

PROTEOMICS

**Supporting Information
for Proteomics**

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**Shotgun identification of proteins from uredospores of the bean
rust *Uromyces appendiculatus***

1 **Table 1.** List of assembled proteins with matching peptides from *U. appendiculatus*.

2 Proteins are grouped by their GO Biological Processes and their parsimony

3 designations are indicated

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| GO Biological Process ^{a)} | Accession no. | Protein description | Number of Peptides | Parsimony ^{b)} | |
|-------------------------------------|--|--|---|-------------------------|----|
| Acetyl-CoA metabolism (c) | gi 41408120 | MAP2022 (<i>Mycobacterium avium</i>) acetyl coA dehydrogenase | 1 | ds | |
| | gi 13430788 | Putative pyruvate dehydrogenase e1 alpha subunit (<i>Ar. thaliana</i>) | 1 | eq | |
| | gi 48142522 | Similar to ENSANGP00000010866 (<i>Apis mellifera</i>) | 1 | ds | |
| Amino acid metabolism (c) | gi 41726279 | COG0427: Acetyl-CoA hydrolase (<i>Dechloromonas aromatica</i> RCB) | 1 | ds | |
| | gi 35186990 | PlmS3 (<i>Streptomyces</i> sp. HK803) | 1 | ds | |
| | gi 40744738 | AN1993.2 (<i>A. nidulans</i> FGSC A4) glutamate oxaloacetate transaminase | 1 | eq | |
| | gi 40741005 | AN4430.2 (<i>A. nidulans</i> FGSC A4) acetolactate synthase | 1 | ds | |
| | gi 13473715 | 3-Isopropylmalate dehydratase small subunit (<i>Mesorhizobium loti</i> MAFF303099) | 1 | eq | |
| | gi 57229785 | 5-Methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase | 1 | ds | |
| | gi 47214847 | Unnamed protein (<i>Tetraodon nigroviridis</i>) S-adenosylhomocystein hydrolase | 1 | ds | |
| | gi 1200230 | S-Adenosyl-L-homocysteine hydrolase (<i>Drosophila melanogaster</i>) | 1 | eq | |
| | gi 46435344 | CaO19.8272 (<i>Candida albicans</i> SC5314) S-adenosylmethionine synthetase | 1 | sb | |
| | gi 46909377 | Methionine adenosyltransferase (<i>Stylochus</i> sp. KJP-2004) | 1 | ds | |
| | gi 46909383 | Methionine adenosyltransferase (<i>Mytilus edulis</i>) | 2 | df | |
| | gi 50749162 | Similar to S-adenosylmethionine synthetase alpha and beta forms (<i>Gallus gallus</i>) | 1 | ds | |
| | gi 1064970 | Chain B, Triosephosphate isomerase (<i>G. gallus</i>) | 1 | eq | |
| | gi 45357954 | Aspartate aminotransferase (<i>Methanococcus maripaludis</i> S2) | 1 | ds | |
| | gi 105387 | Aspartate transaminase (EC 2.6.1.1) – human | 1 | eq | |
| gi 6492282 | Phosphoribosyl anthranilate isomerase (<i>Buchnera aphidico</i>) | 1 | ds | | |
| gi 57226570 | Adenosylhomocysteinase (<i>C. neoformans</i>) | 1 | ds | | |
| gi 46100325 | UM04584.1 (<i>Us. maydis</i> 521) tryptophan synthetase | 1 | ds | | |
| gi 51770401 | Similar to caspase recruitment domain protein 12 (<i>Mus musculus</i>) | 1 | ds | | |
| Apoptosis (b) | gi 10543 | Triosephosphate isomerase (<i>Trypanosoma brucei</i>) | 1 | eq | |
| Carbohydrate metabolism (i) | gi 15896708 | Endoglucanase family 5 (<i>Clostridium acetobutylicum</i> ATCC 824) | 1 | ds | |
| Cell cycle (g) | gi 47459237 | Glycogen synthase (<i>Mycoplasma mobile</i> 163K) | 1 | ds | |
| | gi 1764133 | PIG8 (<i>Uromyces fabae</i>) Probable NADP-dependent mannitol dehydrogenase | 1 | ds | |
| | gi 24215617 | Alpha-galactosidase (<i>Leptospira interrogans</i> serovar Lai str. 56601) | 1 | eq | |
| | gi 50918707 | Unnamed protein (<i>Oryza sativa</i>) similar to beta-glucosidase | 1 | ds | |
| | gi 48845676 | COG3206: exopolysaccharide biosynthesis (<i>Geobacter metallireducens</i>) | 1 | ds | |
| | gi 20090664 | MA1813 (<i>Methanosarcina acetivorans</i> C2A) cdc48 | 1 | eq | |
| | gi 50259101 | CNBC4800 (<i>C. neoformans</i> var. <i>neoformans</i> B-3501A) cdc | 1 | eq | |
| | gi 56470483 | Conserved protein (<i>Entamoeba histolytica</i> HM-1:IMSS) similar ti rice mct-1/cdc | 1 | ds | |
| | gi 23478257 | Cell division cycle protein 48 homolog (<i>Plasmodium yoelii yoelii</i>) | 1 | eq | |
| | gi 56467577 | cdc48-like protein (<i>E. histolytica</i> HM-1:IMSS) | 1 | eq | |
| | gi 46100727 | UM05761.1 (<i>Us. maydis</i> 521) EB1-like | 1 | ds | |
| | gi 31088222 | SMC1 alpha (<i>Oryzias latipes</i>) | 1 | ds | |
| | gi 50746703 | Similar to fat-like cadherin FATJ protein (<i>G. gallus</i>) | 1 | ds | |
| | Cell physiology (f) | gi 38347763 | Myosin-heavy chain (<i>Lethenteron japonicum</i>) | 1 | eq |
| | Chemotaxis (j) | gi 21242494 | Chemotaxis protein (<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306) | 1 | ds |
| Chorismate biosynthesis (c) | gi 19113854 | Phospho-2-dehydro-3-deoxyheptonate aldolase (<i>Schizosaccharomyces pombe</i>) | 1 | eq | |
| Citrate metabolism (c) | gi 10800928 | Mitochondrial citrate synthase (<i>Podospira anserina</i>) | 1 | eq | |
| | gi 46096782 | UM01005.1 (<i>Us. maydis</i> 521) ATP citrate lyase | 1 | eq | |
| Cytoskeleton organization (d) | gi 57227836 | Actin-lateral binding protein (<i>C. neoformans</i>) | 1 | ds | |
| | gi 57097681 | PREDICTED: similar to centaurin (<i>Canis familiaris</i>) | 1 | ds | |
| | gi 113249 | Actin 3-sub 1 (<i>Dictyostelium discoideum</i>) | 5 | sb | |
| | gi 2289975 | Cytoplasmic actin CyII (<i>Heliocidaris tuberculata</i>) | 6 | eq | |
| | gi 460993 | Actin (<i>Puccinia graminis</i>) | 5 | df | |
| | gi 31581450 | Actin (<i>Saccharomyces spencerorum</i>) | 4 | df | |
| | gi 32423714 | Actin (<i>Haemaphysalis longicornis</i>) | 4 | sb | |
| | gi 2289965 | Cytoplasmic actin LvC4 (<i>Lytechinus variegatus</i>) | 3 | sb | |
| | gi 31581448 | Actin (<i>Kluyveromyces lodderae</i>) | 3 | sb | |
| | gi 31581482 | Actin (<i>Kluyveromyces polysporus</i>) | 3 | df | |
| | gi 32127373 | Actin (<i>Saccharomyces exiguus</i>) | 3 | sb | |
| | gi 50980792 | Actin (<i>Paxillus involutus</i>) | 3 | sb | |
| | gi 5702223 | Type 1 actin (<i>Pleurochrysis carterae</i>) | 3 | eq | |

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|------------------------------------|-------------|---|---|----|
| | gi 33355923 | Actin (<i>Phaseolus acutifolius</i>) | 2 | sb |
| | gi 56112394 | Beta-actin (<i>Macrobrachium rosenbergii</i>) | 2 | df |
| | gi 8895929 | Actin (<i>Staurouteuthis syrtensis</i>) | 2 | sb |
| | gi 11276981 | Actin-related protein ro-4 (imported) – <i>N. crassa</i> | 1 | eq |
| | gi 27475931 | Beta-actin 1 (<i>Meloidogyne javanica</i>) | 1 | ds |
| | gi 50355625 | Actin (<i>Ulva pertusa</i>) | 1 | ds |
| | gi 7197 | Unnamed protein (<i>D. discoideum</i>) similar to actin | 1 | ds |
| | gi 39579169 | CBG24444 (<i>Caenorhabditis briggsae</i>) similar to actin | 2 | eq |
| Deadenyl-depen decap (c) | gi 49651952 | Unnamed protein (<i>Yarrowia lipolytica</i> CLIB99) similar to mrna decapping enzyme | 1 | ds |
| Dethiobiotin biosynthesis (c) | gi 53800777 | COG0132: Dethiobiotin synthetase (<i>Xylella fastidiosa</i> Dixon) | 1 | ds |
| Dihydroliipoamide metabolism (c) | gi 100037 | Dihydroliipoamide dehydrogenase (EC 1.8.1.4) precursor – garden pea | 1 | eq |
| DNA repair (c) | gi 26342218 | Unnamed protein (<i>Mu. musculus</i>) similar to DNA helicase | 1 | eq |
| | gi 40738551 | AN5992.2 (<i>A. nidulans</i> FGSC A4) DNA helicase | 1 | ds |
| | gi 53721883 | BPSS0856 (<i>Burkholderia pseudomallei</i> K96243) rad3 dna helicase | 1 | ds |
| | gi 20091202 | ATP-dependent DNA helicase (<i>M. acetivorans</i> C2A) | 1 | ds |
| | gi 40741072 | Hypothetical protein AN8713.2 (<i>A. nidulans</i> FGSC A4) rad16 | 1 | ds |
| | gi 17545141 | Probable SS binding protein (<i>Ralstonia solanacearum</i>) | 1 | ds |
| | gi 17548680 | Putative RHS-related protein (<i>R. solanacearum</i> GMI1000) | 1 | ds |
| | gi 49237293 | COG0632: Holliday junction resolvase (<i>Moorella thermoacetica</i>) | 1 | ds |
| DNA topological change (c) | gi 17227937 | DNA topoisomerase chain A (<i>Nostoc</i> sp. PCC 7120) | 1 | ds |
| | gi 48784351 | COG0188: Type IIA topoisomerase (<i>Burkholderia fungorum</i> LB400) | 1 | ds |
| | gi 23128095 | COG0188: Type IIA topoisomerase (<i>Nostoc punctiforme</i> PCC 73102) | 1 | ds |
| | gi 17342640 | TraI (IncN plasmid R46) | 1 | ds |
| Electron transport (c) | gi 17536191 | Cytochrome P450 (ccp-13A7) (<i>Caenorhabditis elegans</i>) | 1 | ds |
| | gi 57227949 | Electron transporter (<i>C. neoformans</i> var. <i>neoformans</i> JEC21) | 1 | ds |
| Entner–Doudoroff pathway (c) | gi 47228814 | Unnamed protein (<i>T. nigroviridis</i>) similar to phosphogluconate dehydrogen | 1 | eq |
| ER to Golgi transport (d) | gi 47156986 | SEC18-like vesicular fusion protein (<i>Antonospora locustae</i>) | 1 | ds |
| Ergosterol biosynthesis (c) | gi 19112579 | Putative delta-sterol c-methyltransferase (<i>S. pombe</i>) | 1 | eq |
| Exopolysaccharide synthesis (c) | gi 28828901 | Similar to Amylovoran biosynthesis protein amsF precursor (<i>Dictyostelium</i>) | 1 | ds |
| Fermentation (c) | gi 17551266 | Atp citrate lyase (XC101) (<i>Cae. elegans</i>) | 1 | eq |
| | gi 46098122 | Hypothetical protein UM02233.1 (<i>Us. maydis</i> 521) alcohol dehydrogenase | 1 | ds |
| Folic acid metabolism (c) | gi 17568737 | Methylenetetrahydrofolate dehydrogenase (XI700) (<i>Cae. elegans</i>) | 1 | eq |
| | gi 57045140 | Predicted: similar to methylenetetrahydrofolate reductase (<i>Ca. familiaris</i>) | 1 | ds |
| Fumarate metabolism (c) | gi 46100568 | Hypothetical protein UM04971.1 (<i>Us. maydis</i> 521) fumarate reductase | 2 | df |
| Gene transcription (c) | gi 15894705 | Possible transcriptional regulator, leucine-rich protein (<i>Clostridium</i>) | 1 | ds |
| | gi 21355909 | CG8301-PA (<i>D. melanogaster</i>) zinc finger | 1 | Ds |
| | gi 24372994 | DNA-binding response regulator (<i>Shewanella oneidensis</i> MR-1) | 1 | ds |
| | gi 42601441 | KIAA1007 protein-like protein (<i>Oikopleura dioica</i>) | 1 | ds |
| | gi 46321703 | COG1167: Transcriptional regulators (<i>Burkholderia cepacia</i>) | 1 | ds |
| | gi 52010008 | COG0583: Transcriptional regulator (<i>Silicibacter</i> sp. TM1040) | 1 | ds |
| | gi 15673959 | Transcription regulator (<i>Lactococcus lactis</i> ssp. <i>lactis</i> I11403) | 1 | ds |
| | gi 48787762 | COG2183: Transcriptional accessory protein (<i>B. fungorum</i> LB400) | 1 | ds |
| | gi 53793087 | MYB transcription factor like [<i>O. sativa</i> (japonica cultivar-group)] | 1 | ds |
| Gluconeogenesis (c) | gi 46097771 | UM05130.1 (<i>Us. maydis</i> 521) phosphoenolpyruvate carboxykinase | 1 | ds |
| | gi 57228862 | Phosphoenolpyruvate carboxykinase (<i>C. neoformans</i>) | 1 | ds |
| | gi 16519317 | Fructose 1,6-bisphosphatase (<i>Galdieria sulphuraria</i>) | 1 | ds |
| Glutathione metabolism (c) | gi 15674854 | Putative glutathione reductase (GR) (<i>Streptococcus pyogenes</i> M1 GAS) | 1 | eq |
| | gi 22073900 | Putative glutathione/thioredoxin peroxidase (<i>Toxoplasma gondii</i>) | 1 | eq |
| Glycerol metabolism (c) | gi 47213952 | Unnamed protein product (<i>T. nigroviridis</i>) dihydroxyacetone kinase | 1 | ds |
| Glycerophospholipid catabolism (c) | gi 17432518 | Lys-49 phospholipase A2-like protein (<i>Bothriechis schlegelii</i>) | 1 | ds |
| Glycolysis (c) | gi 46099053 | UM03299.1 (<i>Us. maydis</i> 521) triosephosphate isomerase | 1 | eq |
| | gi 2209089 | Glyceraldehyde-3-phosphate dehydrogenase (<i>Colletotrichum lindemuthianum</i>) | 2 | eq |
| | gi 166331 | Glyceraldehyde-3-phosphate dehydrogenase (<i>Agaricus bisporus</i>) | 1 | ds |
| | gi 2078386 | Glyceraldehyde-3-phosphate dehydrogenase (<i>Selaginella lepidophylla</i>) | 1 | eq |
| | gi 41394407 | Glyceraldehyde-3-phosphate dehydrogenase (<i>Lithobius</i> sp. SBH266126) | 2 | df |
| | gi 41394409 | Glyceraldehyde-3-phosphate dehydrogenase (<i>Diplopoda</i> sp. SBH266145) | 1 | ds |
| | gi 2494643 | Glyceraldehyde-3-phosphate dehydrogenase (<i>Hypocrea lixii</i>) | 2 | sb |
| | gi 1002616 | Enolase (<i>Schistosoma mansoni</i>) | 2 | df |
| | gi 8919600 | Enolase (<i>Euglena gracilis</i>) | 1 | eq |
| | gi 19552199 | Enolase (<i>Corynebacterium glutamicum</i> ATCC 13032) | 1 | eq |
| | gi 37681795 | Enolase 1 (<i>Danio rerio</i>) | 1 | sb |
| | gi 37702655 | Enolase (<i>Davidiella tassiana</i>) | 2 | eq |
| | gi 15595003 | Phosphoglycerate mutase (gpmA) (<i>Borrelia burgdorferi</i> B31) | 1 | eq |
| | gi 16904828 | Phosphoglycerate mutase (<i>Schistosoma japonicum</i>) | 1 | eq |
| | gi 15677454 | Phosphoglycerate mutase (<i>Neisseria meningitidis</i> MC58) | 1 | eq |

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|----------------------------------|-------------|--|---|----|
| | gi 46101355 | UM05339.1 (<i>Us. maydis</i> 521) Phosphoglycerate mutase | 1 | ds |
| | gi 10383781 | 3-Phosphoglycerate kinase (<i>Saccharomyces cerevisiae</i>) | 1 | eq |
| | gi 51860718 | Chloroplast phosphoglycerate kinase precursor (<i>Eu. gracilis</i>) | 1 | ds |
| | gi 1078667 | Phosphoglycerate kinase (EC 2.7.2.3) – <i>N. crassa</i> | 1 | eq |
| | gi 1084489 | Phosphoglycerate kinase (EC 2.7.2.3) – <i>Rhizopus niveus</i> | 1 | eq |
| Glycoprotein binding (c) | gi 1125065 | Laminin-binding protein (<i>Homo sapiens</i>) | 1 | eq |
| Glyoxylate cycle (d) | gi 46310643 | COG2225: Malate synthase (<i>B. cepacia</i> R18194) | 1 | eq |
| Golgi to PM transport (c) | gi 49524140 | Unnamed protein (<i>Candida glabrata</i> CBS138) sec9 | 1 | ds |
| Hydrolase activity (l) | gi 38107465 | MG07908.4 (<i>M. grisea</i> 70-15) cellobiohydrolase | 1 | ds |
| | gi 48782226 | Metal-dependent hydrolase (<i>B. fungorum</i> LB400) | 1 | ds |
| Intracellular signal cascade (a) | gi 57089531 | Similar to Rho guanine nucleotide exchange factor (<i>Ca. familiaris</i>) | 1 | ds |
| Lipopolysaccharide biosynth (c) | gi 50260058 | CNBB1690 (<i>C. neoformans</i>) phosphoglucose isomerase | 1 | eq |
| Lipoprotein (d) | gi 15925817 | Lipoprotein (<i>Staphylococcus aureus</i> ssp. Aureus N315) | 1 | ds |
| | gi 56478459 | Putative enoyl-CoA hydratase/isomerase (<i>Azoarcus</i> sp. EbN1) | 1 | ds |
| Microtubule-based process (d) | gi 15865475 | Beta-tubulin (<i>Uromyces viciae-fabae</i>) | 7 | df |
| | gi 23263900 | Beta-tubulin (<i>Cladonia rigida</i>) | 4 | df |
| | gi 16209262 | Beta-tubulin (<i>Grifola frondosa</i>) | 3 | df |
| | gi 21396469 | Beta-tubulin (<i>Suillus bovinus</i>) | 3 | eq |
| | gi 23263876 | Beta-tubulin (<i>Cladonia lepidophora</i>) | 3 | sb |
| | gi 20429150 | Putative beta-tubulin (<i>Piriformospora indica</i>) | 2 | df |
| | gi 31790276 | Beta-tubulin (<i>Sclerotinia sclerotiorum</i>) | 2 | sb |
| | gi 52626592 | Beta tubulin (<i>Glomus claroideum</i>) | 2 | df |
| | gi 6424951 | Beta tubulin (<i>Gigaspora rosea</i>) | 2 | sb |
| | gi 16517097 | Beta tubulin (<i>Gillichthys mirabilis</i>) | 1 | df |
| | gi 17506073 | Tubulin (<i>Cae. elegans</i>) | 1 | eq |
| | gi 27372943 | Alpha-tubulin I2 (<i>Oi. dioica</i>) | 1 | eq |
| | gi 32967398 | Alpha-tubulin (<i>Leucosolenia</i> sp.) | 1 | ds |
| | gi 49650011 | Unnamed protein (<i>Y. lipolytica</i> CLIB99) alpha tubulin | 1 | ds |
| | gi 46100156 | Hypothetical protein UM04507.1 (<i>Us. maydis</i> 521) kinesin | 1 | ds |
| Mitochondrial electron trans (c) | gi 1041980 | Succinate-ubiquinone oxidoreductase; fumarate reductase (<i>Dirofilaria immitis</i>) | 1 | eq |
| | gi 12056150 | NADH dehydrogenase subunit 5 (<i>Takakia lepidiozoides</i>) | 1 | eq |
| | gi 33519790 | Succinate dehydrogenase iron-sulfur protein (<i>Candidatus blochmannia</i>) | 1 | ds |
| | gi 40644750 | Succinate dehydrogenase (<i>Uromyces viciae-fabae</i>) | 1 | ds |
| | gi 46096723 | Hypothetical protein UM01172.1 (<i>Us. maydis</i> 521) succinate dehydrogenase | 2 | df |
| Mitochondrion organization (d) | gi 46098715 | Hypothetical protein UM02899.1 (<i>Us. maydis</i> 521) aconitase | 1 | eq |
| | gi 10637996 | Mitochondrial aconitase (<i>Rattus norvegicus</i>) | 1 | eq |
| | gi 45383738 | Aconitase 2 (<i>G. gallus</i>) | 1 | eq |
| MRNA processing (c) | gi 6321344 | Pan2p-Pan3p poly(A)-ribonuclease subunit (<i>Sa. cerevisiae</i>) | 1 | ds |
| | gi 19115173 | Putative ATP-dependent RNA helicase (<i>S. pombe</i>) | 1 | eq |
| Nonribosomal peptide synth (c) | gi 29606807 | Putative nonribosomal peptide synthetase (<i>Streptomyces avermitilis</i> MA-4680) | 1 | eq |
| Nuclear migration (d) | gi 57223619 | Conserved protein (<i>C. neoformans</i>) microtubule-associated | 1 | ds |
| Nucleic acid binding (c) | gi 40226353 | KUB3 protein (<i>H. sapiens</i>) ku70 binding protein | 1 | eq |
| | gi 28853522 | TPR domain protein (<i>Pseudomonas syringae</i> pv. tomato str. DC3000) | 1 | eq |
| Nucleic acid metabolism (c) | gi 143579 | adk gene product (<i>Bacillus subtilis</i>) | 1 | eq |
| | gi 46132282 | Guanosine polyphosphate pyrophosphohydrolases (<i>Ralstonia eutropha</i>) | 1 | ds |
| | gi 48854452 | Glutamine phosphoribosylpyrophosphate amidotransferase (<i>Cytophaga</i>) | 1 | ds |
| | gi 46098724 | UM02908.1 (<i>Us. maydis</i> 521) dUTP Pyrophosphatase | 1 | ds |
| | gi 11498284 | Adenylate kinase (adk) (<i>Archaeoglobus fulgidus</i> DSM 4304) | 1 | eq |
| Nucleosome assembly (d) | gi 15529616 | Histone H2B variant 1 (<i>To. gondii</i>) | 1 | eq |
| | gi 46097327 | H2B_AGABI Histone H2B (<i>Us. maydis</i> 521) | 1 | eq |
| | gi 122030 | Histone H2B.2 (<i>Psammochinus miliaris</i>) | 1 | eq |
| | gi 48994796 | Histone H2A.2 (<i>To. gondii</i>) | 1 | ds |
| | gi 10953803 | Histone H4 (<i>Sc. mansoni</i>) | 1 | eq |
| Oxidation/reduction (m) | gi 45382879 | Aldo-keto reductase (<i>G. gallus</i>) | 1 | eq |
| | gi 54022639 | Putative oxidoreductase (<i>Nocardia farcinica</i> IFM 10152) | 1 | eq |
| | gi 26553933 | Oxidoreductase (<i>Mycoplasma penetrans</i> HF-2) | 1 | eq |
| | gi 42573620 | FAD-dependent oxidoreductase family protein (<i>Ar. thaliana</i>) | 1 | eq |
| Pentose phosphate pathway (c) | gi 28564918 | TAL1 (<i>Saccharomyces castellii</i>) | 1 | eq |
| | gi 11251352 | Probable phosphogluconate dehydrogenase – fission yeast | 1 | eq |
| Peptidoglycan biosynthesis (d) | gi 21218688 | SCO0128 (<i>Streptomyces coelicolor</i>) UDP-N-acetylglucosamine enolpyruvyl transf. | 1 | ds |
| | gi 46435278 | CaO19.3672 (<i>Ca. albicans</i> SC5314) UDP glucose-4-epimerase | 1 | ds |
| | gi 27379181 | Alanine racemase (<i>Bradyrhizobium japonicum</i> USDA 110) | 1 | ds |
| | gi 10720387 | UDP-N-acetylhexosamine pyrophosphorylase (<i>H. sapiens</i>) | 1 | eq |
| | gi 38568026 | OSJNBa0070C17.21 (<i>O. sativa</i>) UDP acetylglucosamine pyrophosphorylase | 1 | eq |
| Peroxisome organization (d) | gi 130357 | Peroxisomal membrane protein PMP47A (<i>Candida boidinii</i>) | 1 | eq |
| Phosphate metabolism (c) | gi 2903 | Unnamed protein (<i>Kluyveromyces lactis</i>) inorganic pyrophosphatase | 2 | eq |

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|-------------------------------------|-------------|---|---|----|
| | gi 40744363 | Conserved protein (<i>A. nidulans</i> FGSC A4) inorganic pyrophosphatase | 2 | sb |
| | gi 19114548 | Inorganic pyrophosphatase (EC 3.6.1.1) (<i>S. pombe</i>) | 2 | eq |
| Phosphatidylinositol biosynth. (c) | gi 42734012 | Phosphatidylinositol 3-kinase 2 (<i>D. discoideum</i>) | 1 | ds |
| Phospholipid biosynthesis (c) | gi 42560708 | Cardiolipin synthetase (<i>Mycoplasma mycoides</i> ssp. <i>mycoides</i> SC str. PG1) | 1 | eq |
| Polyadenylation/nuclear export (d) | gi 49257242 | MGC81363 protein (<i>Xenopus laevis</i>) | 1 | ds |
| PHA biosynthesis (c) | gi 57229093 | Polyadenylate-binding protein (<i>C. neoformans</i>) | 1 | ds |
| Posttranslation protein folding (c) | gi 11096251 | Beta-ketothiolase (<i>Ectothiorhodospira shaposhnikovii</i>) | 1 | ds |
| | gi 13897312 | Luminal binding protein (<i>Scherffelia dubia</i>) | 3 | df |
| | gi 27699626 | Similar to T-cell receptor alpha chain (<i>R. norvegicus</i>) | 1 | eq |
| | gi 429116 | Glucose regulated protein/BiP (<i>Phytophthora cinnamomi</i>) | 2 | eq |
| Protein a.a. ADP ribosylation (c) | gi 53757019 | GTP-binding protein (<i>Methylococcus capsulatus</i> str. Bath) | 1 | ds |
| Protein a.a. dephosphoryl (c) | gi 46102000 | Hypothetical protein UM06376.1 (<i>Us. maydis</i> 521) gtp binding protein | 1 | ds |
| | gi 10880267 | Protein phosphatase 2a (<i>Emericella nidulans</i>) | 1 | eq |
| | gi 1280027 | Protein phosphatase 1gamma (<i>Mu. musculus</i>) | 1 | eq |
| Protein a.a. glycosylation (c) | gi 13096544 | 2-Mannosidase (<i>H. sapiens</i>) | 1 | ds |
| | gi 32410755 | Mannose-1-phosphate guanylyltransferase (<i>Hypocrea jecorina</i>) | 1 | eq |
| | gi 3323397 | Mannose-1-phosphate guanylyltransferase (<i>H. jecorina</i>) | 1 | eq |
| Protein a.a. phosphorylation (c) | gi 15072452 | Protein kinase 1 (<i>Cryphonectria parasitica</i>) | 1 | eq |
| | gi 39636592 | Myosin light chain polypeptide kinase isoform 2 (<i>H. sapiens</i>) | 1 | eq |
| | gi 46401522 | Arginine kinase (<i>Epicephala</i> sp. E110AT) | 2 | df |
| | gi 51770328 | Similar to Adenylate kinase isoenzyme 1 (<i>Mu. musculus</i>) | 1 | ds |
| Protein biosynthesis (c) | gi 47208623 | Unnamed protein product (<i>T. nigroviridis</i>) casein kinase | 1 | eq |
| | gi 32403896 | Hypothetical protein (<i>N. crassa</i>) 40S ribosomal | 1 | eq |
| | gi 19112932 | 40S ribosomal protein s0 (<i>S. pombe</i>) | 2 | eq |
| | gi 10383793 | Ribosomal protein 59 of the 40S ribosomal subunit (<i>Sa. cerevisiae</i>) | 1 | eq |
| | gi 13794317 | 40S ribosomal protein S11 (<i>Guillardia theta</i>) | 1 | eq |
| | gi 46100286 | Hypothetical protein UM04662.1 (<i>Us. maydis</i> 521) 19S ribosomal | 1 | ds |
| | gi 50260434 | CNBA6160 (<i>C. neoformans</i> var. <i>neoformans</i> B-3501A) 60S ribosomal | 1 | eq |
| | gi 16943769 | Putative ribosomal protein S19 (<i>Pleurotus ostreatus</i>) | 2 | df |
| | gi 21215170 | Large subunit ribosomal protein L3 (<i>Aspergillus fumigatus</i>) | 2 | eq |
| | gi 1707876 | Ribosomal protein L23a (<i>Pu. graminis</i>) | 1 | df |
| | gi 303853 | Ribosomal protein L3 [<i>O. (japonica</i> cultivar-group)] | 1 | eq |
| | gi 42565416 | Ribosomal protein L3 (<i>Hyacinthus orientalis</i>) | 1 | ds |
| | gi 7417236 | Ribosomal protein L3 (<i>Trypanoplasma borreli</i>) | 1 | ds |
| | gi 11276520 | Ribosomal protein S4 – fission yeast (<i>S. pombe</i>) (fragment) | 1 | eq |
| | gi 18267 | Ribosomal protein L27 (<i>Pyrobotrys stellata</i>) | 1 | ds |
| | gi 18312189 | Ribosomal protein L2 (<i>Pyrobaculum aerophilum</i> str. IM2) | 1 | ds |
| | gi 19075893 | Putative 60s acidic ribosomal protein p0 (<i>S. pombe</i>) | 1 | eq |
| | gi 28436071 | Cytoplasmic ribosomal protein S14 (<i>Brassica napus</i>) | 1 | eq |
| | gi 31202717 | ENSANGP00000015322 (<i>Anopheles gambiae</i>) ribosomal | 1 | eq |
| | gi 32420189 | Hypothetical protein (<i>N. crassa</i>) | 1 | ds |
| | gi 32490929 | WGLp180 (<i>Wigglesworthia glossinidia</i>) ribosomal | 1 | ds |
| | gi 34879387 | Similar to ribosomal protein S27a (<i>R. norvegicus</i>) | 1 | ds |
| | gi 38048297 | Similar to <i>D. melanogaster</i> CG4759 (<i>D. yakuba</i>) ribosomal | 1 | eq |
| | gi 3861468 | Ribosomal protein L3 (<i>Tetrahymena thermophila</i>) | 1 | ds |
| | gi 40738432 | Hypothetical protein AN6679.2 (<i>A. nidulans</i> FGSC A4) ribosomal | 1 | eq |
| | gi 49650247 | Unnamed protein product (<i>Y. lipolytica</i> CLB99) ribosomal | 1 | ds |
| | gi 57242431 | Ribosomal protein S12 (<i>Campylobacter upsaliensis</i> RM3195) | 1 | ds |
| | gi 46096569 | Hypothetical protein UM01060.1 (<i>Us. maydis</i> 521) ribosomal | 1 | ds |
| Protein folding (c) | gi 20260809 | Hsp70 protein 2 (<i>Rhizopus stolonifer</i>) | 5 | eq |
| | gi 40743120 | HS70_TRIRU Heat shock 70 kDa protein (<i>A. nidulans</i> FGSC A4) | 6 | sb |
| | gi 4097891 | Heat shock protein 70 (<i>Pneumocystis carinii</i>) | 5 | sb |
| | gi 38489932 | Heat shock protein 70 (<i>Phytophthora nicotianae</i>) | 4 | eq |
| | gi 11993663 | Inducible heat shock 70 kDa protein (<i>Leptinotarsa decemlineata</i>) | 3 | eq |
| | gi 1620388 | 70 kD heat shock protein (<i>Takifugu rubripes</i>) | 3 | df |
| | gi 1842232 | Heat shock protein 70 (<i>Babesia microti</i>) | 3 | sb |
| | gi 2529289 | Heat shock protein 70 (<i>Biomphalaria glabrata</i>) | 3 | eq |
| | gi 51012459 | Hsp70 (<i>Naegleria fowleri</i>) | 3 | sb |
| | gi 51849654 | Heat shock protein 70 (<i>Chironomus yoshimatsui</i>) | 3 | df |
| | gi 9652348 | HSP70-1 protein (<i>Or. latipes</i>) | 3 | sb |
| | gi 21427250 | Hsp70 protein (<i>Odontaspis ferox</i>) | 2 | eq |
| | gi 21427292 | Hsp70 protein (<i>Lamna ditropis</i>) | 2 | sb |
| | gi 32394421 | Muscle-specific heat shock protein Hsc70-1 (<i>Cyprinus carpio</i>) | 2 | eq |
| | gi 32394423 | Heat shock protein Hsp70 (<i>Cy. carpio</i>) | 2 | df |
| | gi 8918240 | Hsp70 (<i>Blastocystis hominis</i>) | 2 | sb |
| | gi 10946282 | Heat shock protein Hsp70Aa (<i>Drosophila simulans</i>) | 2 | df |
| | gi 12045161 | Heat shock protein 70 (dnaK) (<i>Mycoplasma genitalium</i> G-37) | 1 | eq |
| | gi 12653415 | Heat shock 70 kDa protein 9B (<i>H. sapiens</i>) | 1 | eq |

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|----------------------------|-------------|---|---|----|
| | gi 13431500 | Chaperone protein dnaK (heat shock protein 70) (<i>Rhodothermus marinus</i>) | 1 | eq |
| | gi 15620767 | Heat shock protein (Hsp70) (<i>Moneuplotes crassus</i>) | 1 | ds |
| | gi 1854623 | 70-kDa heat shock protein (unidentified soil organism) | 1 | ds |
| | gi 1885336 | Heat shock 70 protein (<i>Gu. theta</i>) | 1 | ds |
| | gi 25229080 | Heat shock protein 70 (<i>Cryptosporidium parvum</i>) | 1 | eq |
| | gi 3169833 | Heat shock protein 70 (<i>Euplotes aediculatus</i>) | 1 | eq |
| | gi 3169841 | Heat shock protein 70 (<i>Eu. aediculatus</i>) | 1 | ds |
| | gi 640325 | Heat shock 70 kD (<i>Bos taurus</i>) | 1 | ds |
| | gi 881932 | HSS1 (<i>Pu. graminis</i> f. sp. tritici) | 5 | sb |
| | gi 46099593 | Hypothetical protein UM03791.1 (<i>Us. maydis</i> 521) hsp70 | 4 | df |
| | gi 54637782 | GA19632-PA (<i>Drosophila pseudoobscura</i>) hsp70 | 2 | sb |
| | gi 1165012 | Heat shock protein hsp70 (<i>Drosophila auraria</i>) | 3 | eq |
| | gi 17647515 | CG8937-PA Hsc70-1 (<i>D. melanogaster</i>) | 4 | eq |
| | gi 2814 | Unnamed protein product (<i>K. lactis</i>) Hsp70 | 2 | eq |
| | gi 3098140 | Heat shock protein 70 (<i>To. gondii</i>) | 3 | eq |
| | gi 4324942 | Heat shock 70 protein (<i>Entodinium caudatum</i>) | 2 | sb |
| | gi 48766851 | Heat shock protein 70 (<i>Litopenaeus vannamei</i>) | 2 | sb |
| | gi 1708308 | Heat shock protein 70 2 (<i>Pichia angusta</i>) | 4 | df |
| | gi 29468050 | 70 kDa heat shock protein (<i>Balanus amphitrite</i>) | 3 | df |
| | gi 38882982 | HSP70 (<i>Dicentrarchus labrax</i>) | 4 | sb |
| | gi 19114157 | Hsp70 family (<i>S. pombe</i>) | 2 | eq |
| | gi 6466324 | Unknown; Hsp70-type chaperone (<i>Cyanidium caldarium</i>) | 1 | ds |
| | gi 4235279 | Heat shock protein 70 (<i>Setaria digitata</i>) | 3 | eq |
| | gi 37596276 | Heat shock protein 68 (<i>Drosophila lummei</i>) | 3 | df |
| | gi 33591251 | Heat shock protein 68 (<i>Drosophila vulcana</i>) | 3 | eq |
| | gi 2119717 | dnaK-type molecular chaperone hsp70 – <i>Oxytricha nova</i> | 2 | eq |
| | gi 51704984 | Similar to heat shock cognate 71 kDa protein (<i>Mu. musculus</i>) | 1 | ds |
| | gi 109893 | dnaK-type molecular chaperone grp78 precursor – mouse | 2 | eq |
| | gi 15839736 | dnaK protein (<i>Mycobacterium tuberculosis</i> CDC1551) | 2 | df |
| | gi 15828694 | Heat shock protein dnaK (<i>Mycoplasma pulmonis</i> UAB CTIP) | 1 | ds |
| | gi 407521 | Chaperone (<i>Sa. cerevisiae</i>) | 3 | df |
| | gi 23121081 | COG0443: Molecular chaperone (<i>Desulfotobacterium hafniense</i>) | 1 | ds |
| | gi 46308682 | COG0443: Molecular chaperone (<i>Ehrlichia canis</i> str. Jake) | 1 | ds |
| | gi 53691007 | COG0326: Molecular chaperone (<i>Desulfovibrio desulfuricans</i> G20) | 1 | ds |
| | gi 21228607 | Chaperone protein (<i>Methanosarcina mazei</i> Go1) | 1 | eq |
| | gi 1066808 | Heat shock protein 82 (<i>Anopheles albimanus</i>) | 2 | eq |
| | gi 23480384 | Heat shock protein (<i>Pl. yoelii yoelii</i>) | 2 | eq |
| | gi 2908 | Heat shock protein (<i>Kluyveromyces marxianus</i>) | 2 | eq |
| | gi 6466104 | Heat shock protein (<i>Littorina plena</i>) | 1 | ds |
| | gi 46229711 | Heat shock protein (<i>Cr. parvum</i>) | 3 | sb |
| | gi 50261009 | Hypothetical protein CNBA3060 (<i>C. neoformans</i>) heat shock protein | 1 | eq |
| | gi 51233244 | Heat shock protein (<i>Aspergillus niger</i>) | 2 | sb |
| | gi 39937873 | Heat shock protein HtpG (<i>Rhodospseudomonas palustris</i> CGA009) | 1 | ds |
| | gi 31982974 | Heat shock protein 90 (<i>Amastigomonas marina</i>) | 2 | df |
| | gi 15827855 | Heat shock protein Hsp90 family (<i>Mycobacterium leprae</i> TN) | 1 | eq |
| | gi 25986825 | Heat shock protein 90 (<i>Bodo saliens</i>) | 1 | ds |
| | gi 38885054 | Heat shock protein 90 (<i>Oxyrrhis marina</i>) | 1 | ds |
| | gi 49654585 | Unnamed protein product (<i>Debaryomyces hansenii</i> CBS767) hsp90 | 2 | df |
| | gi 14198259 | Unknown (protein for IMAGE:3584589) (<i>Mu. musculus</i>) hsp90 | 1 | eq |
| | gi 56466097 | Heat shock protein 90 (<i>E. histolytica</i>) | 1 | eq |
| | gi 13507533 | Cro r II (<i>Cronartium ribicola</i>) | 2 | df |
| | gi 17738165 | CG5436-PA (<i>D. melanogaster</i>) | 2 | eq |
| | gi 1729877 | T-complex protein 1 chaperone (<i>Tetrahymena pyriformis</i>) | 1 | eq |
| | gi 31242551 | ENSANGP00000015826 (<i>An. gambiae</i>) | 1 | eq |
| | gi 312352 | Unnamed protein product (<i>Sa. cerevisiae</i>) hsp70 | 4 | eq |
| | gi 32417574 | Hypothetical protein (<i>N. crassa</i>) | 2 | df |
| | gi 40647591 | Mitochondrial 60 kDa heat shock protein (<i>Anemonia viridis</i>) | 1 | ds |
| | gi 50309731 | Unnamed protein product (<i>K. lactis</i>) | 3 | df |
| Protein-nucleus export (d) | gi 54657254 | Exportin 1 (chromosome region maintenance protein 1) (<i>Cryptosporidium</i>) | 1 | ds |
| Proteolysis (c) | gi 56464290 | 26s protease regulatory subunit (<i>E. histolytica</i> HM-1:IMSS) | 1 | eq |
| | gi 12697366 | Protease (Human immunodeficiency virus 1) | 1 | ds |
| | gi 13094662 | Neonatal thrombolytic agent alpha-form (<i>H. sapiens</i>) | 1 | eq |
| | gi 6523898 | M43L (<i>Myxoma virus</i>) cystein protease | 1 | ds |
| Proton transport (e) | gi 114575 | ATP synthase beta chain (<i>Sa. cerevisiae</i>) | 6 | eq |
| | gi 46909269 | ATP synthase beta subunit (<i>Priapulus caudatus</i>) | 4 | sb |
| | gi 19114063 | ATP synthase beta chain (<i>S. pombe</i>) | 3 | sb |
| | gi 46909251 | ATP synthase beta subunit (<i>Obelia</i> sp. KJP-2004) | 3 | sb |
| | gi 48844974 | COG0055: F0F1-type ATP synthase (<i>G. metallireducens</i>) | 3 | df |
| | gi 56808123 | COG0055: F0F1-type ATP synthase (<i>S. pyogenes</i>) | 3 | df |
| | gi 23480551 | V-type ATPase (<i>Pl. yoelii yoelii</i>) | 2 | eq |

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|----------------------------------|-------------|---|---|----|
| | gi 23502652 | ATP synthase F1(<i>Brucella suis</i> 1330) | 2 | df |
| | gi 28625015 | F1F0-ATPase subunit beta (<i>Pediococcus parvulus</i>) | 2 | eq |
| | gi 30023337 | ATP synthase beta chain (<i>Bacillus cereus</i> ATCC 14579) | 2 | eq |
| | gi 37721023 | ATP synthase beta subunit (<i>Muscaria comosum</i>) | 2 | df |
| | gi 534854 | ATPase subunit beta (<i>Geobacillus stearothermophilus</i>) | 2 | df |
| | gi 57227561 | ATP synthase alpha chain (<i>C. neoformans</i> var. <i>neoformans</i> JEC21) | 2 | sb |
| | gi 587526 | ATPase beta-subunit (<i>Stigmatella aurantiaca</i>) | 2 | df |
| | gi 11266659 | ATPase subunit 1(<i>D. discoideum</i>) mitochondrion | 1 | eq |
| | gi 11558456 | ATP synthase subunit B (<i>Platycrater arguta</i>) | 1 | eq |
| | gi 14718191 | ATP synthase beta subunit (<i>Portulaca grandiflora</i>) | 1 | ds |
| | gi 14718214 | ATP synthase beta subunit (<i>Schoepfia schreberi</i>) | 1 | ds |
| | gi 15829170 | ATP synthase beta chain (<i>My. pulmonis</i> UAB CTIP) | 1 | ds |
| | gi 17939849 | Mitochondrial F1 ATP synthase beta subunit (<i>Ar. thaliana</i>) | 1 | eq |
| | gi 20467367 | ATPase beta subunit (<i>Ephedra viridis</i>) | 1 | eq |
| | gi 29726132 | ATP synthase beta subunit (<i>Glaucium flavum</i>) | 1 | eq |
| | gi 48785443 | COG0055: F0F1-type ATP synthase (<i>B. fungorum</i> LB400) | 1 | eq |
| | gi 9799480 | ATP synthase beta subunit (<i>Crassula</i> aff. <i>Perforata</i> Fishbein 377) | 1 | ds |
| | gi 28436792 | Atp5b-prov protein (<i>X. laevis</i>) | 4 | eq |
| | gi 39997547 | Copper-translocating P-type ATPase (<i>Geobacter sulfurreducens</i> PCA) | 1 | ds |
| | gi 15920578 | Hypothetical SAV protein (<i>Sulfolobus tokodaii</i> str. 7) | 1 | eq |
| | gi 15889877 | Hypothetical protein AGR_C_4754 (<i>Agrobacterium tumefaciens</i> str. C58) atpase | 2 | eq |
| | gi 55980983 | Hypothetical protein TTHA1014 (<i>Thermus thermophilus</i> HB8) ATPase | 1 | ds |
| Pycocyanobilin metabolism (c) | gi 2493308 | Phycocyanobilin lyase beta subunit (<i>Pseudanabaena</i> sp.) | 1 | ds |
| Pyruvate metabolism (c) | gi 46100630 | Hypothetical protein UM04919.1 (<i>Us. maydis</i> 521) malate dehydrogenase | 2 | df |
| | gi 49652763 | Unnamed protein(<i>Deb. hansenii</i> CBS767) malate dehydrogenase | 1 | ds |
| | gi 23308437 | At3g47520/F1P2_70 (<i>Ar. thaliana</i>) malate dehydrogenase | 2 | eq |
| | gi 2605782 | Malate dehydrogenase (<i>T. brucei</i>) | 2 | df |
| | gi 10444078 | Mitochondrial malate dehydrogenase precursor (<i>Nucella lapillus</i>) | 1 | eq |
| | gi 30313545 | Mitochondrial malate dehydrogenase precursor (<i>Monodonta lineata</i>) | 1 | ds |
| Regulation of ecdysteroid (c) | gi 13752282 | Aldoketoreductase-like protein (<i>Orconectes limosus</i>) | 1 | eq |
| Response to copper ion (j) | gi 50291291 | Unnamed protein product (<i>Ca. glabrata</i>) multicopper ferro-O2-oxidoreductase | 1 | ds |
| Response to oxidative stress (c) | gi 46097168 | Hypothetical protein UM01947.1 (<i>Us. maydis</i> 521) cytochrome C peroxidase | 1 | ds |
| Response to stress (k) | gi 39590943 | Hypothetical protein CBG01908 (<i>Cae. briggsae</i>) GST | 1 | ds |
| | gi 49646106 | Unnamed protein product (<i>Y. lipolytica</i> CLIB99) rehydrin-like | 1 | ds |
| Ribonucleotide biosynthesis (c) | gi 49651979 | Unnamed protein product (<i>Y. lipolytica</i> CLIB99) ribonucleotide reductase | 1 | ds |
| RNA transcription (c) | gi 21225387 | Putative RNA polymerase sigma factor (<i>St. coelicolor</i> A3(2)) | 1 | ds |
| RNA-dependent DNA rep. (c) | gi 28569876 | Reverse transcriptase (<i>An. gambiae</i>) | 1 | ds |
| Shikimate metabolism (c) | gi 12515712 | 3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase (<i>Escherichia coli</i>) | 1 | eq |
| Succinyl-CoA metabolism (c) | gi 15596786 | Succinyl-CoA synthetase alpha chain (<i>Pseudomonas aeruginosa</i> PAO1) | 1 | eq |
| | gi 23480460 | Succinyl-CoA synthetase alpha subunit (<i>Pl. yoelii yoelii</i>) | 1 | eq |
| Telomere maintenance (d) | gi 25150725 | Putative telomere binding protein CLK-2 (<i>Cae. elegans</i>) | 1 | ds |
| Transcriptional initiation | gi 32141103 | Putative sigma factor (<i>St. coelicolor</i> A3(2)) | 1 | eq |
| | gi 1616770 | Putative poly(A)-binding protein FabM (<i>Em. nidulans</i>) | 1 | eq |
| Translational elongation (c) | gi 12007188 | Elongation factor 1 alpha (<i>Chramesus asperatus</i>) | 4 | eq |
| | gi 20335323 | Elongation factor-1 alpha (<i>Apalocnemis</i> sp. NCSU-95051121) | 4 | eq |
| | gi 10637881 | EF-1-alpha (<i>Pi. indica</i>) | 3 | eq |
| | gi 11078158 | Translation elongation factor 1-alpha (<i>Dichotomocladium elegans</i>) | 3 | eq |
| | gi 11078162 | Translation elongation factor 1-alpha (<i>Dissophora decumbens</i>) | 3 | eq |
| | gi 11118941 | Elongation factor-1 alpha (<i>Teloglabus milleri</i>) | 3 | df |
| | gi 11118957 | Elongation factor-1 alpha (<i>Diasemopsis elongata</i>) | 3 | eq |
| | gi 20302635 | Elongation factor-1 alpha (<i>Antherina suraka</i>) | 3 | df |
| | gi 29028184 | Elongation factor-1 alpha (<i>Manataria maculata</i>) | 3 | eq |
| | gi 32563304 | Translation elongation factor 1-alpha (<i>Saccharomyces bulderi</i>) | 3 | df |
| | gi 50660714 | Translation elongation factor 1 alpha (<i>Phytophthora boehmeriae</i>) | 3 | eq |
| | gi 13925370 | Elongation factor 2 (<i>N. crassa</i>) | 2 | eq |
| | gi 2723461 | Elongation factor 1 alpha (<i>Trichomonas tenax</i>) | 2 | eq |
| | gi 34869419 | Similar to Elongation factor 1-alpha 1 (<i>R. norvegicus</i>) | 2 | df |
| | gi 32263549 | Elongation factor-1 alpha (<i>Hypolimnas bolina</i>) | 1 | eq |
| | gi 47176812 | Translation elongation factor (<i>Candida norvegica</i>) | 1 | ds |
| | gi 46100008 | Hypothetical protein UM04152.1 (<i>Us. maydis</i> 521) elongation factor 3 | 1 | ds |
| | gi 50258869 | CNBD0200 (<i>C. neoformans</i>) Elongation factor Tu GTP binding domain | 2 | eq |
| | gi 14150797 | Elongation factor 1-alpha (<i>Platypus compertus</i>) | 1 | ds |
| | gi 14150843 | Elongation factor 1-alpha (<i>Coccidioides immitis</i>) | 2 | df |
| | gi 2367625 | Protein synthesis elongation factor 1-alpha (<i>Rhodotorula mucilaginosa</i>) | 3 | sb |
| | gi 27960791 | Translation elongation factor 1 alpha (<i>Nectria cinnabarina</i>) | 3 | df |

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| | gi 32400746 | Elongation factor-1 alpha 2 (<i>Oi. dioica</i>) | 3 | df |
| | gi 32563270 | Translation elongation factor-1 alpha (<i>Kluyveromyces africanus</i>) | 3 | eq |
| | gi 33330181 | Translation elongation factor-1 alpha (<i>Hypocrea dichromospora</i>) | 3 | df |
| | gi 34880372 | Elongation factor-1 alpha (<i>Liparthrum pilosum</i>) | 3 | sb |
| | gi 55420654 | Elongation factor-1 alpha (<i>Cithaerias aurora</i>) | 3 | df |
| | gi 9230401 | Translation elongation factor-1 alpha (<i>Fusarium fujikuroi</i>) | 2 | df |
| Translational initiation (c) | gi 46101778 | Hypothetical protein UM06129.1 (<i>Us. maydis</i> 521) translation initiation | 1 | eq |
| | gi 32414453 | EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) (EIF4A) (<i>N. crassa</i>) | 1 | eq |
| | gi 49657334 | Unnamed protein product (<i>Deb. hansenii</i> CBS767) translation initiation | 1 | ds |
| Translational termination (c) | gi 13959455 | Peptide chain release factor 2 (RF-2) (<i>B. aphidicola</i>) | 1 | eq |
| Transport (h) | gi 100424 | ADP (<i>Solanum tuberosum</i>) | 1 | eq |
| | gi 15805504 | Sodium:solute symporter protein (<i>Deinococcus radiodurans</i> R1) | 1 | ds |
| | gi 23113787 | COG1122: ABC-type cobalt transport system (<i>De. hafniense</i>) | 1 | ds |
| | gi 23467060 | COG4143: ABC-type thiamine transport system (<i>Haemophilus somnus</i> 129PT) | 1 | eq |
| | gi 27368873 | MRP-like ABC transporter [<i>O. sativa</i> (japonica cultivar-group)] | 1 | eq |
| | gi 53611401 | COG1879: ABC-type sugar transport system (<i>Azotobacter vinelandii</i>) | 1 | ds |
| | gi 57226726 | Importin alpha subunit (<i>C. neoformans</i>) | 1 | ds |
| | gi 24642252 | CG9281-PC ABC transporter (<i>D. melanogaster</i>) | 1 | eq |
| TRNA metabolism (c) | gi 42520059 | Glycyl-tRNA synthetase (<i>Wolbachia</i>) | 1 | ds |
| | gi 54026023 | Putative tRNA pseudouridine synthase (<i>Noc. farcinica</i> IFM 10152) | 1 | ds |
| | gi 46096696 | Hypothetical protein UM00855.1 (<i>Us. maydis</i> 521) tRNA synthetase | 1 | ds |
| Ubiquitin-dep protein catabol (c) | gi 57229614 | MMS2 (<i>C. neoformans</i>) | 2 | df |
| | gi 14719687 | Ubiquitin conjugating enzyme Chain B (<i>Sa. cerevisiae</i>) | 1 | eq |
| | gi 44983899 | AER254Wp (<i>Ashbya gossypii</i> ATCC 10895) | 1 | eq |
| | gi 46100237 | Hypothetical protein UM04547.1 (<i>Us. maydis</i> 521) 26S proteasome | 2 | df |
| | gi 11265288 | Proteasome protein p45/SUG (imported) – rat (fragment) | 1 | eq |
| | gi 32421185 | 26S protease regulatory subunit 6B homolog (<i>N. crassa</i>) | 1 | eq |
| | gi 50939243 | Alpha 1-2 subunit of 20S proteasome [<i>O. sativa</i> (japonica cultivar-group)] | 1 | ds |
| | gi 17945503 | RE23388p (<i>D. melanogaster</i>) | 1 | eq |
| | gi 20466790 | 26S proteasome regulatory subunit (<i>Ar. thaliana</i>) | 1 | eq |
| | gi 28436479 | Putative polyubiquitin (<i>Ar. thaliana</i>) | 2 | df |
| | gi 28436485 | Putative polyubiquitin (<i>Ar. thaliana</i>) | 2 | df |
| | gi 3789940 | Tetra-ubiquitin (<i>Saccharum</i> hybrid cultivar H32-8560) | 2 | df |
| | gi 433970 | Polyubiquitin (<i>Acetabularia cliftonii</i>) | 1 | ds |
| Undefined (n) | gi 40741757 | Conserved protein (<i>A. nidulans</i> FGSC A4) proteasome alpha | 1 | ds |
| | gi 46098213 | UM02408.1 (<i>Us. maydis</i> 521) G-protein beta-like WD repeat protein | 2 | df |
| | gi 15966040 | Hypothetical protein SMC01543 (<i>Simorhizobium meliloti</i> 1021) | 1 | ds |
| | gi 23023793 | COG5283: Phage-related tail protein (<i>Leuconostoc mesenteroides</i>) | 1 | ds |
| | gi 23481602 | Hypothetical protein (<i>Pl. yoelii yoelii</i>) | 1 | ds |
| | gi 23482166 | Hypothetical protein (<i>Pl. yoelii yoelii</i>) | 1 | eq |
| | gi 23508785 | PFL0440c (<i>Plasmodium falciparum</i> 3D7) membrane protein PFEMP3 | 1 | eq |
| | gi 32402980 | Hypothetical protein (<i>N. crassa</i>) | 1 | ds |
| | gi 38100976 | Hypothetical protein MG09149.4 (<i>M. grisea</i> 70-15) putative secreted | 1 | ds |
| | gi 38108199 | Hypothetical protein MG02246.4 (<i>M. grisea</i> 70-15) | 1 | ds |
| | gi 39581580 | Hypothetical protein CBG01490 (<i>Cae. briggsae</i>) | 1 | ds |
| | gi 40741178 | Hypothetical protein AN4798.2 (<i>A. nidulans</i> FGSC A4) | 1 | ds |
| | gi 45359012 | MMP1449 (<i>M. maripaludis</i> S2) membrane protein | 1 | ds |
| | gi 46098152 | Hypothetical protein UM02347.1 (<i>Us. maydis</i> 521) | 1 | eq |
| | gi 46141893 | Hypothetical protein Mbur03002539 (<i>Methanococcoides burtonii</i> DSM 6242) | 1 | ds |
| | gi 47223235 | Unnamed protein (<i>T. nigroviridis</i>) filensin (beaded filament structural protein) | 1 | ds |
| | gi 4929011 | Unknown (<i>Klebsiella oxytoca</i>) | 1 | ds |
| | gi 49650040 | Unnamed protein product (<i>Y. lipolytica</i> CLIB99) G-protein WD-40 receptor | 1 | ds |
| | gi 49651831 | Unnamed protein product (<i>Y. lipolytica</i> CLIB99) | 1 | ds |
| | gi 50913231 | Hypothetical protein [<i>O. sativa</i> (japonica cultivar-group)] | 1 | ds |
| | gi 53687088 | Hypothetical protein Npun02007157 (<i>No. punctiforme</i> PCC 73102) | 1 | ds |
| | gi 53689536 | Hypothetical protein Lmes02000590 (<i>Leuconostoc mesenteroides</i>) | 1 | ds |
| | gi 54294882 | Hypothetical protein lpl1961 (<i>Legionella pneumophila</i> str. Lens) | 1 | ds |
| | gi 55168281 | Hypothetical protein [<i>O. sativa</i> (japonica cultivar-group)] | 1 | ds |
| | gi 31077315 | GLP_93_34057_37386 (<i>Giardia lamblia</i> ATCC 50803) | 1 | ds |
| | gi 41618034 | TPA: HDC09922 (<i>D. melanogaster</i>) | 1 | ds |
| | gi 46250104 | MGC81264 protein (<i>X. laevis</i>) | 1 | eq |
| | gi 54638031 | GA11256-PA (<i>Dr. pseudoobscura</i>) | 1 | ds |
| | gi 55245133 | ENSANGP00000019556 (<i>An. gambiae</i> str. PEST) | 1 | ds |
| | gi 57105430 | Similar to Centaurin gamma 2 (ARF-GAP with GTP-binding protein-like | 1 | ds |
| | gi 15620933 | KIAA1937 protein (<i>H. sapiens</i>) | 1 | eq |
| | gi 21673216 | Hypothetical protein CT0377 (<i>Chlorobium tepidum</i> TLS) | 1 | ds |
| | gi 23013187 | Uncharacterized conserved protein (<i>Magnetospirillum magnetotacticum</i> MS-1) | 1 | ds |
| | gi 24583097 | CG15828-PA (<i>D. melanogaster</i>) | 1 | eq |
| | gi 24640695 | CG12662-PA (<i>D. melanogaster</i>) | 1 | ds |

| | | | |
|-------------|--|---|----|
| gi 29347085 | Conserved protein (<i>Bacteroides thetaiotaomicron</i>) | 1 | ds |
| gi 33597585 | BPP3049 (<i>Bordetella parapertussis</i> 12822) phosphate acetyltransferase | 1 | ds |
| gi 39595905 | Hypothetical protein CBG12894 (<i>Cae. briggsae</i>) | 1 | ds |
| gi 7270928 | Hypothetical protein (<i>Ar. thaliana</i>) | 1 | ds |

1

2 a) Letter in parenthesis is the hierarchal GO Biological Process category shown in

3 Fig. 3.

4 b) ds, distinct protein; df, differentiable protein; eq, equivalent protein; sb,

5 subsumable protein.

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