMEL24_SKIN
LOXIMVI_SKIN
HS695T_SKIN
A2058_SKIN
WM115_SKIN
HS294T_SKIN
RPMI7951_SKIN
More Drug Sensitive
More Drug Resistant
-2
Z-score
2

Figure 77

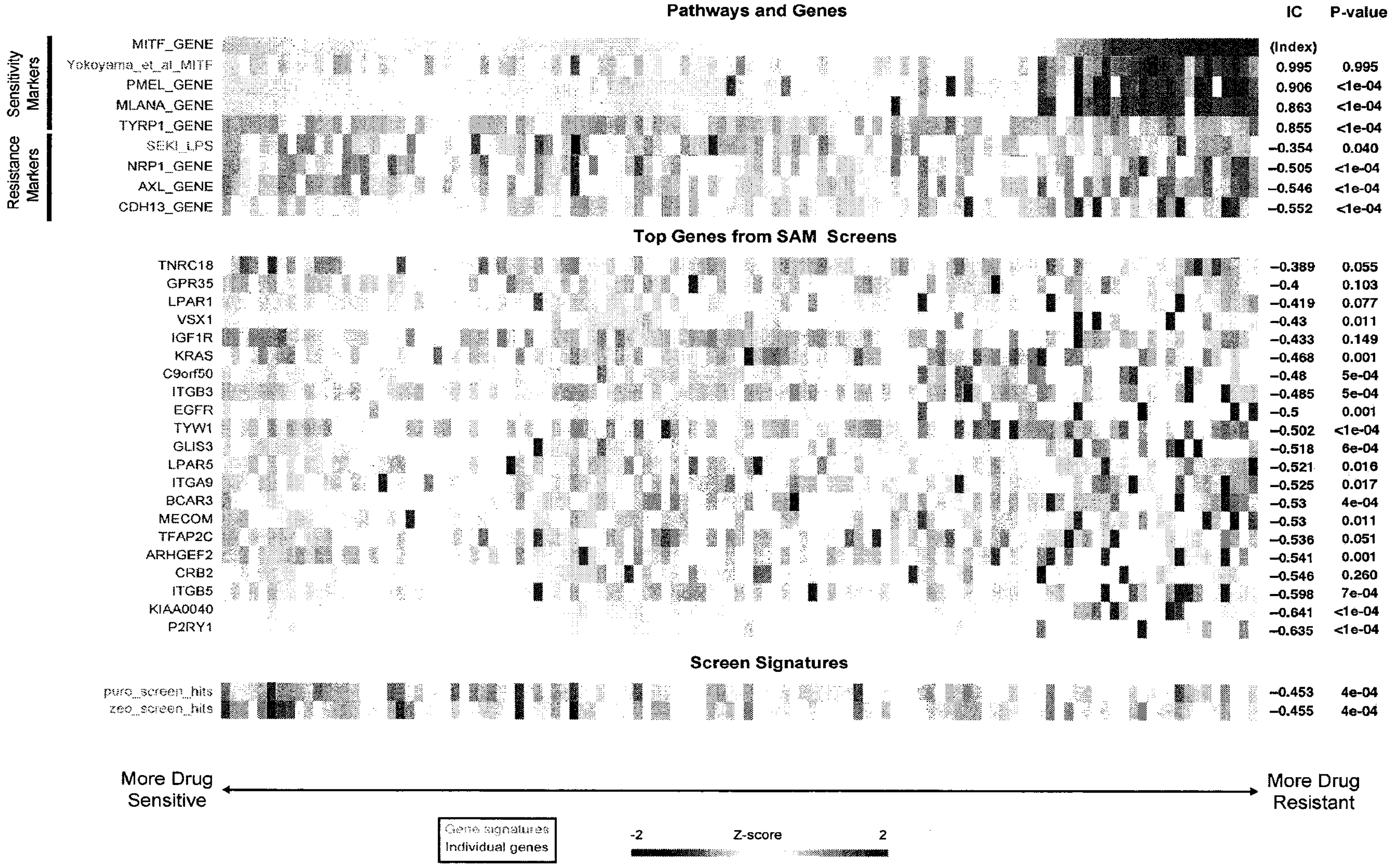

Pathways and Genes
IC
P-value
Sensitivity Markers
Resistance Markers
MITF_GENE (Index)
Yokoyama_et_al_MITF 0.995 0.995
PMEL_GENE 0.906 <1e-04
MLANA_GENE 0.863 <1e-04
TYRP1_GENE 0.855 <1e-04
SEKI_LPS −0.354 0.040
NRP1_GENE −0.505 <1e-04
AXL_GENE −0.546 <1e-04
CDH13_GENE −0.552 <1e-04
Top Genes from SAM Screens
TNRC18 −0.389 0.055
GPR35 −0.4 0.103
LPAR1 −0.419 0.077
VSX1 −0.43 0.011
IGF1R −0.433 0.149
KRAS −0.468 0.001
C9orf50 −0.48 5e-04
ITGB3 −0.485 5e-04
EGFR −0.5 0.001
TYW1 −0.502 <1e-04
GLIS3 −0.518 6e-04
LPAR5 −0.521 0.016
ITGA9 −0.525 0.017
BCAR3 −0.53 4e-04
MECOM −0.53 0.011
TFAP2C −0.536 0.051
ARHGEF2 −0.541 0.001
CRB2 −0.546 0.260
ITGB5 −0.598 7e-04
KIAA0040 −0.641 <1e-04
P2RY1 −0.635 <1e-04
Screen Signatures
puro_screen_hits −0.453 4e-04
zeo_screen_hits −0.455 4e-04
More Drug Sensitive
More Drug Resistant
Gene signatures
Individual genes
-2
Z-score
2

Figure 78

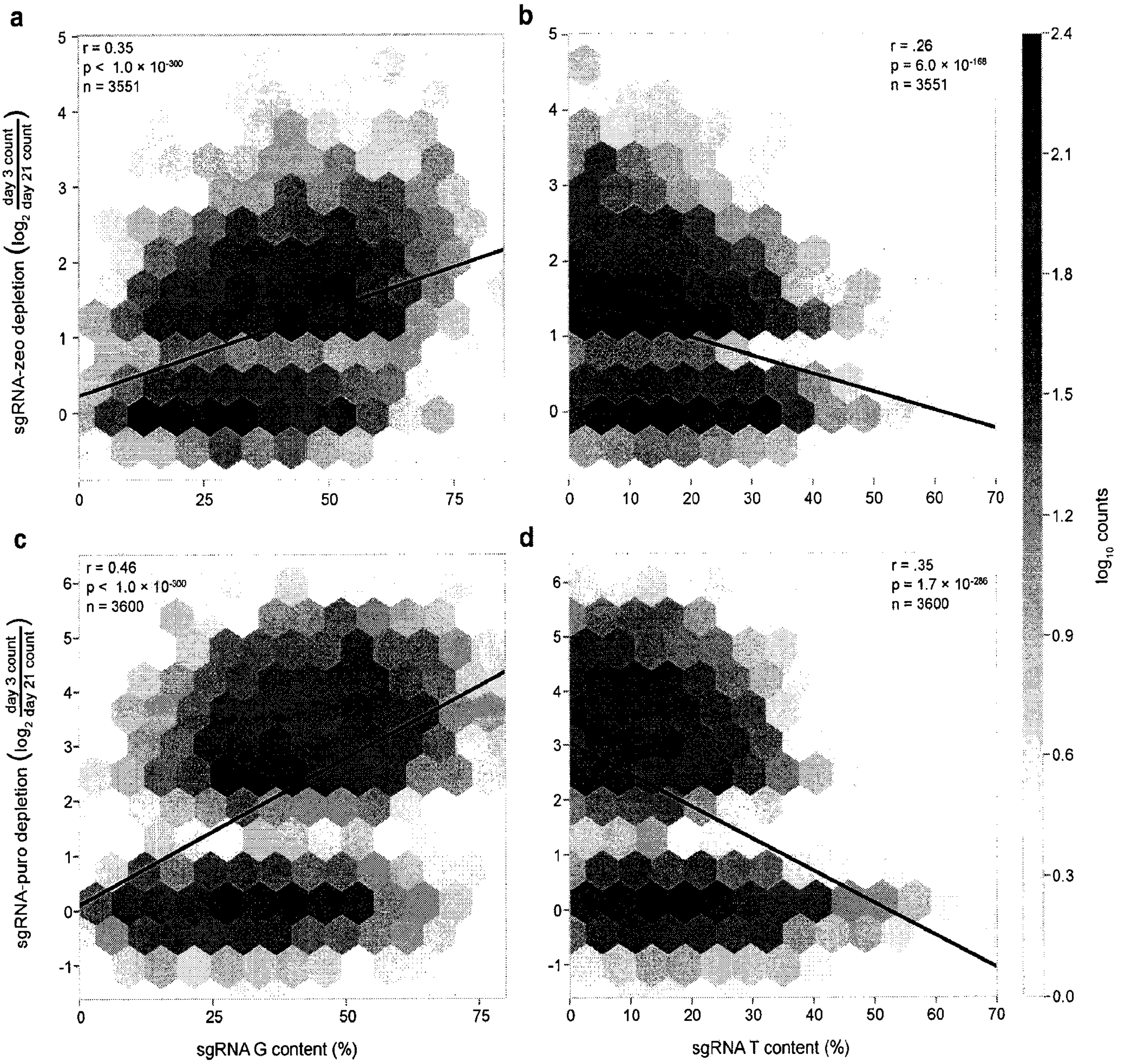

a
r = 0.35
p < 1.0 × 10^-300
n = 3551
sgRNA-zeo depletion (log2 (day 3 count / day 21 count))
5
4
3
2
1
0
0
25
50
75
b
r = .26
p = 6.0 × 10^-168
n = 3551
5
4
3
2
1
0
0
10
20
30
40
50
60
70
c
r = 0.46
p < 1.0 × 10^-300
n = 3600
sgRNA-puro depletion (log2 (day 3 count / day 21 count))
6
5
4
3
2
1
0
-1
0
25
50
75
sgRNA G content (%)
d
r = .35
p = 1.7 × 10^-286
n = 3600
6
5
4
3
2
1
0
-1
0
10
20
30
40
50
60
70
sgRNA T content (%)
log10 counts
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0.3
0.0

FIG. 79A-D

1 SgRNA Scaffolds

1.1 Standard guide scaffold (sgRNA 1.0)

NNNNNNNNNNNNNNNNNNNNGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTT
ATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTT

1.2 Tetraloop MS2 stem loop insertion sgRNA scaffold (sgRNA 1.1)

NNNNNNNNNNNNNNNNNNNNGTTTTAGAGCTAGGCCAACATGAGGATCACCCATGTCTGCAGGG
CCTAGCAAGTTAAAATAAGGCTAGTCCGTTATCACGCCGAAAGGCGGGCACCGAGTCGGTGCTT
TTT

1.3 Loop 2 MS2 stem loop insertion sgRNA scaffold (sgRNA 1.2)

NNNNNNNNNNNNNNNNNNNNGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTT
ATCAACTTGGCCAACATGAGGATCACCCATGTCTGCAGGGCCAAGTGGCACCGAGTCGGTGCTT
TTT

1.4 Tetraloop and Loop 2 MS2 stem loop insertion sgRNA scaffold (sgRNA 2.0)

NNNNNNNNNNNNNNNNNNNNGTTTTAGAGCTAGGCCAACATGAGGATCACCCATGTCTGCAGGG
CCTAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGGCCAACATGAGGATCACCCATGTCT
GCAGGGCCAAGTGGCACCGAGTCGGTGCTTTTT

2 MS2 Constructs

FIG. 80A

2.1 MS2-NLS-VP64

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTACAGCGCTGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCGGACCTA
AGAAAAAGAGGAAGGTGGCGGCCGCTGGATCCGGACGGGCTGACGCATTGGACGATTTTGATCT
GGATATGCTGGGAAGTGACGCCCTCGATGATTTTGACCTTGACATGCTTGGTTCGGATGCCCTT
GATGACTTTGACCTCGACATGCTCGGCAGTGACGCCCTTGATGATTTCGACCTGGACATGCTGA
TTAAC

2.1.1 MS2

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTAC

2.1.2 NLS

GGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCT

2.1.3 VP64

GGACGGGCTGACGCATTGGACGATTTTGATCTGGATATGCTGGGAAGTGACGCCCTCGATGATT
TTGACCTTGACATGCTTGGTTCGGATGCCCTTGATGACTTTGACCTCGACATGCTCGGCAGTGA
CGCCCTTGATGATTTCGACCTGGACATGCTGATTAAC

FIG. 80B

2.2 MS2-NLS-P65

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTACAGCGCTGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCGGACCTA
AGAAAAAGAGGAAGGTGGCGGCCGCTGGATCCCCTTCAGGGCAGATCAGCAACCAGGCCCTGGC
TCTGGCCCCTAGCTCCGCTCCAGTGCTGGCCCAGACTATGGTGCCCTCTAGTGCTATGGTGCCT
CTGGCCCAGCCACCTGCTCCAGCCCCTGTGCTGACCCCAGGACCACCCCAGTCACTGAGCGCTC
CAGTGCCCAAGTCTACACAGGCCGGCGAGGGGACTCTGAGTGAAGCTCTGCTGCACCTGCAGTT
CGACGCTGATGAGGACCTGGGAGCTCTGCTGGGGAACAGCACCGATCCCGGAGTGTTCACAGAT
CTGGCCTCCGTGGACAACTCTGAGTTTCAGCAGCTGCTGAATCAGGGCGTGTCCATGTCTCATA
GTACAGCCGAACCAATGCTGATGGAGTACCCCGAAGCCATTACCCGGCTGGTGACCGGCAGCCA
GCGGCCCCCCGACCCCGCTCCAACTCCCCTGGGAACCAGCGGCCTGCCTAATGGGCTGTCCGGA
GATGAAGACTTCTCAAGCATCGCTGATATGGACTTTAGTGCCCTGCTGTCACAGATTTCCTCTA
GTGGGCAG

2.2.1 MS2

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTAC

2.2.2 NLS

GGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCT

FIG. 80C

2.2.3 P65

CCTTCAGGGCAGATCAGCAACCAGGCCCTGGCTCTGGCCCCTAGCTCCGCTCCAGTGCTGGCCC
AGACTATGGTGCCCTCTAGTGCTATGGTGCCTCTGGCCCAGCCACCTGCTCCAGCCCCTGTGCT
GACCCCAGGACCACCCCAGTCACTGAGCGCTCCAGTGCCCAAGTCTACACAGGCCGGCGAGGGG
ACTCTGAGTGAAGCTCTGCTGCACCTGCAGTTCGACGCTGATGAGGACCTGGGAGCTCTGCTGG
GGAACAGCACCGATCCCGGAGTGTTCACAGATCTGGCCTCCGTGGACAACTCTGAGTTTCAGCA
GCTGCTGAATCAGGGCGTGTCCATGTCTCATAGTACAGCCGAACCAATGCTGATGGAGTACCCC
GAAGCCATTACCCGGCTGGTGACCGGCAGCCAGCGGCCCCCCGACCCCGCTCCAACTCCCCTGG
GAACCAGCGGCCTGCCTAATGGGCTGTCCGGAGATGAAGACTTCTCAAGCATCGCTGATATGGA
CTTTAGTGCCCTGCTGTCACAGATTTCCTCTAGTGGGCAG

2.3 MS2-NLS-P65-HSF1

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTACAGCGCTGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCGGACCTA
AGAAAAAGAGGAAGGTGGCGGCCGCTGGATCCCCTTCAGGGCAGATCAGCAACCAGGCCCTGGC
TCTGGCCCCTAGCTCCGCTCCAGTGCTGGCCCAGACTATGGTGCCCTCTAGTGCTATGGTGCCT
CTGGCCCAGCCACCTGCTCCAGCCCCTGTGCTGACCCCAGGACCACCCCAGTCACTGAGCGCTC
CAGTGCCCAAGTCTACACAGGCCGGCGAGGGGACTCTGAGTGAAGCTCTGCTGCACCTGCAGTT
CGACGCTGATGAGGACCTGGGAGCTCTGCTGGGGAACAGCACCGATCCCGGAGTGTTCACAGAT
CTGGCCTCCGTGGACAACTCTGAGTTTCAGCAGCTGCTGAATCAGGGCGTGTCCATGTCTCATA
GTACAGCCGAACCAATGCTGATGGAGTACCCCGAAGCCATTACCCGGCTGGTGACCGGCAGCCA
GCGGCCCCCCGACCCCGCTCCAACTCCCCTGGGAACCAGCGGCCTGCCTAATGGGCTGTCCGGA
GATGAAGACTTCTCAAGCATCGCTGATATGGACTTTAGTGCCCTGCTGTCACAGATTTCCTCTA
GTGGGCAGGGAGGAGGTGGAAGCGGCTTCAGCGTGGACACCAGTGCCCTGCTGGACCTGTTCAG
CCCCTCGGTGACCGTGCCCGACATGAGCCTGCCTGACCTTGACAGCAGCCTGGCCAGTATCCAA
GAGCTCCTGTCTCCCCAGGAGCCCCCCAGGCCTCCCGAGGCAGAGAACAGCAGCCCGGATTCAG
GGAAGCAGCTGGTGCACTACACAGCGCAGCCGCTGTTCCTGCTGGACCCCGGCTCCGTGGACAC
CGGGAGCAACGACCTGCCGGTGCTGTTTGAGCTGGGAGAGGGCTCCTACTTCTCCGAAGGGGAC
GGCTTCGCCGAGGACCCCACCATCTCCCTGCTGACAGGCTCGGAGCCTCCCAAAGCCAAGGACC
CCACTGTCTCC

FIG. 80D

2.3.1 MS2

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTAC

2.3.2 NLS

GGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCT

2.3.3 P65

CCTTCAGGGCAGATCAGCAACCAGGCCCTGGCTCTGGCCCCTAGCTCCGCTCCAGTGCTGGCCC
AGACTATGGTGCCCTCTAGTGCTATGGTGCCTCTGGCCCAGCCACCTGCTCCAGCCCCTGTGCT
GACCCCAGGACCACCCCAGTCACTGAGCGCTCCAGTGCCCAAGTCTACACAGGCCGGCGAGGGG
ACTCTGAGTGAAGCTCTGCTGCACCTGCAGTTCGACGCTGATGAGGACCTGGGAGCTCTGCTGG
GGAACAGCACCGATCCCGGAGTGTTCACAGATCTGGCCTCCGTGGACAACTCTGAGTTTCAGCA
GCTGCTGAATCAGGGCGTGTCCATGTCTCATAGTACAGCCGAACCAATGCTGATGGAGTACCCC
GAAGCCATTACCCGGCTGGTGACCGGCAGCCAGCGGCCCCCCGACCCCGCTCCAACTCCCCTGG
GAACCAGCGGCCTGCCTAATGGGCTGTCCGGAGATGAAGACTTCTCAAGCATCGCTGATATGGA
CTTTAGTGCCCTGCTGTCACAGATTTCCTCTAGTGGGCAG

2.3.4 HSF1

GGCTTCAGCGTGGACACCAGTGCCCTGCTGGACCTGTTCAGCCCCTCGGTGACCGTGCCCGACA
TGAGCCTGCCTGACCTTGACAGCAGCCTGGCCAGTATCCAAGAGCTCCTGTCTCCCCAGGAGCC
CCCCAGGCCTCCCGAGGCAGAGAACAGCAGCCCGGATTCAGGGAAGCAGCTGGTGCACTACACA
GCGCAGCCGCTGTTCCTGCTGGACCCCGGCTCCGTGGACACCGGGAGCAACGACCTGCCGGTGC
TGTTTGAGCTGGGAGAGGGCTCCTACTTCTCCGAAGGGGACGGCTTCGCCGAGGACCCCACCAT
CTCCCTGCTGACAGGCTCGGAGCCTCCCAAAGCCAAGGACCCCACTGTCTCC

FIG. 80E

2.4 MS2-NLS-P65-Myod1

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTACAGCGCTGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCGGACCTA
AGAAAAAGAGGAAGGTGGCGGCCGCTGGATCCCCTTCAGGGCAGATCAGCAACCAGGCCCTGGC
TCTGGCCCCTAGCTCCGCTCCAGTGCTGGCCCAGACTATGGTGCCCTCTAGTGCTATGGTGCCT
CTGGCCCAGCCACCTGCTCCAGCCCCTGTGCTGACCCCAGGACCACCCCAGTCACTGAGCGCTC
CAGTGCCCAAGTCTACACAGGCCGGCGAGGGGACTCTGAGTGAAGCTCTGCTGCACCTGCAGTT
CGACGCTGATGAGGACCTGGGAGCTCTGCTGGGGAACAGCACCGATCCCGGAGTGTTCACAGAT
CTGGCCTCCGTGGACAACTCTGAGTTTCAGCAGCTGCTGAATCAGGGCGTGTCCATGTCTCATA
GTACAGCCGAACCAATGCTGATGGAGTACCCCGAAGCCATTACCCGGCTGGTGACCGGCAGCCA
GCGGCCCCCCGACCCCGCTCCAACTCCCCTGGGAACCAGCGGCCTGCCTAATGGGCTGTCCGGA
GATGAAGACTTCTCAAGCATCGCTGATATGGACTTTAGTGCCCTGCTGTCACAGATTTCCTCTA
GTGGGCAGGGAGGAGGTGGAAGCATGGAGCTTCTTTCTCCTCCTCTGCGGGATGTTGACCTGAC
TGCGCCCGACGGCTCTCTTTGCTCCTTCGCCACAACCGACGACTTCTACGATGATCCATGTTTT
GACAGCCCCGATCTCAGGTTCTTTGAGGATCTCGATCCTAGACTGATGCACGTGGGCGCACTGC
TCAAACCTGAGGAACATAGC

2.4.1 MS2

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTAC

2.4.2 NLS

GGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCT

FIG. 80F

2.4.3 P65

CCTTCAGGGCAGATCAGCAACCAGGCCCTGGCTCTGGCCCCTAGCTCCGCTCCAGTGCTGGCCC
AGACTATGGTGCCCTCTAGTGCTATGGTGCCTCTGGCCCAGCCACCTGCTCCAGCCCCTGTGCT
GACCCCAGGACCACCCCAGTCACTGAGCGCTCCAGTGCCCAAGTCTACACAGGCCGGCGAGGGG
ACTCTGAGTGAAGCTCTGCTGCACCTGCAGTTCGACGCTGATGAGGACCTGGGAGCTCTGCTGG
GGAACAGCACCGATCCCGGAGTGTTCACAGATCTGGCCTCCGTGGACAACTCTGAGTTTCAGCA
GCTGCTGAATCAGGGCGTGTCCATGTCTCATAGTACAGCCGAACCAATGCTGATGGAGTACCCC
GAAGCCATTACCCGGCTGGTGACCGGCAGCCAGCGGCCCCCCGACCCCGCTCCAACTCCCCTGG
GAACCAGCGGCCTGCCTAATGGGCTGTCCGGAGATGAAGACTTCTCAAGCATCGCTGATATGGA
CTTTAGTGCCCTGCTGTCACAGATTTCCTCTAGTGGGCAG

2.4.4 Myodl

ATGGAGCTTCTTTCTCCTCCTCTGCGGGATGTTGACCTGACTGCGCCCGACGGCTCTCTTTGCT
CCTTCGCCACAACCGACGACTTCTACGATGATCCATGTTTTGACAGCCCCGATCTCAGGTTCTT
TGAGGATCTCGATCCTAGACTGATGCACGTGGGCGCACTGCTCAAACCTGAGGAACATAGC

3 dCas9 Constructs

3.1 dCas9(D10A, H840A)-NLS-VP64

GACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCG
ACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAA
GAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAG
AGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCA
GCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGA
AGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCAC
GAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACC
TGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGG
CGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAAC
CAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCA
GACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGG
CCTGTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGAC
CTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGC

FIG. 80G

TGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCAT

CCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATG

ATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGC

TGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGA

CGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGC

ACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACA

ACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGA

TTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCC

TACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGG

AAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCAT

CGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTG

CTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGA

GAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAA

CCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCC

GTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGA

AAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGT

GCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCAC

CTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGA

GCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAA

GTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAA

GAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATC

TGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGT

GAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACC

ACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGC

TGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTA

CCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTG

TCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACA

AGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGT

GAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTC

GACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGA

GACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAA

CACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAG

CTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACC

ACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCT

GGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGC

GAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCA

FIG. 80H

AGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGA
AACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATG
CCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC
TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGG
CGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAG
TCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCG
AGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCAT
CAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCC
GGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGG
CCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGA
ACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATC
CTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCA
GAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTT
CAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCC
ACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAG
GCGACAGCGCTGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCGGACCTAA
GAAAAAGAGGAAGGTGGCGGCCGCTGGATCCGGACGGGCTGACGCATTGGACGATTTTGATCTG
GATATGCTGGGAAGTGACGCCCTCGATGATTTTGACCTTGACATGCTTGGTTCGGATGCCCTTG
ATGACTTTGACCTCGACATGCTCGGCAGTGACGCCCTTGATGATTTCGACCTGGACATGCTGAT
TAAC

3.1.1 dCas9(D10A, H840A)

GACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCG
ACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAA
GAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAG
AGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCA
GCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGA
AGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCAC
GAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACC
TGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGG
CGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAAC
CAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCA
GACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGG
CCTGTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGAC
CTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGC

FIG. 80I

TGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCAT
CCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATG
ATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGC
TGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGA
CGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGC
ACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACA
ACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGA
TTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCC
TACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGG
AAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCAT
CGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTG
CTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGA
GAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAA
CCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCC
GTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGA
AAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGT
GCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCAC
CTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGA
GCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAA
GTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAA
GAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATC
TGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGT
GAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACC
ACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGC
TGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTA
CCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTG
TCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACA
AGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGT
GAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTC
GACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGA
GACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAA
CACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAG
CTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACC
ACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCT
GGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGC
GAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCA

FIG. 80J

AGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGA
AACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATG
CCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC
TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGG
CGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAG
TCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCG
AGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCAT
CAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCC
GGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGG
CCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGA
ACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATC
CTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCA
GAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTT
CAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCC
ACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAG
GCGAC

3.1.2 NLS

GGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCT

3.1.3 VP64

GGACGGGCTGACGCATTGGACGATTTTGATCTGGATATGCTGGGAAGTGACGCCCTCGATGATT
TTGACCTTGACATGCTTGGTTCGGATGCCCTTGATGACTTTGACCTCGACATGCTCGGCAGTGA
CGCCCTTGATGATTTCGACCTGGACATGCTGATTAAC

3.2 dCas9(D10A, H840A)-NLS-P65

GACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCG
ACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAA
GAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAG
AGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCA
GCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGA
AGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCAC
GAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACC

FIG. 80K

TGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGG
CGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAAC
CAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCA
GACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGG
CCTGTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGAC
CTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGC
TGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCAT
CCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATG
ATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGC
TGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGA
CGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGC
ACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACA
ACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGA
TTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCC
TACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGG
AAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCAT
CGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTG
CTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGA
GAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAA
CCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCC
GTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGA
AAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGT
GCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCAC
CTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGA
GCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAA
GTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAA
GAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATC
TGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGT
GAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACC
ACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGC
TGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTA
CCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTG
TCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACA
AGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGT
GAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTC
GACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGA

FIG. 80L

GACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAA
CACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAG
CTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACC
ACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCT
GGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGC
GAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCA
AGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGA
AACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATG
CCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC
TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGG
CGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAG
TCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCG
AGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCAT
CAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCC
GGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGG
CCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGA
ACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATC
CTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCA
GAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTT
CAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCC
ACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAG
GCGACAGCGCTGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCGGACCTAA
GAAAAAGAGGAAGGTGGCGGCCGCTGGATCCCCTTCAGGGCAGATCAGCAACCAGGCCCTGGCT
CTGGCCCCTAGCTCCGCTCCAGTGCTGGCCCAGACTATGGTGCCCTCTAGTGCTATGGTGCCTC
TGGCCCAGCCACCTGCTCCAGCCCCTGTGCTGACCCCAGGACCACCCCAGTCACTGAGCGCTCC
AGTGCCCAAGTCTACACAGGCCGGCGAGGGGACTCTGAGTGAAGCTCTGCTGCACCTGCAGTTC
GACGCTGATGAGGACCTGGGAGCTCTGCTGGGGAACAGCACCGATCCCGGAGTGTTCACAGATC
TGGCCTCCGTGGACAACTCTGAGTTTCAGCAGCTGCTGAATCAGGGCGTGTCCATGTCTCATAG
TACAGCCGAACCAATGCTGATGGAGTACCCCGAAGCCATTACCCGGCTGGTGACCGGCAGCCAG
CGGCCCCCCGACCCCGCTCCAACTCCCCTGGGAACCAGCGGCCTGCCTAATGGGCTGTCCGGAG
ATGAAGACTTCTCAAGCATCGCTGATATGGACTTTAGTGCCCTGCTGTCACAGATTTCCTCTAG
TGGGCAG

FIG. 80M

3.2.1 dCas9(D10A, H840A)

GACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCG
ACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAA
GAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAG
AGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCA
GCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGA
AGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCAC
GAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACC
TGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGG
CGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAAC
CAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCA
GACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGG
CCTGTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGAC
CTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGC
TGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCAT
CCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATG
ATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGC
TGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGA
CGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGC
ACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACA
ACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGA
TTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCC
TACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGG
AAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCAT
CGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTG
CTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGA
GAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAA
CCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCC
GTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGA
AAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGT
GCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCAC
CTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGA
GCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAA
GTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAA
GAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATC

FIG. 80N

TGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGT
GAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACC
ACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGC
TGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTA
CCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTG
TCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACA
AGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGT
GAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTC
GACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGA
GACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAA
CACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAG
CTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACC
ACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCT
GGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGC
GAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCA
AGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGA
AACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATG
CCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC
TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGG
CGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAG
TCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCG
AGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCAT
CAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCC
GGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGG
CCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGA
ACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATC
CTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCA
GAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTT
CAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCC
ACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAG
GCGAC

3.2.2 NLS

GGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCT

FIG. 80O

3.2.3 P65

CCTTCAGGGCAGATCAGCAACCAGGCCCTGGCTCTGGCCCCTAGCTCCGCTCCAGTGCTGGCCC
AGACTATGGTGCCCTCTAGTGCTATGGTGCCTCTGGCCCAGCCACCTGCTCCAGCCCCTGTGCT
GACCCCAGGACCACCCCAGTCACTGAGCGCTCCAGTGCCCAAGTCTACACAGGCCGGCGAGGGG
ACTCTGAGTGAAGCTCTGCTGCACCTGCAGTTCGACGCTGATGAGGACCTGGGAGCTCTGCTGG
GGAACAGCACCGATCCCGGAGTGTTCACAGATCTGGCCTCCGTGGACAACTCTGAGTTTCAGCA
GCTGCTGAATCAGGGCGTGTCCATGTCTCATAGTACAGCCGAACCAATGCTGATGGAGTACCCC
GAAGCCATTACCCGGCTGGTGACCGGCAGCCAGCGGCCCCCCGACCCCGCTCCAACTCCCCTGG
GAACCAGCGGCCTGCCTAATGGGCTGTCCGGAGATGAAGACTTCTCAAGCATCGCTGATATGGA
CTTTAGTGCCCTGCTGTCACAGATTTCCTCTAGTGGGCAG

4 Lentiviral Vectors

4.1 pFUGW-EF1α-NLS(SV40)-dCas9(N863)-NLS-VP64-P2A-Blast

TGCAAAGATGGATAAAGTTTTAAACAGAGAGGAATCTTTGCAGCTAATGGACCTTCTAGGTCTT
GAAAGGAGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCC
GAGAAGTTGGGGGGAGGGGTCGGCAATTGAACCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACT
GGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAG
TGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTAAGTGCC
GTGTGTGGTTCCCGCGGGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATTACTT
CCACTGGCTGCAGTACGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTCG
AGGCCTTGCGCTTAAGGAGCCCCTTCGCCTCGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGGG
GCCGCCGCGTGCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAGC
CATTTAAAATTTTTGATGACCTGCTGCGACGCTTTTTTTCTGGCAAGATAGTCTTGTAAATGCG
GGCCAAGATCTGCACACTGGTATTTCGGTTTTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCGT
CCCAGCGCACATGTTCGGCGAGGCGGGGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGTA
GTCTCAAGCTGGCCGGCCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTGG
GCGGCAAGGCTGGCCCGGTCGGCACCAGTTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTG
CTGCAGGGAGCTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGGTGAGTCACCCACACA
AAGGAAAAGGGCCTTTCCGTCCTCAGCCGTCGCTTCATGTGACTCCACGGAGTACCGGGCGCCG
TCCAGGCACCTCGATTAGTTCTCGAGCTTTTGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGGT
TTTATGCGATGGAGTTTCCCCACACTGAGTGGGTGGAGACTGAAGTTAGGCCAGCTTGGCACTT
GATGTAATTCTCCTTGGAATTTGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAAGCCTCAG

FIG. 80P

ACAGTGGTTCAAAGTTTTTTTCTTCCATTTCAGGTGTCGTGACGTACGGCCACCCATGAGCCCC
AAGAAGAAGAGAAAGGTGGAGGCCAGCGACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCA
ACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCT
GGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGC
GAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACC
GGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCA
CAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGC
AACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAAC
TGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAA
GTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTG
TTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCG
TGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGC
CCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTG
ACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACA
CCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCT
GGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATC
ACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCC
TGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAG
CAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATC
AAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACC
TGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCT
GCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATC
GAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGAT
TCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGA
CAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAAC
GAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCA
AAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGC
CATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTAC
TTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCT
CCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGA
AAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATC
GAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGC
GGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTC
CGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTG
ATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCG
ATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCA

FIG. 80Q

GACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTG
ATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGA
AGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAA
CACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTG
GACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACCACATCGTGCCTCAGAGCT
TTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGGCCCGGGGCAAGAG
CGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAAC
GCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCG
AACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGT
GGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAA
GTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACA
AAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAAC
CGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTAC
GACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCT
TCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAA
GCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTT
GCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGA
CAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAA
GAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTG
GTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGA
TCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTA
CAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAAC
GGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCT
CCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGA
TAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAG
ATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCT
ACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCT
GACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTAC
ACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGA
CACGGATCGACCTGTCTCAGCTGGGAGGCGACAGCGCTGGAGGAGGTGGAAGCGGAGGAGGAGG
AAGCGGAGGAGGAGGTAGCGGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCTGGATCCGGACGG
GCTGACGCATTGGACGATTTTGATCTGGATATGCTGGGAAGTGACGCCCTCGATGATTTTGACC
TTGACATGCTTGGTTCGGATGCCCTTGATGACTTTGACCTCGACATGCTCGGCAGTGACGCCCT
TGATGATTTCGACCTGGACATGCTGATTAACTGTACAGGCAGTGGAGAGGGCAGAGGAAGTCTG
CTAACATGCGGTGACGTCGAGGAGAATCCTGGCCCAATGGCCAAGCCTTTGTCTCAAGAAGAAT
CCACCCTCATTGAAAGAGCAACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGT

FIG. 80R

CGCCAGCGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATCATTTTACT
GGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGA
CTTGTATCGTCGCGATCGGAAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACA
GGTGCTTCTCGATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACG
GCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAA

4.1.1 EF1α

TGCAAAGATGGATAAAGTTTTAAACAGAGAGGAATCTTTGCAGCTAATGGACCTTCTAGGTCTT
GAAAGGAGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCC
GAGAAGTTGGGGGGAGGGGTCGGCAATTGAACCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACT
GGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAG
TGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTAAGTGCC
GTGTGTGGTTCCCGCGGGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATTACTT
CCACTGGCTGCAGTACGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTCG
AGGCCTTGCGCTTAAGGAGCCCCTTCGCCTCGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGGG
GCCGCCGCGTGCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAGC
CATTTAAAATTTTTGATGACCTGCTGCGACGCTTTTTTTCTGGCAAGATAGTCTTGTAAATGCG
GGCCAAGATCTGCACACTGGTATTTCGGTTTTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCGT
CCCAGCGCACATGTTCGGCGAGGCGGGGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGTA
GTCTCAAGCTGGCCGGCCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTGG
GCGGCAAGGCTGGCCCGGTCGGCACCAGTTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTG
CTGCAGGGAGCTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGGTGAGTCACCCACACA
AAGGAAAAGGGCCTTTCCGTCCTCAGCCGTCGCTTCATGTGACTCCACGGAGTACCGGGCGCCG
TCCAGGCACCTCGATTAGTTCTCGAGCTTTTGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGGT
TTTATGCGATGGAGTTTCCCCACACTGAGTGGGTGGAGACTGAAGTTAGGCCAGCTTGGCACTT
GATGTAATTCTCCTTGGAATTTGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAAGCCTCAG
ACAGTGGTTCAAAGTTTTTTTCTTCCATTTCAGGTGTCGTGA

4.1.2 NLS(SV40)

ATGAGCCCCAAGAAGAAGAGAAAGGTGGAGGCCAGC

FIG. 80S

4.1.3 dCas9(N863)

GACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCG
ACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAA
GAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAG
AGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCA
GCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGA
AGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCAC
GAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACC
TGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGG
CGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAAC
CAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCA
GACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGG
CCTGTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGAC
CTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGC
TGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCAT
CCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATG
ATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGC
TGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGA
CGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGC
ACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACA
ACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGA
TTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCC
TACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGG
AAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCAT
CGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTG
CTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGA
GAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAA
CCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCC
GTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGA
AAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGT
GCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCAC
CTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGA
GCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAA
GTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAA
GAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATC

FIG. 80T

TGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGT
GAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACC
ACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGC
TGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTA
CCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTG
TCCGACTACGATGTGGACCACATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACA
AGGTGCTGACCAGAAGCGACAAGGCCCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGT
GAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTC
GACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGA
GACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAA
CACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAG
CTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACC
ACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCT
GGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGC
GAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCA
AGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGA
AACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATG
CCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC
TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGG
CGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAG
TCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCG
AGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCAT
CAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCC
GGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGG
CCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGA
ACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATC
CTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCA
GAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTT
CAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCC
ACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAG
GCGAC

4.1.4 NLS

GGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCT

FIG. 80U

4.1.5 VP64

GGACGGGCTGACGCATTGGACGATTTTGATCTGGATATGCTGGGAAGTGACGCCCTCGATGATT
TTGACCTTGACATGCTTGGTTCGGATGCCCTTGATGACTTTGACCTCGACATGCTCGGCAGTGA
CGCCCTTGATGATTTCGACCTGGACATGCTGATTAAC

4.1.6 P2A

GGCAGTGGAGAGGGCAGAGGAAGTCTGCTAACATGCGGTGACGTCGAGGAGAATCCTGGCCCA

4.1.7 Blast

ATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAACA
GCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACGGCCGCATCTT
CACTGGTGTCAATGTATATCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACT
GCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAACAGGGGCA
TCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCCAT
AGTGAAGGACAGTGATGGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTAT
GTGTGGGAGGGCTAA

4.2 pFUGW-EF1α-MS2-NLS-p65-HSF1-P2A-Hygro

TGCAAAGATGGATAAAGTTTTAAACAGAGAGGAATCTTTGCAGCTAATGGACCTTCTAGGTCTT
GAAAGGAGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCC
GAGAAGTTGGGGGGAGGGGTCGGCAATTGAACCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACT
GGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAG
TGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTAAGTGCC
GTGTGTGGTTCCCGCGGGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATTACTT
CCACCTGGCTGCAGTACGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTC
GAGGCCTTGCGCTTAAGGAGCCCCTTCGCCTCGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGG
GGCCGCCGCGTGCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAG
CCATTTAAAATTTTTGATGACCTGCTGCGACGCTTTTTTTCTGGCAAGATAGTCTTGTAAATGC
GGGCCAAGATCTGCACACTGGTATTTCGGTTTTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCG
TCCCAGCGCACATGTTCGGCGAGGCGGGGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGT
AGTCTCAAGCTGGCCGGCCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTG
GGCGGCAAGGCTGGCCCGGTCGGCACCAGTTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCT
GCTGCAGGGAGCTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGGTGAGTCACCCACAC

FIG. 80V

AAAGGAAAAGGGCCTTTCCGTCCTCAGCCGTCGCTTCATGTGACTCCACGGAGTACCGGGCGCC
GTCCAGGCACCTCGATTAGTTCTCGAGCTTTTGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGG
TTTTATGCGATGGAGTTTCCCCACACTGAGTGGGTGGAGACTGAAGTTAGGCCAGCTTGGCACT
TGATGTAATTCTCCTTGGAATTTGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAAGCCTCA
GACAGTGGTTCAAAGTTTTTTTCTTCCATTTCAGGTGTCGTGACGTACGGCCACCATGGCTTCA
AACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGGCTCCTTCTA
ATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTACAAGGTGAC
ATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAGGTCCCCAAA
GTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCTACCTGAACA
TGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAAGGCAATGCA
GGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGTATCTACAGC
GCTGGAGGAGGTGGAAGCGGAGGAGGAGGAAGCGGAGGAGGAGGTAGCGGACCTAAGAAAAAGA
GGAAGGTGGCGGCCGCTGGATCCCCTTCAGGGCAGATCAGCAACCAGGCCCTGGCTCTGGCCCC
TAGCTCCGCTCCAGTGCTGGCCCAGACTATGGTGCCCTCTAGTGCTATGGTGCCTCTGGCCCAG
CCACCTGCTCCAGCCCCTGTGCTGACCCCAGGACCACCCCAGTCACTGAGCGCTCCAGTGCCCA
AGTCTACACAGGCCGGCGAGGGGACTCTGAGTGAAGCTCTGCTGCACCTGCAGTTCGACGCTGA
TGAGGACCTGGGAGCTCTGCTGGGGAACAGCACCGATCCCGGAGTGTTCACAGATCTGGCCTCC
GTGGACAACTCTGAGTTTCAGCAGCTGCTGAATCAGGGCGTGTCCATGTCTCATAGTACAGCCG
AACCAATGCTGATGGAGTACCCCGAAGCCATTACCCGGCTGGTGACCGGCAGCCAGCGGCCCCC
CGACCCCGCTCCAACTCCCCTGGGAACCAGCGGCCTGCCTAATGGGCTGTCCGGAGATGAAGAC
TTCTCAAGCATCGCTGATATGGACTTTAGTGCCCTGCTGTCACAGATTTCCTCTAGTGGGCAGG
GAGGAGGTGGAAGCGGCTTCAGCGTGGACACCAGTGCCCTGCTGGACCTGTTCAGCCCCTCGGT
GACCGTGCCCGACATGAGCCTGCCTGACCTTGACAGCAGCCTGGCCAGTATCCAAGAGCTCCTG
TCTCCCCAGGAGCCCCCCAGGCCTCCCGAGGCAGAGAACAGCAGCCCGGATTCAGGGAAGCAGC
TGGTGCACTACACAGCGCAGCCGCTGTTCCTGCTGGACCCCGGCTCCGTGGACACCGGGAGCAA
CGACCTGCCGGTGCTGTTTGAGCTGGGAGAGGGCTCCTACTTCTCCGAAGGGGACGGCTTCGCC
GAGGACCCCACCATCTCCCTGCTGACAGGCTCGGAGCCTCCCAAAGCCAAGGACCCCACTGTCT
CCTGTACAGGCAGTGGAGAGGGCAGAGGAAGTCTGCTAACATGCGGTGACGTCGAGGAGAATCC
TGGCCCAACCATGAAAAAGCCTGAACTCACCGCTACCTCTGTCGAGAAGTTTCTGATCGAAAAG
TTCGACAGCGTCTCCGACCTGATGCAGCTCTCCGAGGGCGAAGAATCTCGGGCTTTCAGCTTCG
ATGTGGGAGGGCGTGGATATGTCCTGCGGGTGAATAGCTGCGCCGATGGTTTCTACAAAGATCG
CTATGTTTATCGGCACTTTGCATCCGCCGCTCTCCCTATTCCCGAAGTGCTTGACATTGGGGAG
TTCAGCGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCACCTTGCAAGACCTGC
CTGAAACCGAACTGCCCGCTGTTCTCCAGCCCGTCGCCGAGGCCATGGATGCCATCGCTGCCGC
CGATCTTAGCCAGACCAGCGGGTTCGGCCCATTCGGACCTCAAGGAATCGGTCAATACACTACA
TGGCGCGATTTCATCTGCGCTATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACG

FIG. 80W

ACACCGTCAGTGCCTCCGTCGCCCAGGCTCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCC
CGAAGTCCGGCACCTCGTGCACGCCGATTTCGGCTCCAACAATGTCCTGACCGACAATGGCCGC
ATAACAGCCGTCATTGACTGGAGCGAGGCCATGTTCGGGGATTCCCAATACGAGGTCGCCAACA
TCTTCTTCTGGAGGCCCTGGTTGGCTTGTATGGAGCAGCAGACCCGCTACTTCGAGCGGAGGCA
TCCCGAGCTTGCAGGATCTCCTCGGCTCCGGGCTTATATGCTCCGCATTGGTCTTGACCAACTC
TATCAGAGCTTGGTTGACGGCAATTTCGATGATGCAGCTTGGGCTCAGGGTCGCTGCGACGCAA
TCGTCCGGTCCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGCAGAAGCGCTGCCGTCTG
GACCGATGGCTGTGTGGAAGTGCTCGCCGATAGTGGAAACAGACGCCCCAGCACTCGTCCTAGG
GCAAAGGATCTGCAGTAATGA

4.2.1 EF1α

TGCAAAGATGGATAAAGTTTTAAACAGAGAGGAATCTTTGCAGCTAATGGACCTTCTAGGTCTT
GAAAGGAGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCC
GAGAAGTTGGGGGGAGGGGTCGGCAATTGAACCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACT
GGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAG
TGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTAAGTGCC
GTGTGTGGTTCCCGCGGGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATTACTT
CCACCTGGCTGCAGTACGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTC
GAGGCCTTGCGCTTAAGGAGCCCCTTCGCCTCGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGG
GGCCGCCGCGTGCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAG
CCATTTAAAATTTTTGATGACCTGCTGCGACGCTTTTTTTCTGGCAAGATAGTCTTGTAAATGC
GGGCCAAGATCTGCACACTGGTATTTCGGTTTTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCG
TCCCAGCGCACATGTTCGGCGAGGCGGGGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGT
AGTCTCAAGCTGGCCGGCCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTG
GGCGGCAAGGCTGGCCCGGTCGGCACCAGTTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCT
GCTGCAGGGAGCTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGGTGAGTCACCCACAC
AAAGGAAAAGGGCCTTTCCGTCCTCAGCCGTCGCTTCATGTGACTCCACGGAGTACCGGGCGCC
GTCCAGGCACCTCGATTAGTTCTCGAGCTTTTGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGG
TTTTATGCGATGGAGTTTCCCCACACTGAGTGGGTGGAGACTGAAGTTAGGCCAGCTTGGCACT
TGATGTAATTCTCCTTGGAATTTGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAAGCCTCA
GACAGTGGTTCAAAGTTTTTTTCTTCCATTTCAGGTGTCGTGA

FIG. 80X

4.2.2 MS2

ATGGCTTCAAACTTTACTCAGTTCGTGCTCGTGGACAATGGTGGGACAGGGGATGTGACAGTGG
CTCCTTCTAATTTCGCTAATGGGGTGGCAGAGTGGATCAGCTCCAACTCACGGAGCCAGGCCTA
CAAGGTGACATGCAGCGTCAGGCAGTCTAGTGCCCAGAAGAGAAAGTATACCATCAAGGTGGAG
GTCCCCAAAGTGGCTACCCAGACAGTGGGCGGAGTCGAACTGCCTGTCGCCGCTTGGAGGTCCT
ACCTGAACATGGAGCTCACTATCCCAATTTTCGCTACCAATTCTGACTGTGAACTCATCGTGAA
GGCAATGCAGGGGCTCCTCAAAGACGGTAATCCTATCCCTTCCGCCATCGCCGCTAACTCAGGT
ATCTAC

4.2.3 NLS

GGACCTAAGAAAAAGAGGAAGGTGGCGGCCGCT

4.2.4 p65

CCTTCAGGGCAGATCAGCAACCAGGCCCTGGCTCTGGCCCCTAGCTCCGCTCCAGTGCTGGCCC
AGACTATGGTGCCCTCTAGTGCTATGGTGCCTCTGGCCCAGCCACCTGCTCCAGCCCCTGTGCT
GACCCCAGGACCACCCCAGTCACTGAGCGCTCCAGTGCCCAAGTCTACACAGGCCGGCGAGGGG
ACTCTGAGTGAAGCTCTGCTGCACCTGCAGTTCGACGCTGATGAGGACCTGGGAGCTCTGCTGG
GGAACAGCACCGATCCCGGAGTGTTCACAGATCTGGCCTCCGTGGACAACTCTGAGTTTCAGCA
GCTGCTGAATCAGGGCGTGTCCATGTCTCATAGTACAGCCGAACCAATGCTGATGGAGTACCCC
GAAGCCATTACCCGGCTGGTGACCGGCAGCCAGCGGCCCCCCGACCCCGCTCCAACTCCCCTGG
GAACCAGCGGCCTGCCTAATGGGCTGTCCGGAGATGAAGACTTCTCAAGCATCGCTGATATGGA
CTTTAGTGCCCTGCTGTCACAGATTTCCTCTAGTGGGCAG

4.2.5 HSF1

GGCTTCAGCGTGGACACCAGTGCCCTGCTGGACCTGTTCAGCCCCTCGGTGACCGTGCCCGACA
TGAGCCTGCCTGACCTTGACAGCAGCCTGGCCAGTATCCAAGAGCTCCTGTCTCCCCAGGAGCC
CCCCAGGCCTCCCGAGGCAGAGAACAGCAGCCCGGATTCAGGGAAGCAGCTGGTGCACTACACA
GCGCAGCCGCTGTTCCTGCTGGACCCCGGCTCCGTGGACACCGGGAGCAACGACCTGCCGGTGC
TGTTTGAGCTGGGAGAGGGCTCCTACTTCTCCGAAGGGGACGGCTTCGCCGAGGACCCCACCAT
CTCCCTGCTGACAGGCTCGGAGCCTCCCAAAGCCAAGGACCCCACTGTCTCC

FIG. 80Y

4.2.6 P2A

GGCAGTGGAGAGGGCAGAGGAAGTCTGCTAACATGCGGTGACGTCGAGGAGAATCCTGGCCCA

4.2.7 Hygro

ACCATGAAAAAGCCTGAACTCACCGCTACCTCTGTCGAGAAGTTTCTGATCGAAAAGTTCGACA
GCGTCTCCGACCTGATGCAGCTCTCCGAGGGCGAAGAATCTCGGGCTTTCAGCTTCGATGTGGG
AGGGCGTGGATATGTCCTGCGGGTGAATAGCTGCGCCGATGGTTTCTACAAAGATCGCTATGTT
TATCGGCACTTTGCATCCGCCGCTCTCCCTATTCCCGAAGTGCTTGACATTGGGGAGTTCAGCG
AGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCACCTTGCAAGACCTGCCTGAAAC
CGAACTGCCCGCTGTTCTCCAGCCCGTCGCCGAGGCCATGGATGCCATCGCTGCCGCCGATCTT
AGCCAGACCAGCGGGTTCGGCCCATTCGGACCTCAAGGAATCGGTCAATACACTACATGGCGCG
ATTTCATCTGCGCTATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACACCGT
CAGTGCCTCCGTCGCCCAGGCTCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTC
CGGCACCTCGTGCACGCCGATTTCGGCTCCAACAATGTCCTGACCGACAATGGCCGCATAACAG
CCGTCATTGACTGGAGCGAGGCCATGTTCGGGGATTCCCAATACGAGGTCGCCAACATCTTCTT
CTGGAGGCCCTGGTTGGCTTGTATGGAGCAGCAGACCCGCTACTTCGAGCGGAGGCATCCCGAG
CTTGCAGGATCTCCTCGGCTCCGGGCTTATATGCTCCGCATTGGTCTTGACCAACTCTATCAGA
GCTTGGTTGACGGCAATTTCGATGATGCAGCTTGGGCTCAGGGTCGCTGCGACGCAATCGTCCG
GTCCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGCAGAAGCGCTGCCGTCTGGACCGAT
GGCTGTGTGGAAGTGCTCGCCGATAGTGGAAACAGACGCCCCAGCACTCGTCCTAGGGCAAAGG
ATCTGCAGTAATGA

4.3 pFUGW-U6-sgRNA-EF1α-Zeo

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAGATAA
TTGGAATTAATTTGACTGTAAACACAAAGATATTAGTACAAAATACGTGACGTAGAAAGTAATA
ATTTCTTGGGTAGTTTGCAGTTTTAAAATTATGTTTTAAAATGGACTATCATATGCTTACCGTA
ACTTGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGACGAAACACCGGAGACG
GGATACCGTCTCTGTTTTAGAGCTAGGCCAACATGAGGATCACCCATGTCTGCAGGGCCTAGCA
AGTTAAAATAAGGCTAGTCCGTTATCAACTTGGCCAACATGAGGATCACCCATGTCTGCAGGGC
CAAGTGGCACCGAGTCGGTGCTTTTTTTGGATCCTGCAAAGATGGATAAAGTTTTAAACAGAGA
GGAATCTTTGCAGCTAATGGACCTTCTAGGTCTTGAAAGGAGTGGGAATTGGCTCCGGTGCCCG
TCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGA
TCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCC
TTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCG

FIG. 80Z

CAACGGGTTTGCCGCCAGAACACAGGTAAGTGCCGTGTGTGGTTCCCGCGGGCCTGGCCTCTTT
ACGGGTTATGGCCCTTGCGTGCCTTGAATTACTTCCACTGGCTGCAGTACGTGATTCTTGATCC
CGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTCGAGGCCTTGCGCTTAAGGAGCCCCTTCGCCT
CGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGGGGCCGCCGCGTGCGAATCTGGTGGCACCTTC
GCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAGCCATTTAAAATTTTTGATGACCTGCTGCGAC
GCTTTTTTTCTGGCAAGATAGTCTTGTAAATGCGGGCCAAGATCTGCACACTGGTATTTCGGTT
TTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCGTCCCAGCGCACATGTTCGGCGAGGCGGGGCC
TGCGAGCGCGGCCACCGAGAATCGGACGGGGGTAGTCTCAAGCTGGCCGGCCTGCTCTGGTGCC
TGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTGGGCGGCAAGGCTGGCCCGGTCGGCACCAGTT
GCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTGCTGCAGGGAGCTCAAAATGGAGGACGCGGC
GCTCGGGAGAGCGGGCGGGTGAGTCACCCACACAAAGGAAAAGGGCCTTTCCGTCCTCAGCCGT
CGCTTCATGTGACTCCACGGAGTACCGGGCGCCGTCCAGGCACCTCGATTAGTTCTCGAGCTTT
TGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGGTTTTATGCGATGGAGTTTCCCCACACTGAGT
GGGTGGAGACTGAAGTTAGGCCAGCTTGGCACTTGATGTAATTCTCCTTGGAATTTGCCCTTTT
TGAGTTTGGATCTTGGTTCATTCTCAAGCCTCAGACAGTGGTTCAAAGTTTTTTTCTTCCATTT
CAGGTGTCGTGATGTACAATGGCCAAGTTGACCAGTGCCGTTCCGGTGCTCACCGCGCGCGACG
TCGCCGGAGCGGTCGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACGA
CTTCGCCGGTGTGGTCCGGGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGACCAGGTGGTG
CCGGACAACACCCTGGCCTGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGG
AGGTCGTGTCCACGAACTTCCGGGACGCCTCCGGGCCGGCCATGACCGAGATCGGCGAGCAGCC
GTGGGGGCGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGCACTTCGTGGCCGAGGAG
CAGGACTGA

4.3.1 U6

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAGATAA
TTGGAATTAATTTGACTGTAAACACAAAGATATTAGTACAAAATACGTGACGTAGAAAGTAATA
ATTTCTTGGGTAGTTTGCAGTTTTAAAATTATGTTTTAAAATGGACTATCATATGCTTACCGTA
ACTTGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGACGAAACACC

4.3.2 sgRNA

GTTTTAGAGCTAGGCCAACATGAGGATCACCCATGTCTGCAGGGCCTAGCAAGTTAAAATAAGG
CTAGTCCGTTATCAACTTGGCCAACATGAGGATCACCCATGTCTGCAGGGCCAAGTGGCACCGA
GTCGGTGC

FIG. 80AA

4.3.3 EF1α

TGCAAAGATGGATAAAGTTTTAAACAGAGAGGAATCTTTGCAGCTAATGGACCTTCTAGGTCTT
GAAAGGAGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCC
GAGAAGTTGGGGGGAGGGGTCGGCAATTGATCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACT
GGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAG
TGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTAAGTGCC
GTGTGTGGTTCCCGCGGGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATTACTT
CCACTGGCTGCAGTACGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTCG
AGGCCTTGCGCTTAAGGAGCCCCTTCGCCTCGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGGG
GCCGCCGCGTGCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAGC
CATTTAAAATTTTTGATGACCTGCTGCGACGCTTTTTTTCTGGCAAGATAGTCTTGTAAATGCG
GGCCAAGATCTGCACACTGGTATTTCGGTTTTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCGT
CCCAGCGCACATGTTCGGCGAGGCGGGGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGTA
GTCTCAAGCTGGCCGGCCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTGG
GCGGCAAGGCTGGCCCGGTCGGCACCAGTTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTG
CTGCAGGGAGCTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGGTGAGTCACCCACACA
AAGGAAAAGGGCCTTTCCGTCCTCAGCCGTCGCTTCATGTGACTCCACGGAGTACCGGGCGCCG
TCCAGGCACCTCGATTAGTTCTCGAGCTTTTGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGGT
TTTATGCGATGGAGTTTCCCCACACTGAGTGGGTGGAGACTGAAGTTAGGCCAGCTTGGCACTT
GATGTAATTCTCCTTGGAATTTGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAAGCCTCAG
ACAGTGGTTCAAAGTTTTTTTCTTCCATTTCAGGTGTCGTGA

4.3.4 Zeo

ATGGCCAAGTTGACCAGTGCCGTTCCGGTGCTCACCGCGCGCGACGTCGCCGGAGCGGTCGAGT
TCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACGACTTCGCCGGTGTGGTCCG
GGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGACCAGGTGGTGCCGGACAACACCCTGGCC
TGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGTCCACGAACT
TCCGGGACGCCTCCGGGCCGGCCATGACCGAGATCGGCGAGCAGCCGTGGGGGCGGGAGTTCGC
CCTGCGCGACCCGGCCGGCAACTGCGTGCACTTCGTGGCCGAGGAGCAGGACTGA

4.4 pFUGW-U6-sgRNA-EF1α-Puro

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAGATAA
TTGGAATTAATTTGACTGTAAACACAAAGATATTAGTACAAAATACGTGACGTAGAAAGTAATA
ATTTCTTGGGTAGTTTGCAGTTTTAAAATTATGTTTTAAAATGGACTATCATATGCTTACCGTA

FIG. 80BB

ACTTGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGACGAAACACCGGAGACG
GGATACCGTCTCTGTTTTAGAGCTAGGCCAACATGAGGATCACCCATGTCTGCAGGGCCTAGCA
AGTTAAAATAAGGCTAGTCCGTTATCAACTTGGCCAACATGAGGATCACCCATGTCTGCAGGGC
CAAGTGGCACCGAGTCGGTGCTTTTTTTGGATCCTGCAAAGATGGATAAAGTTTTAAACAGAGA
GGAATCTTTGCAGCTAATGGACCTTCTAGGTCTTGAAAGGAGTGGGAATTGGCTCCGGTGCCCG
TCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGA
TCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCC
TTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCG
CAACGGGTTTGCCGCCAGAACACAGGTAAGTGCCGTGTGTGGTTCCCGCGGGCCTGGCCTCTTT
ACGGGTTATGGCCCTTGCGTGCCTTGAATTACTTCCACCGGCTGCAGTACGTGATTCTTGATCC
CGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTCGAGGCCTTGCGCTTAAGGAGCCCCTTCGCCT
CGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGGGGCCGCCGCGTGCGAATCTGGTGGCACCTTC
GCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAGCCATTTAAAATTTTTGATGACCTGCTGCGAC
GCTTTTTTTCTGGCAAGATAGTCTTGTAAATGCGGGCCAAGATCTGCACACTGGTATTTCGGTT
TTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCGTCCCAGCGCACATGTTCGGCGAGGCGGGGCC
TGCGAGCGCGGCCACCGAGAATCGGACGGGGGTAGTCTCAAGCTGGCCGGCCTGCTCTGGTGCC
TGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTGGGCGGCAAGGCTGGCCCGGTCGGCACCAGTT
GCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTGCTGCAGGGAGCTCAAAATGGAGGACGCGGC
GCTCGGGAGAGCGGGCGGGTGAGTCACCCACACAAAGGAAAAGGGCCTTTCCGTCCTCAGCCGT
CGCTTCATGTGACTCCACGGAGTACCGGGCGCCGTCCAGGCACCTCGATTAGTTCTCGAGCTTT
TGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGGTTTTATGCGATGGAGTTTCCCCACACTGAGT
GGGTGGAGACTGAAGTTAGGCCAGCTTGGCACTTGATGTAATTCTCCTTGGAATTTGCCCTTTT
TGAGTTTGGATCTTGGTTCATTCTCAAGCCTCAGACAGTGGTTCAAAGTTTTTTTCTTCCATTT
CAGGTGTCGTGATGTACAATGACCGAGTACAAGCCCACGGTGCGCCTCGCCACCCGCGACGACG
TCCCCAGGGCCGTACGCACCCTCGCCGCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGT
CGATCCGGACCGCCACATCGAGCGGGTCACCGAGCTGCAAGAACTCTTCCTCACGCGCGTCGGG
CTCGACATCGGCAAGGTGTGGGTCGCGGACGACGGCGCCGCCGTGGCGGTCTGGACCACGCCGG
AGAGCGTCGAAGCGGGGGCGGTGTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGCGGTTC
CCGGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCGGCCCAAGGAGCCCGCG
TGGTTCCTGGCCACCGTCGGAGTCTCGCCCGACCACCAGGGCAAGGGTCTGGGCAGCGCCGTCG
TGCTCCCCGGAGTGGAGGCGGCCGAGCGCGCCGGGGTGCCCGCCTTCCTGGAGACCTCCGCGCC
CCGCAACCTCCCCTTCTACGAGCGGCTCGGCTTCACCGTCACCGCCGACGTCGAGGTGCCCGAA
GGACCGCGCACCTGGTGCATGACCCGCAAGCCCGGTGCCTGA

FIG. 80CC

4.4.1 U6

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAGATAA
TTGGAATTAATTTGACTGTAAACACAAAGATATTAGTACAAAATACGTGACGTAGAAAGTAATA
ATTTCTTGGGTAGTTTGCAGTTTTAAAATTATGTTTTAAAATGGACTATCATATGCTTACCGTA
ACTTGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGACGAAACACC

4.4.2 sgRNA

GTTTTAGAGCTAGGCCAACATGAGGATCACCCATGTCTGCAGGGCCTAGCAAGTTAAAATAAGG
CTAGTCCGTTATCAACTTGGCCAACATGAGGATCACCCATGTCTGCAGGGCCAAGTGGCACCGA
GTCGGTGC

4.4.3 EF1α

TGCAAAGATGGATAAAGTTTTAAACAGAGAGGAATCTTTGCAGCTAATGGACCTTCTAGGTCTT
GAAAGGAGTGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCC
GAGAAGTTGGGGGGAGGGGTCGGCAATTGATCCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACT
GGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAG
TGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTAAGTGCC
GTGTGTGGTTCCCGCGGGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATTACTT
CCACCGGCTGCAGTACGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTCG
AGGCCTTGCGCTTAAGGAGCCCCTTCGCCTCGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGGG
GCCGCCGCGTGCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAGC
CATTTAAAATTTTTGATGACCTGCTGCGACGCTTTTTTTCTGGCAAGATAGTCTTGTAAATGCG
GGCCAAGATCTGCACACTGGTATTTCGGTTTTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCGT
CCCAGCGCACATGTTCGGCGAGGCGGGGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGTA
GTCTCAAGCTGGCCGGCCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTGG
GCGGCAAGGCTGGCCCGGTCGGCACCAGTTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTG
CTGCAGGGAGCTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGGTGAGTCACCCACACA
AAGGAAAAGGGCCTTTCCGTCCTCAGCCGTCGCTTCATGTGACTCCACGGAGTACCGGGCGCCG
TCCAGGCACCTCGATTAGTTCTCGAGCTTTTGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGGT
TTTATGCGATGGAGTTTCCCCACACTGAGTGGGTGGAGACTGAAGTTAGGCCAGCTTGGCACTT
GATGTAATTCTCCTTGGAATTTGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAAGCCTCAG
ACAGTGGTTCAAAGTTTTTTTCTTCCATTTCAGGTGTCGTGA

FIG. 80DD

4.4.4 Puro

ATGACCGAGTACAAGCCCACGGTGCGCCTCGCCACCCGCGACGACGTCCCCAGGGCCGTACGCA
CCCTCGCCGCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGATCCGGACCGCCACAT
CGAGCGGGTCACCGAGCTGCAAGAACTCTTCCTCACGCGCGTCGGGCTCGACATCGGCAAGGTG
TGGGTCGCGGACGACGGCGCCGCCGTGGCGGTCTGGACCACGCCGGAGAGCGTCGAAGCGGGGG
CGGTGTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGCGGTTCCCGGCTGGCCGCGCAGCA
ACAGATGGAAGGCCTCCTGGCGCCGCACCGGCCCAAGGAGCCCGCGTGGTTCCTGGCCACCGTC
GGAGTCTCGCCCGACCACCAGGGCAAGGGTCTGGGCAGCGCCGTCGTGCTCCCCGGAGTGGAGG
CGGCCGAGCGCGCCGGGGTGCCCGCCTTCCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTA
CGAGCGGCTCGGCTTCACCGTCACCGCCGACGTCGAGGTGCCCGAAGGACCGCGCACCTGGTGC
ATGACCCGCAAGCCCGGTGCCTGA

FIG. 80EE

Target guide sequences used in this paper

Gene	**Target Sequence**
Neurog2	TGGTTCAGTGGCTGCGTGTC
ASCL1	GCAGCCGCTCGCTGCAGCAG
MYOD1	GGGCCCCTGCGGCCACCCCG
SOX2	GCCGGCCGCGCGGGGGAGGC
SOX2	CCATGTGACGGGGGCTGTCA
SOX2	GGCAGGCGAGGAGGGGGAGG
SOX2	GCTGCCGGGTTTTGCATGAA
SOX2	GTATCCCCTCTCGCAGCAAC
SOX2	AGGAGCCGCCGCGCGCTGAT
SOX2	TTTACCCACTTCCTTCGAAA
SOX2	GCAGGGTACTTAAATGAGGA
NANOG	CGCCAGGAGGGGTGGGTCTA
NANOG	GATTAACTGAGAATTCACAA
NANOG	TCTAGTTCCCCACCTAGTCT
NANOG	GCCTTGGTGAGACTGGTAGA
NANOG	TGTCTTCAGGTTCTGTTGCT
NANOG	TGATTTAAAAGTTGGAAACG
NANOG	CATATTCCTGATTTAAAAGT
NANOG	TCCCAATTTACTGGGATTAC
KLF4	GCGCGCTCCACACAACTCAC
KLF4	AAGGAACGCGCGCCGGCGGC
KLF4	ATGGGAGAAGGCGGAGGAAA
KLF4	GCAACGATGGAAGGGAGCCT
KLF4	GCGCACGTGGGGGCGGGGGA
KLF4	GCCTGGCTGGCGTCACGGCC
KLF4	GCCGCCGACACCACTGCCGC
KLF4	CGGTTCCTCGCGCCCCGCGC
POU5F1 (OCT4)	GACACAACTGGCGCCCCTCC
POU5F1 (OCT4)	GGGGGGAGAAACTGAGGCGA
POU5F1 (OCT4)	TCTGTGGGGGACCTGCACTG
POU5F1 (OCT4)	GGCACAGTGCCAGAGGTCTG

FIG. 81A

POU5F1 (OCT4)	GGTGAAATGAGGGCTTGCGA
POU5F1 (OCT4)	TCAAGGCTAGTGGGTGGGAC
POU5F1 (OCT4)	GGTGGTGGCAATGGTGTCTG
POU5F1 (OCT4)	ACAGGAATTCAAGACCAGCC
VEGFA	GCAAAGAGGGAACGGCTCTC
VEGFA	ACAGAGTTTCCGGGGGCGGA
VEGFA	CCCTTCATTGCGGCGGGCTG
VEGFA	GGCCCGAGCCGCGTGTGGAA
VEGFA	GCGGGCCGGGGGCGGGGTCC
VEGFA	TTTAAAAGTCGGCTGGTAGC
HBG1	TCCCTGAACTTTTCAAAAAT
HBG1	CACTGGAGCTAGAGACAAGA
HBG1	GTATCCTCTATGATGGGAGA
HBG1	AAAAACTGGAATGACTGAAT
HBG1	AAAATTAGCAGTATCCTCTT
HBG1	ATGCAAATATCTGTCTGAAA
HBG1	CTTGACCAATAGCCTTGACA
HBG1	GGCTAGGGATGAAGAATAAA
TERT	GCCGCACGCACCTGTTCCCA
TERT	CTGCACCCTGGGAGCGCGAG
TERT	GCCCGGAGCAGCTGCGCTGT
TERT	CCAGGACCGCGCTTCCCACG
TERT	GAGCTGGAAGGTGAAGGGGC
TERT	CCCGACCCCTCCCGGGTCCC
TERT	GGAAAGGAAGGGGAGGGGCT
TERT	GCGGCCCCGCCCTCTCCTCG
IL1B	TTAGTATATGTGGGACAAAG
IL1B	GAAAATCCAGTATTTTAATG
IL1B	GAAAACAATGCATATTTGCA
IL1B	CTCTGGTTCATGGAAGGGCA
IL1B	AGTATTGGTGGAAGCTTCTT
IL1B	TTTAACTTGATTGTGAAATC
IL1B	TGGCTTTCAAAAGCAGAAGT
IL1B	AAAAACAGCGAGGGAGAAAC
IL1R2	AAACTCCACAATCTAGAATA
IL1R2	TTAACAGTTAAAAATCATAC

FIG. 81B

IL1R2	TGGAAAACCAACTCTTCCAC
IL1R2	AGCATCTTTTTCTCTTTAAT
IL1R2	ATCACTTTAAAACCACCTCT
IL1R2	AAACTTATGCGGCGTTTCCT
IL1R2	GAGTACATGATCACCCAGAT
IL1R2	GACCCAGCACTGCAGCCTGG
ZFP42 (REX1)	TAGCAATACAGTCACATTAA
ZFP42 (REX1)	GCCGGGCGTCTGGGCTCTGG
ZFP42 (REX1)	TGCCCGGCGGCCGGGCTGAG
ZFP42 (REX1)	GCCTGGGGGCCCCGGGCTGA
ZFP42 (REX1)	CCGGGCAGAGAGTGAACGCG
ZFP42 (REX1)	GCGGCGCCCCAGGGCGGGGC
ZFP42 (REX1)	ACCCTGGCGGAGCTGATGGG
ZFP42 (REX1)	GGGTCTTGGGAGGGGGGCGCA
MYC	GGCCCCACGGAAGCCTGAGC
MYC	CAGTGCGTTCTCGGTGTGGA
MYC	TTTGTCAAACAGTACTGCTA
MYC	GCGCGCGTAGTTAATTCATG
MYC	AGCTAGAGTGCTCGGCTGCC
MYC	GGTTCCCAAAGCAGAGGGCG
MYC	TCTCGCTAATCTCCGCCCAC
MYC	CCCTTTATAATGCGAGGGTC
LIN28A	AGAAGCAGGCCGCGCATTCC
LIN28A	GCGGGTCAGCTCCAAGCAGC
LIN28A	TCTGATTGGCCAGCGCCGCC
LIN28A	CCCATCTCCAGTTGTGCGTG
LIN28A	TCTGAGAAGGGACACCCCAG
LIN28A	CGGAGGGAAAGGGAGGGGAA
LIN28A	GGGGCTGCCCGCGGGGGGTT
LIN28A	GGGAGCCTTTGAAAAGCCGT
TINCR	TGGGCAGGCCCGGCCCGGCG
TINCR	GCGCACTCTGGGGCCAGCAG
TINCR	GGCTGGGATGACCTCGCTGA
TINCR	TGATCTTTTTAAGGACAGGC
TINCR	TCTCAAGTAGCTGGGACTAC
TINCR	CAGGTGCGGTGGCTCATGCC

FIG. 81C

TINCR	CTCACTGCAACCTCTGTCTG
HOTTIP	GGTGGGGCAGGGAAGGAAGG
HOTTIP	GCACCATTCACCCGGGGGAG
HOTTIP	TGCACCCGTCGTCCCCGCCG
HOTTIP	GTGGGCGGAGCGGGGGGGCC
HOTTIP	GCGCGCTCTTCACTTCTTGG
HOTTIP	TCGTAGAGAAACATGACGGT
HOTTIP	CGCGGCTGCGGCGGCGGCCG
HOTTIP	TTGGCGGCCTCTGCGCCCGC
PCAT-1	TCGGAGCCACTCCCTCCTCT
PCAT-1	AATTTGTCATAGTCTTGAGT
PCAT-1	TCTTTTTACATTGACTGATA
PCAT-1	TGCTTTTGAATGAACACCCA
PCAT-1	TTGGGGTCTACTCACAATTT
PCAT-1	GTTCTGTGAAGTCCAGTCCC
PCAT-1	AGCAAGTACTCAATATATTT
PCAT-1	AGTAGAGAGGCCAGGCACAG
LINC00925	TAAAATAGAGCGGAGATATC
LINC00925	CCTTCTTGAAGGTGCACTCA
LINC00925	CAGGCTGTGGTTGTGACCTG
LINC00925	TTTCTCTCCTGCGTCCTGGG
LINC00925	CACGCTTCCAGCCACCCGCT
LINC00925	CGATGCGCTTGCTGGGTCGC
LINC00925	GGCTCCCAGCCCCAGCCCCC
LINC00925	ACCAGCTGCCTTCTTCCCCC
LINC00514	CAGCCCCTCCTTCTACCCTT
LINC00514	GGGCAGGAGGTGGAGTGTCA
LINC00514	GGGGGCCGGAGGGGGAGAGG
LINC00514	GCAGGCTGAGAAGGGTGGGC
LINC00514	TCTCATCAAGTGTCCACTCA
LINC00514	GTCTCCCATCTCTCCTGCCC
LINC00514	GGGTGTGGAAAGCCTGGTCT
LINC00514	TGACTCTAGGCAGAGTGGGA
LINC00028	TCGCGGCTGGAGGACGCTGC
LINC00028	CGCCCCAGCCCCGGGGGACG
LINC00028	CAGGGACACGATGGTCCAAA

FIG. 81D

LINC00028	GTCAGGAGTTTCCAGCCCGA
LINC00028	CCCAGGAGGAGGCTGGGCCC
LINC00028	GAGTGAGTTGGATTAAACTG
LINC00028	CTGCTATACGCGAAGTTGCC
LINC00028	ACGTTCTAGATTCACATGTC
Scrambled guide 1	CTGAAAAAGGAAGGAGTTGA
Scrambled guide 2	AAGATGAAAGGAAAGGCGTT

FIG. 81E

Top 300 depleted genes for A375. Mean depletion for each gene is given as the log2 ratio of Day 21 vs. Day 3 averaged over all sgRNAs for the gene.

Gene	**Mean_Depletion**	**Rank**
CDKN1A	-2.992660039	1
MXI1	-2.897744853	2
STRBP	-2.829748727	3
ZNF619	-2.804758127	4
SPANXF1	-2.726815579	5
FAM129B	-2.719695757	6
CDKN1A	-2.656298721	7
ARPP21	-2.653166497	8
NFATC1	-2.629949555	9
ADAMTS12	-2.590207051	10
SYNCRIP	-2.543127112	11
DUSP9	-2.525451884	12
JUNB	-2.490663237	13
YAF2	-2.448742407	14
SLC19A1	-2.448391667	15
MYBL1	-2.447625101	16
MEX3A	-2.409240548	17
TRIB1	-2.398434141	18
CHST8	-2.335622871	19
ENOX2	-2.304989857	20
RNPEP	-2.279404126	21
GRB10	-2.278152274	22
NKX2-1	-2.277268968	23
RTFDC1	-2.276773205	24
PRKAG2	-2.257706064	25
DUSP5	-2.257470856	26
CPEB4	-2.257275333	27
PRAME	-2.253782388	28
ZNF583	-2.236146291	29

FIG. 82A

NTRK2	-2.187236566	30
MEIS3	-2.18329438	31
CRY1	-2.181419445	32
GPR137B	-2.153058431	33
TTLL12	-2.14262453	34
EEF1A1	-2.136133061	35
SPNS2	-2.130267043	36
BAG1	-2.12875898	37
PRDM1	-2.126237386	38
NAT8L	-2.11667318	39
HSD17B8	-2.106531573	40
GALNT7	-2.095244894	41
WNT3A	-2.090472623	42
TGFBR2	-2.074145064	43
RBM47	-2.071991956	44
LOXL4	-2.061797982	45
JADE3	-2.038321308	46
TMSB4Y	-2.026889341	47
CHPF	-2.025890484	48
MSRB3	-2.02586623	49
ZNF641	-2.023295975	50
DUX4L2	-2.015241148	51
BLOC1S2	-2.002638012	52
FAM49A	-2.001061567	53
AUP1	-1.997624613	54
CDKN1C	-1.995664305	55
SLC1A1	-1.990961882	56
ASB10	-1.989066237	57
WNK2	-1.977746737	58
ITGA5	-1.954342921	59
NFIC	-1.953212838	60
KLK11	-1.948539824	61
WDR91	-1.938490545	62
S100A13	-1.935432269	63
PXDC1	-1.927854467	64
NDNF	-1.921200613	65

FIG. 82B

BRI3	-1.911739793	66
TMEM220	-1.903966859	67
DUSP14	-1.898023448	68
NAA35	-1.885506504	69
ZNF395	-1.878461929	70
MIA3	-1.870671759	71
KCNK10	-1.867897168	72
IGF2BP3	-1.859186347	73
ATP6V0A1	-1.848977641	74
POU3F3	-1.848092491	75
LMNA	-1.847152595	76
LHFPL3	-1.8465067	77
ZNF665	-1.84640875	78
DYM	-1.837513747	79
KLHL8	-1.836730363	80
WNT7A	-1.836730124	81
SEC61A1	-1.832537638	82
TCF7L2	-1.827830567	83
GPRASP2	-1.823465993	84
CACNA1C	-1.821967953	85
INO80	-1.819581697	86
MEX3C	-1.818591589	87
ERG	-1.808903306	88
ESPL1	-1.801783358	89
KLF2	-1.798003457	90
COL1A1	-1.795687915	91
RCC2	-1.789402047	92
PAK1	-1.781478474	93
GALNT13	-1.779304272	94
TMCC3	-1.779143425	95
WDR45B	-1.769033944	96
RNF111	-1.768775527	97
BCL3	-1.76223965	98
FAM110B	-1.760460731	99
LATS2	-1.753053715	100
GRTP1	-1.749316218	101

FIG. 82C

41891	-1.740174795	102
SPIRE2	-1.737385676	103
BIVM-ERCC5	-1.73527893	104
HOXC13	-1.727592439	105
SKI	-1.727146495	106
HEXDC	-1.726799679	107
BTG2	-1.723525381	108
EID2B	-1.719706185	109
NELL2	-1.718412006	110
CELF1	-1.710704793	111
FXYD1	-1.709774577	112
GATA1	-1.703530563	113
AGPAT6	-1.703304319	114
PDGFRB	-1.702489783	115
EFHB	-1.699297265	116
OTX1	-1.69840649	117
CLIC1	-1.698145729	118
GNAO1	-1.69117871	119
TSPAN5	-1.690531306	120
GLB1	-1.688687106	121
PHF2	-1.688502906	122
MIIP	-1.687831215	123
BFSP1	-1.685843655	124
PKDCC	-1.681959775	125
UCN3	-1.681603774	126
AKAP11	-1.681106799	127
STK3	-1.680125551	128
DOT1L	-1.679505143	129
CRHR1	-1.678232195	130
PLEKHO1	-1.674893272	131
ANKEF1	-1.674522971	132
EBF2	-1.671684092	133
COPE	-1.667505883	134
USP28	-1.666943424	135
KMT2B	-1.664730943	136
RIMS4	-1.664556738	137

FIG. 82D

ADAMTS7	-1.664444631	138
FAM9A	-1.661881924	139
EPHA2	-1.65846104	140
REEP6	-1.657571504	141
SIAH1	-1.656570969	142
FPR2	-1.651081286	143
AVL9	-1.650350499	144
SP3	-1.649187872	145
PCNXL3	-1.646537811	146
SHROOM4	-1.645105253	147
HNRNPAB	-1.642348412	148
CACNA2D1	-1.639847135	149
FGFRL1	-1.63856667	150
SHB	-1.632097534	151
CA2	-1.631971681	152
CAMK2N1	-1.629137656	153
ARHGAP4	-1.62825701	154
CPLX2	-1.626599879	155
HOXC11	-1.626203388	156
ITM2C	-1.625957387	157
TRNT1	-1.624893641	158
DNAAF2	-1.624882836	159
GCC2	-1.624354479	160
TTC9	-1.624140349	161
IFT81	-1.622920533	162
PLEKHF1	-1.62180107	163
C10orf82	-1.620405891	164
KIAA0753	-1.619239696	165
WDR89	-1.617607367	166
CRCP	-1.611109935	167
ADRA1A	-1.602361316	168
TXLNG	-1.601904094	169
ANKZF1	-1.601604975	170
EFHD2	-1.599046924	171
SERPINI1	-1.598621083	172
MIB1	-1.597274936	173

FIG. 82E

MEAF6	-1.593894564	174
HLCS	-1.59025755	175
ING2	-1.589728576	176
PYROXD2	-1.589535269	177
PPARGC1A	-1.587408566	178
ANKRD30A	-1.586667965	179
BTBD2	-1.586118313	180
IGSF8	-1.580902664	181
FAM69C	-1.577696726	182
PAXIP1	-1.576009399	183
PAOX	-1.575951644	184
ZNF667	-1.572756871	185
TCF3	-1.56874959	186
IMPA2	-1.567559877	187
UBE3D	-1.566869169	188
SPATA31A1	-1.566628243	189
SLCO4A1	-1.562067095	190
PAPOLB	-1.561157727	191
RHOBTB2	-1.557854541	192
WWC1	-1.557454101	193
MLXIP	-1.556308378	194
MSH6	-1.555493523	195
TEX28	-1.555077182	196
TLR7	-1.554718342	197
TBC1D22A	-1.553299902	198
COBL	-1.552319793	199
ZBTB40	-1.551377333	200
EBAG9	-1.551195482	201
BHLHE23	-1.549931838	202
CCNE1	-1.549380807	203
FOSL2	-1.548586206	204
KANK1	-1.545495013	205
UBE2G1	-1.545073693	206
CTSZ	-1.544508991	207
PIK3R1	-1.541543206	208
PLCD1	-1.540526535	209

FIG. 82F

CFHR1	-1.540322263	210
EAPP	-1.539559841	211
FOXN2	-1.536894335	212
NRXN3	-1.536756987	213
PRRG4	-1.536411123	214
AURKA	-1.535632929	215
POLR2I	-1.535013569	216
TEX38	-1.534957213	217
SNRPF	-1.534928953	218
FZD6	-1.534873785	219
CHRDL2	-1.53363039	220
CAMK1D	-1.532738633	221
TSPAN4	-1.532033491	222
ZNF514	-1.53035277	223
CTAG1A	-1.528262121	224
TSPY1	-1.518969471	225
FAM45A	-1.515966792	226
PHF23	-1.514788961	227
NRD1	-1.514485943	228
UBR5	-1.514476856	229
GTPBP10	-1.51320279	230
PLEKHM3	-1.512593991	231
TMEM181	-1.512024763	232
ANKRD44	-1.510607784	233
SULT4A1	-1.510256216	234
PDGFC	-1.509051383	235
CDYL	-1.508799208	236
CDC42EP2	-1.508624776	237
KCNMB3	-1.507843102	238
FOXI1	-1.507819638	239
FHL1	-1.507785919	240
JRK	-1.507056803	241
FAM110C	-1.506457203	242
NPEPPS	-1.506442168	243
CNKSR3	-1.505895119	244
SYNGR1	-1.50378579	245

FIG. 82G

LIG1	-1.50220227	246
UCK1	-1.498574732	247
PLEKHG3	-1.498493459	248
SHANK2	-1.496266754	249
SYNGR2	-1.495929066	250
FRMPD2	-1.495810709	251
SCAP	-1.494636312	252
RGS22	-1.493115397	253
GALNT18	-1.49152462	254
GPAT2	-1.491059745	255
TRIM6-TRIM34	-1.490703347	256
AJUBA	-1.488388821	257
GAS8	-1.486564139	258
PLXNA2	-1.486492818	259
RPN2	-1.485389319	260
RBMX	-1.485222602	261
FOXF2	-1.484610716	262
ARHGAP31	-1.483785576	263
PNMA5	-1.4816382	264
SLAMF6	-1.481389938	265
HIST1H3J	-1.479761902	266
HHAT	-1.479346095	267
KCNC3	-1.478985068	268
PFKM	-1.477414591	269
CDHR5	-1.476532282	270
GABRB3	-1.476436096	271
POLR1D	-1.476282564	272
TTYH2	-1.475655292	273
TMEM198	-1.475348451	274
NRP2	-1.474615777	275
UBE3B	-1.474189706	276
ZNF618	-1.471872622	277
PYGO1	-1.471843021	278
SLFN11	-1.470539972	279
LONRF3	-1.470166863	280
TSPAN17	-1.468806125	281

FIG. 82H

STARD8	-1.468402107	282
HFE2	-1.467933276	283
LTBP1	-1.466001082	284
ENKD1	-1.464456854	285
PIGP	-1.462758078	286
CHTF8	-1.462614997	287
EHD2	-1.462454773	288
ST6GAL1	-1.460732993	289
ZNF527	-1.45924688	290
SLC22A17	-1.459181743	291
C17orf62	-1.458600852	292
POLR2G	-1.457145699	293
WDR88	-1.455886365	294
USP32	-1.455612942	295
CTNNA2	-1.452748274	296
LCOR	-1.452523453	297
HDAC9	-1.450768923	298
WNT7B	-1.449752179	299
LRRC4B	-1.449610591	300

FIG. 82I

Top 100 genes from the output of the RIGER algorithm for the sgRNA-Zeo PLX screen comparing PLX (mean of the two replicates at Day 21) to DMSO control (mean of the two replicates at Day 21). The Kolmogorov-Smirnov method was used to score genes.

Gene	**NES**	**Gene rank**	**p-value**	**p-value rank**
EGFR	1.9319	1	0.00000001	1
LPAR5	1.9292	2	0.00000001	2
GPR35	1.9277	3	0.0000001	3
LPAR1	1.9262	4	0.00000045	4
P2RY8	1.9248	5	0.00000045	5
ARHGEF1	1.9184	6	0.0000009	6
ITGB3	1.9116	7	0.0000031	7
ITGA9	1.894	8	0.0000201	8
ITGB5	1.89	9	0.000026	9
CRB2	1.8895	10	0.00002695	10
TYW1	1.8833	11	0.00003825	11
VSX1	1.8752	12	0.00005925	12
LOC102724862	1.8698	13	0.0000772	13
BCAR3	1.8552	14	0.0001412	14
PCDH7	1.8521	15	0.0001584	15
KIAA0040	1.8506	16	0.0001687	16
TFAP2C	1.8468	17	0.0001934	17
PHB	1.6441	112	0.0002845	18
IGF1R	1.8125	18	0.0005271	19
CGB8	1.8105	19	0.0005533	20
RNF223	1.8075	20	0.0005983	21
TFEB	1.7961	21	0.0007757	22
TOR3A	1.7826	22	0.00103	23
MRFAP1	1.7815	23	0.001049	24
WNT7A	1.7763	24	0.001158	25
MEIS2	1.775	25	0.001189	26
KCTD20	1.7703	26	0.001303	27
SHB	1.7691	27	0.001331	28

FIG. 83A

PLEKHG5	1.7665	28	0.001393	29
DAG1	1.7612	29	0.00153	30
RAPGEF1	1.7575	30	0.001632	31
SSC5D	1.7571	31	0.001645	32
PSMF1	1.7564	32	0.001665	33
ZNF747	1.7539	33	0.001736	34
SIGIRR	1.7537	34	0.001741	35
ISLR2	1.7503	35	0.001843	36
AARSD1	1.7439	36	0.002044	37
SLC32A1	1.7418	37	0.002115	38
PLXDC2	1.7393	38	0.002204	39
FGF17	1.7376	39	0.002262	40
SLC25A20	1.7366	40	0.002296	41
DCAF7	1.7365	41	0.002299	42
CA12	1.7364	42	0.002303	43
MSRB3	1.7356	43	0.002335	44
TRIM7	1.7353	44	0.002345	45
RRAS2	1.7338	45	0.002397	46
OSBPL1A	1.7278	46	0.002622	47
CEP63	1.7275	47	0.002638	48
PHC2	1.7252	48	0.002725	49
SPHK1	1.7246	49	0.00275	50
ACP6	1.7206	50	0.002914	51
NEIL3	1.7182	51	0.003017	52
TNNC1	1.7141	52	0.003201	53
KIAA1804	1.7133	53	0.003233	54
MAP3K11	1.7131	54	0.003242	55
ZNF582	1.7128	55	0.003256	56
SNX13	1.7111	56	0.003333	57
CPLX2	1.7104	57	0.003366	58
FGD1	1.7102	58	0.003377	59
DTX3	1.7093	59	0.003416	60
IFNGR1	1.7078	60	0.003484	61
LRRC10B	1.7075	61	0.003499	62
UBE2E3	1.7048	62	0.003629	63
VKORC1	1.7028	63	0.003727	64

FIG. 83B

PPDPF	1.6994	64	0.003893	65
CCND2	1.697	65	0.004017	66
TEAD4	1.6967	66	0.004032	67
TMEM26	1.6961	67	0.004065	68
HMGXB3	1.6959	68	0.004074	69
PDCD4	1.6936	69	0.004192	70
COA3	1.6924	70	0.004258	71
LAMP5	1.6918	71	0.004287	72
NEK5	1.6912	72	0.004322	73
MRPS35	1.6901	73	0.004382	74
TAPBP	1.6892	74	0.004431	75
FGF8	1.689	75	0.00444	76
GBE1	1.6887	76	0.004455	77
KCND1	1.6887	77	0.004458	78
TRIB1	1.6883	78	0.004475	79
SEBOX	1.688	79	0.004493	80
ATP10A	1.6859	80	0.004614	81
RNF41	1.6849	81	0.004673	82
PROM1	1.6848	82	0.004676	83
BCAP29	1.6819	83	0.004845	84
EFNA1	1.6783	84	0.005063	85
ZNF83	1.6778	85	0.005091	86
MAGEB6	1.6774	86	0.005119	87
TAS2R19	1.6766	87	0.005166	88
BCAR1	1.6744	88	0.005307	89
STAT4	1.6739	89	0.005336	90
RPS16	1.6721	90	0.005454	91
FICD	1.6718	91	0.005475	92
CPEB1	1.6713	92	0.005503	93
TMEM133	1.6694	93	0.005625	94
SNED1	1.6693	94	0.005635	95
TCEA2	1.6684	95	0.005691	96
GSR	1.6667	96	0.005808	97
IQGAP3	1.6618	97	0.006145	98
RAB42	1.6617	98	0.006149	99
ADORA1	1.6603	99	0.006254	100

FIG. 83C

Top 100 genes from the output of the RIGER algorithm for the sgRNA-Puro PLX screen comparing PLX (mean of the two replicates at Day 21) to DMSO control (mean of the two replicates at Day 21). The Kolmogorov-Smirnov method was used to score genes.

Gene	**NES**	**Gene rank**	**p-value**	**p-value rank**
EGFR	1.8164	3	0.00000001	1
LPAR5	1.8175	1	0.00000001	2
P2RY8	1.8165	2	0.00000001	3
MECOM	1.8111	4	0.0000003	4
CRB2	1.8109	5	0.00000035	5
GLIS3	1.7914	6	0.000014	6
PCDH7	1.7879	7	0.00002015	7
TFAP2C	1.7749	8	0.00005425	8
C9orf50	1.7679	9	0.00008335	9
LPAR1	1.7678	10	0.000084	10
CNR1	1.758	11	0.0001413	11
BCAR3	1.7565	12	0.0001516	12
ITGB3	1.7542	13	0.000169	13
CGNL1	1.7529	14	0.0001793	14
ZASP	1.747	15	0.0002318	15
P2RY1	1.7435	16	0.0002672	16
TNRC18	1.7352	17	0.000363	17
GPR35	1.7297	18	0.0004385	18
ARHGEF2	1.7293	19	0.0004437	19
KRAS	1.7254	20	0.000504	20
PBX2	1.7227	21	0.0005528	21
PYGO1	1.719	22	0.0006131	22
RASSF5	1.7167	23	0.0006551	23
AKR1B1	1.7122	24	0.000745	24
ZFHX4	1.7106	25	0.0007778	25
ACVR2A	1.7104	26	0.0007828	26
ITGB5	1.7078	27	0.0008385	27
LOC730183	1.7072	28	0.0008523	28

FIG. 84A

COL25A1	1.7057	29	0.0008865	29
EPAS1	1.7044	30	0.0009167	30
RPS16	1.7022	31	0.0009716	31
CST5	1.7015	32	0.000991	32
CHN2	1.6984	33	0.001067	33
RAPGEF1	1.6968	34	0.001111	34
ABLIM2	1.6921	35	0.001241	35
GAB2	1.69	36	0.001305	36
INHBA	1.6861	37	0.001424	37
C11orf21	1.6851	38	0.001456	38
NEFM	1.6843	39	0.001484	39
C19orf18	1.6841	40	0.00149	40
SLC19A2	1.681	41	0.001591	41
DYRK3	1.6775	42	0.001718	42
ARHGAP6	1.6742	43	0.001842	43
FOXO4	1.6723	44	0.001913	44
EIF4EBP2	1.6711	45	0.001955	45
TMEM199	1.6694	46	0.002024	46
ZCCHC11	1.6692	47	0.00203	47
CHID1	1.668	48	0.002082	48
MGAT3	1.6669	49	0.002129	49
CHST15	1.6667	50	0.002138	50
C14orf39	1.6649	51	0.002214	51
FSD1	1.6636	52	0.002271	52
STAU2	1.6629	53	0.002296	53
TRIM65	1.6579	54	0.002526	54
JUN	1.6571	55	0.002561	55
MMRN2	1.6555	56	0.002639	56
TMEM129	1.6532	57	0.002748	57
BRINP1	1.6507	58	0.002872	58
BCL7C	1.6494	59	0.002938	59
NFS1	1.6492	60	0.002947	60
AP4B1	1.6487	61	0.002971	61
41885	1.6474	62	0.003039	62
B4GALNT2	1.6472	63	0.003052	63
MDK	1.6447	64	0.003186	64

FIG. 84B

PABPC5	1.6424	65	0.003309	65
TNFRSF1B	1.6404	66	0.003425	66
MLLT6	1.6398	67	0.003458	67
IER3IP1	1.6344	68	0.003784	68
PBX1	1.6325	69	0.003907	69
BCAS3	1.631	70	0.003993	70
HDX	1.6291	71	0.00412	71
RNF6	1.6271	72	0.00425	72
MAP3K11	1.6268	73	0.00427	73
CA3	1.62	74	0.004741	74
APBB1	1.6196	75	0.004776	75
FOXJ1	1.6179	76	0.004905	76
LYPD2	1.6162	77	0.005023	77
DNASE1L2	1.6151	78	0.005103	78
BRI3	1.6132	79	0.005249	79
GCK	1.6112	80	0.0054	80
PRKCE	1.6081	81	0.005637	81
GCNT1	1.6074	82	0.005693	82
CDR2	1.6071	83	0.005713	83
DDX11	1.6059	84	0.005807	84
SLC2A3	1.6015	85	0.00618	85
PAK7	1.5993	86	0.006366	86
TCF7L1	1.599	87	0.006387	87
SOCS6	1.5969	88	0.006578	88
C19orf68	1.594	89	0.006839	89
C3orf27	1.5938	90	0.006853	90
NBL1	1.592	91	0.007023	91
ARHGEF5	1.5909	92	0.007126	92
GABRQ	1.5879	93	0.007405	93
ANKRD29	1.5877	94	0.007428	94
ZNF704	1.586	95	0.007587	95
RHOG	1.5853	96	0.007657	96
HOXB4	1.5849	97	0.007701	97
CCER1	1.5836	98	0.007833	98
ATL1	1.5832	99	0.007874	99
RASGRF1	1.5831	100	0.00788	100

FIG. 84C

TaqMan qPCR probe ID's used to quantify relative RNA expression levels for each gene (Life Technologies)

Gene	**Probe ID**
ASCL1	Hs00269932_m1
HBG1/HBG2	Hs00361131_g1
HOTTIP	Hs00955374_s1
IL1B	Hs01555410_m1
IL1R2	Hs01030384_m1
KLF4	Hs00358836_m1
LIN28A	Hs00702808_s1
LINC00028	Hs04233790_s1
LINC00514	Hs04273769_m1
LINC00925	Hs00288663_m1
MYC	Hs00153408_m1
MYOD1	Hs02330075_g1
NANOG	Hs04260366_g1
NEUROG2	Mm00437603_g1
PCAT-1	Hs04275836_s1
POU5F1	Hs00999632_g1
SOX2	Hs01053049_s1
TERT	Hs00972656_m1
TINCR	Hs00542141_m1
VEGFA	Hs00900055_m1
ZFP42	Hs00399279_m1

FIG. 85

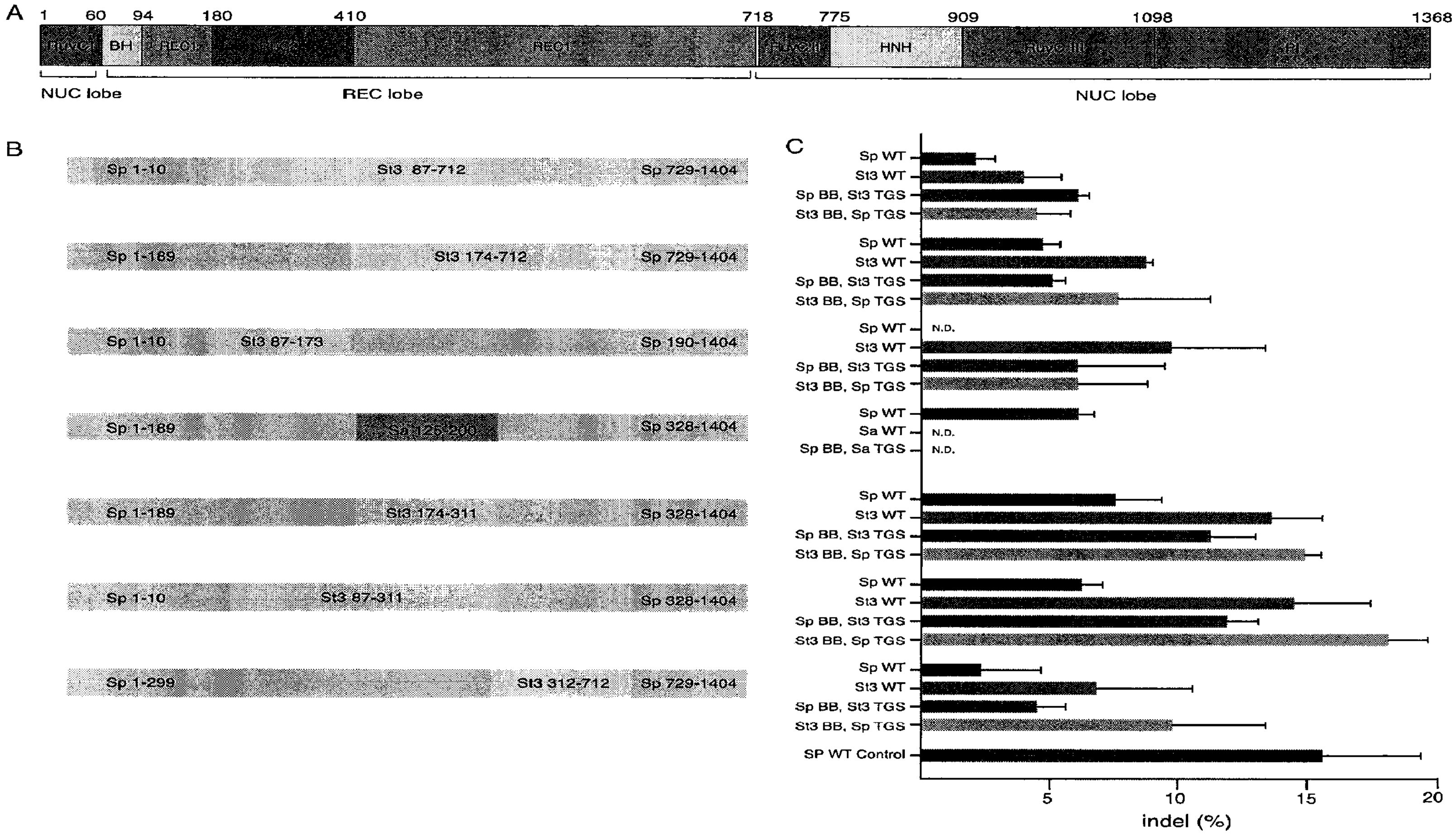

A
1
60
94
180
410
718
775
909
1098
1368
RuvC I
BH
REC1
REC1
RuvC II
HNH
RuvC III
PI
NUC lobe
REC lobe
NUC lobe
B
Sp 1-10
St3 87-712
Sp 729-1404
Sp 1-169
St3 174-712
Sp 729-1404
Sp 1-10
St3 87-173
Sp 190-1404
Sp 1-189
Sa 125-200
Sp 328-1404
Sp 1-189
St3 174-311
Sp 328-1404
Sp 1-10
St3 87-311
Sp 328-1404
Sp 1-299
St3 312-712
Sp 729-1404
C
Sp WT
St3 WT
Sp BB, St3 TGS
St3 BB, Sp TGS
Sp WT
St3 WT
Sp BB, St3 TGS
St3 BB, Sp TGS
Sp WT
N.D.
St3 WT
Sp BB, St3 TGS
St3 BB, Sp TGS
Sp WT
Sa WT
N.D.
Sp BB, Sa TGS
N.D.
Sp WT
St3 WT
Sp BB, St3 TGS
St3 BB, Sp TGS
Sp WT
St3 WT
Sp BB, St3 TGS
St3 BB, Sp TGS
Sp WT
St3 WT
Sp BB, St3 TGS
St3 BB, Sp TGS
SP WT Control
5
10
15
20
indel (%)

FIG. 86