Genome-wide survey of remote homologues for protein domain superfamilies of known structure reveals unequal distribution across structural classes

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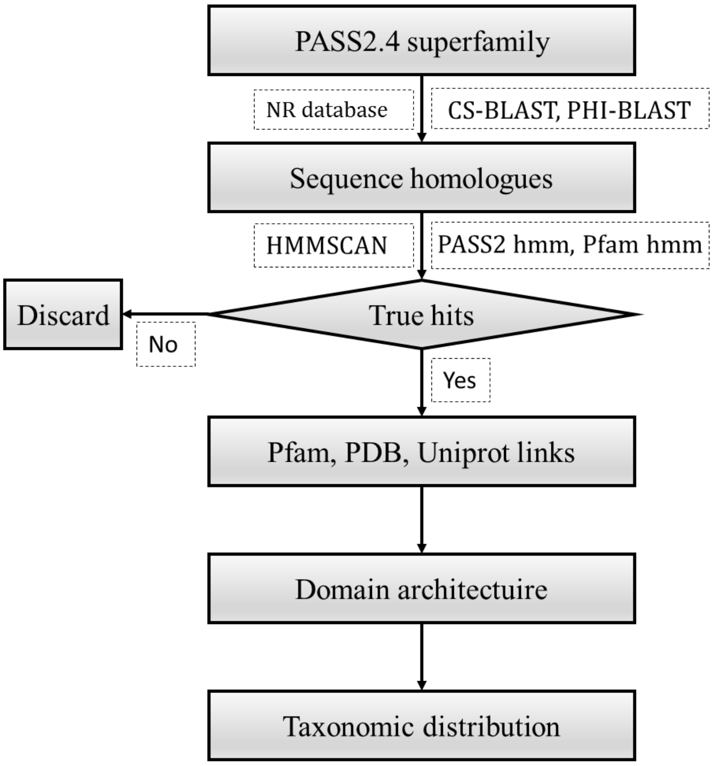
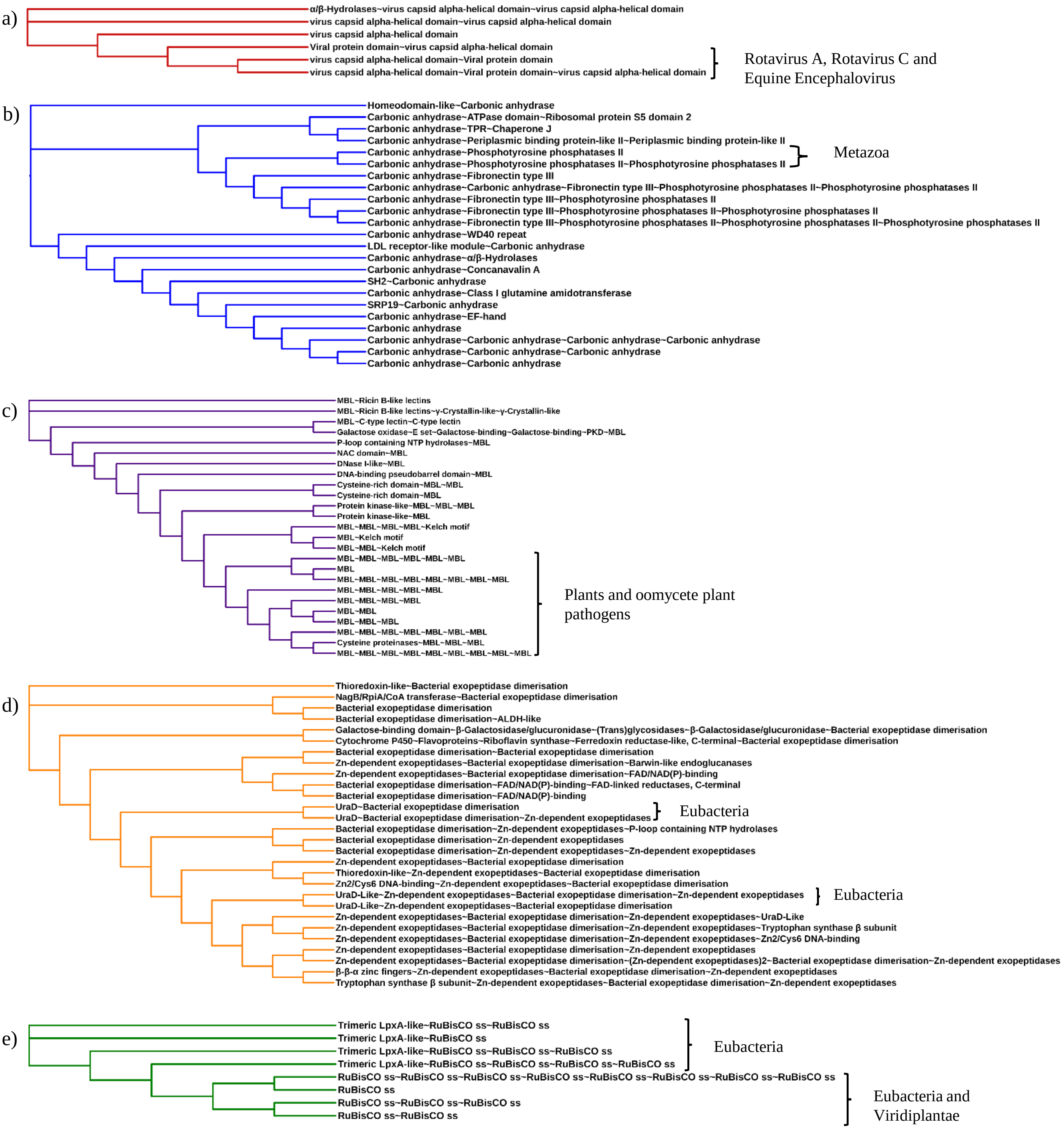


Supplementary Figure 1: The work-flow followed in the paper has been illustrated. Each hit identified by sequence searches undergoes the following steps- validation using superfamily HMMs, DA determination at SCOP and Pfam level, finding the taxonomic occurrence.



Supplementary Figure 2: The phylogenetic trees obtained using the DA for the superfamilies a) 48345 (red) b) 55239 (green) c) 51069 (blue) d) 51101 (purple) e) 55031 (orange) are shown. We see that that similar DA like domain repeats (51101) and same pair of domains associated with other domains (55239 and 51161) are clustered and unrelated domains are well-separated. The taxonomic distribution of the different DA is indicated.

Supplementary Table 1: The HMM library was created using all the PASS2.4 member sequences and the superfamily alignments. PASS2.4 is divided into different categories based on the number of PASS2.4 members in the superfamily into Single-membered (SMS), Two-membered (TMS) and multi-membered superfamilies (MMS). PASS2.4 also provides structure-based sequence alignments for all the superfamilies. Since, SMS have only a single member, the SF-HMM is a single sequence HMM. There were in total 1080 SF-HMMs and 10569 SQ-HMMs, 11649 total HMMs. We used the superfamily alignments and the member sequences to create a HMM library with a total of 11,749 HMMs. SF-HMM – PASS2.4 superfamily alignment HMM, SQ-HMM – Single query HMM.

Type of HMM library	**Number of SMS HMM**	**Number of TMS HMM**	**Number of MMS HMM**	**Total**
SF-HMM	-	366	714	1180
SQ-HMM	864	732	8973	10,569
Total	864	1098	9687	11,749

Supplementary Table 2: Number of sequence search (PHI-BLAST and CS-BLAST) and validation (HMMSCAN) runs carried out in the study.

Sequence search method	**Number of runs in SMS**	**Number of runs in TMS**	**Number of runs in MMS**	**Total**
CS-BLAST	864	732	8,970	10,566
PHI-BLAST	4,425	4,405	4,662	13,492
Total	5,289	5,137	13,632	24, 058

Sequence search method	**HMM library**	**Number of runs in SMS**	**Number of runs in TMS**	**Number of runs in MMS**	**Total**
CS-BLAST	PASS2.4 HMM	847	363	730	1,940
	Pfam HMM	847	363	730	1,940
PHI-BLAST	PASS2.4 HMM	686	338	697	1,721
	Pfam HMM	686	338	697	1,721
Total	Total	3,066	1,402	2,854	7,322

Supplementary Table 3: The comparison of the MP and MQ approach for the superfamily test dataset. MQ approach picks up more hits whereas the MP approach has a better Positive Prediction Value (PPV). MP-Multi-Pattern, MQ- Multi-Query, TP- True Positive, FP- False positive

SCOP Superfamily	**Superfamily description**	**Total**	**TP_total**	**FP_total**	**Total PPV**	**MP_total**	**MP_TP**	**MP_FP**	**MP PPV**	**MQ_total**	**MQ_TP**	**MQ_FP**	**MQ PPV**
47336	ACP-like	24330	21394	2936	0.88	2125	2114	11	0.99	23883	20949	2934	0.88
47565	Insect Pheromone-OBPs	2549	2306	243	0.91	707	698	9	0.99	2548	2306	242	0.91
48345	A virus capsid protein alpha helical domain	1693	1055	638	0.62	785	755	30	0.96	1692	1055	637	0.62
50203	Bacterial Enterotoxins	2908	2633	275	0.91	764	678	86	0.89	2900	2633	267	0.91
51101	Carbonic anhydrase	3121	1790	1331	0.57	673	658	15	0.98	3120	1790	1330	0.57
51069	Mannose-binding lectins	7563	7464	99	0.99	777	777	0	1	7561	7464	97	0.99
55031	Triosephosphate isomerase	32235	25309	6926	0.79	570	439	131	0.77	32084	25204	6880	0.79
55239	Bacterial-luciferase like	2642	1944	698	0.74	694	570	124	0.82	2641	1944	697	0.74
55307	Nucleotide-binding domain	15953	15815	138	0.99	3323	3315	8	0.99	15582	15454	128	0.99
51351		7599	7568	31	0.99	562	552	10	0.98	7052	7032	20	0.99
51679	Bacterial exopeptidase dimerisation	24813	22089	2724	0.89	1880	1724	156	0.92	24391	21794	2597	0.89
51971	RuBisCo-small subunit	29134	12631	16503	0.43	2393	1449	944	0.61	27608	11616	15992	0.42

Supplementary Table 4: The number of hits obtained for each superfamily using the different sequence search approaches has been provided with the taxonomic distribution. The SCOP class and fold code have also been provided. The numbers indicate the number of true positive hits for the different taxa.

CLASS	FOLD	SF	SUPERFAMILY DESCRIPTION	CSBLAST HITS	PHIBLAST HITS	CSBLAST TP HITS	PHIBLAST TP LIST	PHIBLAST PDB COUNT	CSBLAST PDB COUNT	ALL PDB COUNT	PFAM UNIQUE DA	PASS2 UNIQUE DA	TAXID	CELLULAR ORGANISMS	VIRUS	UNCHARACTERISED	ENVIRONMENTAL SAMPLE	BACTERIA	ARCHAEA	PLANT	METAZOA	PROTEOBACTERIA	ACTINOBACTERIA	FIRMICUTES	SAR	FUNGI
46456	46457	46458	Globin-like	26176	1603	22203	1479	995	2824	2824	131	59	6399	6394	0	12	19	4787	87	111	980	2324	1180	688	33	294
46456	46457	46548	alpha-helical ferredoxin	10853	529	6154	529	20	114	114	43	39	3910	3909	0	17	19	2957	107	72	313	2229	628	13	59	336
46456	46556	46557	GreA transcript cleavage protein, N-terminal domain	5583	2634	5581	2626	19	1	19	4	6	4638	4637	0	10	148	4632	0	0	4	2383	632	955	0	0
46456	46556	46561	Ribosomal protein L29 (L29p)	4925	1096	4901	1094	76	395	395	6	8	4204	4202	0	14	200	3590	195	52	156	1520	725	983	21	169
46456	46556	46565	Chaperone J-domain	28574	813	27587	749	5	56	57	292	159	8737	8631	104	62	366	7455	158	88	324	2838	1226	1601	88	464
46456	116730	46575	DNA polymerase III theta subunit-like	770	651	693	0	7	7	7	2	4	273	270	3	0	0	268	0	0	1	268	0	0	0	1
46456	46556	46579	Prefoldin	5353	1916	1033	769	7	2	7	13	9	883	880	0	44	52	5	376	62	202	0	0	0	39	176
46456	46556	46585	HR1 repeat	3464	871	1330	849	5	5	5	34	22	302	301	0	0	0	0	0	1	264	0	0	0	0	36
46456	46556	46589	tRNA-binding arm	16027	1093	8453	1066	10	30	32	9	20	4232	4229	0	9	142	4173	50	3	3	2155	162	1495	0	0
46456	46556	46596	Eukaryotic DNA topoisomerase I, dispensable insert domain	1122	965	472	3	15	15	15	6	9	437	437	0	0	0	0	0	0	437	0	0	0	0	0
46456	46556	46600	C-terminal UvrC-binding domain of UvrB	5000	783	2999	782	4	2	4	5	9	1606	1606	0	3	33	1604	0	0	1	1359	3	167	0	1
46456	46556	46604	Epsilon subunit of F1F0-ATP synthase C-terminal domain	842	1357	834	956	22	22	22	3	7	795	794	0	4	4	595	0	0	198	589	1	1	0	1
46456	46556	46609	Fe,Mn superoxide dismutase (SOD), N-terminal domain	10292	1690	10284	1671	17	222	227	25	20	6270	6266	1	36	76	5223	192	145	344	2497	654	966	48	292
46456	46625	46626	Cytochrome c	61639	1032	37802	905	7	729	729	287	77	6394	6388	0	46	67	5356	9	109	360	3840	36	437	111	376
46456	46688	46689	Homeodomain-like	215768	1504	176340	1502	2	734	736	7	398	11984	11949	6	40	276	10012	86	401	780	4883	1761	2161	90	533
46456	46688	46767	Methylated DNA-protein cysteine methyltransferase, C-terminal domain	7467	2602	7467	2590	10	4	12	26	32	3914	3912	1	8	93	3757	106	2	17	2061	492	740	0	29
46456	46688	46774	ARID-like	5801	639	5584	639	5	18	18	83	33	743	742	0	0	0	0	0	63	276	0	0	0	5	388
46456	46688	46785	Winged helix DNA-binding domain	427550	674	282586	674	12	1550	1550	6	403	15596	15484	57	164	541	13379	463	284	628	5891	1992	3244	98	570
46456	46688	46894	C-terminal effector domain of the bipartite response regulators	67583	674	61405	668	3	111	111	400	111	8764	8754	0	29	333	8724	2	2	10	3578	1845	2285	1	2
46456	46688	46906	Ribosomal protein L11, C-terminal domain	5554	2067	5546	2060	135	226	273	7	10	4752	4749	0	29	230	4415	223	66	3	1388	777	1113	26	0
46456	46688	46911	Ribosomal protein S18	5000	1429	4960	71	272	382	382	3	9	4160	4159	0	11	222	4041	0	75	0	1282	681	1016	24	6
46456	46688	46915	Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3	6973	2330	4709	72	7	26	26	41	45	3165	3165	0	6	87	2871	0	54	240	1228	1097	344	0	0
46456	46688	46919	N-terminal Zn binding domain of HIV integrase	5000	1686	5000	1676	12	0	12	30	38	37	0	33	0	0	0	0	0	0	0	0	0	0	0
46456	46688	46924	RNA polymerase subunit RPB10	887	606	850	597	126	127	127	3	6	749	738	8	28	35	1	281	65	80	1	0	0	37	235
46456	46928	46929	DNA helicase RuvA subunit, C-terminal domain	2467	745	2413	490	7	28	28	6	11	1689	1688	0	2	57	1686	1	0	0	938	214	30	0	1
46456	46928	46934	UBA-like	22958	1253	19302	1187	5	130	130	273	130	4788	4786	0	13	202	3720	0	99	310	1649	262	1129	84	516
46456	46928	46938	CRAL/TRIO N-terminal domain	7018	810	4204	477	13	36	36	40	27	761	760	0	0	0	1	0	77	276	1	0	0	16	359
46456	46928	46942	Elongation factor TFIIS domain 2	3602	976	437	409	8	13	13	11	9	388	388	0	0	0	0	0	26	42	0	0	0	1	317
46456	81297	46946	S13-like H2TH domain	12237	1345	11882	1211	2	469	469	23	29	6619	6615	2	42	254	6263	141	29	177	2762	1082	1398	1	1
46456	46928	46950	Double-stranded DNA-binding domain	1216	1025	1197	946	3	5	5	17	9	1032	1031	0	33	38	1	310	68	241	0	0	0	48	325
46456	46954	46955	Putative DNA-binding domain	29703	938	26128	933	14	91	91	140	87	6878	6860	15	18	153	6184	1	6	293	3203	800	1676	8	354
46456	46965	46966	Spectrin repeat	11241	670	9925	670	1	47	47	887	593	686	685	0	0	0	0	0	0	519	0	0	0	0	154
46456	46965	46973	Enzyme IIa from lactose specific PTS, IIa-lac	4506	1061	4340	1056	14	38	38	5	7	1404	1404	0	0	20	1403	0	0	0	380	54	891	0	1
46456	46965	46977	Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain	13685	1208	13635	1048	18	115	115	30	32	6236	6233	0	21	128	5410	104	71	241	3400	870	539	30	344
46456	46965	46984	Smac/diablo	1129	406	323	0	3	3	3	1	4	180	180	0	0	0	0	0	0	180	0	0	0	0	0
46456	46965	46988	Tubulin chaperone cofactor A	823	861	781	10	4	5	5	5	5	665	664	0	0	0	0	0	69	235	0	0	0	38	296
46456	46965	46992	Ribosomal protein S20	5191	2003	5184	98	377	378	378	1	5	4406	4405	0	12	172	4324	0	56	1	1852	809	904	16	0
46456	46996	46997	Bacterial immunoglobulin/albumin-binding domains	3693	725	3282	723	21	62	62	453	65	793	769	0	0	0	767	0	0	1	0	0	767	0	1
46456	47004	47005	Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex	7123	1302	7122	1301	24	22	24	21	27	2756	2755	0	6	7	2323	18	59	193	1460	39	628	21	124
46456	47013	47014	Protozoan pheromone proteins	5	3	5	0	2	3	3	1	4	1	1	0	0	0	0	0	0	0	0	0	0	1	0
46456	47026	47027	Acyl-CoA binding protein	5102	1961	4538	1941	30	30	30	72	25	1373	1371	1	3	3	503	3	85	310	333	36	0	71	363
46456	47026	47031	Second domain of FERM	16107	1226	14982	1224	42	90	90	269	167	334	333	0	0	0	1	0	5	300	1	0	0	2	2
46456	47039	47040	Kix domain of CBP (creb binding protein)	1568	704	937	700	9	10	10	49	37	267	267	0	0	0	0	0	0	265	0	0	0	0	1
46456	47044	47045	RAP domain-like	332	354	329	257	9	9	9	6	7	237	236	0	0	0	0	0	0	236	0	0	0	0	0
46456	47049	47050	VHP, Villin headpiece domain	5021	1879	4937	64	26	21	31	47	35	367	366	0	0	0	0	0	64	276	0	0	0	5	1
46456	47054	47055	TAF(II)230 TBP-binding fragment	458	557	56	0	1	1	1	4	6	27	27	0	0	0	0	0	0	27	0	0	0	0	0
46456	47059	47060	S15/NS1 RNA-binding domain	11636	890	11620	889	3	141	144	79	66	10269	4326	5942	13	223	4062	1	4	243	1806	525	1159	12	0
46456	47071	47072	Cysteine alpha-hairpin motif	840	1080	592	6	10	9	10	8	9	441	440	0	0	0	1	0	57	218	1	0	0	13	144
46456	47076	47077	T4 endonuclease V	238	557	207	0	7	7	7	1	4	138	67	71	1	1	67	0	0	0	60	1	0	0	0
46456	47081	47082	Fertilization protein	73	82	48	0	11	11	11	1	4	36	36	0	0	0	0	0	0	36	0	0	0	0	0
46456	47089	47090	PGBD-like	12762	1009	10700	993	1	30	30	236	108	3410	3377	32	9	158	2991	13	62	304	1219	463	1032	0	6
46456	47094	47095	HMG-box	21340	0	21074	0	0	66	66	227	121	1724	1712	8	0	0	5	0	96	777	2	2	1	74	721
46456	47112	47113	Histone-fold	30010	582	28106	574	10	926	926	289	115	3674	3646	12	1	1	128	101	216	2309	17	87	1	113	714
46456	47143	47144	HSC20 (HSCB), C-terminal oligomerisation domain	2679	632	1635	625	3	11	11	5	7	942	941	0	2	2	917	0	7	4	913	1	1	0	12
46456	47143	47148	Diol dehydratase, gamma subunit	571	557	554	0	20	20	20	2	5	312	312	0	1	4	309	3	0	0	101	55	126	0	0
46456	47143	47152	Methane monooxygenase hydrolase, gamma subunit	29	29	29	0	58	58	58	1	4	24	24	0	0	0	24	0	0	0	21	3	0	0	0
46456	47143	47157	Mitochondrial import receptor subunit Tom20	791	635	434	3	22	22	22	4	6	282	281	0	0	0	0	0	0	253	0	0	0	0	26
46456	47161	47162	Apolipoprotein	2972	836	554	32	24	30	30	7	7	185	184	0	0	0	0	0	0	183	0	0	0	1	0
46456	47161	47170	Aspartate receptor, ligand-binding domain	5000	1004	2585	0	14	15	15	9	6	522	522	0	0	0	520	0	0	1	519	1	0	0	1
46456	47161	47175	Cytochromes	4063	0	2794	0	0	243	243	10	9	1521	1520	0	4	4	1517	0	0	2	1504	0	1	0	1
46456	47161	47188	Hemerythrin-like	4157	1380	1887	1181	49	52	52	51	20	949	948	0	3	37	912	16	0	18	509	1	274	0	0
46456	47161	47195	TMV-like viral coat proteins	348	646	325	16	62	62	62	1	4	60	0	60	0	0	0	0	0	0	0	0	0	0	0
46456	47363	47203	Acyl-CoA dehydrogenase C-terminal domain-like	36698	1601	34120	1600	1	215	216	90	65	6606	6600	0	75	163	5494	239	87	291	2318	1267	1102	41	418
46456	47161	47212	FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)	1252	590	1198	0	26	26	26	42	11	858	857	0	0	0	0	0	68	269	0	0	0	40	435
46456	47161	47216	Proteasome activator	968	767	764	0	91	91	91	8	7	336	335	0	0	0	0	1	0	254	0	0	0	24	27
46456	47161	47220	alpha-catenin/vinculin-like	6554	573	3005	572	2	82	82	38	57	295	294	0	0	0	0	0	0	282	0	0	0	0	2
46456	47161	47226	Histidine-containing phosphotransfer domain, HPT domain	22409	1100	14026	468	2	48	48	396	137	4464	4463	0	6	57	3959	105	78	3	2850	18	731	0	313
46456	47161	47233	Bacterial GAP domain	419	416	391	0	8	8	8	6	8	93	92	0	0	0	92	0	0	0	92	0	0	0	0
46456	47239	47240	Ferritin-like	62685	818	49796	436	2	2671	2671	90	44	10870	10506	356	52	365	9082	320	156	457	3902	1533	1933	67	378
46456	47265	47266	4-helical cytokines	11821	1212	9157	1106	18	364	364	72	32	659	621	32	0	0	2	0	0	618	0	0	2	0	1
46456	47322	47323	Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases	42913	1507	35922	1001	2	83	83	65	92	9470	9466	0	45	386	8746	293	12	123	3380	1381	2304	2	287
46456	47335	47336	ACP-like	23884	2126	20949	2114	8	108	108	2082	2695	7409	7399	5	23	258	6563	4	99	232	2508	1457	1447	76	370
46456	47335	47345	Colicin E immunity proteins	892	600	779	0	48	49	49	3	5	227	225	0	0	0	225	0	0	0	217	1	4	0	0
46456	47335	47353	Retrovirus capsid dimerization domain-like	15384	1520	15383	1510	17	2615	2632	531	187	232	119	106	0	0	0	0	0	119	0	0	0	0	0
46456	47161	47364	Domain of the SRP/SRP receptor G-proteins	12270	869	10775	804	2	23	25	15	21	6179	6178	0	7	275	5481	1	63	394	2062	1033	1485	16	214
46456	47363	47370	Bromodomain	8238	704	8236	702	3	341	341	203	128	820	819	0	0	0	0	0	75	288	0	0	0	35	407
46456	47379	47380	ROP protein	380	499	369	89	37	37	37	2	5	132	129	0	1	1	127	1	0	1	112	2	8	0	0
46456	47379	47384	Homodimeric domain of signal transducing histidine kinase	15000	969	14009	969	7	27	29	164	402	4853	4849	0	8	68	4782	55	2	3	3181	9	1044	1	5
46456	47390	47391	Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit	845	1337	845	201	48	48	48	17	19	289	288	0	0	0	0	0	4	275	0	0	0	3	0
46456	47395	47396	Transcription factor IIA (TFIIA), alpha-helical domain	1695	781	1677	32	4	8	8	23	14	749	749	0	0	0	1	0	89	278	1	0	0	3	370
46456	47400	47401	Ectatomin subunits	1	1	1	0	1	1	1	1	4	1	1	0	0	0	0	0	0	1	0	0	0	0	0
46456	47405	47406	SinR repressor dimerisation domain-like	277	349	277	56	6	6	6	6	5	197	197	0	0	0	197	0	0	0	0	0	197	0	0
46456	47412	47413	lambda repressor-like DNA-binding domains	76821	1244	60611	1048	14	327	328	351	100	10033	9912	83	26	308	9340	158	12	362	4058	1427	2741	1	38
46456	47445	47446	Signal peptide-binding domain	7225	610	7223	591	6	14	14	12	15	5116	5115	0	5	213	4476	34	35	468	1444	1072	1234	9	91
46456	47453	47454	A DNA-binding domain in eukaryotic transcription factors	3138	1960	3082	1823	10	15	15	16	14	293	290	1	0	0	1	0	0	288	1	0	0	0	0
46456	47458	47459	HLH, helix-loop-helix DNA-binding domain	17367	1120	15313	1004	2	9	11	110	74	1431	1416	12	0	0	0	0	104	859	0	0	0	0	448
46456	47472	47473	EF-hand	61475	0	56632	0	0	1405	1405	1848	464	2441	2386	2	0	0	424	0	267	626	19	352	0	118	887
46456	47472	47565	Insect pheromone/odorant-binding proteins	2549	708	2306	58	44	130	130	9	11	237	236	0	0	0	0	0	0	236	0	0	0	0	0
46456	47472	47571	Cloroperoxidase	1665	880	538	5	19	19	19	10	6	216	216	0	0	0	0	0	0	0	0	0	0	5	211
46456	47575	47576	Calponin-homology domain, CH-domain	19053	656	18473	656	1	71	71	658	493	1096	1095	0	0	0	2	0	76	431	2	0	0	68	485
46456	47586	47587	Domain of poly(ADP-ribose) polymerase	1942	1220	1604	1158	70	70	70	97	68	636	635	0	0	0	4	0	62	269	1	0	3	31	236
46456	47591	47592	SWIB/MDM2 domain	4743	999	3946	916	1	163	163	63	36	988	986	1	1	1	195	0	77	280	133	0	0	51	371
46456	47597	47598	Ribbon-helix-helix	9753	751	7320	750	13	194	194	25	15	2756	2750	4	7	25	2539	210	0	0	2107	132	99	0	1
46456	47615	47616	GST C-terminal domain-like	54173	777	46546	746	10	1047	1047	10	128	6054	6010	0	29	38	4330	99	199	788	3480	400	182	66	492
46456	47643	47644	Methionine synthase domain	5000	757	5000	751	7	7	7	13	24	2586	2586	0	4	5	2552	0	3	4	2146	181	5	18	2
46456	47643	47648	Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain	11648	662	11633	660	6	40	40	16	23	5669	5667	0	16	205	5499	121	37	4	2292	1129	1618	4	1
46456	47654	47655	STAT	7607	883	1545	844	9	14	14	37	23	238	236	0	0	0	0	0	0	230	0	0	0	0	0
46456	47654	47661	t-snare proteins	9171	608	5431	589	12	24	24	51	29	982	981	0	0	0	0	0	77	386	0	0	0	65	425
46456	47667	47668	N-terminal domain of cbl (N-cbl)	923	600	819	19	38	46	46	21	16	263	261	1	0	0	0	0	0	258	0	0	0	0	0
46456	47667	47672	Transferrin receptor-like dimerisation domain	3046	1037	1736	961	87	89	89	14	12	502	501	0	1	1	40	0	59	235	0	7	7	12	153
46456	47667	47676	Conserved domain common to transcription factors TFIIS, elongin A, CRSP70	3800	1424	2005	999	3	3	3	37	21	719	718	0	0	0	0	0	66	271	0	0	0	42	326
46456	47680	47681	C-terminal domain of B transposition protein	321	329	279	0	1	1	1	4	6	133	129	4	0	0	129	0	0	0	129	0	0	0	0

46456	47685	47686	Anaphylotoxins (complement system)	1104	712	907	32	46	50	50	68	21	201	200	0	0	0	0	0	0	200	0	0	0	0	0
46456	47693	47694	Cytochrome c oxidase subunit h	1089	688	1022	24	53	53	53	10	9	610	609	0	0	0	1	0	74	220	1	0	0	12	287
46456	47698	47699	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin	8347	808	5512	778	7	58	58	19	10	424	423	0	0	0	1	0	419	2	0	0	1	0	1
46456	47718	47719	p53 tetramerization domain	205	294	205	108	104	46	104	6	7	138	136	1	0	0	0	0	1	135	0	0	0	0	0
46456	47723	47724	Domain of early E2A DNA-binding protein, ADDBP	211	220	181	0	7	7	7	2	6	113	0	113	0	0	0	0	0	0	0	0	0	0	0
46456	47728	47729	IHF-like DNA-binding proteins	9034	747	8999	744	7	58	58	7	14	4156	4151	3	13	192	4139	3	1	4	2413	38	1097	2	0
46456	47740	47741	CO dehydrogenase ISP C-domain like	7287	661	7284	646	68	104	104	58	64	3065	3061	0	17	49	2388	70	72	273	1343	532	364	19	224
46456	47751	47752	Protein HNS-dependent expression A; HdeA	173	639	152	6	15	9	15	2	5	100	100	0	0	0	99	0	0	1	99	0	0	0	0
46456	47756	47757	Chemotaxis receptor methyltransferase CheR, N-terminal domain	5000	749	3504	745	2	2	2	5	7	1929	1928	0	2	9	1920	3	1	2	1647	22	88	0	2
46456	47761	47762	PAH2 domain	2498	678	1743	672	7	11	11	36	17	791	790	0	0	0	1	0	70	261	1	0	0	22	421
46456	47768	47769	SAM/Pointed domain	28287	1332	25681	1290	5	126	129	697	191	976	973	2	0	0	109	0	62	329	108	0	0	21	436
46456	47768	47781	RuvA domain 2-like	38469	1953	36366	1841	9	51	51	142	85	10265	10258	3	64	402	9376	311	68	253	3902	1639	2279	31	195
46456	47768	47789	C-terminal domain of RNA polymerase alpha subunit	6316	1267	6316	1266	129	76	205	19	22	4898	4896	0	12	242	4891	0	1	2	2199	765	1261	1	0
46456	47768	47794	Rad51 N-terminal domain-like	5720	652	5411	648	8	51	51	73	51	3523	3520	2	47	64	2359	361	77	271	2276	3	4	65	333
46456	47768	47798	Barrier-to-autointegration factor, BAF	374	385	323	0	13	13	13	4	6	195	195	0	0	0	0	0	0	193	0	0	0	0	0
46456	47768	47802	DNA polymerase beta, N-terminal domain-like	5195	920	3753	845	305	345	345	64	38	2010	1990	19	10	12	1119	166	63	238	157	134	461	24	350
46456	47768	47807	5' to 3' exonuclease, C-terminal subdomain	17513	2112	14706	2092	3	51	51	38	26	8761	8667	91	61	372	7422	381	70	254	2489	1422	1877	72	425
46456	47768	47819	HRDC-like	19464	642	15568	624	7	107	107	86	33	7574	7571	0	37	204	6410	311	73	281	3146	1306	1014	54	404
46456	47768	47823	lambda integrase-like, N-terminal domain	20024	1051	11440	731	58	72	72	13	12	5732	5708	4	21	197	5696	0	2	1	2902	724	1085	0	9
46456	47768	47831	Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain	5000	629	4963	625	21	23	23	19	22	2579	2579	0	2	103	2575	0	2	1	1145	19	1234	0	1
46456	47835	47836	Retroviral matrix proteins	6474	2449	6298	2435	23	15	37	156	84	295	89	197	0	0	1	0	0	87	0	0	0	0	0
46456	47851	47852	Hepatitis B viral capsid (hbcag)	5000	739	5000	729	8	8	8	6	6	50	0	49	0	0	0	0	0	0	0	0	0	0	0
46456	47856	47857	Apolipophorin-III	4487	3826	36	67	3	3	3	1	7	57	57	0	0	0	3	0	0	54	1	1	0	0	0
46456	47861	47862	Saposin	2389	1003	1924	23	21	32	32	144	24	407	406	0	0	0	1	0	94	289	1	0	0	0	3
46456	47861	47869	Bacteriocin AS-48	22	27	22	5	13	13	13	1	4	17	17	0	0	0	17	0	0	0	0	2	15	0	0
46456	47873	47874	Annexin	5298	1325	5139	1256	15	94	94	44	22	667	666	0	0	0	1	0	111	314	1	0	0	14	215
46456	47894	47895	Transducin (alpha subunit), insertion domain	5340	642	5181	596	19	133	133	12	18	752	751	0	1	1	0	0	24	358	0	0	0	5	348
46456	47911	47912	Wiscott-Aldrich syndrome protein, WASP, C-terminal domain	3598	620	232	231	5	12	12	8	7	114	113	0	0	0	0	0	0	112	0	0	0	0	1
46456	47916	47917	C-terminal domain of alpha and beta subunits of F1 ATP synthase	10000	2276	9996	2246	232	315	315	24	28	7424	7422	0	10	65	4229	2	2490	316	2191	769	887	33	323
46456	47916	47923	Ypt/Rab-GAP domain of gyp1p	7054	1210	2254	32	5	5	5	11	9	864	863	0	0	0	0	0	81	270	0	0	0	62	409
46456	47927	47928	N-terminal domain of the delta subunit of the F1F0-ATP synthase	5000	592	2702	587	2	8	8	5	8	1892	1889	0	6	12	1791	0	7	56	1604	0	132	16	10
46456	47932	47933	ERP29 C domain-like	837	709	680	0	14	14	14	12	9	526	526	0	0	0	0	0	70	212	0	0	0	12	202
46456	47937	47938	Functional domain of the splicing factor Prp18	3167	802	65	61	2	10	10	3	4	59	59	0	0	0	0	0	0	0	0	0	0	2	57
46456	47942	47943	Retrovirus capsid protein, N-terminal core domain	21456	1571	21309	1545	7	42	49	169	85	305	115	181	0	0	0	0	0	114	0	0	0	0	0
46456	47953	47954	Cyclin-like	18644	1240	16871	1220	17	316	319	139	48	1683	1639	41	97	108	4	441	164	369	0	0	0	90	518
46456	47972	47973	Ribosomal protein S7	7725	3190	7651	3181	296	462	465	14	16	6479	6476	0	50	237	4148	333	80	1508	1707	646	1112	50	300
46456	47978	47979	Iron-dependent repressor protein, dimerization domain	5820	1220	5367	1210	59	105	105	19	9	3256	3255	0	45	143	2955	299	0	1	130	1113	1047	0	0
46456	47985	47986	DEATH domain	20425	690	10508	672	18	238	238	880	86	355	345	9	0	0	1	0	0	344	0	0	0	0	0
46456	48007	48008	GntR ligand-binding domain-like	21600	1539	4920	1497	17	9	17	7	7	2394	2394	0	2	34	2390	4	0	0	1272	669	379	0	0
46456	48012	48013	NusB-like	11208	945	11130	941	7	32	32	21	15	5595	5593	0	10	174	5589	0	0	3	2235	1234	1502	0	1
46456	48018	48019	post-AAA+ oligomerization domain-like	28340	1425	24341	1415	15	119	119	102	43	8571	8560	7	55	332	7245	361	77	285	3460	1046	1606	71	482
46456	48023	48024	N-terminal domain of DnaB helicase	5000	607	5000	606	5	53	53	12	13	3139	3131	8	5	12	3128	0	0	3	1589	844	607	0	0
46456	48370	48029	FliG	5000	769	4873	768	5	9	9	7	6	3210	3210	0	7	59	3208	0	0	2	2037	118	779	0	0
46456	48033	48034	Guanido kinase N-terminal domain	2918	1370	2329	138	67	134	134	30	23	1105	1104	0	1	1	19	0	0	1039	16	0	0	27	0
46456	48044	48045	Scaffolding protein gpD of bacteriophage procapsid	178	183	107	0	14	14	14	2	4	53	31	21	1	1	28	0	0	0	18	0	5	0	3
46456	48049	48050	Hemocyanin, N-terminal domain	1008	711	652	38	55	58	58	11	13	183	183	0	0	0	0	0	0	183	0	0	0	0	0
46456	48055	48056	Di-copper centre-containing domain	6638	752	1622	0	44	154	154	37	31	446	445	0	0	0	46	0	135	254	21	10	1	1	6
46456	48064	48065	DBL homology domain (DH-domain)	16910	605	16755	531	6	74	74	687	610	619	618	0	0	0	0	0	0	287	0	0	0	0	320
46456	48075	48076	LigA subunit of an aromatic-ring-opening dioxygenase LigAB	858	648	638	0	22	22	22	3	6	400	400	0	2	2	400	0	0	0	341	55	1	0	0
46456	48080	48081	Methyl-coenzyme M reductase alpha and beta chain C-terminal domain	5147	1029	2003	0	59	62	62	4	5	229	227	0	59	62	2	225	0	0	0	0	0	0	0
46456	48091	48092	Transcription factor STAT-4 N-domain	1883	854	1602	828	3	3	3	31	22	252	250	0	0	0	0	0	0	248	0	0	0	0	0
46456	48096	48097	Regulator of G-protein signaling, RGS	12289	743	11372	659	17	109	109	158	72	616	615	0	0	0	1	0	46	310	1	0	0	20	222
46456	48107	48108	Carbamoyl phosphate synthetase, large subunit connection domain	5000	621	4989	620	40	40	40	16	113	2967	2967	0	8	12	2884	13	62	7	2500	4	149	0	0
46456	48112	48113	Heme-dependent peroxidases	19071	592	16716	584	218	736	736	158	60	4378	4374	2	14	18	3144	128	266	328	1846	692	131	27	444
46456	48139	48140	Ribosomal protein L19 (L19e)	1640	1011	1463	37	82	140	140	19	13	1066	1065	0	36	41	3	338	79	213	3	0	0	50	335
46456	48144	48145	Influenza virus matrix protein M1	4553	562	4286	547	6	69	69	4	5	4222	0	4222	0	0	0	0	0	0	0	0	0	0	0
46456	48149	48150	DNA-glycosylase	26032	783	25929	779	6	131	131	61	53	8846	8841	0	50	277	7731	314	72	265	3679	1086	1903	50	392
46456	48162	48163	An anticodon-binding domain of class I aminoacyl-tRNA synthetases	16661	3972	8319	703	21	37	37	9	8	5670	5669	0	42	183	5383	220	13	8	1971	989	1067	3	41
46456	48167	48168	R1 subunit of ribonucleotide reductase, N-terminal domain	9869	1900	9807	1897	70	103	103	27	19	5065	4856	206	8	17	4359	1	16	118	2320	728	899	8	353
46456	48172	48173	Cryptochrome/photolyase FAD-binding domain	6395	950	6395	501	11	31	31	20	21	3466	3464	0	11	12	2934	86	102	81	2030	175	203	11	243
46456	48178	48179	6-phosphogluconate dehydrogenase C-terminal domain-like	74431	1488	69871	1450	20	302	304	161	122	11144	11109	26	74	376	9834	289	95	320	4441	1492	2376	67	450
46456	48200	48201	Uteroglobin-like	524	708	423	144	12	12	12	6	5	115	114	0	0	0	0	0	0	114	0	0	0	0	0
46456	48207	48208	Six-hairpin glycosidases	48473	1541	31846	1460	23	283	283	56	159	7385	7379	1	27	241	6360	88	117	300	2588	1120	1545	26	472
46456	48207	48225	Seven-hairpin glycosidases	5117	2271	4203	2175	19	25	25	48	28	871	871	0	0	0	27	0	72	277	11	6	0	23	456
46456	48207	48230	Chondroitin AC/alginate lyase	8495	1118	3000	1083	26	69	69	96	27	1177	1177	0	1	30	1168	2	0	0	208	318	437	0	3
46456	48207	48239	Terpenoid cyclases/Protein prenyltransferases	19752	866	13588	859	45	343	343	270	77	2759	2757	0	6	7	1315	17	396	409	449	406	265	78	489
46456	48255	48256	Citrate synthase	20000	643	14970	642	21	104	104	19	13	7407	7406	0	44	221	6340	236	89	244	2969	1277	1147	60	400
46456	48263	48264	Cytochrome P450	43697	816	42882	802	18	920	920	119	126	4574	4564	2	25	30	3262	102	234	426	1140	1253	454	26	489
46456	46688	48295	TrpR-like	8972	1708	7028	1705	9	51	60	10	9	4365	4364	0	7	50	4356	0	0	6	2863	526	864	0	1
46456	48299	48300	Ribosomal protein L7/12, oligomerisation (N-terminal) domain	1	271	1	268	52	0	52	3	7	197	196	0	1	2	196	0	0	0	188	0	1	0	0
46456	48304	48305	Class II MHC-associated invariant chain ectoplasmic trimerization domain	356	357	333	0	3	3	3	7	7	163	162	0	0	0	0	0	0	162	0	0	0	0	0
46456	48309	48310	Aldehyde ferredoxin oxidoreductase, C-terminal domains	2725	933	1783	916	10	10	10	5	8	686	683	0	18	24	472	211	0	0	194	14	156	0	0
46456	48316	48317	Acid phosphatase/Vanadium-dependent haloperoxidase	20047	641	1327	627	22	50	50	1	5	731	730	0	3	9	694	1	1	0	459	40	35	4	24
46456	48333	48334	DNA repair protein MutS, domain III	17455	2008	14630	2007	34	52	52	60	35	7708	7707	0	29	338	6650	175	65	267	3314	5	1851	21	486
46456	48339	48340	Interferon-induced guanylate-binding protein 1 (GBP1), C-terminal domain	4209	751	861	728	2	2	2	10	11	109	108	0	0	0	0	0	0	108	0	0	0	0	0
46456	48344	48345	A virus capsid protein alpha-helical domain	1693	786	1055	731	54	86	86	4	9	193	0	185	0	0	0	0	0	0	0	0	0	0	0
46456	48349	48350	GTPase activation domain, GAP	15745	770	14954	723	8	25	25	210	153	749	748	0	0	0	0	0	0	278	0	0	0	13	437
46456	48365	48366	Ras GEF	5000	555	1884	551	24	29	29	54	38	672	672	0	0	0	0	0	1	266	0	0	0	1	386
46456	48370	48371	ARM repeat	88801	0	46755	0	0	776	776	1057	195	3590	3586	1	8	24	2183	148	134	414	560	508	661	91	554
53931	74651	48403	Ankyrin repeat	9555	890	9521	890	8	102	110	3358	429	507	499	6	6	7	68	11	6	269	39	0	5	11	126
46456	48370	48425	Sec7 domain	5259	648	5252	618	16	36	36	52	28	866	865	0	0	0	3	0	74	276	3	0	0	31	467
46456	48370	48431	Lipovitellin-phosvitin complex, superhelical domain	15934	895	685	57	1	92	92	30	17	250	250	0	0	0	0	0	0	250	0	0	0	0	0
46456	48370	48435	Bacterial muramidases	5000	558	3484	557	3	3	3	6	6	1649	1648	0	4	5	1646	0	1	1	1642	1	2	0	0
46456	48370	48439	Protein prenylyltransferase	5473	1722	104	1318	151	127	153	33	21	746	746	0	0	0	4	0	64	269	0	0	0	26	363
46456	48370	48445	14-3-3 protein	4357	1451	3498	1448	59	158	158	30	21	974	973	0	0	0	1	0	134	326	1	0	0	78	383
46456	48370	48452	TPR-like	77879	679	31295	661	10	260	270	4561	241	5977	5969	4	50	135	4854	152	90	311	2442	881	243	74	442
46456	48370	48464	ENTH/VHS domain	17693	604	13215	604	11	118	118	122	60	977	976	0	0	0	1	0	79	283	1	0	0	62	504
46456	48370	48479	Cytochrome c oxidase subunit E	782	618	750	0	53	53	53	6	6	613	612	0	0	0	0	0	0	291	0	0	0	0	317
46456	48483	48484	Lipoxigenase	4040	1861	2701	29	69	71	71	22	18	469	468	0	0	0	128	0	120	188	70	7	0	3	23
46456	48492	48493	gene 59 helicase assembly protein	145	145	129	0	1	1	1	3	4	102	3	99	1	1	3	0	0	0	2	1	0	0	0
46456	48497	48498	Tetracyclin repressor-like, C-terminal domain	74762	945	31040	588	25	266	266	54	28	5361	5330	0	8	12	5223	99	2	4	2841	1364	713	0	2
46456	48507	48508	Nuclear receptor ligand-binding domain	15878	838	15324	815	91	1367	1367	80	39	685	663	2	0	0	1	0	0	662	1	0	0	0	0
46456	48536	48537	Phospholipase C/P1 nuclease	3824	697	1846	47	25	37	37	7	9	859	859	0	1	14	542	0	74	1	196	0	105	12	208
46456	48551	48552	Serum albumin-like	1048	918	1006	905	158	159	159	17	15	228	226	1	0	0	1	0	0	225	1	0	0	0	0
46456	48556	48557	L-aspartase-like	23245	819	23148	811	5	167	167	38	30	7635	7628	0	53	266	6415	251	248	261	3265	235	1704	26	396
46456	48575	48576	Terpenoid synthases	25799	1316	20488	987	40	575	575	67	40	7290	7288	0	27	233	5809	186	432	287	2945	562	1379	46	487
46456	48591	48592	GroEL equatorial domain-like	10000	1410	3358	202	878	960	960	22	31	1543	1540	0	23	40	478	227	69	277	296	1	29	67	375
46456	48599	48600	Chorismate mutase II	11209	1102	9588	976	1	57	57	40	31	5324	5322	0	17	153	4778	108	78	8	2626	760	872	14	328
46456	48607	48608	Peridinin-chlorophyll protein	234	234	226	0	9	9	9	2	5	28	28	0	0	0	0	0	0	1	0	0	0	27	0
46456	48612	48613	Heme oxygenase-like	15985	1091	12192	1042	3	241	241	53	30	5258	5245	7	42	68	4302	193	87	216	2053	1010	727	20	400
46456	48618	48619	Phospholipase A2, PLA2	4934	1088	3880	999	290	466	467	20	12	785	783	1	0	0	235	0	0	467	0	218	0	0	81
46456	48646	48647	Fungal elicitin	405	463	329	3	16	16	16	4	6	46	45	0	0	0	0	0	1	0	0	0	0	44	0
46456	48651	48652	Tetraspanin	872	610	327	0	4	4	4	1	4	168	167	0	0	0	0	0	0	167	0	0	0	0	0
46456	48656	48657	FinO-like	3181	1878	1470	0	7	7	7	4	4	558	557	1	1	2	557	0	0	0	553	1	2	0	0
46456	48661	48662	Ribosomal protein L39e	0	637	0	572	78	0	78	8	9	327	325	0	3	3	1	40	45	130	1	0	0	22	84
46456	48661	48666	Methanol dehydrogenase subunit	123	124	123	123	31	31	31	1	4	110	110	0	2	2	110	0	0	0	108	0	0	0	0
46456	48661	48670	Transducin (heterotrimeric G protein), gamma chain	1386	960	1189	10	27	27	27	11	16	276	275	0	0	0	0	0	0	274	0	0	0	0	0
46456	48661	48674	Fe-only hydrogenase smaller subunit	1992	864	41	28	8	12	12	8	7	32	32	0	0	0	32	0	0	0	24	0	8	0	0
46456	48661	48678	Moesin tail domain	1641	778	1199	742	2	4	4	17	14	283	282	0	0	0	0	0	0	279	0	0	0	0	0
46456	48661	48686	Proteinase A inhibitor IA3	0	8	0	8	3	0	3	1	4	6	6	0	0	0	0	0	0	0	0	0	0	0	6
46456	48661	48690	Epsilon subunit of mitochondrial F1F0-ATP synthase	560	621	389	58	13	13	13	3	5	301	301	0	0	0	0	0	62	194	0	0	0	3	34
46456	48694	48695	Multiheme cytochromes	39491	1735	4788	761	62	306	306	70	20	1983	1982	0	13	30	1970	12	0	0	1331	41	106	0	0
48724	48725	48726	Immunoglobulin	162544	810	159315	802	9	10523	10523	6239	2506	1660	1559	75	0	0	24	0	2	1531	5	0	8	0	0
48724	48725	49265	Fibronectin type III	56187	603	54162	603	1	470	471	4292	2589	2286	2282	2	4	22	1461	14	9	769	183	596	418	21	0
48724	48725	49299	PKD domain	6915	670	4906	657	1	34	34	847	204	1436	1432	0	27	41	1099	149	0	183	256	270	158	0	0
48724	48725	49303	beta-Galactosidase/glucuronidase domain	19125	570	8018	556	8	370	370	115	79	2820	2729	2	9	113	2279	18	21	234	837	489	380	1	175
48724	48725	49309	Transglutaminase, two C-terminal domains	2403	745	2313	13	25	45	45	26	25	281	280	0	0	0	0	0	0	279	0	0	0	0	0
48724	48725	49313	Cadherin-like	24504	693	21506	676	1	103	104	1115	286	410	409	0	0	1	63	0	0	343	45	0	0	0	1
48724	48725	49319	Actinoxanthin-like	632	474	79	9	27	27	27	1	4	53	52	0	0	0	52	0	0	0	0	52	0	0	0
48724	48725	49329	Cu,Zn superoxide dismutase-like	7177	1341	6957	1336	11	574	574	24	18	3500	3387	112	4	15	2312	11	198	472	1338	264	412	23	359
48724	48725	49344	CBD9-like	6161	1063	1197	426	3	15	15	132	67	577	574	0	6	14	305	27	0	0	12	53	172	0	242
48724	48725	49348	Clathrin adaptor appendage domain	6983	687	6226	684	5	50	50	68	36	898	897	0	0	0	1	0	73	274	1	0	0	78	426
48724	48725	49354	PapD-like	11966	1023	10679	1006	29	115	127	51	28	2193	2192	0	0	2	1437	0	77	294	1434	1	1	55	315
48724	48725	49363	Purple acid phosphatase, N-terminal domain	5000	670	1058	7	36	39	39	9	8	199	199	0	1	1	54	0	78	43	36	17	0	15	4
48724	48725	49367	Superoxide reductase-like	1595	1067	1361	0	93	93	93	12	7	1069	1069	0	8	103	942	122	0	0	155	43	524	0	0

48724	48725	49373	Invasin/intimin cell-adhesion fragments	12080	721	4839	657	1	18	18	207	53	965	964	0	1	13	962	2	0	0	851	25	57	0	0
48724	49379	49380	Diphtheria toxin, C-terminal domain	24	24	19	0	14	14	14	2	5	6	5	1	0	0	5	0	0	0	0	5	0	0	0
48724	49379	49384	Carbohydrate-binding domain	10389	850	8655	844	2	119	119	476	247	1357	1352	0	5	14	1326	18	0	6	416	614	245	2	0
48724	49379	49401	Bacterial adhesins	22422	612	14175	606	30	249	249	98	32	2038	2037	0	0	2	2035	0	0	1	1000	21	1014	0	1
48724	49379	49410	Alpha-macroglobulin receptor domain	3934	737	2557	697	9	72	72	121	38	327	326	0	0	0	0	0	0	326	0	0	0	0	0
48724	49379	49417	p53-like transcription factors	17445	530	14329	521	2	423	423	198	71	648	644	2	0	0	0	0	1	513	0	0	0	0	119
48724	49379	49441	Cytochrome f, large domain	1305	742	1253	35	19	36	36	6	8	1117	1117	0	2	2	204	0	837	0	2	0	2	46	0
48724	49379	49447	Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor	5000	1271	3044	1221	33	36	36	47	34	981	980	0	0	0	1	0	80	385	1	0	0	67	395
48724	49451	49452	Starch-binding domain-like	11917	997	5044	991	70	127	127	209	128	2010	2009	0	3	23	1517	9	75	89	307	431	616	27	273
48724	49451	49464	Carboxypeptidase regulatory domain-like	10834	880	5037	863	2	10	10	79	134	1040	1037	0	1	69	779	0	0	256	4	7	7	0	0
48724	49451	49468	VHL	592	566	215	201	88	88	88	3	6	163	163	0	0	0	0	0	0	163	0	0	0	0	0
48724	49451	49472	Transthyretin (synonym: prealbumin)	5000	874	3355	799	541	555	555	10	9	1897	1895	0	2	15	1478	15	7	266	1021	298	38	9	110
48724	49451	49478	Cna protein B-type domain	8039	755	2702	728	3	43	43	118	48	910	909	0	13	52	908	1	0	0	12	124	750	0	0
48724	49451	49482	Aromatic compound dioxygenase	8932	693	8021	693	145	438	438	21	11	2306	2304	0	4	4	2009	0	0	4	1278	633	19	0	291
48724	49492	49493	HSP40/DnaJ peptide-binding domain	19823	1718	17814	1702	1	22	22	57	53	7230	7224	3	31	283	6066	143	93	358	2601	1118	1218	87	421
48724	49497	49498	alpha-Amylase inhibitor tendamistat	62	155	52	3	7	7	7	2	5	46	46	0	0	0	46	0	0	0	0	46	0	0	0
48724	49502	49503	Cupredoxins	64326	611	55723	610	20	1270	1270	347	110	12292	12255	33	121	129	6978	270	188	4141	3974	1123	886	24	639
48724	49561	49562	C2 domain (Calcium/lipid-binding domain, CaLB)	43585	557	37948	542	4	284	284	727	352	1044	1042	1	0	0	3	0	114	363	1	0	0	37	478
48724	49561	49584	Periplasmic chaperone C-domain	7410	840	7351	838	20	89	89	6	8	1357	1357	0	0	2	1353	0	0	2	1350	1	2	0	2
48724	49561	49590	PHL pollen allergen	3499	1235	882	635	13	13	13	6	11	88	88	0	0	0	4	0	84	0	0	4	0	0	0
48724	49561	49594	Rab geranylgeranyltransferase alpha-subunit, insert domain	170	173	149	0	3	3	3	12	9	110	110	0	0	0	0	0	0	110	0	0	0	0	0
48724	49598	49599	TRAF domain-like	9900	571	6426	569	52	130	130	96	33	579	573	5	0	0	2	0	83	474	2	0	0	3	4
48724	49605	49606	Neurophysin II	481	503	462	6	29	29	29	5	4	224	224	0	0	0	0	0	0	224	0	0	0	0	0
48724	49694	49695	gamma-Crystallin-like	5490	1395	4886	1194	67	124	124	122	59	595	594	0	2	7	366	4	12	204	137	120	47	2	5
48724	49722	49723	Lipase/lipooxygenase domain (PLAT/LH2 domain)	7671	833	3955	797	27	98	98	127	75	440	439	0	0	0	54	1	124	223	7	6	34	33	1
48724	88632	49742	PHM/PNGase F	2779	651	1852	637	19	36	36	38	12	358	357	0	0	0	57	0	10	288	9	0	0	0	1
48724	88632	49749	Group II dsDNA viruses VP	3405	526	1209	484	67	167	167	9	6	350	4	346	0	2	1	0	0	1	0	0	0	1	0
48724	49757	49758	Calpain large subunit, middle domain (domain III)	5000	1062	3698	998	8	9	9	74	47	337	335	1	0	0	0	0	34	285	0	0	0	0	8
48724	49763	49764	HSP20-like chaperones	14560	1397	13895	1393	18	101	119	174	70	3961	3960	0	13	78	2789	104	190	303	1183	719	345	87	439
48724	49771	49772	Ecotin, trypsin inhibitor	1249	681	1167	651	37	37	37	1	4	575	574	0	1	1	556	0	0	1	480	1	1	0	0
48724	49776	49777	PEBP-like	9307	1402	7820	1379	20	42	42	38	24	3525	3518	5	17	27	2449	119	226	284	1244	910	30	31	399
48724	49784	49785	Galactose-binding domain-like	95872	545	50161	538	3	1070	1070	2179	811	7161	7065	2	49	260	5889	78	99	368	1787	1238	1629	73	520
48724	49817	49818	Viral protein domain	27663	1120	26199	1120	3	649	649	9	10	24787	0	24784	0	0	0	0	0	0	0	0	0	0	0
48724	49829	49830	ENV polyprotein, receptor-binding domain	1025	1573	104	0	3	3	3	4	7	30	7	22	0	0	0	0	0	7	0	0	0	0	0
48724	49834	49835	Virus attachment protein globular domain	629	453	602	315	171	373	373	19	10	216	11	203	0	0	11	0	0	0	2	1	6	0	0
48724	49841	49842	TNF-like	9661	584	9352	582	130	390	390	69	39	402	399	1	1	1	0	0	0	399	0	0	0	0	0
48724	49853	49854	Spermadhesin, CUB domain	8138	923	8138	913	14	37	37	831	1018	300	299	0	0	0	2	0	0	297	0	0	0	0	0
48724	49862	49863	Hyaluronate lyase-like, C-terminal domain	3027	815	2229	574	9	47	47	68	22	825	825	0	1	28	814	2	0	0	83	235	318	0	6
48724	49869	49870	Osmotin, thaumatin-like protein	3577	912	2702	710	94	97	97	30	18	324	323	0	0	0	47	0	171	18	0	47	0	0	86
48724	49878	49879	SMAD/FHA domain	36249	861	21383	503	14	143	143	355	128	3673	3671	0	8	92	2823	2	77	319	550	1472	465	29	395
48724	49888	49889	Soluble secreted chemokine inhibitor, VCCI	131	132	71	0	7	7	7	1	4	16	0	15	0	0	0	0	0	0	0	0	0	0	0
48724	49893	49894	Baculovirus p35 protein	39	39	32	0	10	10	10	1	4	15	0	15	0	0	0	0	0	0	0	0	0	0	0
48724	49898	49899	Concanavalin A-like lectins/glucanases	98675	1521	55607	1383	663	2222	2222	2619	1206	5017	4569	438	19	120	3069	29	253	495	1003	563	995	47	615
48724	49993	49998	Amine oxidase catalytic domain	5019	1414	4483	27	85	238	238	53	33	1438	1437	0	0	0	774	12	82	172	307	394	22	24	368
48724	50011	50012	EV matrix protein	91	91	90	0	16	16	16	1	5	18	0	18	0	0	0	0	0	0	0	0	0	0	0
48724	50016	50017	gp9	188	938	63	0	79	79	79	2	4	63	1	62	0	0	1	0	0	0	0	1	0	0	0
48724	50021	50022	ISP domain	32124	1854	28556	1155	15	443	443	108	46	7109	7104	0	64	81	6028	162	110	309	3577	1318	445	72	389
48724	50036	50037	C-terminal domain of transcriptional repressors	8810	1256	4222	549	4	122	122	19	17	2437	2432	0	9	59	2392	39	0	1	1137	718	335	0	0
48724	50036	50044	SH3-domain	52374	1395	51705	1369	12	463	464	1583	844	927	909	14	0	0	3	0	1	348	2	0	0	21	502
48724	50036	50084	Myosin S1 fragment, N-terminal domain	5916	668	5320	666	42	167	167	83	26	340	339	0	0	0	0	0	0	316	0	0	0	0	14
48724	50036	50090	Electron transport accessory proteins	2780	921	1662	796	66	156	156	8	6	925	920	3	5	5	762	5	84	1	419	126	11	40	0
48724	50036	50104	Translation proteins SH3-like domain	36663	1037	33337	1035	142	1173	1173	119	59	9854	9848	1	129	428	7560	437	714	472	2826	1298	1736	108	463
48724	50036	50118	Cell growth inhibitor/plasmid maintenance toxic component	7485	614	7025	603	8	70	70	18	14	3605	3582	4	12	180	3508	69	1	3	1148	660	1260	0	1
48724	50036	50122	DNA-binding domain of retroviral integrase	5128	1812	5127	1687	14	10	14	63	51	103	34	65	0	0	0	0	0	34	0	0	0	0	0
48724	50128	50129	GroES-like	91758	1219	87245	1083	2	525	525	233	354	10872	10813	51	101	264	9251	291	297	363	4376	1699	1820	43	527
48724	50128	50151	SacY-like RNA-binding domain	4935	827	4547	6	2	5	5	7	9	1530	1530	0	0	43	1528	0	0	1	247	145	1110	0	1
48724	50155	50156	PDZ domain-like	76048	1029	69204	213	2	604	604	911	463	7894	7887	0	39	234	7358	107	56	340	3820	916	1321	15	2
48724	50175	50176	N-terminal domains of the minor coat protein g3p	129	306	113	0	14	14	14	9	10	37	24	6	0	0	24	0	0	0	24	0	0	0	0
48724	50181	50182	Sm-like ribonucleoproteins	23639	736	22421	718	43	959	959	153	82	5026	5024	0	46	114	3709	317	88	307	2710	2	666	88	462
48724	50192	50193	Ribosomal protein L14	6175	1666	6157	1645	145	447	447	9	13	5088	5084	0	42	235	3599	280	606	227	1298	557	951	69	247
48724	50198	50199	Staphylococcal nuclease	5000	661	4002	641	251	251	251	24	10	2075	2070	1	9	29	1961	81	10	1	707	153	624	3	4
48724	50198	50203	Bacterial enterotoxins	2901	765	2633	662	126	761	761	25	14	365	349	9	1	1	349	0	0	0	57	0	292	0	0
48724	50198	50242	TIMP-like	5959	796	3016	494	1	84	84	169	72	353	352	0	0	0	32	1	0	318	1	0	22	0	0
48724	50198	50249	Nucleic acid-binding proteins	215787	0	169742	0	0	2094	2094	768	438	16024	15603	397	248	632	13080	591	769	363	5636	1695	3002	138	558
48724	50198	50324	Inorganic pyrophosphatase	7112	1344	6971	1224	67	183	183	20	17	4539	4538	0	10	94	3478	196	82	278	1836	857	175	63	397
48724	50198	50331	MOP-like	20226	942	16636	495	2	117	117	21	17	5248	5245	0	13	138	5028	213	0	3	2469	963	1199	0	1
48724	50198	50341	CheW-like	9999	3227	9825	697	14	12	14	37	56	3277	3276	0	6	52	3207	67	0	1	2179	3	804	0	1
48724	50345	50346	PRC-barrel domain	11602	1382	5624	9	1	134	134	19	13	3046	3044	0	10	65	2754	3	2	263	1846	23	845	19	1
48724	50352	50353	Cytokine	7064	801	5749	732	293	396	396	31	26	413	358	53	0	0	0	0	0	358	0	0	0	0	0
48724	50352	50370	Ricin B-like lectins	15329	689	13204	618	4	193	193	570	221	1895	1889	2	8	39	1461	19	32	284	407	701	251	21	66
48724	50352	50382	Agglutinin	244	1041	160	153	16	31	43	7	8	26	26	0	0	0	0	0	26	0	0	0	0	0	0
48724	50352	50386	STI-like	1729	785	1536	737	61	163	163	10	10	187	180	2	0	0	11	0	169	0	0	1	10	0	0
48724	50352	50405	Actin-crosslinking proteins	3117	661	1188	594	14	41	41	49	29	436	427	3	1	1	106	3	52	249	11	13	58	1	5
48724	50412	50443	FucI/AraA C-terminal domain-like	5856	1459	4095	1397	15	36	36	8	6	1951	1950	0	2	116	1948	2	0	0	466	440	652	0	0
48724	50412	50447	Translation proteins	66173	2256	59118	2255	32	841	841	245	182	18875	18868	1	184	511	8813	683	149	6586	3920	1353	2139	145	2078
48724	50464	50465	EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain	19246	900	19184	899	14	163	177	70	68	10375	10372	0	53	171	4296	344	160	2338	2843	560	441	103	3025
48724	50474	50475	FMN-binding split barrel	52181	1132	36607	1086	6	212	212	82	50	8538	8533	0	43	295	7643	237	73	249	3587	1366	1425	21	293
48724	50485	50486	FMT C-terminal domain-like	12794	856	12405	69	14	45	45	31	23	5821	5819	0	23	168	5465	47	55	241	2338	923	1584	3	6
48724	50493	50494	Trypsin-like serine proteases	71358	779	69184	779	54	2842	2842	970	587	10364	9320	1017	44	265	8347	102	72	658	3722	1353	1568	25	111
48724	50609	50610	mu transposase, C-terminal domain	1767	821	250	0	5	5	5	5	11	132	130	2	0	0	130	0	0	0	130	0	0	0	0
48724	50614	50615	N-terminal domain of alpha and beta subunits of F1 ATP synthase	9999	2112	9999	2111	220	379	379	39	29	6316	6315	0	6	34	2262	2	3288	313	954	2	874	62	357
48724	50614	50621	Alanine racemase C-terminal domain-like	20303	2248	20146	2232	13	151	152	31	37	7813	7810	1	26	219	7073	109	41	267	3108	1376	1823	11	291
48724	50629	50630	Acid proteases	32402	2754	31096	2741	184	919	1103	163	126	3006	2649	352	4	12	1452	8	161	384	1096	72	1	83	545
48724	50676	50677	ValRS/IleRS/LeuRS editing domain	17088	1229	13046	292	8	27	35	26	50	5670	5670	0	14	300	5502	70	59	32	1586	843	2020	5	1
48724	50684	50685	Barwin-like endoglucanases	11631	1462	7824	689	7	45	45	44	27	2793	2765	26	11	21	2344	0	204	24	2167	1	2	8	170
48724	50684	50692	ADC-like	32672	676	31279	676	4	240	240	151	58	8522	8516	2	68	198	7225	394	77	277	3830	1268	1089	82	409
48724	50714	50715	Ribosomal protein L25-like	11522	1232	9484	1229	194	334	334	11	39	5895	5893	0	16	195	5887	0	1	4	2696	972	967	1	0
48724	50722	50723	Core binding factor beta, CBF	360	405	237	233	36	36	36	4	5	143	142	0	0	0	0	0	0	142	0	0	0	0	0
48724	50728	50729	PH domain-like	123065	592	94233	592	7	609	609	2308	1175	2313	2309	3	0	15	1191	1	81	396	276	239	509	78	509
48724	50783	50784	Transcription factor IIA (TFIIA), beta-barrel domain	1929	817	1871	31	3	8	8	25	15	773	773	0	0	0	1	0	89	280	1	0	0	2	388
48724	50788	50789	Herpes virus serine proteinase, assemblin	266	266	266	0	53	53	53	2	5	96	0	95	0	0	0	0	0	0	0	0	0	0	0
48724	50799	50800	PK beta-barrel domain-like	12249	756	8378	637	2	331	331	27	27	4145	4144	0	4	111	3431	4	80	283	1406	837	892	53	246
48724	50808	50809	XRCC4, N-terminal domain	324	328	277	164	32	32	32	3	6	166	165	0	0	0	0	0	0	165	0	0	0	0	0
48724	50813	50814	Lipocalins	21857	922	18069	888	147	888	888	97	56	4971	4964	6	4	124	4322	0	77	489	1749	842	1276	28	38
48724	50875	50876	Avidin/streptavidin	772	667	691	0	485	535	535	33	31	183	180	0	0	0	93	0	0	83	71	20	0	0	4
48724	50875	50882	beta-Barrel protease inhibitors	1059	634	501	18	3	12	12	5	4	212	211	0	1	1	211	0	0	0	192	0	17	0	0
48724	50875	50886	D-aminopeptidase, middle and C-terminal domains	157	157	157	0	1	1	1	4	7	127	127	0	0	0	63	0	0	0	63	0	0	0	64
48724	50890	50891	Cyclophilin-like	24437	941	22143	939	8	279	279	168	120	6169	6166	0	27	132	4924	118	159	364	2434	635	1386	91	455
48724	50903	50904	Oncogene products	349	353	327	0	6	6	6	3	6	110	110	0	0	0	0	0	0	110	0	0	0	0	0
48724	50910	50911	Mannose 6-phosphate receptor domain	4045	854	955	670	49	52	52	53	38	462	462	0	0	0	0	0	1	253	0	0	0	5	187
48724	50915	50916	Rap30/74 interaction domains	1720	1415	623	0	12	12	12	9	10	258	257	0	0	0	0	0	0	252	0	0	0	0	4
48724	50922	50923	Hemopexin-like domain	5211	971	4474	881	7	31	31	100	55	345	342	2	0	0	19	0	0	322	7	9	0	0	0
48724	50933	50934	Tachylectin-2	4157	1255	21	22	20	1	20	3	6	16	15	0	0	0	10	0	0	5	0	7	0	0	0
48724	50938	50939	Sialidases	21328	1590	16625	1514	70	388	388	126	39	11204	1336	9867	2	58	1087	1	0	182	63	404	228	1	44
48724	50938	50952	Soluble quinoprotein glucose dehydrogenase	5000	789	364	363	9	13	13	5	6	94	94	0	0	1	93	1	0	0	62	12	2	0	0
48724	50938	50956	Thermostable phytase (3-phytase)	5000	558	1117	538	7	11	11	29	13	771	769	0	1	1	692	0	0	0	379	52	61	0	78
48724	50938	50960	TolB, C-terminal domain	5000	794	4041	768	20	20	20	16	13	2754	2752	0	11	23	2745	3	0	3	2678	5	4	0	1
48724	50964	50965	Galactose oxidase, central domain	5000	1182	618	615	13	54	54	67	21	399	399	0	0	0	276	0	2	0	127	130	0	1	120
48724	50964	50969	YVTN repeat-like/Quinoprotein amine dehydrogenase	6253	1210	383	613	144	2	146	116	57	564	564	0	1	1	472	27	0	0	356	40	4	3	60
48724	50964	50974	Nitrous oxide reductase, N-terminal domain	5000	693	1927	606	32	32	32	6	5	801	800	0	46	47	768	32	0	0	518	0	31	0	0
48724	50964	50978	WD40 repeat-like	20795	1373	16934	1317	17	201	218	910	300	1924	1923	0	5	6	899	10	77	326	163	443	4	53	510
48724	50964	50985	RCC1/BLIP-II	6141	1069	2400	754	19	35	35	586	80	724	724	0	2	4	150	2	66	252	30	33	48	27	219
48724	50964	50989	Clathrin heavy-chain terminal domain	1648	599	1492	572	40	40	40	80	12	824	824	0	0	0	0	0	69	252	0	0	0	73	380
48724	50964	50993	Peptidase/esterase 'gauge' domain	10000	1038	3053	850	29	43	43	7	11	1696	1695	0	4	23	1317	0	66	234	529	126	11	29	41
48724	50997	50998	Quinoprotein alcohol dehydrogenase-like	5185	1078	2888	672	31	38	38	107	7	1104	1102	0	15	15	1101	0	0	1	1018	31	13	0	0
48724	50997	51004	C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase	5000	877	425	0	42	42	42	4	7	259	259	0	5	5	259	0	0	0	228	0	0	0	0
48724	51010	51011	Glycosyl hydrolase domain	58060	1021	28771	125	66	867	867	347	142	7217	7208	0	36	234	6102	87	111	540	2241	1123	1768	6	347
48724	51044	51045	WW domain	11250	904	11246	877	56	70	74	277	222	865	864	0	0	0	0	0	73	293	0	0	0	55	434
48724	51044	51055	Carbohydrate binding domain	2782	890	2607	394	48	64	71	149	114	942	936	1	1	5	859	6	0	1	332	356	160	0	70
48724	51063	51064	Head domain of nucleotide exchange factor GrpE	5000	996	4882	27	2	6	6	2	7	3271	3270	0	8	99	3159	10	57	7	1892	8	1052	7	28
48724	51068	51069	Carbonic anhydrase	7562	778	7464	776	14	599	599	26	26	1370	1367	2	2	3	961	0	73	320	712	21	138	3	5
48724	51080	51081	Bacteriochlorophyll A protein	83	83	69	0	7	7	7	1	4	28	28	0	1	6	28	0	0	0	0	0	0	0	0
48724	51086	51087	Outer surface protein	426	441	347	0	32	32	32	1	4	26	25	0	1	1	25	0	0	0	0	0	0	0	0
48724	51091	51092	Vitelline membrane outer protein-I (VMO-I)	457	816	344	10	2	2	2	7	9	188	188	0	0	0	10	0	1	175	8	0	0	1	0
48724	51091	51096	delta-Endotoxin (insectocide), middle domain	814	542	620	441	19	23	23	13	10	48	46	0	1	3	45	0	1	0	1	0	44	0	0

48724	51091	51101	Mannose-binding lectins	3121	674	1790	648	172	215	215	89	28	362	361	0	0	0	110	0	97	89	43	41	6	10	51
48724	51109	51110	alpha-D-mannose-specific plant lectins	5654	972	709	177	71	72	77	64	30	471	463	6	0	0	336	1	83	10	61	230	9	3	24
48724	51125	51120	beta-Roll	5000	594	750	554	28	28	28	24	8	210	210	0	1	1	210	0	0	0	208	0	0	0	0
48724	51125	51126	Pectin lyase-like	50473	737	20582	701	13	175	175	642	79	3139	3097	39	3	64	2485	22	185	20	1366	357	375	18	364
48724	51125	51156	Insect cysteine-rich antifreeze protein	165	1919	63	59	3	3	3	5	6	9	9	0	0	0	1	0	0	8	0	0	0	0	0
48724	51160	51161	Trimeric LpxA-like enzymes	53278	1137	40342	1118	22	420	420	319	52	9363	9355	5	44	288	8352	195	149	243	4120	789	1845	20	370
48724	51160	51177	An insect antifreeze protein	24	34	7	0	11	11	11	1	4	1	1	0	0	0	0	0	0	1	0	0	0	0	0
48724	51181	51182	RmlC-like cupins	126795	809	73057	651	12	661	666	235	73	10991	10974	11	70	389	9504	352	264	298	3974	1391	2200	38	461
48724	51181	51197	Clavaminate synthase-like	60413	1259	32689	831	11	385	394	140	92	6723	6717	4	29	124	5505	10	538	247	3002	1054	543	27	358
48724	51181	51206	cAMP-binding domain-like	31258	1461	31055	1459	98	346	346	363	202	6617	6610	0	25	98	5611	1	115	340	2449	952	1042	87	416
48724	51181	51215	Regulatory protein AraC	5000	536	696	4	10	10	10	5	5	373	371	0	0	7	371	0	0	0	314	9	39	0	0
48724	51181	51219	TRAP-like	6368	1912	5363	6	1	265	265	13	6	2947	2944	0	19	113	2482	186	62	0	478	599	964	15	191
48724	51224	51225	Fibre shaft of virus attachment proteins	270	135	122	82	30	30	30	18	7	40	1	37	0	0	1	0	0	0	1	0	0	0	0
48724	51229	51230	Single hybrid motif	35711	1069	35692	1069	10	123	133	89	120	8560	8551	0	61	247	7453	191	103	284	3616	1143	1458	49	433
48724	51229	51246	Rudiment single hybrid motif	28696	763	21466	763	13	208	208	73	134	8037	8034	0	34	241	6375	140	795	261	3306	779	1134	10	443
48724	51229	51261	Duplicated hybrid motif	25000	2253	5264	129	17	25	25	22	14	1690	1689	0	2	45	1688	0	0	0	534	59	1061	0	1
48724	51268	51269	AFP III-like domain	4486	893	3420	809	43	20	51	21	15	1819	1818	0	7	38	1571	49	2	195	740	45	403	0	1
48724	51268	51274	Head decoration protein D (gpD, major capsid protein D)	784	734	663	0	18	18	18	2	4	136	129	4	0	0	129	0	0	0	128	0	0	0	0
48724	51268	51278	Urease, beta-subunit	4759	1233	4575	1223	11	60	60	18	17	2948	2948	0	18	32	2486	63	63	11	1282	660	274	15	307
48724	51268	51283	dUTPase-like	16857	1360	15902	1354	26	374	374	91	62	8392	7944	445	44	339	6917	267	70	262	2826	1285	1435	59	345
48724	51268	51289	Tlp20, baculovirus telokin-like protein	77	88	73	0	1	1	1	1	4	57	0	57	0	0	0	0	0	0	0	0	0	0	0
48724	51293	51294	Hedgehog/intein (Hint) domain	10750	841	2845	589	6	52	52	307	98	1459	1425	29	5	18	894	125	3	290	118	330	120	9	91
48724	51305	51306	LexA/Signal peptidase	16137	919	16004	884	14	47	47	31	21	6651	6607	25	19	225	6601	1	1	2	3562	1137	1214	0	1
48724	51315	51316	Mss4-like	11707	1338	7014	1337	8	51	51	33	24	3690	3689	0	5	40	2844	18	86	317	1101	186	1115	56	328
48724	51321	51322	Cyanovirin-N	735	550	304	1	59	59	59	8	8	164	163	0	0	0	18	0	2	0	4	0	0	0	142
48724	51326	51327	Head-binding domain of phage P22 tailspike protein	724	599	706	0	11	11	11	12	8	257	241	16	0	0	241	0	0	0	241	0	0	0	0
48724	51331	51332	E2 regulatory, transactivation domain	737	636	723	479	11	13	13	3	5	337	1	335	0	0	1	0	0	0	0	0	0	0	0
48724	51337	51338	Composite domain of metallo-dependent hydrolases	72186	1691	10734	15	2	435	437	41	34	4531	4530	0	16	79	4048	46	28	174	1965	819	808	14	208
48724	51343	51344	Epsilon subunit of F1F0-ATP synthase N-terminal domain	5002	1006	4995	1001	22	14	27	6	11	4090	4088	0	10	43	3084	1	800	171	1923	270	606	2	1
51349	51350	51351	Triosephosphate isomerase (TIM)	7053	563	7032	552	24	219	243	21	19	5507	5504	0	41	293	4395	330	91	274	1068	876	1382	51	316
51349	51350	51366	Ribulose-phoshate binding barrel	61890	777	55480	756	37	878	878	106	72	10700	10690	0	95	380	9279	398	98	267	3983	1463	2156	65	515
51349	51350	51391	Thiamin phosphate synthase	5466	1704	5460	1694	20	52	52	23	34	3390	3388	0	14	189	2843	148	67	4	625	197	1298	4	317
51349	51350	51395	FMN-linked oxidoreductases	54779	2074	49832	2055	16	555	557	137	121	10331	10327	0	81	358	8985	371	103	273	3935	1442	2117	60	469
51349	51350	51412	Inosine monophosphate dehydrogenase (IMPDH)	7143	630	7136	22	10	125	125	14	11	4838	4835	0	10	167	4328	1	11	240	1509	775	1264	21	221
51349	51350	51419	PLP-binding barrel	27076	598	26975	598	2	185	185	49	53	8595	8561	31	18	267	7569	67	94	288	3163	1360	1819	49	443
51349	51350	51430	NAD(P)-linked oxidoreductase	32083	1035	32037	974	27	457	457	55	58	7026	7022	0	23	98	6056	81	92	300	2846	1188	1188	30	418
51349	51350	51445	(Trans)glycosidases	252735	3297	177656	3272	8	3074	3074	2113	783	14177	13939	128	148	509	11735	203	361	813	4575	1847	3108	60	715
51349	51350	51556	Metallo-dependent hydrolases	116595	579	107766	578	1	982	982	223	120	12758	12746	0	85	451	11360	356	81	290	4805	1655	2704	79	532
51349	51350	51569	Aldolase	109203	998	97989	963	22	1671	1671	202	145	12841	12776	53	143	485	11199	432	129	341	4808	1651	2520	99	510
51349	51350	51604	Enolase C-terminal domain-like	32042	3136	31694	3130	30	787	791	74	42	8619	8611	1	32	155	6560	213	96	1081	3052	1295	1123	161	451
51349	51350	51621	Phosphoenolpyruvate/pyruvate domain	43532	2491	39731	2491	3	560	560	95	63	9700	9690	0	115	422	8379	317	165	244	3802	1409	1758	51	462
51349	51350	51645	Malate synthase G	5000	804	3319	803	12	21	21	2	5	1886	1885	0	12	12	1880	0	0	2	1473	268	129	1	1
51349	51350	51649	RuBisCo, C-terminal domain	7827	2021	7827	2005	113	46	159	6	10	7927	7924	0	8	10	776	116	7029	0	423	32	107	2	0
51349	51350	51658	Xylose isomerase-like	34183	733	23957	720	3	362	362	26	19	7142	7137	0	48	312	6268	184	64	208	2542	1019	1631	64	341
51349	51350	51679	Bacterial luciferase-like	24392	1881	21794	1712	18	41	43	54	108	4336	4330	0	35	36	4029	253	0	3	1724	1312	649	0	45
51349	51350	51690	Nicotinate/Quinolinate PRTase C-terminal domain-like	15826	1177	15662	1177	2	133	133	21	29	7509	7506	1	20	298	6481	276	65	217	2688	936	1805	49	373
51349	51350	51695	PLC-like phosphodiesterases	20921	1278	15504	1270	9	114	114	171	74	5050	5040	9	6	77	4264	72	70	291	1821	733	1128	17	304
51349	51350	51703	Cobalamin (vitamin B12)-dependent enzymes	7736	580	7320	573	15	110	110	14	16	3715	3712	0	51	128	3276	202	3	192	1141	833	517	17	4
51349	51350	51713	tRNA-guanine transglycosylase	5315	2629	5315	2599	120	112	120	7	9	3978	3977	0	38	120	3638	333	0	4	2441	4	1001	0	1
51349	51350	51717	Dihydropteroate synthetase-like	11287	1187	11287	1182	16	111	115	28	40	5318	5317	0	8	141	5224	8	37	25	2828	477	1358	6	16
51349	51350	51726	UROD/MetE-like	11375	2058	11365	2008	2	45	45	17	14	4892	4888	0	9	42	4119	21	91	229	2402	587	400	20	376
51349	51350	51730	FAD-linked oxidoreductase	10550	1014	10548	1014	11	60	60	12	18	4609	4608	0	3	63	4034	0	66	152	2993	604	252	18	325
51349	51734	51735	NAD(P)-binding Rossmann-fold domains	610245	2584	516238	2568	12	5242	5246	2687	2719	19364	19261	48	539	916	16138	686	611	885	6920	2590	3510	141	672
51349	51904	51905	FAD/NAD(P)-binding domain	219788	667	138831	643	2	1489	1489	508	395	13486	13472	1	143	467	11780	403	168	378	5321	1918	2514	90	582
51349	51970	51971	Nucleotide-binding domain	27609	2394	11616	1448	12	202	204	93	121	5517	5507	8	24	214	4772	42	18	232	2038	1132	932	18	404
51349	51983	51984	MurCD N-terminal domain	10244	575	9799	572	20	28	28	27	50	4981	4980	0	7	206	4971	1	5	3	2276	906	1510	0	0
51349	51988	51989	Glycosyl hydrolases family 6, cellulases	2850	1345	2620	0	50	63	63	45	38	1067	1065	0	4	4	844	0	0	0	96	689	27	17	203
51349	51997	51998	PFL-like glycyl radical enzymes	31099	1627	26408	248	4	160	160	44	20	8495	8171	320	18	328	7259	116	72	245	2695	1336	2182	56	385
51349	52008	52009	Phosphohistidine domain	10000	1446	9235	1439	29	34	34	15	32	5208	5203	0	45	320	4887	147	89	2	1878	637	1626	23	2
51349	52008	52016	LeuD/IlvD-like	23209	796	20208	770	6	35	35	39	32	7820	7817	0	93	296	6647	301	84	295	3441	993	1130	47	409
51349	52008	52021	Carbamoyl phosphate synthetase, small subunit N-terminal domain	5000	592	5000	589	40	40	40	6	55	3359	3358	0	8	72	3327	1	22	6	2066	438	515	2	0
51349	52008	52025	PA domain	5175	1235	2474	1155	87	92	92	25	19	839	838	0	2	2	141	0	54	242	33	10	8	11	384
51349	52008	52029	GroEL apical domain-like	11268	786	10987	646	335	970	970	44	54	4322	4320	0	76	96	2961	404	76	294	2513	1	3	77	447
51349	52037	52038	Barstar-related	2900	1106	1254	799	46	46	46	6	6	818	818	0	0	12	814	3	0	0	492	73	169	0	0
51349	52037	52042	Ribosomal protein L32e	1765	1091	1406	1058	81	138	138	25	15	1097	1095	0	36	42	0	351	75	255	0	0	0	52	316
51349	52046	52047	RNI-like	29915	2961	4804	1292	18	50	51	151	53	768	767	0	1	1	12	0	82	287	7	0	0	21	335
51349	52046	52058	L domain-like	47004	1205	33799	990	13	312	312	2740	490	1935	1931	2	2	16	706	5	158	479	102	26	343	69	466
51349	52046	52075	Outer arm dynein light chain 1	5000	844	10	550	2	0	2	23	40	314	314	0	0	0	2	0	9	228	1	0	0	36	13
51349	52079	52080	Ribosomal proteins L15p and L18e	8996	1583	7903	1574	78	557	559	13	10	6140	6136	0	50	296	5046	361	76	263	1856	864	1257	60	297
51349	52086	52087	CRAL/TRIO domain	7310	575	6415	574	13	36	36	48	41	820	819	0	0	0	0	0	79	283	0	0	0	54	376
51349	52086	52091	SpoIIaa-like	7238	1798	6469	131	16	27	29	21	19	2964	2964	0	5	170	2933	31	0	0	612	744	1021	0	0
51349	52095	52096	ClpP/crotonase	71688	1261	53327	1242	20	851	859	174	140	12024	12018	0	141	413	8583	300	150	2379	3955	1333	1658	79	473
51349	52112	52113	BRCT domain	16000	2548	14017	2544	3	136	136	404	135	4250	4249	0	6	84	3341	2	76	293	1672	595	679	41	460
51349	52120	52121	Lumazine synthase	5676	2158	5673	2150	295	375	375	11	16	4263	4262	0	9	133	3811	18	70	3	1459	370	942	17	337
51349	52128	52129	Caspase-like	14018	1352	5523	1231	252	561	561	141	47	775	774	0	3	7	415	1	0	356	315	0	11	1	0
51349	52140	52141	Uracil-DNA glycosylase-like	19097	990	13826	978	52	92	92	28	20	7137	7129	5	55	316	6316	348	54	253	2882	821	1320	8	141
51349	52150	52151	FabD/lysophospholipase-like	16488	986	7647	862	18	35	38	143	1566	4557	4554	0	9	113	4266	0	71	24	1888	772	896	4	189
51349	52155	52156	Initiation factor IF2/eIF5b, domain 3	5000	950	2855	925	20	19	20	33	19	1774	1772	0	29	55	639	315	72	258	71	5	548	65	390
51349	52160	52161	Ribosomal protein L13	6414	1968	6410	76	248	420	420	19	17	5280	5276	0	43	189	4220	333	79	257	1719	747	1089	54	306
51349	52165	52166	Ribosomal protein L4	7960	2148	7882	2148	193	455	455	12	12	6161	6158	0	44	279	4983	343	77	285	1725	924	1277	53	359
51349	52171	52172	CheY-like	81084	606	79431	606	8	248	248	1299	578	10311	10303	0	47	331	9691	205	22	10	4383	1669	2228	1	339
51349	52171	52200	Toll/Interleukin receptor TIR domain	5000	1075	4861	80	12	14	14	222	29	441	441	0	0	0	0	0	0	441	0	0	0	0	0
51349	52171	52206	Hypothetical protein MTH538	12157	0	7	0	0	14	14	1	4	6	6	0	0	0	0	6	0	0	0	0	0	0	0
51349	52171	52210	Succinyl-CoA synthetase domains	16052	941	15995	941	5	63	68	73	52	6346	6341	0	64	103	5157	363	76	280	2975	748	547	60	354
51349	52171	52218	Flavoproteins	53548	1811	48657	1803	28	560	560	163	143	9937	9898	33	45	321	8605	279	120	315	3759	1325	2166	38	489
51349	52171	52242	Cobalamin (vitamin B12)-binding domain	16460	1074	15625	1069	10	79	79	35	37	6218	6216	0	28	191	5749	208	5	204	2693	1028	1035	16	11
51349	52171	52255	N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)	5000	909	5000	902	17	66	78	8	15	3724	3722	0	7	64	3472	34	53	3	1322	655	840	18	137
51349	52171	52266	SGNH hydrolase	38312	2051	30724	2008	27	130	130	400	141	8651	8528	117	34	269	7740	41	79	243	3203	1355	1849	23	381
51349	52171	52279	Beta-D-glucan exohydrolase, C-terminal domain	5000	636	2348	594	22	28	28	31	24	1107	1105	0	5	37	1011	7	81	1	388	242	72	0	4
51349	52171	52283	Formate/glycerate dehydrogenase catalytic domain-like	37385	0	28310	0	0	343	343	60	63	8554	8548	1	71	219	7396	309	91	291	3243	1300	1452	37	376
51349	52171	52304	Type II 3-dehydroquinate dehydratase	5761	3299	5761	331	411	469	471	10	10	4236	4235	0	11	110	4098	0	0	2	2139	808	484	0	135
51349	52171	52309	N-(deoxy)ribosyltransferase-like	5586	590	1674	460	32	268	268	8	5	796	792	3	1	5	575	9	0	189	341	7	215	0	2
51349	52171	52313	Ribosomal protein S2	6761	1840	6754	621	134	193	193	15	13	5173	5170	0	33	195	4108	334	75	249	1723	866	1353	48	318
51349	52171	52317	Class I glutamine amidotransferase-like	114163	1105	84118	1105	13	607	607	144	201	12042	12032	1	95	432	10665	386	83	288	4840	1612	2394	73	481
51349	52334	52335	Methylglyoxal synthase-like	15916	2225	15886	2224	2	107	109	26	93	6413	6411	0	20	252	5865	155	47	213	2808	269	1658	4	124
51349	52342	52343	Ferredoxin reductase-like, C-terminal NADP-linked domain	38357	1012	38252	951	3	189	189	205	193	8949	8942	0	33	309	7728	165	154	328	3703	1166	1678	44	473
51349	52373	52374	Nucleotidylyl transferase	110628	2652	98964	2627	3	710	710	203	255	12798	12780	12	216	588	11276	480	91	285	4620	1702	2623	86	511
51349	52373	52402	Adenine nucleotide alpha hydrolases-like	109795	0	86310	0	0	279	279	201	113	11908	11874	29	138	503	10452	477	106	293	4564	1496	2530	61	437
51349	52373	52413	UDP-glucose/GDP-mannose dehydrogenase C-terminal domain	10000	1519	4262	1319	14	33	33	10	12	2185	2167	18	4	118	2156	7	1	3	1155	256	510	0	0
51349	52417	52418	Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain	10466	1189	10460	1189	22	52	52	15	25	5547	5545	0	13	189	5285	183	42	10	2357	742	1698	15	5
51349	52424	52425	Cryptochrome/photolyase, N-terminal domain	7696	619	7662	48	11	52	52	22	20	4014	4012	0	10	11	3321	102	110	243	2223	428	53	6	223
51349	52439	52440	PreATP-grasp domain	55462	690	44211	689	13	324	324	141	265	9751	9742	0	106	376	8429	344	94	298	3898	1334	1713	63	468
51349	52466	52467	DHS-like NAD/FAD-binding domain	44877	993	43885	966	62	366	366	147	92	10590	10581	0	140	440	8962	453	188	291	4065	1496	1867	85	524
51349	52489	52490	Tubulin nucleotide-binding domain-like	13023	1622	12998	1612	24	386	388	53	43	5811	5809	0	18	185	3427	248	183	455	358	1044	1281	289	1044
51349	52498	52499	Isochorismatase-like hydrolases	30799	957	30083	870	4	116	116	105	54	7507	7504	0	23	100	6470	251	81	257	3193	1314	1146	24	375
51349	52506	52507	Homo-oligomeric flavin-containing Cys decarboxylases, HFCD	11384	1081	11258	1016	7	20	20	23	26	5832	5825	4	27	193	5022	174	66	257	2809	246	1193	31	260
51349	52517	52518	Thiamin diphosphate-binding fold (THDP-binding)	65442	1474	65144	1454	80	494	496	276	123	11704	11691	3	81	409	10218	336	167	292	4518	1625	2379	98	494
51349	52539	52540	P-loop containing nucleoside triphosphate hydrolases	858969	2091	735348	1949	44	5428	5428	30	1884	28024	26533	1226	512	908	18267	732	2312	3337	8671	2349	3864	273	1222
51349	52727	52728	PTS IIb component	5000	1387	4980	1348	9	12	12	6	7	1420	1420	0	2	33	1419	0	0	0	490	67	826	0	1
51349	52732	52733	Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)	5109	2095	5109	2081	38	44	44	12	13	3038	3037	0	4	94	3032	4	1	0	1319	616	645	0	0
51349	52737	52738	Methylesterase CheB, C-terminal domain	5000	614	5000	613	3	4	4	6	33	2547	2544	0	5	15	2511	32	0	0	1782	22	524	0	1
51349	52742	52743	Subtilisin-like	23397	1491	19774	1430	5	308	308	445	157	4669	4664	1	51	119	3382	229	67	308	978	802	1000	40	608
51349	52767	52768	Arginase/deacetylase	21300	1158	20426	1158	8	496	496	70	40	5706	5700	0	23	47	4508	149	81	362	2191	959	878	64	479
51349	52776	52777	CoA-dependent acyltransferases	40318	587	29843	566	58	133	133	1456	1111	6981	6962	0	58	102	6015	30	72	301	3597	853	686	27	479
51349	52787	52788	Phosphotyrosine protein phosphatases I	11156	2234	11139	2198	4	64	64	30	29	6005	6001	0	23	128	5349	74	54	228	2224	966	1094	4	277
51349	52787	52794	PTS system IIB component-like	15000	1252	13328	1240	8	15	15	23	15	2999	2999	0	1	97	2995	0	1	2	885	310	1600	0	1
51349	52798	52799	(Phosphotyrosine protein) phosphatases II	48571	821	37819	592	11	493	493	443	336	3562	3492	68	26	62	2449	49	83	313	1002	703	488	74	468
51349	52820	52821	Rhodanese/Cell cycle control phosphatase	39467	1959	38327	1897	2	89	89	200	129	8977	8966	8	54	204	7759	263	89	295	3493	1369	1565	38	475
51349	52832	52833	Thioredoxin-like	224108	1126	198235	894	1	2764	2764	6	318	14692	14524	97	200	565	12134	467	316	828	5449	1682	2505	113	574
51349	52832	52913	RNA 3'-terminal phosphate cyclase, RPTC, insert domain	2513	671	899	231	15	24	24	3	5	384	383	0	1	1	381	0	0	2	367	0	0	0	0
51349	52921	52922	TK C-terminal domain-like	24901	846	24899	843	20	172	176	164	68	8483	8479	0	40	280	7442	152	79	273	3471	1142	1594	61	409
51349	52934	52935	PK C-terminal domain-like	24745	895	7672	893	212	356	356	19	23	3898	3897	0	2	96	2957	115	82	272	930	372	1322	57	355
51349	52934	52943	ATP synthase (F1-ATPase), gamma subunit	6705	653	6655	652	5	43	43	7	10	4805	4803	0	10	61	4147	1	75	258	1920	781	881	27	277
51349	52948	52949	Macro domain-like	14524	1613	11304	10	8	95	95	99	71	5096	4946	149	12	114	4103	97	73	285	1888	704	963	25	334

51349	52953	52954	Class II aaRS ABD-related	30993	2057	12354	642	5	132	136	84	58	6233	6228	0	71	322	4924	384	75	277	1675	698	1404	74	439
51349	52953	52964	TolB, N-terminal domain	4160	616	3644	616	20	20	20	13	7	2447	2445	0	3	12	2442	0	0	2	2422	1	4	0	1
51349	52953	52968	B12-dependent dehydatase associated subunit	1099	728	1057	716	10	26	26	3	6	370	370	0	1	7	367	3	0	0	126	61	152	0	0
51349	52953	52972	ITPase-like	15651	932	15471	932	11	70	70	36	30	6946	6944	2	37	312	5971	326	65	236	2797	376	1625	30	281
51349	52979	52980	Restriction endonuclease-like	58876	1080	23809	461	10	385	385	117	44	7268	7098	158	53	236	5947	371	69	256	3036	597	1291	56	366
51349	52979	53032	tRNA-intron endonuclease catalytic domain-like	2780	776	1646	642	38	40	40	19	15	916	915	0	39	44	2	361	56	256	0	1	0	39	177
51349	52979	53036	Eukaryotic RPB5 N-terminal domain	1074	636	892	28	113	113	113	15	11	632	632	0	0	0	0	0	79	173	0	0	0	44	309
51349	53040	53041	Resolvase-like	5000	1531	4990	1412	20	20	22	12	6	2009	1995	8	5	8	1989	2	1	0	1250	302	309	0	2
51349	53040	53056	beta-carbonic anhydrase, cab	10020	792	9950	792	6	161	161	24	15	4875	4873	0	7	56	4381	38	108	4	2443	662	667	19	300
51349	53061	53062	PTS system fructose IIA component-like	8481	1209	8339	49	8	41	41	14	17	3333	3333	0	5	42	3303	28	0	1	1486	637	1015	0	1
51349	53066	53067	Actin-like ATPase domain	124837	818	113125	814	2	1140	1140	275	200	15843	15798	29	100	475	11896	278	360	1601	4992	1671	2801	419	961
51349	53066	53092	Creatinase/prolidase N-terminal domain	12424	1957	8570	1691	12	84	84	12	10	4341	4339	0	24	54	3903	78	54	24	2035	189	1044	8	270
51349	53066	53098	Ribonuclease H-like	131411	752	87172	389	30	1064	1064	521	239	12665	12362	287	72	425	10937	378	81	295	5025	1584	2509	87	526
51349	53066	53137	Translational machinery components	15071	906	13342	906	115	817	817	31	29	7144	7131	12	87	350	5223	433	603	275	2007	644	1377	118	393
51349	53066	53146	Nitrogenase accessory factor-like	5212	971	4277	971	5	14	14	24	19	1851	1848	0	12	103	1686	162	0	0	682	41	623	0	0
51349	53066	53150	DNA repair protein MutS, domain II	5653	2275	5610	2248	34	34	34	15	18	3540	3539	0	17	195	3399	133	2	5	1915	2	497	0	0
51349	53066	53155	Methylated DNA-protein cysteine methyltransferase domain	5282	1167	2876	1163	1	16	16	26	18	1501	1497	0	4	4	1347	24	0	125	1254	5	5	0	1
51349	53162	53163	HybD-like	5894	1905	4095	761	9	13	13	9	10	2412	2412	0	9	173	2298	113	1	0	826	352	904	0	0
51349	53162	53167	Purine and uridine phosphorylases	28647	941	27446	940	50	1082	1082	40	27	9226	9221	2	48	394	8097	323	39	297	3111	1265	2077	64	356
51349	53162	53178	Peptidyl-tRNA hydrolase-like	6677	2101	6677	2037	12	53	53	8	10	4628	4626	0	8	242	4548	1	70	6	1635	750	1479	0	1
51349	53162	53182	Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)	5000	1004	3547	1004	54	68	68	10	10	1985	1984	0	12	50	1639	64	46	203	533	331	635	12	11
51349	53162	53187	Zn-dependent exopeptidases	116214	848	65454	372	2	677	677	404	186	10401	10387	10	58	369	9079	314	82	374	3865	1042	2399	25	493
51349	53162	53213	LigB-like	7950	1383	6021	1318	23	23	23	12	16	3330	3328	0	2	11	3107	19	75	5	1870	645	308	2	111
51349	53217	53218	Molybdenum cofactor biosynthesis proteins	16553	1925	15771	1924	35	147	147	53	53	6700	6699	0	43	117	5751	313	71	245	3007	1157	956	20	284
51349	53222	53223	Aminoacid dehydrogenase-like, N-terminal domain	40008	576	39614	575	4	407	407	92	88	9751	9745	0	78	358	8498	379	126	297	3718	1221	2001	48	346
51349	53243	53244	MurD-like peptide ligases, peptide-binding domain	37286	1442	36068	1433	1	62	62	67	75	9355	9352	0	24	364	9226	98	11	8	3837	1339	2178	1	8
51349	53253	53254	Phosphoglycerate mutase-like	23227	1755	21650	1728	41	250	250	84	64	6458	6456	0	8	184	5421	26	77	309	1978	1243	1332	70	509
51349	53270	53271	PRTase-like	60298	910	58719	888	13	482	482	107	73	11135	11123	5	90	409	9785	353	83	316	3878	1610	2405	74	454
51349	53299	53300	vWA-like	29524	949	23882	743	4	317	317	1310	619	4070	4054	14	14	92	2310	44	78	994	1188	88	76	65	510
51349	53322	53323	Pyruvate-ferredoxin oxidoreductase, PFOR, domain III	5000	939	4957	932	20	20	20	130	29	2292	2291	0	7	230	2249	1	3	6	617	113	919	8	1
51349	53327	53328	Formyltransferase	12959	798	12959	796	15	98	98	40	71	5134	5132	0	25	239	4799	71	0	260	2889	30	1419	0	1
51349	53334	53335	S-adenosyl-L-methionine-dependent methyltransferases	311483	0	191416	0	0	1364	1364	811	271	15987	15425	532	228	603	13337	525	390	451	5891	1893	3126	96	549
51349	53382	53383	PLP-dependent transferases	156687	821	155591	821	6	1205	1205	234	297	14240	14221	0	166	512	11746	452	197	1094	5138	1736	2745	106	547
51349	53447	53448	Nucleotide-diphospho-sugar transferases	97866	820	66466	534	1	733	733	348	128	10858	10853	2	43	374	9462	276	171	305	4233	1145	2234	54	526
51349	53473	53474	alpha/beta-Hydrolases	162537	1371	130298	1232	2	1918	1920	1055	847	12236	12167	18	101	334	10545	309	110	490	4777	1831	1964	58	605
51349	53589	53590	Nucleoside hydrolase	5980	1445	5976	1420	49	67	67	5	10	2468	2467	0	3	34	2344	5	61	6	1100	386	694	3	10
51349	53596	53597	Dihydrofolate reductase-like	16279	1209	16224	1208	1	627	627	54	41	6982	6912	61	19	181	6019	196	72	256	2799	639	1393	83	274
51349	53612	53613	Ribokinase-like	44260	1370	43019	1354	17	253	255	59	82	9241	9237	0	32	335	8144	279	92	270	3498	1013	2297	26	379
51349	53612	53623	MurD-like peptide ligases, catalytic domain	25750	2167	25504	2165	3	49	50	33	70	7135	7134	0	11	290	7102	14	6	6	3511	322	2031	0	6
51349	53632	53633	Carbamate kinase-like	21861	655	21624	654	18	138	138	41	53	7932	7929	0	59	346	7562	232	76	6	3231	1213	1683	24	1
51349	53638	53639	AraD/HMP-PK domain-like	10830	564	10604	564	49	87	87	22	26	4420	4419	0	28	188	4099	317	0	3	1501	823	1173	0	0
51349	53648	53649	Alkaline phosphatase-like	29755	657	22556	649	1	254	255	58	44	6600	6590	0	14	283	6009	52	2	288	2773	726	1449	9	220
51349	53658	53659	Isocitrate/Isopropylmalate dehydrogenase-like	38983	3505	37179	3340	13	263	264	42	42	9584	9578	0	34	310	8440	212	92	321	3943	1385	1833	66	396
51349	53670	53671	Aspartate/ornithine carbamoyltransferase	20048	811	20032	811	15	303	303	61	82	8708	8694	8	78	336	7500	376	75	260	3014	1208	1854	49	395
51349	53670	53681	Aspartate/glutamate racemase	12312	1191	12268	8	21	71	71	7	17	5988	5987	0	16	217	5850	66	25	3	2208	917	1698	0	43
51349	53685	53686	Tryptophan synthase beta subunit-like PLP-dependent enzymes	27146	2136	26930	2136	12	195	207	51	69	8822	8815	0	61	319	7759	351	95	168	3391	1300	1722	20	407
51349	53696	53697	SIS domain	26880	1780	25064	1780	9	115	124	42	52	8596	8589	4	37	341	8029	304	116	11	3284	1188	1878	37	86
51349	53705	53706	Formate dehydrogenase/DMSO reductase, domains 1-3	10000	0	9990	0	0	20	20	97	47	3269	3268	0	9	27	3114	148	2	3	2103	289	605	0	1
51349	53719	53720	ALDH-like	15000	7678	14748	7671	56	345	401	45	91	6285	6279	0	15	177	5154	184	96	310	2307	867	1201	21	495
51349	53731	53732	Aconitase iron-sulfur domain	14106	926	14060	924	6	23	23	29	21	6063	6058	0	50	132	5063	162	77	291	3099	308	738	36	406
51349	53737	53738	Phosphoglucomutase, first 3 domains	14145	1026	11339	1026	15	44	44	35	28	5331	5329	0	12	58	4434	71	88	277	2911	947	161	46	376
51349	53742	53743	FucI/AraA N-terminal and middle domains	6330	1955	4000	1943	30	36	36	12	6	1935	1934	0	2	109	1932	2	0	0	437	460	645	0	0
51349	53747	53748	Phosphoglycerate kinase	13671	3914	12455	3801	42	66	66	29	24	8435	8432	0	37	331	7126	328	161	313	2839	1142	1567	81	362
51349	53755	53756	UDP-Glycosyltransferase/glycogen phosphorylase	40599	5940	32936	4881	20	119	119	89	59	9252	9241	8	33	274	8257	193	343	78	3531	1270	1936	30	326
51349	53773	53774	Glutaminase/Asparaginase	5000	1673	4978	1665	5	109	114	10	11	3249	3247	0	30	126	2728	353	0	8	1208	32	1008	3	147
51349	53783	53784	Phosphofructokinase	14412	1337	10736	579	42	89	89	17	13	5547	5536	9	17	300	4661	19	72	295	924	948	1528	59	402
51349	53789	53790	Tetrapyrrole methylase	6320	801	6313	774	164	172	172	19	43	3250	3249	0	21	52	2277	227	71	246	1449	2	725	57	337
51349	53794	53795	PEP carboxykinase-like	4998	743	3405	743	10	60	70	4	17	2528	2526	0	12	58	2121	61	1	327	808	1050	101	1	2
51349	53799	53800	Chelatase	14644	858	9781	792	54	91	91	22	15	5926	5925	0	13	111	5119	127	74	230	2488	1013	1093	21	345
51349	53799	53807	Helical backbone metal receptor	38148	962	30627	871	57	271	271	33	22	7324	7322	0	19	124	7082	178	55	4	3195	911	1823	0	1
51349	53821	53822	Periplasmic binding protein-like I	57045	777	44094	737	2	330	330	162	79	7444	7417	0	21	130	6980	120	13	300	3695	1012	1675	0	2
51349	53849	53850	Periplasmic binding protein-like II	188008	1447	158727	1403	23	1864	1876	242	177	13215	13176	18	102	399	11964	376	82	420	5795	1716	2699	18	298
51349	53900	53901	Thiolase-like	45278	2990	44788	2989	13	575	582	99	2245	10383	10373	0	90	324	8532	328	743	285	3877	1252	1970	41	416
51349	53919	53920	Fe-only hydrogenase	5000	1132	2887	1011	4	12	12	141	36	1459	1457	0	6	159	1079	3	70	246	116	35	710	17	12
51349	53926	53927	Cytidine deaminase-like	37948	939	30684	924	18	219	219	97	80	9421	9292	111	53	392	8189	254	77	275	3394	1014	2246	41	433
53931	53932	53933	Microbial ribonucleases	3297	668	2761	420	135	353	353	42	14	1704	1698	0	1	15	1440	5	0	0	556	571	199	0	253
53931	53954	53955	Lysozyme-like	48153	596	32808	596	3	1922	1922	184	66	7515	7285	225	33	73	6584	3	192	455	4127	1294	788	18	28
53931	54000	54001	Cysteine proteinases	100563	0	46943	0	0	889	889	520	254	5425	5178	243	17	113	3659	20	218	534	1255	791	861	112	551
53931	54059	54060	His-Me finger endonucleases	15002	713	7479	711	11	116	116	103	27	3452	3125	325	4	91	2598	7	3	258	1424	105	295	12	243
53931	54075	54076	RNase A-like	2358	856	2167	680	416	531	531	3	6	334	333	0	0	0	0	0	0	333	0	0	0	0	0
53931	54097	54098	Prion-like	1088	699	957	625	27	94	94	10	5	328	327	0	0	0	0	0	0	327	0	0	0	0	0
53931	54105	54106	LysM domain	7113	1973	6326	1731	26	13	26	201	91	3216	3207	9	14	93	3203	0	1	1	1748	63	781	0	1
53931	54110	54111	Urease, gamma-subunit	4031	1134	3881	1133	40	69	69	15	16	2654	2653	0	18	31	2223	62	64	10	1066	647	249	14	277
53931	54116	54117	Interleukin 8-like chemokines	6248	1043	6141	1021	36	308	308	24	19	276	256	17	0	0	0	0	0	256	0	0	0	0	0
48724	50036	54160	Chromo domain-like	14975	1321	9029	1309	24	199	200	240	84	985	984	0	0	0	0	11	82	349	0	0	0	62	452
53931	54170	54171	DNA-binding domain	10578	739	7954	736	3	30	30	75	42	884	879	4	0	26	426	0	237	214	183	5	234	1	0
53931	54183	54184	Penicillin-binding protein 2x (pbp-2x), c-terminal domain	5642	901	2227	863	18	18	18	8	9	631	631	0	1	18	631	0	0	0	3	0	548	0	0
53931	54188	54189	Ribosomal proteins S24e, L23 and L15e	9985	2032	9544	2029	191	629	629	48	27	5663	5654	0	47	252	3922	374	417	387	1412	798	1128	96	383
53931	54196	54197	HIT-like	29046	766	25527	73	10	173	173	98	52	9256	9249	2	95	407	7929	387	76	292	2958	1487	1734	68	451
53931	54210	54211	Ribosomal protein S5 domain 2-like	128695	1291	120788	1236	76	1515	1515	353	287	17077	16802	32	248	619	14311	574	174	631	6042	2425	3001	276	680
53931	54235	54236	Ubiquitin-like	57139	1440	42147	1439	168	1309	1309	722	375	1691	1579	101	1	3	76	2	209	537	26	10	13	153	524
53931	54235	54277	CAD & PB1 domains	9931	950	5940	698	14	70	70	190	68	759	758	0	0	0	0	0	69	295	0	0	0	13	370
53931	54235	54285	MoaD/ThiS	17696	1860	15614	1777	11	57	58	33	28	6441	6438	0	51	157	5467	320	68	225	3043	766	845	34	278
53931	54235	54292	2Fe-2S ferredoxin-like	41384	888	39697	886	4	371	375	275	167	7916	7888	20	44	144	6614	163	132	325	3779	1363	556	113	438
53931	54235	54328	Staphylokinase/streptokinase	412	322	393	287	10	22	22	4	7	48	44	3	0	0	44	0	0	0	0	0	43	0	0
53931	54235	54334	Superantigen toxins, C-terminal domain	2786	815	2514	798	22	233	233	5	5	313	309	3	1	1	309	0	0	0	1	0	307	0	0
53931	54235	54358	Immunoglobulin-binding domains	144	148	143	0	164	164	164	22	23	38	30	1	0	0	29	0	0	1	1	0	28	0	0
53931	54235	54364	Translation initiation factor IF3, N-terminal domain	5000	876	4998	873	1	1	1	7	8	4164	4163	0	6	175	4146	0	4	4	1334	890	1259	0	1
53931	54235	54368	Glutamine synthetase, N-terminal domain	5000	680	5000	680	114	187	187	2	5	3628	3626	0	12	20	3618	4	0	3	2261	945	117	1	0
53931	54372	54373	FAD-linked reductases, C-terminal domain	61359	2550	28439	271	6	757	757	175	108	6784	6778	1	29	54	5674	68	105	333	2986	1276	753	63	496
53931	54402	54403	Cystatin/monellin	7856	623	4747	589	36	159	159	37	16	832	829	2	0	1	327	0	126	357	4	0	321	6	0
53931	54402	54416	Amine oxidase N-terminal region	4647	692	3732	679	6	238	238	44	29	1274	1273	0	1	1	679	13	82	145	312	293	22	8	343
53931	54402	54423	DsbC/DsbG N-terminal domain-like	4486	524	2873	514	17	42	42	5	8	1177	1177	0	3	5	1177	0	0	0	1171	1	1	0	0
53931	54402	54427	NTF2-like	81999	1068	42167	910	159	743	743	198	91	7401	7396	0	35	82	6262	139	79	303	3585	1264	598	73	497
53931	54402	54441	Uracil-DNA glycosylase inhibitor protein	3	3	3	0	41	41	41	0	4	2	0	2	0	0	0	0	0	0	0	0	0	0	0
53931	54446	54447	ssDNA-binding transcriptional regulator domain	1642	727	1470	22	21	61	61	25	9	866	865	0	1	8	211	0	78	226	2	0	5	24	287
53931	54451	54452	MHC antigen-recognition domain	18237	1254	17350	1231	34	1084	1118	40	32	392	385	6	0	0	0	0	0	385	0	0	0	0	0
53931	54494	54495	UBC-like	29334	671	24481	662	4	361	361	320	128	1220	1197	22	1	3	7	6	142	339	6	0	1	100	536
53931	54505	54506	Diaminopimelate epimerase-like	26730	1289	25085	836	2	85	85	38	23	7512	7509	0	23	255	6706	168	74	203	3456	890	1360	20	309
53931	54510	54511	GFP-like	2934	769	2308	507	268	1172	1172	428	209	816	361	6	0	0	7	0	0	350	6	1	0	4	8
53931	54517	54518	Tubby C-terminal domain-like	6286	1531	2530	602	5	10	10	20	12	480	480	0	0	0	52	0	76	263	0	44	8	25	60
53931	54522	54523	Pili subunits	30420	1061	12109	773	21	113	113	792	17	3231	3226	4	9	12	3221	0	1	2	3049	3	15	0	1
53931	54528	54529	Mitochondrial glycoprotein MAM33-like	1535	929	552	0	6	14	14	5	7	365	365	0	0	0	0	0	65	207	0	0	0	27	44
53931	54533	54534	FKBP-like	47019	616	46416	609	19	387	387	247	92	10085	10078	0	91	412	8721	361	89	318	4256	953	1825	71	463
53931	54533	54552	Colicin E3 immunity protein	151	153	137	0	7	7	7	1	4	58	58	0	0	0	58	0	0	0	57	0	0	0	0
53931	54533	54556	Chitinase insertion domain	10133	700	6580	634	1	261	261	150	127	2075	2033	36	4	7	1125	8	53	347	329	470	242	6	482
53931	54564	54565	Ribosomal protein S16	6304	1926	6304	1916	270	380	380	4	7	5269	5267	0	13	255	5067	0	69	3	1895	1000	1159	10	115
53931	54569	54570	Ribosomal protein S19	5000	1355	5000	15	109	383	383	5	13	4276	4274	0	15	231	3725	0	487	1	1280	553	1040	30	0
53931	54574	54575	Ribosomal protein L31e	1567	990	1190	29	131	142	142	6	9	904	902	0	24	29	1	286	83	204	1	0	0	36	259
53931	54579	54580	Allophycocyanin linker chain (domain)	144	144	144	0	2	2	2	1	4	132	132	0	0	0	126	0	0	0	0	0	0	1	0
53931	54584	54585	Cdc48 domain 2-like	4011	1220	2822	729	60	108	108	42	20	1048	1047	0	17	22	1	149	79	282	0	1	0	74	409
53931	54592	54593	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	81646	676	61184	674	16	407	407	127	68	9457	9427	1	95	251	8302	264	102	293	3745	1388	1820	46	390
53931	54610	54611	SecB-like	3423	926	3156	855	9	21	21	3	6	2315	2314	0	7	17	2313	0	1	0	2122	1	176	0	0
53931	54615	54616	DNA-binding domain of Mlu1-box binding protein MBP1	2025	727	1349	717	5	5	5	34	12	465	465	0	0	0	1	0	0	0	1	0	0	0	464
53931	54620	54621	Heme-binding protein A (HasA)	299	302	192	0	43	43	43	1	4	76	75	0	0	0	75	0	0	0	75	0	0	0	0
53931	54625	54626	Chalcone isomerase	3848	726	535	467	23	25	25	7	7	173	173	0	0	0	0	0	170	0	0	0	0	1	0
53931	54630	54631	CBS-domain pair	42931	1825	38235	1631	12	158	158	357	196	9055	9050	0	85	330	7793	419	85	286	3250	1225	1814	29	413
53931	54636	54637	Thioesterase/thiol ester dehydrase-isomerase	91813	661	76357	658	1	795	795	211	97	10925	10913	0	103	379	9704	318	107	277	4465	1616	2059	48	428
53931	54647	54648	DLC	2406	562	2101	0	68	73	73	23	13	681	681	0	0	0	0	0	79	245	0	0	0	66	254
53931	54653	54654	CI-2 family of serine protease inhibitors	1015	619	853	499	58	62	63	9	7	200	199	0	0	0	53	0	97	5	41	12	0	5	37
53931	54664	54665	CO dehydrogenase molybdoprotein N-domain-like	10518	2701	10503	2695	56	132	132	60	61	3759	3755	0	17	50	3045	62	68	335	1642	739	462	15	218
53931	54664	54675	Nicotinate/Quinolinate PRTase N-terminal domain-like	17066	1027	16688	110	2	71	73	18	23	7843	7839	1	36	305	6945	302	75	83	2850	1216	1770	28	361
53931	54664	54680	Pyrimidine nucleoside phosphorylase C-terminal domain	5589	754	5530	747	3	24	24	12	14	3421	3419	0	5	127	3364	1	0	52	825	996	1296	1	1
53931	54664	54686	Ribosomal protein L16p/L10e	7647	778	7383	778	115	438	438	14	16	5991	5988	0	45	252	4158	325	641	336	1467	666	1073	141	317
53931	54664	54690	Molybdopterin synthase subunit MoaE	5000	587	4753	587	10	21	21	11	13	2989	2989	0	18	24	2721	38	59	148	2011	35	389	8	10

53931	54694	54695	POZ domain	16470	1105	14332	1103	5	271	271	222	151	772	765	6	0	0	1	0	75	325	0	0	0	31	310
53931	54712	54713	Elongation factor Ts (EF-Ts), dimerisation domain	7913	1641	7886	1628	27	32	32	19	21	5642	5638	0	14	242	5306	0	69	208	2462	388	1487	18	12
53931	54718	54719	Fe,Mn superoxide dismutase (SOD), C-terminal domain	7091	1240	7091	1233	47	199	240	12	19	4187	4184	1	28	62	3629	92	35	312	1351	480	826	35	49
53931	54735	54736	ClpS-like	10000	2201	9388	2199	59	73	73	19	15	5486	5485	0	27	178	5388	1	61	4	2636	790	1041	11	0
53931	54746	54747	Ribosomal L11/L12e N-terminal domain	6364	1809	6351	72	98	234	234	22	26	4962	4959	0	36	190	4065	130	81	231	1406	714	973	86	315
53931	54751	54752	RecA protein, C-terminal domain	5835	2240	5835	2208	37	89	90	18	19	4462	4458	0	8	103	4448	1	2	5	2351	911	934	0	1
53931	54761	54762	Signal recognition particle alu RNA binding heterodimer, SRP9/14	1266	1185	942	801	17	17	17	16	10	486	486	0	0	0	0	0	68	241	0	0	0	38	122
53931	54767	54768	dsRNA-binding domain-like	22015	656	19090	650	3	225	225	121	54	7541	7514	24	23	307	6659	18	64	319	2614	1026	1629	13	418
53931	54767	54782	Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain	5000	622	4986	609	5	7	7	7	12	2996	2994	0	6	13	2947	1	0	3	1918	40	548	2	34
53931	54767	54786	YcfA/nrd intein domain	3471	1140	2311	6	2	4	4	7	6	1105	1105	0	5	19	1045	59	0	0	435	44	213	0	0
53931	54790	54791	Eukaryotic type KH-domain (KH-domain type I)	37185	703	23938	702	4	112	112	480	153	3828	3827	0	52	216	2440	361	80	330	547	177	1342	73	494
53931	54805	54806	Alpha-lytic protease prodomain	1735	931	677	3	7	7	7	8	12	376	376	0	1	1	376	0	0	0	19	355	1	0	0
53931	54805	54810	GMP synthetase C-terminal dimerisation domain	5000	741	5000	741	4	8	8	15	15	3404	3402	0	10	56	3310	1	0	2	2353	4	134	19	69
53931	54805	54814	Prokaryotic type KH domain (KH-domain type II)	18586	594	18469	589	15	468	468	64	65	7859	7857	0	19	319	7152	43	76	217	2776	1259	1797	49	288
53931	54820	54821	Ribosomal protein S3 C-terminal domain	5000	1412	5000	1412	377	109	377	4	17	4018	4015	0	14	185	3978	1	5	4	1923	502	1086	12	0
53931	54825	54826	Enolase N-terminal domain-like	29472	2523	28287	2505	86	852	882	61	39	7765	7759	2	30	182	6463	188	91	476	3109	952	1336	66	430
53931	54842	54843	Ribosomal protein L22	6719	2047	6625	1083	399	459	459	20	15	5213	5209	0	39	188	3489	329	659	243	1012	714	1002	84	338
53931	54848	54849	GroEL-intermediate domain like	10000	1725	700	75	842	957	957	1	17	473	472	0	6	6	188	10	9	137	162	0	0	6	119
53931	54856	54857	DNA damage-inducible protein DinI	1894	720	1756	694	1	1	1	3	5	455	447	8	0	0	445	0	0	1	445	0	0	0	1
53931	54861	54862	4Fe-4S ferredoxins	72314	0	55310	0	0	307	307	1728	191	11036	11010	3	171	566	9429	431	294	288	4244	1507	2135	62	411
53931	54861	54893	Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain	1865	964	1823	949	133	138	138	8	13	1385	1384	0	35	180	1065	317	0	1	388	44	354	0	1
53931	54861	54897	Protease propeptides/inhibitors	12862	924	3715	803	10	69	69	70	26	1036	1034	0	0	0	545	5	0	311	181	256	77	0	169
53931	54861	54909	Dimeric alpha+beta barrel	71030	1177	42411	1175	6	599	599	92	37	7935	7927	0	43	162	7017	196	76	261	3482	1333	1146	19	340
53931	54861	54913	GlnB-like	15086	1767	14487	1581	11	233	239	38	24	6307	6305	0	48	134	5263	314	64	246	2846	1120	174	47	354
53931	54861	54919	Nucleoside diphosphate kinase, NDK	5609	2029	5603	2002	271	521	521	12	17	3680	3670	7	30	81	2555	276	95	319	594	899	613	56	327
53931	54861	54928	RNA-binding domain, RBD	92740	682	90213	682	8	572	572	1099	499	2825	2823	0	13	27	1471	10	188	443	608	8	55	97	555
53931	54861	54957	Viral DNA-binding domain	876	660	802	613	38	42	42	3	5	346	1	343	0	0	1	0	0	0	0	0	0	0	0
53931	54861	54966	RuBisCO, large subunit, small (N-terminal) domain	11787	2830	11787	2825	28	48	76	8	10	10911	10907	0	8	11	203	41	10655	0	144	3	9	6	0
53931	54861	54975	Acylphosphatase/BLUF domain-like	15120	759	14276	709	9	132	132	61	37	6510	6507	0	45	134	5632	346	60	249	2703	976	1069	34	149
53931	54861	54980	EF-G C-terminal domain-like	17448	1244	13192	1244	10	107	109	87	70	7229	7228	0	56	245	5470	362	86	446	2288	1041	1287	100	468
53931	54861	54984	eEF-1beta-like	2478	1500	2384	15	10	11	11	23	17	1137	1135	0	29	36	0	320	77	303	0	0	0	66	323
53931	54861	54991	Anticodon-binding domain of PheRS	5000	1641	5000	1640	12	25	25	8	36	2996	2995	0	3	197	2993	0	1	1	478	576	1372	0	0
53931	54861	54995	Ribosomal protein S6	5754	1264	5751	88	3	114	114	1	4	4599	4598	0	12	169	4537	0	59	1	2055	742	1029	1	0
53931	54861	54999	Ribosomal protein S10	5000	811	4983	811	268	402	402	10	14	3938	3935	0	27	243	3408	84	77	190	1111	247	884	45	98
53931	54861	55003	PAP/Archaeal CCA-adding enzyme, C-terminal domain	2542	626	1710	592	5	75	75	21	16	846	845	0	3	5	0	179	59	266	0	0	0	4	335
53931	54861	55008	HMA, heavy metal-associated domain	15733	744	15652	744	6	78	79	81	79	5964	5961	0	14	139	4791	151	98	524	2169	830	1356	16	372
53931	54861	55021	ACT-like	62349	1510	43016	1378	2	207	207	165	115	9937	9931	0	95	367	8827	371	83	164	4118	1339	1958	37	409
53931	54861	55031	Bacterial exopeptidase dimerisation domain	32085	571	25204	437	2	68	68	30	31	6972	6970	0	26	221	6597	50	69	6	3443	345	1778	13	219
53931	54861	55035	NAD-binding domain of HMG-CoA reductase	5434	1649	3417	6	112	112	112	24	20	2016	2014	0	24	30	949	195	136	278	405	173	278	15	418
53931	54861	55040	Molybdenum cofactor biosynthesis protein C, MoaC	5000	642	5000	641	9	45	45	15	18	3552	3551	0	11	68	3265	1	61	144	1996	296	671	0	79
53931	54861	55044	TRADD, N-terminal domain	252	1161	230	223	2	2	2	3	5	163	162	0	0	0	0	0	0	162	0	0	0	0	0
53931	54861	55048	Probable ACP-binding domain of malonyl-CoA ACP transacylase	5810	1596	1013	209	22	27	29	7	67	831	831	0	2	50	828	0	0	3	193	99	387	0	0
53931	54861	55052	CheY-binding domain of CheA	3453	1536	2933	1523	15	15	15	23	23	1545	1545	0	1	39	1522	22	0	0	719	2	763	0	1
53931	54861	55056	Killer toxin KP6 alpha-subunit	6	6	6	0	2	2	2	0	4	3	1	2	0	0	0	0	0	0	0	0	0	0	1
53931	54861	55060	GHMP Kinase, C-terminal domain	27286	1066	21652	950	3	117	117	77	50	7825	7820	0	45	259	6620	319	106	278	2468	1016	1922	32	421
53931	54861	55064	Translational regulator protein regA	124	124	124	0	2	2	2	1	4	108	3	105	1	1	3	0	0	0	2	1	0	0	0
53931	54861	55068	Peptide methionine sulfoxide reductase	6859	1645	6832	1623	6	15	15	17	20	4353	4349	0	37	51	3904	173	75	151	2096	982	38	21	15
53931	54861	55073	Nucleotide cyclase	18286	1062	18261	1062	6	87	87	700	239	3961	3955	3	20	41	3171	3	3	304	2118	92	316	5	431
53931	54861	55083	6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK	5000	672	4993	667	55	71	71	17	27	3093	3092	0	5	66	3017	0	0	2	1614	351	876	0	70
53931	54861	55088	Methyl-coenzyme M reductase subunits	2026	698	478	173	31	93	93	5	5	118	118	0	11	12	0	118	0	0	0	0	0	0	0
53931	54861	55103	FAD-linked oxidases, C-terminal domain	30136	623	4253	2	39	113	113	23	19	1636	1636	0	3	4	1414	0	82	4	1166	167	43	0	135
53931	54861	55112	Formylmethanofuran:tetrahydromethanopterin formyltransferase	513	513	499	0	24	24	24	3	5	336	335	0	8	8	238	97	0	0	205	1	4	0	0
53931	54861	55116	Formiminotransferase domain of formiminotransferase-cyclodeaminase.	1452	1030	1347	0	10	10	10	11	8	872	870	0	18	80	586	25	66	183	25	13	208	3	0
53931	100877	55120	Pseudouridine synthase	30896	1066	28431	1066	8	63	63	46	43	7384	7380	0	46	277	6281	323	71	243	3297	494	1978	55	361
53931	54861	55124	Nitrite/Sulfite reductase N-terminal domain-like	24790	1139	10045	263	24	85	85	50	55	4484	4481	1	37	97	3799	150	99	3	1644	914	582	13	409
53931	55128	55129	Ribosomal protein L30p/L7e	7464	2109	5378	370	255	450	450	6	7	4564	4562	0	50	228	4019	337	20	3	1573	722	987	5	163
53931	55135	55136	Probable bacterial effector-binding domain	12932	730	4353	702	1	35	35	28	15	1743	1742	0	5	12	1433	23	77	202	954	42	256	2	0
53931	55143	55144	LigT-like	7490	1229	5164	451	8	36	36	26	12	3356	3352	0	38	64	2717	330	89	172	1193	483	585	2	38
53931	55148	55149	Pepsin inhibitor-3	82	84	7	0	2	2	2	1	4	2	2	0	0	0	0	0	0	2	0	0	0	0	0
53931	55153	55154	CYTH-like phosphatases	9815	646	4388	612	10	41	41	18	14	3120	3115	5	15	181	2409	269	25	173	955	165	491	3	227
53931	55158	55159	eIF1-like	5907	1185	4027	734	7	15	15	19	16	2716	2709	4	24	78	1758	249	93	231	1037	8	0	49	311
53931	55165	55166	Hedgehog/DD-peptidase	18131	1361	6183	859	6	71	71	56	29	3268	3238	27	16	60	2963	0	0	266	1646	464	431	3	1
53931	55173	55174	Alpha-L RNA-binding motif	30010	735	19435	735	5	411	411	16	14	7306	7304	0	46	350	7274	1	21	2	3037	1196	1707	3	2
53931	55185	55186	ThrRS/AlaRS common domain	10866	2140	10866	2131	23	27	33	21	52	5111	5109	0	45	242	4719	340	0	5	2782	29	1549	31	1
53931	55185	55190	Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain	6629	1523	2105	18	6	9	11	16	16	1262	1260	0	3	31	898	19	0	18	365	59	370	0	322
53931	55185	55194	Ribosome recycling factor, RRF	6248	1720	6239	492	2	28	29	4	10	5218	5214	0	12	219	4898	0	67	230	2073	849	1334	5	9
53931	55199	55200	Translation initiation factor IF3, C-terminal domain	5000	572	5000	569	1	2	2	9	10	3922	3920	0	6	56	3911	1	0	6	2134	838	865	0	1
53931	55199	55205	EPT/RTPC-like	18062	812	16078	810	14	216	216	34	39	7019	7017	0	24	209	6018	243	99	200	3170	500	1576	25	410
53931	55220	55221	Yeast killer toxins	149	320	138	1	10	10	10	4	6	63	62	1	0	0	0	0	1	0	0	0	0	0	61
53931	55228	55229	Cell division protein MinE topological specificity domain	1483	785	1462	772	4	6	6	1	4	1139	1138	0	2	3	1137	0	1	0	1133	0	0	0	0
53931	55233	55234	Cyanase C-terminal domain	2011	655	1984	652	90	90	90	5	8	1390	1389	0	1	4	1058	5	61	12	615	265	47	5	246
53931	55238	55239	RuBisCO, small subunit	2642	695	1944	9	19	237	237	18	11	997	994	0	6	6	601	0	222	0	337	59	4	110	0
53931	55247	55248	PCD-like	5226	1312	5150	1204	44	53	53	17	9	3775	3774	0	39	40	3070	161	65	258	1733	519	172	22	169
53931	55247	55252	C-terminal domain of arginine repressor	4947	1132	4871	1	37	74	74	5	8	3163	3163	0	8	196	3159	0	0	2	547	1016	1265	0	2
53931	55247	55257	RBP11-like subunits of RNA polymerase	8686	945	2765	462	94	467	467	31	27	1580	1578	1	14	22	474	283	74	268	417	0	44	53	381
53931	55247	55261	GAD domain-like	6188	1283	3767	770	4	20	22	10	16	2583	2583	0	41	76	2227	351	1	3	1584	2	579	0	1
53931	55266	55267	tRNA-intron endonuclease N-terminal domain-like	370	407	167	5	17	32	33	6	8	159	159	0	8	8	0	159	0	0	0	0	0	0	0
53931	55266	55271	DNA repair protein MutS, domain I	6804	3203	6804	3200	32	26	32	10	33	4138	4138	0	11	145	4018	113	1	5	2172	3	1277	0	0
53931	55276	55277	GYF domain	2972	1534	743	518	9	14	14	19	16	320	320	0	0	0	0	0	59	194	0	0	0	1	55
53931	55281	55282	RL5-like	6709	1096	6674	1084	138	463	463	21	16	5096	5093	0	77	266	4114	392	91	221	1778	641	1192	25	237
53931	55286	55287	RPB5-like RNA polymerase subunit	1404	662	1363	661	113	129	129	15	11	1025	1000	25	31	38	0	313	78	185	0	0	0	52	323
53931	55297	55298	YjgF-like	14092	717	13833	717	1	176	176	33	34	6822	6813	3	30	236	6148	153	67	149	2651	1039	1310	23	249
53931	55297	55307	Tubulin C-terminal domain-like	15583	3324	15454	606	245	388	391	73	46	6130	6128	0	7	110	3836	21	208	471	1048	1095	1109	474	859
53931	55297	55315	L30e-like	21880	597	15329	595	16	416	416	64	49	5575	5567	6	117	294	3994	483	89	371	1824	128	1485	108	453
53931	55297	55326	PurM N-terminal domain-like	29370	735	28829	735	10	66	66	61	94	9186	9181	1	44	201	8185	251	10	262	3959	1336	1594	41	404
53931	55330	55331	Tautomerase/MIF	12689	792	9723	716	226	606	606	33	17	4285	4284	0	10	63	3686	54	70	245	1888	510	949	37	173
53931	55346	55347	Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain	82134	1027	56583	1012	7	565	566	126	89	10759	10754	0	107	404	9411	366	111	314	4199	1566	2034	34	462
53931	55382	55383	Copper amine oxidase, domain N	5000	1115	1628	515	32	32	32	70	30	477	477	0	1	4	476	0	0	1	190	0	281	0	0
53931	55382	55387	Frataxin/Nqo15-like	2853	672	2703	593	16	49	49	9	8	1884	1883	0	2	6	1166	0	66	251	1102	1	0	40	336
53931	55393	55394	Bactericidal permeability-increasing protein, BPI	3815	1410	1963	1064	7	7	7	23	14	299	298	0	0	0	0	0	61	231	0	0	0	1	0
53931	55398	55399	Subtilisin inhibitor	1214	809	905	1	14	14	14	1	4	450	450	0	0	0	450	0	0	0	0	450	0	0	0
53931	55404	55405	RNA bacteriophage capsid protein	186	100	111	34	338	360	360	5	5	23	0	21	0	0	0	0	0	0	0	0	0	0	0
53931	55417	55418	eIF4e-like	4238	895	3334	3	54	79	79	25	13	900	893	6	0	1	1	6	114	291	1	0	0	52	379
53931	55423	55424	FAD/NAD-linked reductases, dimerisation (C-terminal) domain	38401	796	36901	796	2	399	401	94	71	9341	9335	0	43	182	8175	195	103	300	3619	1312	1688	80	423
53931	55423	55447	CO dehydrogenase flavoprotein C-terminal domain-like	12108	1125	9968	918	4	120	120	59	58	3835	3829	0	20	46	2915	72	273	301	1645	715	282	19	235
53931	55454	55455	SRF-like	5676	2356	5676	2281	12	2	12	19	16	1013	1012	0	0	0	0	0	391	278	0	0	0	10	324
53931	55463	55464	Origin of replication-binding domain, RBD-like	11188	925	9239	924	2	80	80	36	10	2470	944	1522	3	3	935	0	3	3	589	238	8	1	1
53931	55468	55469	FMN-dependent nitroreductase-like	28367	1366	26850	1364	3	192	192	79	30	8094	8089	0	37	302	7408	289	2	104	2822	1164	2085	16	256
53931	55480	55481	N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1	1414	560	1347	2	10	18	18	13	15	1052	1045	6	37	43	2	359	74	157	0	0	0	70	334
53931	55485	55486	Metalloproteases ("zincins"), catalytic domain	80695	697	55037	317	28	1080	1080	711	247	9585	9563	17	43	278	8155	246	78	537	3670	1456	1480	26	458
53931	55485	55545	beta-N-acetylhexosaminidase-like domain	12426	961	8195	753	30	136	136	145	50	2843	2841	0	7	93	2425	12	48	178	754	604	314	5	166
53931	55549	55550	SH2 domain	26980	555	21983	555	13	503	503	509	293	406	385	19	0	0	0	0	0	369	0	0	0	0	0
53931	55593	55594	HPr-like	5638	952	5638	950	38	87	87	21	30	3067	3066	0	6	139	3054	8	0	1	1573	52	1137	0	3
53931	55603	55604	Glucose permease domain IIB	5000	1178	5000	1173	6	6	6	8	14	1807	1807	0	1	64	1805	0	0	1	566	60	1096	0	1
53931	55603	55608	Homing endonucleases	8163	940	2314	120	11	151	151	133	71	952	939	4	7	19	338	74	170	30	21	24	97	1	314
53931	55619	55620	Tetrahydrobiopterin biosynthesis enzymes-like	21317	934	16727	934	110	442	442	40	29	6797	6790	4	29	195	5893	83	80	297	2196	1299	1171	48	373
53931	55636	55637	Cell cycle regulatory proteins	1063	739	879	0	28	28	28	10	7	636	635	0	0	0	0	0	70	188	0	0	0	43	298
53931	55647	55648	beta-lactamase-inhibitor protein, BLIP	1777	1227	28	1	30	30	30	1	4	9	9	0	0	0	9	0	0	0	0	9	0	0	0
53931	55652	55653	Ribosomal protein L9 C-domain	6290	1292	6288	1287	109	248	248	4	5	4949	4947	0	11	225	4927	0	17	2	1941	815	1378	1	0
53931	55657	55658	L9 N-domain-like	7565	1820	7344	1316	19	279	280	57	24	5459	5445	12	10	242	4864	3	17	186	2085	599	1396	17	334
53931	55665	55666	Ribonuclease PH domain 2-like	16341	928	15788	710	2	206	206	61	94	7318	7315	0	55	212	6310	240	74	277	2642	1278	1213	61	320
53931	55670	55671	Regulatory factor Nef	5000	1667	5000	1659	18	10	24	4	6	24	1	22	0	0	0	0	0	1	0	0	0	0	0
53931	55675	55676	CytB endotoxin-like	221	224	187	0	17	17	17	3	7	75	74	0	0	0	56	0	0	0	12	28	16	0	18
53931	55680	55681	Class II aaRS and biotin synthetases	89529	1798	84005	1767	11	433	442	220	200	12433	12421	0	155	518	10964	479	74	281	4580	1390	2660	79	477
53931	55710	55711	Subdomain of clathrin and coatomer appendage domain	4197	547	3341	539	11	22	22	41	16	774	773	0	0	0	0	0	72	274	0	0	0	53	346
53931	55717	55718	SCP-like	11726	951	7454	875	3	108	108	67	45	3251	3246	3	10	56	2438	99	64	287	1039	547	659	33	309
53931	55723	55724	Mog1p/PsbP-like	6759	635	2013	492	2	14	14	10	7	988	987	0	0	0	499	0	98	108	235	137	3	36	236
53931	55728	55729	Acyl-CoA N-acyltransferases (Nat)	213486	2032	126681	1693	2	766	766	432	163	12794	12732	23	122	461	11230	354	81	399	4601	1670	2995	88	515
53931	55752	55753	Actin depolymerizing proteins	11390	929	9930	866	7	152	152	192	86	1676	1675	0	0	0	16	1	101	981	0	15	0	68	456
53931	55769	55770	Profilin (actin-binding protein)	2149	713	1890	609	25	50	50	18	14	797	786	10	0	0	14	0	138	277	2	7	0	15	303
53931	55769	55781	GAF domain-like	27247	542	21258	521	12	114	114	250	134	9264	9259	0	19	151	5456	34	3118	277	2337	752	1439	30	310
53931	55769	55785	PYP-like sensor domain (PAS domain)	40015	1736	35177	634	69	234	303	3734	441	6817	6804	0	21	25	5164	185	240	907	3238	478	562	18	282
53931	55796	55797	PR-1-like	6983	1549	6882	1444	3	40	40	82	57	1167	1166	0	1	1	177	0	125	446	102	35	0	8	406
53931	55803	55804	Phoshotransferase/anion transport protein	16665	841	16129	830	12	31	31	57	34	4395	4394	0	3	108	4098	0	0	293	2260	308	1408	0	1
53931	55810	55811	Nudix	86132	652	67880	650	6	349	349	232	118	11768	11745	13	144	491	10322	415	128	289	4445	1706	2253	74	469

53931	55815	55816	5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain	7153	1283	6774	1000	3	26	26	95	43	3475	3472	1	4	32	2951	21	4	250	1280	568	826	0	243
53931	55820	55821	YrdC/RibB	16356	2659	16344	2644	17	23	33	30	26	7543	7541	0	21	294	6867	162	65	7	2907	997	1703	9	407
53931	55825	55826	YbaK/ProRS associated domain	10424	1969	10384	1937	14	15	21	23	17	5117	5115	0	10	266	4746	54	57	169	2155	826	1358	62	4
53931	55830	55831	Thymidylate synthase/dCMP hydroxymethylase	5279	1245	5201	1235	13	226	237	6	12	3941	3929	9	13	173	3828	9	9	76	1679	748	729	5	1
53931	55845	55846	N-acetylmuramoyl-L-alanine amidase-like	16003	617	15214	595	7	211	211	158	36	5692	5573	118	11	174	5258	2	0	299	2780	965	952	0	14
53931	55855	55856	Cytochrome b5-like heme/steroid binding domain	10763	1191	10043	1144	24	110	110	170	135	1482	1477	4	2	3	339	28	172	344	71	16	131	68	480
53931	55868	55869	DNA topoisomerase I domain	73	73	67	0	4	4	4	2	5	38	0	38	0	0	0	0	0	0	0	0	0	0	0
53931	55873	55874	ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase	67564	1648	63213	1578	30	586	586	2430	507	10457	10425	21	38	300	8826	140	118	531	4802	1024	1888	159	527
53931	55889	55890	Sporulation response regulatory protein Spo0B	5000	1886	4	326	10	0	10	6	5	206	206	0	0	0	206	0	0	0	1	0	205	0	0
53931	55894	55895	Ribonuclease Rh-like	5409	1077	4296	39	10	29	29	20	11	1774	1770	4	1	1	957	0	152	256	924	1	0	20	369
53931	55903	55904	Ornithine decarboxylase C-terminal domain	5000	1164	4984	1154	3	16	16	5	7	1592	1591	0	2	19	1584	5	0	1	1418	36	107	0	1
53931	55908	55909	Pentein	19470	748	17289	711	13	171	171	40	26	6640	6610	26	60	206	5410	356	106	289	2223	1110	990	62	343
53931	55919	55920	Creatinase/aminopeptidase	19152	1004	19151	1003	29	196	207	31	51	7345	7341	0	54	188	6153	332	72	271	2994	825	1524	70	394
53931	55930	55931	Glutamine synthetase/guanido kinase	25100	0	19999	0	0	392	392	36	33	8295	8293	0	31	178	6415	35	53	1733	3342	1142	1279	34	2
53931	55944	55945	TATA-box binding protein-like	8616	767	5877	761	38	145	145	37	26	2581	2579	0	48	65	1295	374	85	320	954	253	38	78	380
53931	55944	55957	Phosphoglucomutase, C-terminal domain	12593	940	7353	939	16	43	43	34	22	3847	3846	0	16	69	2887	87	88	278	1947	429	134	44	419
53931	55944	55961	Bet v1-like	60062	887	32006	573	4	583	583	136	71	6696	6689	0	29	43	5511	133	215	323	3210	1226	571	71	389
53931	55972	55973	S-adenosylmethionine synthetase	8326	751	8326	737	24	56	56	14	12	5321	5320	0	8	175	4353	10	157	363	1705	846	1500	53	329
53931	55978	55979	DNA clamp	10594	1110	9836	1110	3	316	316	37	18	6784	6521	259	54	237	5356	363	84	239	2467	1030	1265	75	353
53931	56002	56003	Molybdenum cofactor-binding domain	11862	4172	11179	4058	105	131	131	58	55	4117	4111	0	25	102	3378	88	73	308	1878	783	488	18	234
53931	56013	56014	Nitrite and sulphite reductase 4Fe-4S domain-like	18911	1358	10650	373	18	85	85	51	66	5358	5355	0	41	45	4704	130	103	4	2552	900	530	14	390
53931	56018	56019	The spindle assembly checkpoint protein mad2	2788	840	967	750	42	68	68	5	5	674	673	0	0	0	0	0	69	240	0	0	0	16	316
53931	56023	56024	Phospholipase D/nuclease	28971	709	18276	640	2	69	69	72	42	7821	7818	1	28	205	6935	206	65	266	3162	1216	1331	27	283
53931	56028	56029	Monooxygenase (hydroxylase) regulatory protein	618	575	554	503	26	31	31	1	5	378	378	0	1	1	375	3	0	0	275	91	6	0	0
48724	56036	56037	PheT/TilS domain	10000	3371	7028	2806	16	18	18	16	45	3624	3623	0	9	215	3619	0	0	4	1141	493	1233	0	0
53931	56041	56042	PurM C-terminal domain-like	29709	1214	29349	1214	9	68	68	70	100	9359	9354	1	43	246	8209	309	69	278	4012	1357	1604	41	420
53931	56046	56047	Ribosomal protein S8	6225	1722	6218	208	79	466	466	10	12	5045	5042	0	41	281	4094	311	65	191	1356	752	1151	62	265
53931	56052	56053	Ribosomal protein L6	10346	636	10304	633	115	453	453	20	19	7585	7582	0	49	301	6278	344	89	327	2303	976	1349	100	364
53931	56058	56059	Glutathione synthetase ATP-binding domain-like	87415	1015	78500	976	19	398	398	287	338	13948	13772	5	202	556	10271	496	128	2180	4356	1574	2466	100	513
53931	56058	56091	DNA ligase/mRNA capping enzyme, catalytic domain	23207	936	19532	431	7	84	84	133	60	6962	6682	278	28	50	5318	356	73	328	2526	1039	1068	72	483
53931	56103	56104	SAICAR synthase-like	18509	0	11765	0	0	84	84	53	29	6265	6248	15	24	188	5343	134	46	281	2140	1109	1422	25	403
53931	56111	56112	Protein kinase-like (PK-like)	169498	3675	136998	3649	484	4236	4236	1974	1866	7712	7573	59	18	205	5723	184	272	549	2506	1309	1677	112	654
53931	56175	56176	FAD-binding/transporter-associated domain-like	52766	1098	48783	1075	4	266	266	147	119	10516	10507	0	45	356	8976	175	588	303	4285	1176	1988	28	421
53931	56193	56194	Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain	10000	1309	9097	833	7	14	14	12	17	5728	5728	0	11	264	5690	6	17	4	2632	493	1493	0	11
53931	56198	56199	Methenyltetrahydromethanopterin cyclohydrolase	589	550	502	0	13	13	13	3	4	426	426	0	11	12	232	194	0	0	185	1	18	0	0
53931	56203	56204	Hect, E3 ligase catalytic domain	6548	1700	6539	1644	7	25	25	117	92	801	800	0	0	0	0	0	64	281	0	0	0	32	404
53931	56208	56209	Nitrile hydratase alpha chain	1451	921	1083	872	93	94	94	3	6	707	706	0	5	5	697	5	1	0	475	183	11	2	0
53931	56213	56214	4'-phosphopantetheinyl transferase	11219	883	7711	880	31	60	60	20	19	4639	4637	0	13	117	4288	6	55	184	2041	344	1421	10	86
53931	56218	56219	DNase I-like	43219	884	31308	200	3	205	206	216	94	8455	8448	4	19	275	7329	122	79	303	3383	793	1595	58	498
53931	56227	56228	Aldehyde ferredoxin oxidoreductase, N-terminal domain	2730	1183	2487	1	10	10	10	6	8	868	865	0	18	33	653	212	0	0	326	33	180	0	0
53931	56234	56235	N-terminal nucleophile aminohydrolases (Ntn hydrolases)	82083	871	69250	854	268	4799	4799	206	126	11130	11099	26	149	435	9479	456	132	386	4541	1403	2052	87	496
53931	56265	56266	DmpA/ArgJ-like	10000	1757	7339	1271	60	50	74	12	10	4376	4373	0	18	157	4083	54	12	3	1993	285	1256	0	214
53931	56270	56271	Pyruvoyl-dependent histidine and arginine decarboxylases	807	696	381	0	84	84	84	2	4	295	294	0	6	10	136	158	0	0	26	8	65	0	0
53931	56275	56276	S-adenosylmethionine decarboxylase	5385	843	3217	833	12	75	75	15	8	2206	2188	15	18	39	1521	130	129	192	549	112	499	19	156
53931	56280	56281	Metallo-hydrolase/oxidoreductase	87852	3581	58791	3236	21	513	513	199	104	11177	11167	5	111	464	9823	421	78	278	4049	1451	2260	72	442
53931	56299	56300	Metallo-dependent phosphatases	71174	3951	48483	2079	23	320	334	328	123	9938	9886	45	75	394	8354	389	137	347	3521	961	2230	86	517
53931	56316	56317	Carbon-nitrogen hydrolase	10713	1592	10700	1557	4	56	56	29	35	5320	5285	34	14	125	4400	84	107	266	2474	508	657	23	370
53931	56321	56322	ADC synthase	15687	637	13593	637	4	57	57	17	20	5261	5260	0	15	106	5065	125	45	3	2636	903	1110	5	15
53931	56326	56327	LDH C-terminal domain-like	22848	809	20421	804	109	594	594	35	26	7647	7642	0	35	203	6125	207	148	601	2375	1119	1676	88	387
53931	56348	56349	DNA breaking-rejoining enzymes	26503	1794	23198	1145	58	110	110	57	31	9079	8968	90	54	317	7913	162	84	308	3880	1005	1484	61	404
53931	56365	56366	SMAD MH1 domain	2438	942	1957	809	4	10	10	8	10	297	296	0	0	0	0	0	0	296	0	0	0	0	0
53931	56370	56371	Ribosome inactivating proteins (RIP)	1418	776	976	466	207	258	258	11	14	189	180	6	0	0	81	0	90	1	35	40	0	0	8
53931	56398	56399	ADP-ribosylation	16353	814	8402	647	55	636	636	179	93	3463	3442	15	17	51	2594	133	64	280	1112	649	484	37	299
53931	56419	56420	Peptide deformylase	9308	690	9308	686	18	154	154	5	10	5498	5496	0	18	157	5409	2	62	1	2680	619	1079	19	0
53931	56424	56425	Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain	16043	777	14108	777	12	128	140	53	73	6575	6571	0	22	132	5687	35	74	284	3416	759	702	61	396
53931	56435	56436	C-type lectin-like	36493	1394	31099	1336	34	880	880	1175	733	3003	2978	20	8	15	2426	8	18	515	958	824	122	6	0
53931	56486	56487	SRCR-like	5212	2157	5211	1441	7	4	10	431	346	252	251	0	0	0	0	0	2	249	0	0	0	0	0
53931	56486	56491	A heparin-binding domain	1726	692	1639	645	13	13	13	34	19	254	253	0	0	0	0	0	0	253	0	0	0	0	0
53931	56495	56496	Fibrinogen C-terminal domain-like	5495	1788	5492	1680	178	279	279	465	76	272	271	0	0	0	0	0	0	271	0	0	0	0	0
53931	56501	56502	gp120 core	5000	2066	4492	1504	140	57	140	5	7	17	1	15	0	0	0	0	0	1	0	0	0	0	0
53931	56506	56507	Methionine synthase activation domain-like	5293	1562	5280	915	8	8	8	14	25	3290	3289	0	5	58	3230	0	4	41	2180	159	440	0	7
53931	56511	56512	Nitric oxide (NO) synthase oxygenase domain	2341	1619	2123	1550	715	726	726	30	28	951	950	0	2	2	642	5	3	271	7	191	397	1	26
53931	56518	56519	Penicillin binding protein dimerisation domain	20606	1501	3607	462	43	72	72	12	14	1893	1893	0	6	79	1889	0	0	2	798	96	681	0	1
53931	56523	56524	Oxidoreductase molybdopterin-binding domain	9788	2174	7862	73	45	47	47	42	34	3677	3675	0	19	19	2976	23	106	199	2069	551	47	32	324
53931	56528	56529	FAH	20971	780	20815	750	8	94	94	60	39	5907	5905	0	13	28	4949	194	71	272	2551	1158	544	25	367
53931	56533	56534	Aromatic aminoacid monoxygenases, catalytic and oligomerization domains	4567	1464	4073	1437	36	54	54	17	10	1969	1966	0	7	7	1560	3	8	323	1085	126	70	32	12
53931	56541	56542	Substrate-binding domain of HMG-CoA reductase	5382	1781	2868	0	112	112	112	21	20	1877	1876	0	19	26	913	181	82	229	145	33	465	9	427
53931	56547	56548	Conserved core of transcriptional regulatory protein vp16	90	90	88	0	1	1	1	2	4	41	1	40	0	0	0	0	0	1	0	0	0	0	0
53931	56552	56553	Insert subdomain of RNA polymerase alpha subunit	7244	1352	6355	1313	201	223	223	31	28	4543	4539	1	29	110	3552	239	68	213	1845	720	934	58	360
53931	56557	56558	Baseplate structural protein gp11	70	70	60	0	24	24	24	1	4	60	1	59	0	0	1	0	0	0	0	1	0	0	0
53931	56562	56563	Major capsid protein gp5	5000	569	1130	0	84	84	84	3	5	614	561	52	3	8	561	0	0	0	371	130	37	0	0
53931	56567	56568	Non-globular alpha+beta subunits of globular proteins	440	264	334	167	2	37	37	11	8	154	153	0	0	0	66	0	0	76	66	0	0	0	0
56572	56573	56574	Serpins	7236	1343	7203	1343	14	230	230	15	24	725	702	20	3	6	302	58	25	315	31	125	23	1	0
56572	56595	56596	Replication terminator protein (Tus)	1496	607	1098	0	4	4	4	1	4	418	418	0	0	0	418	0	0	0	418	0	0	0	0
56572	56600	56601	beta-lactamase/transpeptidase-like	88236	874	79833	552	26	1298	1298	196	111	11921	11782	29	76	388	11232	69	6	237	4736	1609	2977	9	218
56572	56633	56634	Heme-dependent catalase-like	10593	676	10571	675	4	368	368	18	14	4596	4596	0	4	21	3901	47	41	294	2026	950	554	22	279
56572	56644	56645	Acyl-CoA dehydrogenase NM domain-like	25754	4278	24525	4263	16	170	171	78	64	6103	6098	0	46	107	5134	191	78	276	2370	1118	996	34	366
56572	56654	56655	Carbohydrate phosphatase	21541	1239	21117	1090	37	312	316	46	37	7235	7228	0	44	112	6191	117	99	300	3447	905	634	44	434
56572	56671	56672	DNA/RNA polymerases	47594	1054	40058	513	42	1247	1247	361	224	8330	6078	2227	32	143	4794	226	75	361	2779	5	1295	74	498
56572	56711	56712	Prokaryotic type I DNA topoisomerase	10342	2726	10340	2629	14	27	38	41	31	4113	4113	0	8	181	4015	96	0	1	1718	22	1812	0	1
56572	56718	56719	Type II DNA topoisomerase	6634	2265	6521	1278	32	56	56	45	26	3793	3743	49	2	11	2867	0	70	258	2364	1	485	73	424
56572	56725	56726	DNA topoisomerase IV, alpha subunit	2356	893	1095	1	7	7	7	10	8	739	739	0	33	38	16	341	70	199	9	0	0	29	75
56572	56730	56731	DNA primase core	6184	1352	6050	578	18	18	18	33	12	3900	3806	93	13	173	3766	0	39	0	2518	2	1037	1	0
56572	56740	56741	Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment	1999	1416	1905	1352	16	17	17	13	15	1301	1297	4	15	15	0	39	84	680	0	0	0	62	394
53931	56746	56747	Prim-pol domain	6243	1080	950	624	20	25	25	13	9	727	726	0	30	35	108	332	17	129	107	0	0	27	88
56572	56751	56752	D-aminoacid aminotransferase-like PLP-dependent enzymes	14581	716	14536	716	18	118	118	18	18	6895	6891	0	56	126	5852	280	56	254	2884	1147	1000	24	388
56572	56761	56762	HydB/Nqo4-like	10115	1855	8303	1776	113	152	152	16	14	4470	4470	0	11	31	3660	73	108	224	2440	719	193	80	290
56572	56769	56770	HydA/Nqo6-like	10000	2533	8273	1785	139	152	152	25	14	4984	4981	0	12	61	3623	63	714	236	2009	673	328	18	307
51349	56783	56784	HAD-like	146483	1303	129234	1299	8	960	960	528	304	13436	13278	148	96	448	11624	399	113	477	4868	1762	2894	86	520
56572	56795	56796	Dehydroquinate synthase-like	22383	3636	21982	3631	8	92	92	25	38	7098	7097	0	18	300	6509	63	65	7	2916	719	1939	8	409
56572	56800	56801	Acetyl-CoA synthetase-like	39139	2104	39022	2101	10	82	82	869	1592	7862	7818	1	48	114	6856	221	167	217	3716	1297	852	18	320
56572	56807	56808	Ribosomal protein L1	6192	1642	6191	1633	109	115	126	11	9	4938	4936	0	23	231	4315	84	76	239	1411	734	1237	43	158
56572	56814	56815	Sec1/munc18-like (SM) proteins	5093	2201	3086	1631	14	21	21	25	18	887	886	0	0	0	0	0	70	276	0	0	0	60	438
56572	56820	56821	Prismane protein-like	5947	726	5077	645	35	77	77	8	8	2311	2309	0	7	153	2157	124	3	3	763	34	933	6	0
56572	56825	56826	Upper collar protein gp10 (connector protein)	45	45	27	0	39	39	39	2	4	20	7	13	0	2	6	0	0	1	0	1	2	0	0
56572	56830	56831	Reovirus inner layer core protein p3	293	14	232	0	2	4	4	2	4	83	0	83	0	0	0	0	0	0	0	0	0	0	0
56835	56836	56837	Colicin	727	580	571	0	7	7	7	8	6	166	165	0	0	0	165	0	0	0	165	0	0	0	0
56835	56836	56845	Diphtheria toxin, middle domain	357	233	32	23	14	47	47	4	7	6	4	1	0	0	4	0	0	0	0	4	0	0	0
56835	56836	56849	delta-Endotoxin (insectocide), N-terminal domain	1400	840	1007	119	23	24	24	23	15	124	121	0	0	2	102	1	3	1	26	1	71	0	9
56835	56836	56854	Bcl-2 inhibitors of programmed cell death	3560	651	2319	554	134	290	290	20	12	334	305	27	0	0	0	0	0	305	0	0	0	0	0
56835	56836	56864	Exotoxin A, middle domain	313	314	294	0	4	4	4	8	10	18	17	0	0	0	17	0	0	0	17	0	0	0	0
56835	56917	56918	Light-harvesting complex subunits	690	365	690	328	101	200	200	2	5	203	202	0	4	4	202	0	0	0	198	0	0	0	0
56835	56924	56925	OMPA-like	15941	1521	7359	296	3	125	125	19	8	1805	1800	5	2	12	1641	0	104	4	1426	0	3	25	1
56835	56924	56931	Outer membrane phospholipase A (OMPLA)	3220	537	2905	526	9	9	9	4	6	1444	1444	0	1	11	1441	0	0	3	1291	0	4	0	0
56835	56924	56935	Porins	38919	707	29682	705	6	237	237	21	12	3838	3836	1	3	16	3832	0	0	2	3735	3	5	0	1
56835	56953	56954	Outer membrane efflux proteins (OEP)	10000	1200	9969	1166	23	30	30	7	11	3130	3128	0	15	26	3122	0	1	4	3080	1	4	0	1
56835	56958	56959	Leukocidin-like	2687	945	1345	839	143	168	168	4	6	335	330	4	0	0	330	0	0	0	2	174	154	0	0
56835	56967	56968	Lipovitellin-phosvitin complex; beta-sheet shell regions	2387	0	578	0	0	2	2	23	17	195	195	0	0	0	0	0	0	195	0	0	0	0	0
56835	56972	56973	Aerolisin/ETX pore-forming domain	1377	741	314	39	14	26	26	4	7	98	96	0	1	1	93	0	1	2	77	0	15	0	0
56835	56977	56978	Perfringolysin	1508	633	738	560	12	18	18	5	6	176	176	0	0	1	175	0	0	0	9	8	141	1	0
56835	56982	56983	Viral glycoprotein, central and dimerisation domains	6191	1304	5741	1240	62	136	152	59	25	121	0	114	0	0	0	0	0	0	0	0	0	0	0
56835	56987	56988	Anthrax protective antigen	5000	1411	147	147	63	71	71	12	11	40	39	0	0	0	39	0	0	0	0	0	39	0	0
56992	56993	56994	Insulin-like	1406	1007	1347	701	568	39	578	8	9	413	410	2	0	0	0	0	2	408	0	0	0	0	0
56992	57006	57007	Heat-stable enterotoxin B	5	5	5	0	1	1	1	1	4	1	1	0	0	0	1	0	0	0	1	0	0	0	0
56992	57006	57011	Neurotoxin B-IV	3	4	3	1	1	0	1	1	4	2	1	0	0	0	0	0	0	1	0	0	0	0	0
56992	57015	57016	Plant lectins/antimicrobial peptides	666	660	495	153	47	11	49	27	32	210	209	0	0	0	0	0	152	0	0	0	0	0	56
56992	57015	57027	Plant inhibitors of proteinases and amylases	11	58	11	58	24	0	24	11	11	28	27	0	0	0	0	0	27	0	0	0	0	0	0
56992	57015	57038	Cyclotides	9	0	9	0	0	0	0	2	4	5	5	0	0	0	0	0	5	0	0	0	0	0	0
56992	57015	57048	Gurmarin-like	1	0	1	0	0	0	0	1	4	1	1	0	0	0	0	0	1	0	0	0	0	0	0
56992	57015	57055	Agouti-related protein	227	560	221	468	4	1	4	2	5	218	218	0	0	0	0	0	0	218	0	0	0	0	0
56992	57015	57059	omega toxin-like	110	89	109	88	3	20	23	11	4	37	36	1	0	0	0	0	13	22	0	0	0	0	1
56992	57015	57095	Scorpion toxin-like	1236	529	1233	450	78	96	103	11	6	250	248	0	0	0	0	0	123	125	0	0	0	0	0
56992	57015	57180	Cellulose-binding domain	2775	1013	2733	991	7	0	7	129	79	348	346	0	1	1	0	0	1	0	0	0	0	13	331
56992	57015	57184	Growth factor receptor domain	10574	833	3843	776	11	62	62	86	85	346	345	0	0	0	0	0	0	341	0	0	0	0	2

56992	57015	57190	Colipase-like	618	408	617	51	2	8	9	6	7	185	184	0	0	0	0	0	0	184	0	0	0	0	0
56992	57015	57196	EGF/Laminin	32550	716	30862	715	4	365	365	5271	4007	530	490	35	0	0	9	0	2	408	9	0	0	63	0
56992	57015	57243	Bromelain inhibitor VI (cysteine protease inhibitor)	0	2	0	2	2	0	2	2	5	1	1	0	0	0	0	0	1	0	0	0	0	0	0
56992	57015	57247	Bowman-Birk inhibitor, BBI	315	471	314	85	23	21	23	6	8	84	82	0	0	0	0	0	82	0	0	0	0	0	0
56992	57015	57256	Elafin-like	203	833	198	473	5	2	5	40	23	150	149	0	0	0	0	0	0	149	0	0	0	0	0
56992	57015	57262	Leech antihemostatic proteins	40	28	40	10	11	19	19	4	6	8	6	0	0	0	0	0	0	6	0	0	0	0	0
56992	57015	57277	Granulin repeat	0	8	0	8	3	0	3	1	4	4	3	0	0	0	0	0	0	3	0	0	0	0	0
56992	57282	57283	PMP inhibitors	2	54	2	52	14	0	14	12	21	24	21	0	2	2	0	2	0	18	0	0	0	0	0
56992	57287	57288	Midkine	537	545	537	2	4	4	4	6	5	174	173	0	0	0	0	0	0	173	0	0	0	0	0
56992	57295	57296	Amb V allergen	1	2	1	1	3	0	3	1	4	1	1	0	0	0	0	0	1	0	0	0	0	0	0
56992	57301	57302	Snake toxin-like	4171	936	2930	805	143	255	262	35	20	353	351	1	0	0	0	0	0	351	0	0	0	0	0
56992	57361	57362	BPTI-like	5448	874	5448	874	10	199	199	597	237	375	372	0	0	0	4	0	1	365	4	0	0	0	0
56992	57391	57392	Defensin-like	275	0	275	0	0	49	49	9	5	98	97	0	0	0	0	0	0	97	0	0	0	0	0
56992	57413	57414	Hairpin loop containing domain-like	1096	619	643	375	42	50	50	25	17	186	185	0	0	0	0	0	0	176	0	0	0	9	0
56992	57418	57419	Neurotoxin III (ATX III)	0	6	0	6	1	0	1	1	4	2	2	0	0	0	0	0	0	2	0	0	0	0	0
56992	57423	57424	LDL receptor-like module	5246	689	5239	678	4	16	17	1590	1731	305	304	0	0	0	0	0	0	303	0	0	0	1	0
56992	57428	57429	Crambin-like	203	261	203	86	47	14	47	2	5	36	36	0	0	0	0	0	36	0	0	0	0	0	0
56992	57439	57440	Kringle-like	8819	772	8703	768	24	142	142	568	414	417	415	0	0	0	1	0	4	360	1	0	0	32	0
56992	57491	57492	Trefoil	1207	894	465	484	23	29	31	30	32	196	195	0	0	0	1	0	1	185	1	0	0	0	3
56992	57500	57501	Cystine-knot cytokines	17790	764	14737	762	20	294	314	59	33	2292	2274	16	0	0	0	0	0	2274	0	0	0	0	0
56992	57534	57535	Complement control module/SCR domain	14497	1119	14028	1119	12	204	204	1224	978	657	616	39	0	0	0	0	0	585	0	0	0	27	0
56992	57545	57546	Crisp domain-like	618	562	589	3	24	23	24	5	8	242	242	0	0	0	0	0	0	242	0	0	0	0	0
56992	57551	57552	Blood coagulation inhibitor (disintegrin)	5545	2237	5462	200	51	16	51	96	29	481	480	0	0	0	0	0	0	377	0	0	0	0	103
56992	57560	57561	Methylamine dehydrogenase, L chain	331	334	316	2	144	144	144	1	4	225	225	0	1	1	225	0	0	0	196	24	0	0	0
56992	57566	57567	Serine protease inhibitors	2612	1684	213	521	6	6	6	145	51	152	150	2	0	0	0	0	0	144	0	0	0	0	6
56992	57580	57581	TB module/8-cys domain	2358	741	2348	709	1	8	8	1049	694	220	219	0	0	0	0	0	0	219	0	0	0	0	0
56992	57585	57586	TNF receptor-like	3617	816	3443	802	9	56	62	37	24	243	217	25	0	0	0	0	0	216	0	0	0	0	0
56992	57592	57593	Heparin-binding domain from vascular endothelial growth factor	380	413	363	21	5	5	5	5	9	163	162	0	0	0	0	0	0	162	0	0	0	0	0
56992	57597	57598	Antifungal protein (AGAFP)	6	6	6	0	1	1	1	1	5	3	3	0	0	0	0	0	0	0	0	0	0	0	3
56992	57602	57603	FnI-like domain	5238	656	4444	60	1	35	35	304	190	266	264	0	0	0	0	0	0	264	0	0	0	0	0
56992	57609	57610	Thyroglobulin type-1 domain	4430	813	4134	803	1	10	10	246	100	324	323	0	0	0	1	0	0	321	1	0	0	0	1
56992	57614	57615	Type X cellulose binding domain, CBDX	297	312	287	10	2	2	2	61	48	27	27	0	1	2	27	0	0	0	25	0	0	0	0
56992	57619	57620	Carboxypeptidase inhibitor	4	4	4	0	8	8	8	0	4	1	1	0	0	0	0	0	0	1	0	0	0	0	0
56992	57624	57625	Invertebrate chitin-binding proteins	2624	1131	56	30	2	5	5	27	20	40	40	0	0	0	1	0	0	39	1	0	0	0	0
56992	57629	57630	GLA-domain	269	143	269	24	4	11	11	9	13	117	117	0	0	0	0	0	0	117	0	0	0	0	0
56992	57641	57642	Cholecystokinin A receptor, N-domain	196	198	192	1	1	1	1	3	6	136	136	0	0	0	0	0	0	136	0	0	0	0	0
56992	57646	57647	HIV-1 VPU cytoplasmic domain	5000	1211	5000	1141	3	2	3	1	4	39	0	38	0	0	0	0	0	0	0	0	0	0	0
56992	57651	57652	HIPIP (high potential iron protein)	706	687	672	26	25	32	32	3	4	402	402	0	2	2	383	19	0	0	362	1	0	0	0
56992	57661	57662	Ferredoxin thioredoxin reductase (FTR), catalytic beta chain	659	617	419	0	9	9	9	5	7	342	340	0	2	2	199	35	73	0	23	0	0	11	0
56992	57666	57667	beta-beta-alpha zinc fingers	46843	1703	42564	1703	3	43	46	3220	592	2973	2968	1	0	0	4	0	74	2327	4	0	0	62	476
56992	57700	57701	Zn2/Cys6 DNA-binding domain	18957	1703	17662	1617	2	0	2	255	138	592	566	0	0	0	0	0	1	0	0	0	0	1	561
56992	57715	57716	Glucocorticoid receptor-like (DNA-binding domain)	74183	930	63254	930	8	816	824	576	272	10061	10003	47	71	298	7576	313	730	659	3188	1242	1697	101	534
56992	57755	57756	Retrovirus zinc finger-like domains	5553	1247	5530	1246	5	0	5	114	126	154	37	115	0	0	0	0	0	37	0	0	0	0	0
56992	57769	57770	Methionyl-tRNA synthetase (MetRS), Zn-domain	5000	916	557	110	13	13	13	5	19	413	413	0	1	8	410	0	0	2	349	2	3	0	1
56992	57769	57774	Microbial and mitochondrial ADK, insert "zinc finger" domain	8493	751	6309	729	36	91	91	28	20	3829	3828	0	11	103	2965	64	73	272	1617	166	1001	61	354
56992	57769	57783	Zinc beta-ribbon	18035	830	17035	829	2	137	137	114	53	5441	5334	106	97	233	3942	455	74	289	2210	167	1268	77	444
56992	57769	57798	Casein kinase II beta subunit	1874	672	1627	29	36	36	36	12	9	714	713	0	0	0	0	0	76	149	0	0	0	66	379
56992	57769	57802	Rubredoxin-like	9357	836	8757	836	47	182	184	65	57	4396	4394	0	18	296	3630	112	79	221	1564	266	956	14	323
56992	57769	57821	Hypothetical protein MTH1184	23	23	23	0	1	1	1	1	4	19	19	0	0	0	0	19	0	0	0	0	0	0	0
56992	57769	57825	Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain	1726	1412	1715	7	138	138	138	6	10	1300	1300	0	36	172	995	304	0	1	388	37	327	0	0
56992	57769	57829	Zn-binding ribosomal proteins	16313	1018	13721	990	130	1229	1229	65	34	6752	6749	0	100	350	4799	415	602	378	1691	839	1270	110	383
56992	57839	57840	Ribosomal protein L36	1112	865	1109	863	144	118	149	6	7	1239	1239	0	1	58	694	0	176	97	47	182	324	39	217
56992	57844	57845	B-box zinc-binding domain	11895	749	10813	717	4	9	12	263	121	333	332	0	0	0	1	0	0	274	1	0	0	3	52
56992	57849	57850	RING/U-box	80135	1180	61055	563	1	132	132	1175	431	5305	5268	34	9	9	755	21	196	3617	157	529	1	87	539
56992	57862	57863	ArfGap/RecO-like zinc finger	10000	724	5121	1	7	24	24	110	72	909	909	0	0	16	372	0	70	274	8	139	182	24	140
56992	57867	57868	Metallothionein	395	587	393	264	1	2	2	4	6	175	173	0	0	0	46	0	0	127	3	0	0	0	0
56992	57878	57879	Zinc domain conserved in yeast copper-regulated transcription factors	677	556	653	4	1	1	1	2	4	386	386	0	0	0	0	0	1	0	0	0	0	0	385
56992	57883	57884	Ada DNA repair protein, N-terminal domain (N-Ada 10)	5000	804	4684	801	5	5	5	19	21	2524	2521	0	3	3	2406	2	0	0	1214	804	293	0	113
56992	57888	57889	Cysteine-rich domain	14334	920	13632	920	2	7	9	396	191	893	891	1	0	0	0	0	98	310	0	0	0	38	434
56992	57902	57903	FYVE/PHD zinc finger	37789	864	30422	495	1	113	113	820	283	1346	1345	0	0	0	1	0	78	670	1	0	0	38	527
56992	57916	57917	Zn-binding domains of ADDBP	222	223	212	0	7	7	7	2	6	138	0	138	0	0	0	0	0	0	0	0	0	0	0
56992	57923	57924	Inhibitor of apoptosis (IAP) repeat	3371	1152	3116	1089	41	258	258	55	25	764	660	103	0	0	0	0	1	317	0	0	0	0	336
56992	57932	57933	TAZ domain	1940	802	1727	794	8	16	16	97	51	375	375	0	0	0	1	0	77	273	1	0	0	21	0
56992	57937	57938	DnaJ/Hsp40 cysteine-rich domain	8822	1510	8821	1474	2	2	2	38	44	5009	5006	1	23	173	4074	49	83	294	2517	199	922	56	400
48724	50412	63380	Riboflavin synthase domain-like	59382	797	50167	788	2	251	251	258	167	9769	9761	0	52	308	8460	137	159	343	3886	1405	1756	72	540
56992	57769	63393	RNA polymerase subunits	856	1336	841	318	122	120	122	13	6	751	749	0	19	24	0	291	40	118	0	0	0	28	262
53931	63410	63411	LuxS/MPP-like metallohydrolase	36325	1640	33211	1620	76	294	294	112	49	9724	9708	11	35	346	8654	25	81	300	3764	1214	1708	87	511
51349	63417	63418	MurE/MurF N-terminal domain	9447	1233	9319	1231	4	13	13	18	32	3977	3977	0	5	184	3965	1	3	8	1848	175	1145	0	0
48724	50036	63433	Fumarylacetoacetate hydrolase, FAH, N-terminal domain	3699	922	3033	857	10	14	14	28	16	1965	1964	0	6	7	1403	3	66	234	658	425	14	19	224
46456	63445	63446	Type I dockerin domain	3069	1348	1515	20	16	31	31	393	124	207	202	0	1	65	189	13	0	0	6	0	152	0	0
46456	63450	63451	LEM domain	1431	787	1262	12	2	6	6	23	10	246	245	0	0	0	0	0	0	244	0	0	0	0	0
46456	46965	63491	BAG domain	6344	1025	1184	23	9	34	34	9	10	317	316	0	0	0	0	0	22	270	0	0	0	0	22
46456	63500	63501	Frizzled cysteine-rich domain	5000	929	4281	902	3	13	13	133	98	312	311	0	0	0	0	0	0	311	0	0	0	0	0
46456	47161	63515	Outer surface protein C (OspC)	1085	626	995	0	9	21	21	1	4	56	56	0	1	1	56	0	0	0	0	0	0	0	0
46456	63519	63520	PTS-regulatory domain, PRD	5450	1064	5405	1058	2	7	7	25	18	1774	1774	0	1	58	1772	0	0	1	279	160	1303	0	1
46456	63561	63562	RPB6/omega subunit-like	5313	1781	1259	843	176	235	235	7	7	1090	1067	23	29	31	257	138	72	173	2	177	32	56	326
46456	63569	63570	PABC (PABP) domain	2928	629	2810	625	1	35	35	48	27	806	806	0	0	0	2	0	81	284	0	2	0	59	344
46456	63591	63592	Flagellar transcriptional activator FlhD	970	719	836	0	10	10	10	2	5	513	513	0	1	1	513	0	0	0	510	1	1	0	0
46456	63599	63600	Telomeric repeat binding factor (TRF) dimerisation domain	625	615	536	0	13	13	13	8	6	174	173	0	0	0	0	0	0	173	0	0	0	0	0
48724	63696	63697	Olfactory marker protein	191	191	186	0	7	7	7	4	6	157	157	0	0	0	0	0	0	157	0	0	0	0	0
48724	63706	63707	Ganglioside M2 (gm2) activator	1088	723	303	0	19	19	19	4	5	188	188	0	0	0	0	0	0	180	0	0	0	0	0
48724	63711	63712	Nicotinic receptor ligand binding domain-like	5000	1177	3839	1176	725	431	801	18	14	335	334	0	0	0	0	0	0	334	0	0	0	0	0
48724	63723	63724	Cytolysin/lectin	340	736	182	0	109	108	109	4	5	91	91	0	0	0	0	0	3	32	0	0	0	0	56
48724	63736	63737	Leukotriene A4 hydrolase N-terminal domain	20000	1330	2568	1099	52	121	121	34	21	1528	1528	0	4	8	719	50	61	259	342	60	4	28	396
48724	50036	63748	Tudor/PWWP/MBT	21305	585	16111	577	14	198	198	409	185	824	823	0	0	0	1	0	74	308	1	0	0	39	385
53931	63762	63763	SAND domain-like	3474	1149	3224	1104	2	6	6	47	29	298	296	1	0	0	0	0	0	296	0	0	0	0	0
48724	63816	63817	Sortase	10498	776	5462	757	12	96	96	20	8	1829	1827	0	2	199	1827	0	0	0	0	281	1531	0	0
48724	50938	63825	YWTD domain	5123	2009	5057	1953	23	23	23	1831	1147	305	304	0	0	0	2	0	0	302	2	0	0	0	0
48724	50938	63829	Calcium-dependent phosphotriesterase	21581	1101	12109	944	24	107	107	97	50	4178	4174	0	20	28	3490	80	36	273	1906	789	289	10	276
48724	63839	63840	Ribonuclease domain of colicin E3	421	526	330	1	7	7	7	19	6	155	154	0	0	0	153	0	0	1	133	11	0	0	0
48724	51125	63848	Cell-division inhibitor MinC, C-terminal domain	5000	953	3105	823	6	6	6	2	7	2203	2202	0	5	79	2186	0	2	0	1188	2	678	14	0
48724	51181	63862	Thiamin pyrophosphokinase, substrate-binding domain	1073	973	929	0	12	12	12	13	11	657	656	0	0	0	0	0	71	237	0	0	0	46	288
48724	51268	63867	MoeA C-terminal domain-like	8158	746	7466	740	1	44	44	33	29	3735	3735	0	18	28	2908	237	67	229	1731	664	411	16	270
48724	63876	63877	Methuselah ectodomain	430	550	187	138	6	6	6	5	5	19	19	0	0	0	0	0	0	19	0	0	0	0	0
48724	63881	63882	MoeA N-terminal region -like	7674	1194	7671	1194	5	44	44	30	35	3607	3607	0	13	33	2978	239	54	191	2006	133	613	12	126
48724	63886	63887	P-domain of calnexin/calreticulin	2541	1185	2508	812	4	4	5	22	23	952	951	0	0	0	1	0	93	402	1	0	0	28	383
51349	51350	63892	Pyridoxine 5'-phosphate synthase	5000	640	4992	639	40	50	50	5	8	3446	3441	0	18	78	3434	1	0	4	2537	1	11	1	1
51349	52171	63965	Precorrin-8X methylmutase CbiC/CobH	4887	2392	4648	4	10	17	17	17	13	3231	3229	0	22	100	3005	224	0	0	1176	670	653	0	0
51349	63991	63992	Dipeptide transport protein	1846	1007	1585	995	5	5	5	3	5	1030	1030	0	2	16	994	35	0	1	234	388	277	0	0
51349	63998	63999	Thiamin pyrophosphokinase, catalytic domain	5906	1018	873	0	12	33	33	13	11	650	650	0	1	2	46	1	66	214	6	0	26	14	298
51349	64004	64005	Undecaprenyl diphosphate synthase	5386	1447	5386	1431	51	55	55	3	7	3753	3751	0	8	155	3747	0	2	2	1666	53	1283	0	0
51349	64042	64043	Cell-division inhibitor MinC, N-terminal domain	24	24	24	0	4	4	4	1	4	20	20	0	0	0	20	0	0	0	0	0	0	0	0
51349	64075	64076	MTH938-like	2888	1304	1888	1125	7	12	12	4	5	1428	1428	0	4	4	1081	69	30	211	1019	23	5	20	9
51349	64152	64153	YjeF N-terminal domain-like	12440	1997	10560	1827	41	47	47	39	20	6787	6785	0	35	233	5738	300	65	235	2667	929	1019	45	358
51349	64157	64158	2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain	5000	730	4996	721	5	9	9	6	11	3341	3341	0	4	214	3129	38	0	6	1101	6	1243	0	168
51349	64166	64167	SurE-like	5163	3226	5163	3189	61	31	63	2	8	3566	3565	0	17	84	3432	131	0	1	2194	14	188	0	0
51349	64181	64182	DHH phosphoesterases	10000	2710	8563	2110	16	28	28	21	17	3734	3734	0	10	177	3587	134	3	1	1196	65	1646	3	0
53931	64209	64210	Head-to-tail joining protein W, gpW	326	485	313	211	3	3	3	2	4	133	126	6	1	1	126	0	0	0	125	0	0	0	0
53931	64233	64234	Photosystem I subunit PsaD	451	452	420	0	13	13	13	2	5	310	309	1	3	3	166	0	73	0	1	0	0	42	0
53931	64262	64263	Prokaryotic ribosomal protein L17	5455	3402	5455	344	322	301	323	10	15	4637	4635	0	9	102	4263	0	68	213	1889	992	643	12	67
53931	64267	64268	PX domain	11310	810	10862	785	4	49	49	206	113	2287	2286	0	0	0	0	0	73	1721	0	0	0	20	456
53931	64287	64288	Chorismate lyase-like	27593	641	26262	641	4	72	72	17	11	6424	6422	0	15	88	6332	79	2	6	3056	1313	1614	2	1
53931	55199	64307	SirA-like	6103	1268	6091	1265	2	7	7	32	28	3397	3396	0	35	120	3207	186	0	3	1931	158	781	0	0
53931	55769	64356	SNARE-like	14939	1119	9540	1086	18	71	71	126	69	953	952	0	0	0	3	0	88	300	2	0	0	75	433
53931	64375	64376	YlxR-like	4241	882	2335	866	1	1	1	2	5	1869	1869	0	1	211	1867	0	1	0	224	43	1413	1	0
53931	55944	64383	Cell-division protein ZipA, C-terminal domain	3612	917	2852	904	12	12	12	1	4	1402	1402	0	2	3	1400	0	0	0	1389	0	8	1	1
53931	64396	64397	Hsp33 domain	6590	612	6563	610	2	7	7	3	6	4296	4293	0	6	181	4274	0	13	1	2398	3	1527	1	1
53931	64437	64438	CNF1/YfiH-like putative cysteine hydrolases	10080	754	9804	754	1	14	14	15	12	4930	4928	0	14	180	4769	155	1	2	2859	309	1152	0	1
53931	64448	64449	YopH tyrosine phosphatase N-terminal domain	87	90	40	29	5	4	5	3	5	10	10	0	0	0	10	0	0	0	10	0	0	0	0
53931	64464	64465	Outer capsid protein sigma 3	243	243	55	0	15	15	15	1	4	11	0	11	0	0	0	0	0	0	0	0	0	0	0
56572	64483	64484	beta and beta-prime subunits of DNA dependent RNA-polymerase	19997	0	10444	0	0	382	382	135	13	5092	5048	41	36	204	3664	142	99	356	3	1390	1692	72	612
53931	64495	64496	DNA-binding domain of intron-encoded endonucleases	700	983	77	33	3	3	3	13	6	65	29	36	0	0	24	0	5	0	0	0	22	0	0
56572	64517	64518	Phase 1 flagellin	5000	664	1461	155	3	5	5	21	7	545	544	0	2	6	543	0	1	0	463	3	75	0	0
56992	57015	64546	Satiety factor CART (cocaine and amphetamine regulated transcript)	245	250	244	231	1	1	1	1	4	125	124	0	0	0	0	0	0	124	0	0	0	0	0

56992	64570	64571	Cellulose docking domain, dockering	81	92	80	32	4	2	4	26	25	16	16	0	0	0	0	0	0	0	0	0	0	0	16
53931	55199	64586	C-terminal domain of ProRS	3922	1179	2631	1108	4	32	32	10	9	2042	2041	0	28	217	1688	268	71	0	54	30	665	6	3
46456	63450	68906	SAP domain	3360	988	3130	782	3	11	11	80	73	669	666	0	28	28	3	25	37	243	0	1	1	26	320
46456	63450	68912	Rho N-terminal domain-like	1227	741	1225	728	51	53	53	6	13	816	815	0	2	2	813	0	0	2	793	1	16	0	0
46456	63450	68918	Recombination endonuclease VII, C-terminal and dimerization domains	49	63	49	1	10	10	10	2	5	47	5	42	0	0	5	0	0	0	4	1	0	0	0
51349	68922	68923	PEP carboxykinase N-terminal domain	9232	1224	8952	1223	8	86	86	11	11	5810	5807	0	27	206	4836	65	134	339	2083	1057	819	60	338
53931	68929	68930	Protein-L-isoaspartyl O-methyltransferase, C-terminal domain	6	6	6	0	2	2	2	1	4	5	5	0	0	0	5	0	0	0	0	0	0	0	0
46456	47143	68989	Hemolysin expression modulating protein HHA	931	754	763	2	5	5	5	1	4	275	275	0	0	1	274	0	0	1	273	0	1	0	0
46456	47161	68993	FAT domain of focal adhesion kinase	1272	573	1176	0	19	36	36	10	24	248	247	0	0	0	0	0	0	246	0	0	0	0	0
46456	47161	69000	FAD-dependent thiol oxidase	2399	1121	1692	1079	32	56	56	19	15	896	827	68	1	3	3	1	71	260	1	0	1	61	396
46456	47161	69008	RecG, N-terminal domain	29	30	26	0	1	1	1	1	4	24	24	0	0	0	24	0	0	0	0	0	0	0	0
46456	47363	69012	alpha-ketoacid dehydrogenase kinase, N-terminal domain	2823	1365	2585	1291	45	55	55	30	18	810	809	0	0	0	1	0	75	290	1	0	0	32	384
46456	47472	69025	Hypothetical protein MTH865	198	204	183	4	1	1	1	1	4	143	143	0	3	3	10	133	0	0	1	0	9	0	0
46456	69035	69036	Bcr-Abl oncoprotein oligomerization domain	296	297	289	0	8	8	8	15	10	132	131	0	0	0	0	0	0	131	0	0	0	0	0
46456	47768	69047	Hypothetical protein YjbJ	1652	697	1608	0	1	2	2	6	4	1154	1153	0	2	3	1151	0	1	0	887	2	34	0	1
46456	47916	69055	1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain	5000	869	4657	857	29	39	39	7	12	3135	3134	0	8	179	3052	0	55	3	1437	64	872	16	1
46456	69059	69060	Arp2/3 complex 21 kDa subunit ARPC3	808	731	770	0	19	19	19	11	11	624	623	0	0	0	1	0	60	210	1	0	0	18	311
46456	69064	69065	RNase III domain-like	8463	1261	8408	1255	33	50	50	12	25	4857	4853	0	11	237	4755	25	66	1	1691	591	1780	3	2
46456	69069	69070	Anti-sigma factor AsiA	43	43	42	0	6	6	6	1	4	42	1	41	0	0	1	0	0	0	0	1	0	0	0
46456	69074	69075	Glutamyl tRNA-reductase dimerization domain	5000	791	39	10	3	2	3	1	6	37	36	0	2	2	17	19	0	0	11	0	1	0	0
46456	48370	69099	Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain	413	414	349	0	14	14	14	5	8	197	197	0	0	0	0	0	0	197	0	0	0	0	0
46456	48370	69103	Arp2/3 complex 16 kDa subunit ARPC5	990	715	737	25	17	19	19	7	7	510	509	0	0	0	0	0	53	241	0	0	0	8	194
46456	69117	69118	AhpD-like	23170	1237	19572	993	4	95	95	38	24	5842	5840	0	14	130	5466	158	2	93	2712	1180	767	1	119
46456	69124	69125	Nuclear receptor coactivator interlocking domain	1782	1271	1697	17	8	9	9	72	29	197	196	0	0	0	0	0	0	196	0	0	0	0	0
46456	48661	69131	Quinohemoprotein amine dehydrogenase C chain	160	160	159	0	4	4	4	1	5	109	109	0	0	0	109	0	0	0	101	0	8	0	0
48724	48725	69179	Integrin domains	7861	590	1271	568	11	121	121	52	25	271	271	0	0	0	0	0	0	271	0	0	0	0	0
48724	69188	69189	Penicillin-binding protein associated domain	6965	959	6021	606	4	37	37	8	9	2546	2545	0	10	15	2542	0	0	2	2104	1	427	0	1
48724	88632	69203	Nucleoplasmin-like core domain	1160	1067	1025	0	65	65	65	17	11	253	252	0	0	0	0	0	1	249	0	0	0	0	0
48724	50198	69255	gp5 N-terminal domain-like	20041	1863	1953	938	7	7	7	22	13	568	436	132	2	4	435	0	0	0	380	2	1	0	1
48724	69278	69279	Phage tail proteins	15707	0	9486	0	0	21	21	50	16	1747	1672	74	4	24	1668	0	2	1	1329	5	314	0	1
48724	69286	69287	Urease metallochaperone UreE, N-terminal domain	2793	1675	2410	1547	37	37	37	5	5	1343	1343	0	5	18	1337	5	0	1	910	83	205	0	0
48724	50875	69298	Quinohemoprotein amine dehydrogenase A chain, domain 3	295	296	280	0	4	4	4	6	10	173	173	0	0	0	173	0	0	0	170	0	3	0	0
48724	50938	69304	Tricorn protease N-terminal domain	5000	1337	1505	1071	24	24	24	29	21	889	888	0	4	41	872	16	0	0	126	442	2	0	0
48724	50964	69318	Integrin alpha N-terminal domain	5000	1154	2057	933	68	80	80	41	10	265	264	0	0	0	0	0	0	264	0	0	0	0	0
48724	50964	69322	Tricorn protease domain 2	5000	779	0	364	24	2	26	7	14	253	253	0	2	4	236	17	0	0	9	220	1	0	0
48724	51125	69336	Alpha subunit of glutamate synthase, C-terminal domain	13109	1631	11999	1566	7	15	15	33	27	6818	6817	0	26	195	6088	97	76	91	3078	1137	966	43	397
48724	51125	69340	C-terminal domain of adenylylcyclase associated protein	3139	1043	1369	49	8	16	16	11	10	835	834	0	0	0	0	0	82	268	0	0	0	60	383
48724	69348	69349	Phage fibre proteins	5591	1486	369	86	51	147	192	22	14	137	44	93	1	1	44	0	0	0	30	1	13	0	0
48724	69359	69360	Cell wall binding repeat	14261	1356	5215	198	17	58	58	475	65	692	679	12	1	57	679	0	0	0	0	69	607	0	0
48724	69368	69369	Cloacin translocation domain	2144	1376	269	0	6	10	10	18	8	83	83	0	0	0	83	0	0	0	79	0	3	0	0
51349	69499	69500	DTD-like	5553	1830	5553	320	14	10	14	10	11	4306	4305	0	14	263	3731	4	58	246	1437	60	1333	10	230
51349	69571	69572	Activating enzymes of the ubiquitin-like proteins	22325	744	15902	744	3	123	123	61	33	7234	7233	0	41	152	5996	312	77	277	3092	1078	917	72	436
51349	69592	69593	Glycerol-3-phosphate (1)-acyltransferase	5000	1550	162	8	2	2	2	3	4	89	89	0	0	0	4	0	81	0	0	0	0	1	0
51349	69617	69618	HemD-like	6803	2260	4954	1977	11	11	11	13	13	3106	3105	0	11	60	2535	81	21	227	269	1026	698	11	226
53931	69634	69635	Type III secretory system chaperone-like	4207	804	1625	498	21	70	70	6	5	491	490	0	0	0	490	0	0	0	329	3	1	0	0
53931	69634	69645	Arp2/3 complex subunits	1809	690	1669	651	19	38	38	24	11	761	760	0	0	0	1	0	71	259	1	0	0	33	360
53931	69651	69652	DNA-binding C-terminal domain of the transcription factor MotA	44	44	42	0	6	6	6	2	5	41	1	40	0	0	1	0	0	0	0	1	0	0	0
53931	69686	69687	Integrin beta tail domain	2112	777	880	591	14	30	30	22	20	191	190	0	0	0	0	0	0	190	0	0	0	0	0
53931	69694	69695	SRP19	1320	1033	1269	0	21	21	21	6	8	1036	1036	0	26	29	0	294	64	234	0	0	0	57	348
53931	69704	69705	Transcription factor NusA, N-terminal domain	6729	1624	6726	1170	5	7	7	33	28	4798	4798	0	7	188	4794	0	0	3	1901	1023	1468	0	0
53931	69720	69721	DsrC, the gamma subunit of dissimilatory sulfite reductase	2284	760	2177	749	14	14	14	4	6	1311	1308	1	19	20	1290	17	0	0	1121	49	52	0	1
53931	54861	69737	Urease metallochaperone UreE, C-terminal domain	2846	1756	2779	1689	14	14	14	6	5	1774	1773	0	5	8	1771	0	0	0	1308	76	180	0	1
53931	54861	69742	Glutamyl tRNA-reductase catalytic, N-terminal domain	5000	2465	4592	2443	1	1	1	12	12	3266	3265	0	17	33	3104	130	26	1	1549	678	584	0	0
53931	69753	69754	Ribosome binding protein Y (YfiA homologue)	5405	2047	5404	43	14	19	19	3	6	3910	3909	0	9	168	3889	0	11	2	1607	575	1349	3	0
53931	69760	69761	GTP cyclohydrolase I feedback regulatory protein, GFRP	207	207	190	0	35	35	35	4	4	151	151	0	0	0	0	0	0	148	0	0	0	3	0
53931	55297	69765	IpsF-like	5322	2158	5322	2151	114	141	165	9	10	4015	4013	0	6	214	3924	0	82	3	2100	44	1067	1	1
53931	69785	69786	YggU-like	3900	1158	2889	1137	3	3	3	11	5	2109	2109	0	11	29	1632	131	60	169	1295	78	42	32	73
53931	69795	69796	Thymidylate synthase-complementing protein Thy1	3930	582	2809	569	84	138	138	4	6	2031	1796	234	11	67	1745	42	0	1	502	611	341	0	0
53931	69818	69819	MTH1598-like	1373	912	1115	0	6	6	6	6	8	930	927	0	39	43	315	315	9	239	130	20	4	33	0
53931	69847	69848	LCCL domain	2442	865	1749	858	1	1	1	53	53	268	267	0	0	0	19	0	1	189	7	7	0	54	4
53931	69863	69864	Argininosuccinate synthetase, C-terminal domain	6909	3466	6909	69	38	38	38	10	17	4848	4846	0	12	141	4344	11	71	172	2263	472	1215	14	217
56572	69902	69903	NSP3 homodimer	991	625	972	19	8	8	8	3	5	134	0	133	0	0	0	0	0	0	0	0	0	0	0
56572	69907	69908	Membrane penetration protein mu1	147	147	135	0	46	46	46	1	4	39	0	39	0	0	0	0	0	0	0	0	0	0	0
56835	56924	69917	OMPT-like	9322	2268	732	668	14	44	49	3	5	266	266	0	1	2	266	0	0	0	257	0	0	0	0
56835	69921	69922	Head and neck region of the ectodomain of NDV fusion glycoprotein	3872	931	2161	911	8	20	20	2	5	130	1	128	0	0	1	0	0	0	0	0	1	0	0
56992	69963	69964	Pheromone ER-23	1	1	1	0	1	1	1	0	4	1	1	0	0	0	0	0	0	0	0	0	0	1	0
48724	49993	74650	Galactose mutarotase-like	52047	0	29513	0	0	603	603	228	117	7694	7637	2	30	267	6843	94	79	251	3245	862	1659	24	308
53931	74652	74653	TolA/TonB C-terminal domain	12751	761	7264	746	2	19	19	28	9	2339	2337	0	3	7	2334	0	1	1	2220	2	33	0	1
46456	63569	74731	Ribosomal protein L20	5000	816	5000	805	116	282	282	7	10	4177	4175	0	16	239	4104	1	36	4	1603	726	1095	23	1
46456	74747	74748	Variable surface antigen VlsE	2794	765	842	83	4	4	4	11	11	38	37	0	0	0	37	0	0	0	0	0	0	0	0
46456	48370	74778	Aconitase B, N-terminal domain	4559	615	4452	615	2	2	2	6	11	2427	2427	0	10	14	2408	3	5	5	2012	1	10	4	0
46456	48370	74784	Translin	1844	846	988	0	56	78	78	6	6	556	555	0	0	0	0	0	61	231	0	0	0	0	252
46456	48370	74788	Cullin repeat-like	11351	648	4308	640	10	41	41	56	30	907	906	0	0	0	1	0	86	279	1	0	0	52	451
48724	48725	74853	Lamin A/C globular tail domain	5622	671	1629	664	8	14	14	20	13	325	323	0	0	0	19	3	0	300	0	2	17	0	0
48724	48725	74863	Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha)	5000	564	4976	563	8	10	10	16	8	2107	2106	0	12	12	2106	0	0	0	2082	3	4	0	0
48724	49502	74877	Major surface antigen p30, SAG1	575	629	475	4	5	5	5	4	7	17	16	0	0	0	0	0	0	0	0	0	0	16	0
48724	49993	74914	V-region of surface antigen I/II (SA I/II, PAC)	1598	1162	312	0	6	6	6	33	4	55	55	0	0	0	55	0	0	0	0	0	55	0	0
48724	50036	74924	Cap-Gly domain	5765	633	5731	629	1	48	48	108	57	804	803	0	0	0	1	0	69	277	1	0	0	25	392
48724	50181	74942	YhbC-like, C-terminal domain	5000	842	1348	839	1	1	1	1	6	903	903	0	1	25	903	0	0	0	12	1	877	0	0
48724	74981	74982	Small protein B (SmpB)	5000	1184	5000	1181	13	13	13	5	6	3935	3933	0	8	178	3932	0	0	0	1414	883	1231	0	1
48724	50875	75001	Dipeptidyl peptidase I (cathepsin C), exclusion domain	512	517	345	0	17	17	17	6	7	205	203	0	0	0	0	0	0	196	0	0	0	0	0
48724	50933	75005	Arabinanase/levansucrase/invertase	19521	913	18108	701	37	186	186	155	84	4832	4814	2	17	209	4244	83	103	14	1224	584	1471	8	349
48724	50964	75011	3-carboxy-cis,cis-mucoante lactonizing enzyme	5000	1483	202	15	8	16	16	7	7	178	178	0	0	0	0	0	0	0	0	0	0	0	178
51349	51350	75098	Monomethylamine methyltransferase MtmB	162	787	89	88	8	5	8	1	4	55	55	0	0	0	15	40	0	0	4	0	9	0	0
51349	63417	75138	HprK N-terminal domain-like	8027	950	4296	943	2	14	14	31	16	2677	2676	0	6	153	2563	111	0	1	507	21	1514	0	1
51349	75168	75169	DsrEFH-like	9449	593	7656	592	3	43	43	6	7	2414	2412	0	25	31	2248	161	0	1	1748	41	196	0	0
51349	75180	75181	Hypothetical protein MTH777 (MT0777)	80	80	79	0	2	2	2	2	4	67	67	0	0	0	0	67	0	0	0	0	0	0	0
51349	75216	75217	alpha/beta knot	39543	889	37007	889	1	126	126	41	37	10108	10104	0	86	443	8939	402	74	240	3637	1305	2318	61	347
51349	75303	75304	Amidase signature (AS) enzymes	21355	1112	19488	1059	4	122	122	54	46	7617	7612	0	47	216	6578	261	69	268	2635	1268	1461	25	396
53931	54196	75347	Rotavirus NSP2 fragment, C-terminal domain	1009	762	985	11	9	21	21	1	5	129	0	129	0	0	0	0	0	0	0	0	0	0	0
53931	74651	75399	Plakin repeat	3299	1374	2734	1372	5	9	9	219	161	189	189	0	0	0	0	0	0	189	0	0	0	0	0
53931	75403	75404	VSV matrix protein	72	72	72	0	3	3	3	1	4	29	0	29	0	0	0	0	0	0	0	0	0	0	0
53931	75411	75412	Hypothetical protein MTH1880	40	40	40	0	2	2	2	1	4	33	33	0	0	0	0	33	0	0	0	0	0	0	0
53931	54805	75420	YhbC-like, N-terminal domain	5000	1149	4492	1114	1	1	1	1	7	3363	3362	0	8	180	3361	0	0	1	1630	158	1449	0	0
53931	54861	75445	D-ribose-5-phosphate isomerase (RpiA), lid domain	5366	1928	5360	1874	19	47	47	11	17	3588	3587	0	22	45	3098	253	10	173	2122	70	545	13	30
53931	55199	75471	YhbY-like	5009	1249	4175	1241	4	4	4	5	6	2929	2928	0	9	163	2795	71	61	1	1419	70	1215	0	0
53931	55593	75500	Putative transcriptional regulator TM1602, C-terminal domain	1616	903	1593	867	1	1	1	10	10	1020	1019	0	1	94	1007	11	0	1	2	27	919	0	0
53931	55769	75516	Pheromone-binding domain of LuxR-like quorum-sensing transcription factors	5000	773	357	288	10	61	61	2	5	183	182	0	0	0	182	0	0	0	182	0	0	0	0
53931	75552	75553	Smc hinge domain	5000	1118	5000	1117	10	10	10	32	23	2937	2937	0	18	215	2147	233	25	179	8	0	1666	10	337
53931	56234	75569	Archaeal IMP cyclohydrolase PurO	677	652	178	0	13	13	13	1	4	158	158	0	4	7	11	147	0	0	6	1	3	0	0
53931	75573	75574	Rotavirus NSP2 fragment, N-terminal domain	1021	809	1012	6	19	21	21	1	5	133	0	133	0	0	0	0	0	0	0	0	0	0	0
56572	75614	75615	Siroheme synthase middle domains-like	5674	1155	3963	819	9	9	9	23	9	2000	1999	0	6	13	1718	29	0	4	1615	6	77	0	248
56572	75619	75620	Release factor	20025	3225	19495	3204	7	23	23	10	13	8916	8912	0	45	360	8779	0	68	16	3555	1242	1998	20	16
56572	75624	75625	YebC-like	5530	2412	5530	2349	3	3	4	4	9	4608	4607	0	14	228	4604	0	0	2	1934	872	968	0	1
56572	75631	75632	Cullin homology domain	5087	1420	4413	1356	17	20	20	58	31	919	918	0	0	0	1	0	87	280	1	0	0	64	445
56992	75688	75689	Zinc-binding domain of translation initiation factor 2 beta	1121	916	514	118	4	4	5	3	7	504	504	0	28	34	2	327	57	19	0	0	0	0	97
53931	54235	81271	TGS-like	15724	591	15126	249	1	12	12	27	32	6304	6296	0	64	236	5880	391	14	5	2894	594	1457	1	1
46456	81274	81273	H-NS histone-like proteins	1584	993	1582	0	14	4	14	2	5	584	584	0	0	0	584	0	0	0	580	0	2	0	0
48724	81278	81277	C-terminal domain of mollusc hemocyanin	74	86	58	0	15	15	15	16	19	25	25	0	0	0	0	0	0	25	0	0	0	0	0
48724	48725	81296	E set domains	120363	531	75728	531	1	1316	1316	1481	563	10053	9800	242	49	272	8258	57	123	640	3604	1460	1938	105	554
56572	81299	81298	Adenylylcyclase toxin (the edema factor)	544	544	36	0	65	65	65	4	5	16	15	0	0	0	15	0	0	0	1	0	14	0	0
53931	81302	81301	Nucleotidyltransferase	59040	595	41539	595	1	541	541	231	126	10729	10692	25	57	385	9382	384	71	320	3594	1515	2581	66	422
56835	81322	81321	Family A G protein-coupled receptor-like	10308	637	6579	635	42	266	266	20	67	3628	3622	0	33	33	324	96	20	2896	126	38	25	5	274
56835	81325	81324	Voltage-gated potassium channels	12401	739	8990	737	87	77	160	68	56	1738	1737	0	1	9	1093	31	10	342	329	424	79	11	246
56835	81328	81327	Small-conductance potassium channel	1256	616	1166	0	10	10	10	17	10	252	251	0	0	0	0	0	0	251	0	0	0	0	0
56835	81331	81330	Gated mechanosensitive channel	5000	904	4795	904	5	5	5	2	6	3465	3464	0	1	133	3458	2	1	1	1161	924	838	1	1
56835	81334	81333	F1F0 ATP synthase subunit C	1962	758	681	742	29	221	223	5	6	1118	1115	0	6	16	893	0	153	1	605	46	96	33	3
56835	81337	81336	F1F0 ATP synthase subunit A	5000	741	2014	707	1	1	1	2	7	1432	1431	0	5	11	1429	0	0	2	1249	40	64	0	0
56835	81339	81338	Aquaporin-like	12388	768	12324	724	22	77	77	33	27	3706	3699	0	7	17	2701	14	213	368	1417	528	433	18	352
56835	81341	81340	Clc chloride channel	5000	568	4902	560	84	88	88	12	19	2781	2780	0	13	115	2720	57	0	1	1089	207	667	0	2
56835	81344	81342	Transmembrane di-heme cytochromes	13917	0	11942	0	0	50	50	15	16	3923	3922	0	6	9	2193	6	323	1357	1914	61	95	8	1
56835	81344	81343	Fumarate reductase respiratory complex transmembrane subunits	14088	853	7610	829	24	138	138	6	7	3437	3436	0	6	13	3124	0	39	159	2831	223	36	8	68
56835	81346	81345	ABC transporter involved in vitamin B12 uptake, BtuC	5000	628	5000	625	12	14	14	3	6	2339	2338	0	6	29	2221	116	0	0	885	394	774	0	1
46456	81384	81382	Skp1 dimerisation domain-like	2219	629	2161	618	58	64	64	34	22	701	672	27	1	1	1	0	113	163	1	0	0	55	303
46456	81385	81383	F-box domain	9024	1179	4822	868	9	23	23	85	40	708	705	2	0	0	8	0	23	281	1	0	0	0	384

56835	81407	81406	Mitochondrial cytochrome c oxidase subunit IV	1011	643	595	510	53	53	53	3	6	320	320	0	0	0	0	0	0	292	0	0	0	0	28
56835	81407	81411	Mitochondrial cytochrome c oxidase subunit VIa	1048	606	805	0	53	53	53	2	5	499	498	0	0	0	1	0	3	260	1	0	0	0	231
56835	81407	81415	Mitochondrial cytochrome c oxidase subunit VIc	397	408	351	1	53	53	53	3	6	219	218	0	0	0	0	0	0	218	0	0	0	0	0
56835	81407	81419	Mitochondrial cytochrome c oxidase subunit VIIa	717	608	649	23	53	53	53	3	5	216	215	0	0	0	0	0	0	214	0	0	0	0	0
56835	81407	81423	Mitochondrial cytochrome c oxidase subunit VIIb	333	338	330	0	53	53	53	2	5	170	169	0	0	0	0	0	0	169	0	0	0	0	0
56835	81407	81427	Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa)	293	553	293	147	53	53	53	5	5	306	305	0	0	0	0	0	0	203	0	0	0	0	102
56835	81407	81431	Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)	181	244	106	45	53	53	53	1	4	94	94	0	0	0	0	0	0	94	0	0	0	0	0
56835	81443	81442	Cytochrome c oxidase subunit I-like	13019	760	13018	755	35	94	94	3	11	7515	7463	0	17	17	3768	109	4	3579	1781	1065	536	1	1
56835	81453	81452	Cytochrome c oxidase subunit III-like	10000	1326	9988	1170	55	55	55	8	5	6715	6713	0	3	3	2974	20	0	3717	1432	876	453	1	1
56835	81334	81464	Cytochrome c oxidase subunit II-like, transmembrane region	11147	1334	11117	1242	24	110	114	23	20	7358	7356	0	3	3	2967	0	183	3781	2476	5	439	277	99
56835	81407	81469	Bacterial aa3 type cytochrome c oxidase subunit IV	77	124	77	121	5	5	5	1	4	114	114	0	1	1	114	0	0	0	114	0	0	0	0
56835	81407	81473	Bacterial ba3 type cytochrome c oxidase subunit IIa	0	6	0	6	35	0	35	1	4	5	5	0	1	1	5	0	0	0	0	0	0	0	0
56835	81484	81483	Bacterial photosystem II reaction centre, L and M subunits	7153	606	7082	604	45	346	346	4	6	3042	2960	79	42	45	592	0	1281	0	359	0	2	586	0
56835	81407	81490	Photosystem II reaction centre subunit H, transmembrane region	185	0	179	0	0	128	128	2	5	145	145	0	3	3	145	0	0	0	143	0	0	0	0
56835	81407	81496	Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor	796	611	781	58	68	68	68	8	8	612	611	0	0	0	2	0	65	194	2	0	0	13	325
56835	81407	81502	ISP transmembrane anchor	1166	601	1112	39	61	86	86	17	12	810	809	0	0	0	164	0	51	281	0	0	0	4	301
56835	81407	81508	Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrom c reductase)	672	682	643	0	68	68	68	8	8	541	541	0	0	0	0	0	0	232	0	0	0	1	299
56835	81407	81514	Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	611	580	600	4	68	68	68	9	8	502	502	0	0	0	0	0	62	183	0	0	0	2	247
56835	81407	81518	Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	254	284	195	15	18	18	18	3	4	158	158	0	0	0	0	0	0	157	0	0	0	0	0
56835	81525	81524	14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	964	860	902	0	68	68	68	4	6	679	678	0	0	0	0	0	70	262	0	0	0	28	306
56835	81532	81531	Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	981	872	934	23	68	68	68	7	7	694	693	0	0	0	0	0	62	253	0	0	0	23	342
56835	81407	81536	Subunit III of photosystem I reaction centre, PsaF	426	434	405	1	13	13	13	1	4	322	322	0	0	0	175	0	76	0	1	0	1	43	0
56835	81407	81540	Subunit VIII of photosystem I reaction centre, PsaI	0	56	0	56	6	0	6	1	4	51	51	0	0	0	50	0	1	0	0	0	0	0	0
56835	81407	81544	Subunit IX of photosystem I reaction centre, PsaJ	0	549	0	549	13	0	13	4	7	520	520	0	1	1	93	0	367	0	0	0	0	31	0
56835	81407	81548	Subunit XII of photosystem I reaction centre, PsaM	0	76	0	76	7	0	7	1	4	67	67	0	0	0	67	0	0	0	0	0	0	0	0
56835	81407	81552	Subunit PsaX of photosystem I reaction centre	0	23	0	23	3	0	3	1	4	23	23	0	0	0	23	0	0	0	0	0	0	0	0
56835	81559	81558	Photosystem I subunits PsaA/PsaB	5000	687	3328	31	11	26	26	4	7	1929	1927	2	6	6	203	0	1368	0	2	0	2	302	0
56835	81564	81563	Photosystem I reaction center subunit X, PsaK	53	275	51	164	7	7	7	1	4	114	114	0	0	0	97	0	0	0	0	0	0	0	0
56835	81569	81568	Photosystem I reaction center subunit XI, PsaL	494	495	461	0	12	12	12	1	5	310	310	0	3	3	173	0	76	0	0	0	1	33	0
56835	81407	81573	F1F0 ATP synthase subunit B, membrane domain	369	832	369	824	1	1	1	2	5	585	584	0	0	0	582	0	0	2	581	0	1	0	0
46456	47768	81585	PsbU/PolX domain-like	7017	836	2151	229	42	388	388	48	29	843	838	4	0	0	164	1	65	240	1	0	4	31	301
46456	47161	81593	Nucleotidyltransferase substrate binding subunit/domain	8052	812	6447	810	1	29	29	18	16	3036	3030	0	10	53	2946	80	1	3	2324	15	340	0	0
56835	81407	81597	Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor	1565	1054	1488	4	2	2	2	8	7	667	667	0	1	2	666	0	0	0	659	2	2	0	1
46456	81602	81601	Protein serine/threonine phosphatase 2C, C-terminal domain	906	571	881	541	7	7	7	6	6	230	230	0	0	0	0	0	0	230	0	0	0	0	0
53931	81607	81606	PP2C-like	10000	1272	9873	1265	12	45	45	55	45	4074	4073	0	4	141	3224	6	103	281	539	1258	1168	31	386
48724	81625	81624	N-terminal domain of MutM-like DNA repair proteins	8360	557	8338	557	9	77	77	12	15	4498	4497	0	20	49	4353	7	0	137	2528	830	837	0	0
46456	81632	81631	PAP/OAS1 substrate-binding domain	10075	1220	7490	1190	12	131	131	133	55	1850	1848	1	36	53	536	377	72	307	24	21	427	66	439
56835	81649	81648	a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	10000	2593	10000	967	43	72	72	6	10	4014	4014	0	2	2	163	0	550	3231	3	0	2	43	0
48724	51181	81653	Calcium ATPase, transduction domain A	5000	590	5000	587	71	71	71	47	61	2246	2245	0	7	78	1497	38	73	292	380	87	876	21	308
53931	81661	81660	Metal cation-transporting ATPase, ATP-binding domain N	19419	674	17667	638	71	119	119	97	75	7396	7393	0	13	122	5184	148	71	1606	2202	800	1599	47	299
56835	81666	81665	Calcium ATPase, transmembrane domain M	5000	754	5	0	71	71	71	3	7	5	5	0	0	0	1	0	0	2	0	0	0	1	1
46456	81602	81698	FF domain	2933	671	2867	668	3	14	14	47	36	812	811	0	0	0	0	0	70	273	0	0	0	57	400
46456	46996	81710	Plasmid maintenance system epsilon/zeta, antidote epsilon subunit	365	72	52	0	4	8	8	1	4	30	30	0	0	0	30	0	0	0	1	0	28	0	0
46456	81729	81730	beta-catenin-interacting protein ICAT	318	332	275	0	3	3	3	4	6	162	161	0	0	0	0	0	0	160	0	0	0	0	0
46456	47161	81736	Group V grass pollen allergen	77	77	75	0	16	16	16	2	6	16	16	0	0	0	0	0	16	0	0	0	0	0	0
46456	47575	81761	X-Prolyl dipeptidyl aminopeptidase PepX, N-terminal domain	1109	709	921	518	1	1	1	3	6	234	234	0	0	4	234	0	0	0	0	0	233	0	0
46456	81766	81767	Pre-protein crosslinking domain of SecA	5000	668	4998	137	12	28	28	22	40	2957	2956	0	11	124	2920	0	30	5	1102	13	1244	0	1
46456	81777	81778	Crustacean CHH/MIH/GIH neurohormone	373	417	265	8	1	1	1	2	4	113	113	0	0	0	0	0	0	113	0	0	0	0	0
46456	81782	81783	C-terminal domain of DFF45/ICAD (DFF-C domain)	242	254	231	10	2	2	2	3	5	168	167	0	0	0	0	0	0	167	0	0	0	0	0
46456	81789	81790	Myosin phosphatase inhibitor 17kDa protein, CPI-17	720	614	542	0	4	4	4	5	7	216	215	0	0	0	0	0	0	214	0	0	0	1	0
46456	47768	81799	Putative methyltransferase TM0872, insert domain	5000	1183	4982	1174	4	5	5	3	12	3337	3336	0	1	185	3314	0	3	18	864	575	1496	1	0
46456	47932	81811	Helical domain of Sec23/24	4768	1569	3131	1562	24	33	33	52	57	938	938	0	0	0	0	0	74	277	0	0	0	69	473
46456	81821	81822	RuBisCo LSMT C-terminal, substrate-binding domain	2134	658	389	371	22	26	26	4	8	253	253	0	0	0	0	0	69	162	0	0	0	14	4
46456	81831	81832	SopE-like GEF domain	247	253	216	0	6	6	6	2	4	60	60	0	0	0	60	0	0	0	60	0	0	0	0
46456	81836	81837	BEACH domain	5000	617	4544	616	6	6	6	93	20	867	866	0	0	0	1	0	69	271	1	0	0	63	415
46456	48207	81853	Family 10 polysaccharide lyase	5060	1767	570	543	7	52	52	19	15	325	324	0	3	27	324	0	0	0	87	0	52	0	0
46456	81871	81872	BRCA2 helical domain	774	623	345	0	4	4	4	36	12	200	199	0	0	0	0	0	0	199	0	0	0	0	0
46456	81877	81878	BRCA2 tower domain	18	30	18	12	4	4	4	5	11	6	6	0	0	0	0	0	0	6	0	0	0	0	0
46456	81885	81886	Helical scaffold and wing domains of SecA	6486	1438	6486	1428	16	25	25	14	37	4069	4069	0	8	58	4064	0	0	4	2024	1085	928	0	0
46456	81890	81891	Poly A polymerase C-terminal region-like	9411	1087	2580	471	4	32	32	28	12	1448	1446	1	4	22	1188	1	0	255	212	21	853	0	0
46456	48370	81901	HCP-like	6914	1209	5314	1004	2	2	3	236	53	1413	1412	0	4	35	1165	8	5	193	861	3	134	5	25
46456	81922	81923	Double Clp-N motif	10793	2544	10745	2542	3	40	40	38	20	5589	5588	0	21	168	5456	12	62	7	3066	877	674	7	44
46456	81929	81930	Orange carotenoid protein, N-terminal domain	391	391	359	0	8	8	8	2	5	134	134	0	0	0	134	0	0	0	0	0	0	0	0
46456	81934	81935	N-terminal domain of bifunctional PutA protein	5000	784	3881	781	14	14	14	5	11	1634	1634	0	1	1	1632	0	0	1	1626	2	1	0	1
48724	48725	81982	Antigen MPT63/MPB63 (immunoprotective extracellular protein)	326	334	265	1	1	1	1	1	4	104	104	0	0	0	104	0	0	0	0	104	0	0	0
48724	48725	81986	Tp47 lipoprotein, middle and C-terminal domains	74	74	11	0	2	2	2	2	5	5	5	0	0	3	5	0	0	0	0	0	3	0	0
48724	49379	81995	beta-sandwich domain of Sec23/24	5012	1864	2470	811	28	33	33	44	60	778	778	0	0	0	0	0	68	268	0	0	0	45	369
48724	82003	82004	N-utilization substance G protein NusG, insert domain	1744	994	127	114	12	17	17	3	7	113	113	0	1	15	112	1	0	0	1	0	79	0	0
48724	82025	82026	Calcium-mediated lectin	214	250	205	9	113	113	113	5	6	59	58	0	0	0	58	0	0	0	56	1	0	0	0
48724	82045	82046	Viral chemokine binding protein m3	9	9	8	0	8	8	8	1	4	3	0	3	0	0	0	0	0	0	0	0	0	0	0
48724	82050	82051	Obg GTP-binding protein N-terminal domain	5000	2874	5000	2873	4	2	4	4	9	3609	3608	0	6	107	3605	0	2	1	2083	35	1121	0	0
48724	50036	82057	Prokaryotic SH3-related domain	5951	1303	5685	1303	2	8	8	74	38	3315	3307	6	7	11	3300	0	2	2	2035	173	555	2	1
48724	50036	82061	BAH domain	5000	1088	142	139	17	22	22	4	4	86	86	0	0	0	0	0	0	0	0	0	0	0	86
48724	50198	82093	Heme chaperone CcmE	3463	739	3104	735	3	4	4	5	6	2083	2083	0	5	8	2068	1	6	1	1959	11	15	0	1
48724	50352	82109	MIR domain	5673	1682	3740	1565	10	35	35	81	17	831	830	0	0	0	4	0	68	282	0	4	0	23	434
48724	50412	82114	Riboflavin kinase-like	8042	670	7934	664	11	39	39	28	18	5722	5721	0	39	153	4810	324	70	244	2073	966	963	15	235
48724	82152	82153	FAS1 domain	5747	1258	5726	1244	1	9	9	137	167	2516	2514	0	9	10	2157	47	7	268	959	592	39	4	28
48724	50997	82171	DPP6 N-terminal domain-like	5184	1701	3656	1498	278	281	281	24	17	1593	1592	0	2	70	869	1	2	285	141	3	3	1	430
48724	51086	82185	Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain	273	273	270	0	39	39	39	6	5	169	169	0	0	0	0	0	0	169	0	0	0	0	0
48724	51268	82199	SET domain	15019	1243	6053	651	12	129	131	200	71	1269	1240	27	1	1	377	21	82	282	148	6	142	40	411
48724	82214	82215	C-terminal autoproteolytic domain of nucleoporin nup98	1776	630	1669	621	8	19	19	23	7	911	911	0	0	0	0	0	94	266	0	0	0	45	483
48724	82219	82220	Tp47 lipoprotein, N-terminal domain	74	74	8	0	2	2	2	1	4	2	2	0	0	0	2	0	0	0	0	0	0	0	0
51349	51350	82282	Homocysteine S-methyltransferase	6693	1688	6669	1608	28	29	29	17	27	3954	3954	0	5	115	3734	1	3	210	1813	545	829	0	1
51349	52008	82317	Swiveling domain of dehydratase reactivase alpha subunit	891	631	872	2	4	6	6	1	5	327	327	0	1	6	324	3	0	0	117	57	127	0	0
51349	82543	82544	GckA/TtuD-like	3468	963	2961	958	3	3	3	9	8	1985	1982	0	31	54	1591	211	0	175	1170	9	100	4	0
51349	82548	82549	DAK1/DegV-like	11697	917	11696	886	4	43	43	16	15	4030	4027	0	8	157	3760	26	62	127	952	778	1769	14	31
53931	82601	82602	Nuclease A inhibitor (NuiA)	317	342	100	1	3	3	3	4	6	82	82	0	0	0	80	0	0	0	2	0	0	0	2
53931	82606	82607	YbaB-like	5000	821	4991	812	5	7	7	6	8	4004	4002	0	16	171	3998	0	1	2	1986	549	1087	0	1
53931	82614	82615	Polo-box domain	2005	947	1500	0	56	59	59	12	11	410	409	0	0	0	1	0	2	275	1	0	0	25	71
53931	82648	82649	SufE/NifU	16735	802	16090	793	3	47	47	33	20	8040	8037	1	43	315	7047	216	74	228	2856	1101	1723	67	364
53931	54805	82653	Probable GTPase Der, C-terminal domain	5000	1058	2183	952	5	5	6	6	7	1511	1511	0	8	130	1449	0	59	1	69	38	1042	1	0
53931	54805	82657	BolA-like	6209	1719	2954	919	21	18	29	13	12	2090	2089	0	3	3	1583	2	61	182	1522	1	2	26	227
53931	54861	82671	SEA domain	759	1171	382	386	1	1	1	32	34	138	138	0	0	0	0	0	0	138	0	0	0	0	0
53931	54861	82679	N-utilization substance G protein NusG, N-terminal domain	5333	2056	5333	2037	14	3	14	4	11	4309	4309	0	13	198	4307	1	0	1	1457	1096	1273	0	0
53931	54861	82689	Mechanosensitive channel protein MscS (YggB), C-terminal domain	5000	1097	4934	1088	35	42	42	7	12	2477	2476	0	6	148	2351	123	0	2	1564	0	307	0	0
53931	54861	82693	Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains	7592	833	7369	806	86	106	106	7	61	2029	2028	0	4	17	2022	0	0	4	1989	2	3	0	2
53931	109622	82697	PurS-like	8489	684	8344	684	8	34	34	16	28	5113	5100	12	32	40	4654	239	0	5	2880	793	520	0	201
53931	55199	82704	AlbA-like	1739	694	1148	671	30	34	34	4	6	361	360	0	36	41	0	217	74	0	0	0	0	43	2
53931	55199	82708	R3H domain	6263	966	3653	564	2	13	13	67	12	420	419	0	0	0	2	0	61	262	2	0	0	6	62
53931	82713	82714	Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains	5934	787	5933	787	86	104	104	5	59	1637	1637	0	2	7	1630	0	0	5	1611	1	3	0	2
53931	55752	82754	C-terminal, gelsolin-like domain of Sec23/24	4702	2309	3807	0	31	33	33	58	60	948	948	0	0	0	0	0	73	278	0	0	0	77	475
53931	82770	82771	GIY-YIG endonuclease	15889	1082	607	524	3	7	7	24	9	427	377	50	1	9	317	2	3	0	92	8	179	2	52
53931	82783	82784	OsmC-like	19413	895	18170	890	8	57	57	11	9	5689	5685	0	22	34	5437	119	1	3	2784	1032	760	2	112
53931	82807	82808	Replication modulator SeqA, C-terminal DNA-binding domain	1000	625	976	0	9	11	11	5	7	561	561	0	0	1	558	0	0	2	555	0	1	0	1
53931	82828	82829	MesJ substrate recognition domain-like	6621	725	1610	440	1	13	13	8	8	706	706	0	1	7	705	0	0	1	647	4	36	0	0
56572	82855	82856	L-A virus major coat protein	27	28	13	0	2	2	2	2	4	7	3	4	0	0	0	0	0	0	0	0	0	0	3
56835	82860	82861	Mechanosensitive channel protein MscS (YggB), transmembrane region	5000	805	4033	7	35	35	35	6	12	2439	2438	0	4	141	2430	6	0	2	1546	2	335	0	0
56835	82865	82866	Multidrug efflux transporter AcrB transmembrane domain	5733	938	5732	935	86	104	104	7	61	1694	1693	0	4	8	1688	0	0	4	1668	1	3	0	1
56992	82894	82895	TSP-1 type 1 repeat	5000	1157	5000	1148	2	0	2	381	311	265	263	1	0	0	0	0	0	263	0	0	0	0	0
56992	82909	82910	Apical membrane antigen 1	1586	1211	1586	1118	5	5	5	2	5	31	30	0	0	0	0	0	0	0	0	0	0	30	0
56992	57769	82919	Zn-finger domain of Sec23/24	4619	1443	4187	1410	20	35	35	57	57	942	942	0	0	0	0	0	76	279	0	0	0	72	469
56992	82926	82927	Cysteine-rich DNA binding domain, (DM domain)	1967	932	1912	904	1	1	1	16	9	381	381	0	0	0	0	0	0	381	0	0	0	0	0
48724	88632	88633	Positive stranded ssRNA viruses	22409	1409	15700	1407	172	1676	1676	121	44	2254	1	2251	0	5	1	0	0	0	0	1	0	0	0
48724	88632	88645	ssDNA viruses	5160	515	2578	485	11	182	182	7	4	318	63	252	1	1	60	0	0	0	36	3	16	0	3
48724	88632	88648	Group I dsDNA viruses	4129	1324	1451	579	386	427	427	4	6	460	2	455	0	0	1	0	0	1	0	0	0	0	0
48724	88632	88650	Satellite viruses	4114	67	76	66	5	100	100	3	4	13	1	12	0	0	0	0	0	1	0	0	0	0	0
46456	46688	88659	Sigma3 and sigma4 domains of RNA polymerase sigma factors	25059	1416	24544	1415	47	103	110	48	32	7487	7484	0	25	280	7468	1	9	3	3030	1558	2030	1	1
46456	46996	88688	Families 57/38 glycoside transferase middle domain	6778	681	2846	668	2	68	70	35	27	1171	1170	0	4	33	758	35	66	270	85	88	180	19	0
48724	88696	88697	PUA domain-like	59521	1326	33307	1319	9	254	254	198	91	9548	9542	0	131	412	8128	450	85	306	3702	838	1884	72	445
51349	51988	88713	Glycoside hydrolase/deacetylase	35152	1502	27611	1497	2	136	136	165	94	7911	7906	0	24	295	7070	132	67	272	2926	1205	1884	28	312
51349	88722	88723	PIN domain-like	45590	1897	27483	1896	3	113	113	66	33	10499	10374	119	83	410	9003	419	72	277	3544	1516	1967	84	471

53931	88797	88798	N-terminal, heterodimerisation domain of RBP7 (RpoE)	1946	1486	1859	1	83	83	83	29	22	1088	1087	0	27	33	0	316	77	249	0	0	0	66	356
53931	54402	88802	Pre-PUA domain	1497	580	990	551	2	15	15	16	11	824	824	0	1	5	0	152	66	203	0	0	0	51	310
53931	88873	88874	Receptor-binding domain of short tail fibre protein gp12	5000	2516	80	85	20	22	23	6	5	69	23	46	1	1	23	0	0	0	14	1	3	0	0
46456	88945	88946	Sigma2 domain of RNA polymerase sigma factors	20540	2675	15498	221	49	105	105	42	21	5972	5958	0	24	122	5952	2	1	1	2824	1435	848	0	2
46456	46928	89000	post-HMGL domain-like	10313	1408	8926	1390	6	41	41	19	16	4062	4061	0	6	156	3936	119	1	5	1428	1240	1049	0	0
46456	46965	89009	GAT-like domain	9007	902	7084	899	1	25	25	35	29	804	803	0	0	0	0	0	73	277	0	0	0	6	433
46456	47239	89028	Cobalamin adenosyltransferase-like	5317	1628	5316	1621	26	39	42	7	9	3752	3749	0	19	66	3439	136	4	151	1533	667	542	6	7
46456	89042	89043	Soluble domain of poliovirus core protein 3a	2142	692	2092	493	2	2	2	25	20	261	0	260	0	0	0	0	0	0	0	0	0	0	0
46456	89063	89064	Replisome organizer (g39p helicase loader/inhibitor protein)	3	256	3	19	3	3	3	2	4	16	14	2	0	0	14	0	0	0	0	0	14	0	0
46456	89068	89069	N-terminal, cytoplasmic domain of anti-sigmaE factor RseA	2021	595	1623	589	2	2	2	4	5	948	948	0	0	0	946	0	1	0	943	0	2	0	1
46456	89081	89082	Antibiotic binding domain of TipA-like multidrug resistance regulators	3864	593	2227	590	3	4	4	6	5	1357	1357	0	0	12	1356	0	0	0	9	702	625	0	1
46456	89094	89095	GatB/YqeY motif	10066	0	10061	0	0	40	40	5	13	5463	5461	0	14	164	5337	56	61	2	2474	509	1262	3	0
46456	89123	89124	Nop domain	3611	2629	3216	0	33	34	34	23	15	1222	1221	0	23	25	3	263	77	283	1	0	0	78	460
46456	89154	89155	TorD-like	8351	702	3711	609	15	25	25	7	7	1179	1178	0	4	6	1137	40	0	0	991	63	54	0	1
46456	89161	89162	Gametocyte protein Pfg27	22	22	20	0	1	1	1	1	4	17	17	0	0	0	0	0	0	0	0	0	0	17	0
48724	89231	89232	Hypothetical protein TM1070	299	302	287	0	25	25	25	1	4	204	204	0	0	0	194	10	0	0	59	26	66	0	0
48724	49853	89260	Collagen-binding domain	876	885	858	803	8	14	14	30	15	174	174	0	0	0	174	0	0	0	20	0	139	0	0
48724	89359	89360	HesB-like domain	8273	790	7786	790	6	12	12	17	25	4390	4387	0	50	54	3683	64	73	210	2232	553	527	14	334
48724	50938	89372	Fucose-specific lectin	5000	828	3	39	30	4	30	3	5	35	35	0	0	0	0	0	0	0	0	0	0	0	35
48724	89391	89392	Prokaryotic lipoproteins and lipoprotein localization factors	11017	721	5425	706	17	33	33	10	9	2257	2256	0	5	10	2248	2	2	3	2065	125	3	0	1
48724	89427	89428	Adsorption protein p2	8	8	8	0	2	2	2	1	4	6	0	6	0	0	0	0	0	0	0	0	0	0	0
48724	89432	89433	Baseplate structural protein gp8	156	157	66	0	26	26	26	1	4	63	1	62	0	0	1	0	0	0	0	1	0	0	0
48724	89441	89442	Hypothetical protein YojF	533	509	525	0	1	1	1	2	5	378	378	0	0	0	378	0	0	0	0	0	376	0	0
48724	89446	89447	AbrB/MazE/MraZ-like	9188	1513	8649	1505	18	45	45	11	5	4665	4658	3	13	251	4651	6	0	1	1379	728	1622	0	0
51349	51988	89550	PHP domain-like	10218	1311	4752	287	8	26	26	25	12	2697	2696	0	12	97	2459	236	0	0	653	473	910	0	1
51349	52008	89562	RraA-like	5000	1051	4996	1040	6	31	31	8	11	2626	2626	0	6	17	2528	11	75	2	1644	555	270	7	1
51349	89622	89623	Ribose/Galactose isomerase RpiB/AlsB	5533	2919	5528	2898	49	65	65	12	13	4039	4039	0	14	271	4001	9	0	2	745	1014	1244	2	0
51349	89732	89733	L-sulfolactate dehydrogenase-like	5554	1067	5518	995	15	50	50	12	9	2422	2420	0	8	47	2075	62	0	97	1209	158	488	3	172
51349	89795	89796	CoA-transferase family III (CaiB/BaiF)	11765	2381	11735	2334	14	61	75	16	17	4036	4034	0	11	23	3404	89	1	231	2005	915	333	6	296
53931	88797	89807	Dodecin-like	1983	870	1798	866	112	124	124	1	4	1390	1389	0	4	12	1324	65	0	0	689	439	38	0	0
53931	88797	89811	Amyloid beta a4 protein copper binding domain (domain 2)	1706	697	1684	0	13	27	27	36	20	255	254	0	0	0	0	0	0	254	0	0	0	0	0
53931	89816	89817	Mago nashi protein	749	613	680	0	17	17	17	7	8	573	573	0	0	0	0	0	75	177	0	0	0	51	237
53931	54235	89837	Doublecortin (DC)	2888	910	2542	883	4	8	8	47	24	309	308	0	0	0	0	0	0	276	0	0	0	23	2
53931	89871	89872	Inhibitor of vertebrate lysozyme, Ivy	1049	769	697	0	8	8	8	1	4	323	322	0	0	0	322	0	0	0	320	1	1	0	0
53931	89889	89890	Proguanylin	302	302	297	0	1	1	1	2	4	167	167	0	0	0	0	0	0	167	0	0	0	0	0
53931	89894	89895	FYSH domain	1591	1327	1283	0	7	7	7	10	10	983	982	0	35	39	2	304	55	189	1	0	0	53	350
53931	89914	89915	DNA-binding protein Tfx	179	1304	172	167	1	1	1	3	4	149	149	0	4	5	0	149	0	0	0	0	0	0	0
53931	54805	89919	Ribosome-binding factor A, RbfA	5617	1454	5615	1423	1	4	4	5	6	4830	4829	0	11	236	4555	1	52	220	1705	877	1340	1	0
53931	54861	89942	eEF1-gamma domain	1575	867	1114	6	1	1	1	18	14	790	789	0	0	0	0	0	68	254	0	0	0	56	372
53931	54861	89946	Hypothetical protein VC0424	1847	645	922	336	1	1	1	3	5	569	569	0	1	2	568	0	0	0	526	0	14	0	1
53931	54861	89957	MTH1187/YkoF-like	3671	798	3591	772	1	35	35	10	8	2547	2547	0	7	34	2066	200	0	0	289	902	671	2	278
53931	54861	89963	YajQ-like	3950	904	3905	897	2	2	2	1	5	2883	2882	0	5	29	2881	0	0	0	1380	807	366	1	0
53931	100886	89975	Hypothetical protein Yml108w	55	55	34	0	1	1	1	1	4	33	33	0	0	0	0	0	0	0	0	0	0	0	33
53931	90001	90002	Hypothetical protein YjiA, C-terminal domain	5000	572	3483	566	5	5	5	12	11	1622	1622	0	2	6	1515	0	72	9	1209	33	81	13	3
53931	90063	90064	Hypothetical protein TM0875	7	7	7	0	1	1	1	1	4	4	4	0	0	0	4	0	0	0	0	0	0	0	0
53931	90072	90073	GCM domain	673	539	490	0	1	1	1	2	5	247	247	0	0	0	0	0	0	245	0	0	0	0	2
56572	90095	90096	Subunits of heterodimeric actin filament capping protein Capz	2284	1193	1997	1121	62	64	64	19	17	802	801	0	0	0	0	0	61	283	0	0	0	53	381
56835	90111	90112	Neurotransmitter-gated ion-channel transmembrane pore	5106	1892	4996	1889	63	77	78	21	41	333	332	0	0	0	0	0	0	332	0	0	0	0	0
56835	90122	90123	ABC transporter transmembrane region	8455	1585	8454	1539	30	34	34	8	41	3993	3991	0	8	129	3981	5	2	2	1699	724	1337	0	1
56992	57015	90148	DPY module	0	58	0	58	1	0	1	19	52	34	34	0	0	0	0	0	1	33	0	0	0	0	0
56992	90182	90183	Mollusk pheromone	4	6	4	2	1	1	1	1	4	5	5	0	0	0	0	0	0	5	0	0	0	0	0
56992	90187	90188	Somatomedin B domain	675	642	574	23	7	0	7	26	16	169	169	0	0	0	0	0	0	169	0	0	0	0	0
56992	90192	90193	Notch domain	115	810	111	187	9	6	9	163	46	124	124	0	0	0	0	0	0	124	0	0	0	0	0
56992	57769	90209	Ran binding protein zinc finger-like	3803	1157	2924	950	1	7	7	85	120	497	496	0	0	0	0	0	60	256	0	0	0	19	158
56992	90228	90229	CCCH zinc finger	2703	636	2696	630	1	1	2	42	66	710	709	0	0	0	0	0	70	419	0	0	0	26	163
56992	90233	90234	Zinc finger domain of DNA polymerase-alpha	250	282	250	24	7	4	7	8	5	181	181	0	0	0	0	0	0	181	0	0	0	0	0
53931	100878	100879	Lesion bypass DNA polymerase (Y-family), little finger domain	14111	813	10153	138	71	138	138	32	19	5843	5841	0	12	161	5100	81	62	219	2053	1024	1120	21	349
56992	100894	100895	Kazal-type serine protease inhibitors	8016	559	5005	558	16	86	87	362	181	443	442	0	1	1	7	4	2	414	1	0	0	14	0
56992	100896	100897	Plant proteinase inhibitors	178	246	178	24	13	11	13	9	12	35	35	0	0	0	0	0	35	0	0	0	0	0	0
46456	48370	100909	IP3 receptor type 1 binding core, domain 2	2840	1044	1330	20	7	32	32	37	10	270	269	0	0	0	0	0	0	264	0	0	0	1	0
46456	48370	100910	Chemosensory protein Csp2	1264	1004	1156	0	9	9	9	7	9	134	134	0	0	0	1	0	0	133	0	1	0	0	0
48724	100919	100920	Heat shock protein 70kD (HSP70), peptide-binding domain	5000	600	5000	600	74	77	79	6	53	3370	3369	0	9	37	2676	2	77	567	2282	0	94	21	2
46456	46996	100934	Heat shock protein 70kD (HSP70), C-terminal subdomain	12907	677	12851	677	1	97	97	37	43	5448	5445	0	13	74	3909	48	157	625	2703	539	370	157	436
48724	100938	100939	SPOC domain-like	6980	813	2621	729	2	6	6	71	22	725	724	0	0	0	1	0	65	279	0	0	0	21	343
51349	100949	100950	NagB/RpiA/CoA transferase-like	65173	1021	58281	1021	16	325	325	129	74	10935	10932	0	82	383	9649	353	78	292	4261	1490	2221	51	451
46456	47405	100957	Dimerization cofactor of HNF-1 alpha	105	147	105	137	18	0	18	8	9	76	75	0	0	0	0	0	0	75	0	0	0	0	0
53931	100965	100966	Translation initiation factor 2 beta, aIF2beta, N-terminal domain	1398	1000	640	588	12	12	12	4	6	522	522	0	13	19	2	231	70	0	0	0	0	2	211
46456	46556	100985	Sporulation inhibitor Sda	133	356	133	323	5	5	5	1	4	225	225	0	0	0	225	0	0	0	0	0	223	0	0
46456	81602	101059	B-form DNA mimic Ocr	59	59	56	0	3	3	3	1	4	21	0	21	0	0	0	0	0	0	0	0	0	0	0
46456	46996	101082	Typo IV secretion system protein TraC	6923	671	531	481	1	1	1	2	4	280	279	0	1	2	278	0	1	0	274	1	0	0	0
46456	46996	101089	Phosphoprotein XD domain	468	525	468	57	4	4	4	3	4	61	0	61	0	0	0	0	0	0	0	0	0	0	0
46456	46996	101094	Staphylocoagulase	815	550	730	0	6	6	6	19	5	93	93	0	0	0	93	0	0	0	0	0	93	0	0
46456	47161	101112	Oxygen-evolving enhancer protein 3,	595	794	391	367	5	6	6	2	5	101	101	0	0	0	11	0	86	0	0	0	0	2	0
46456	47161	101116	Flagellar export chaperone FliS	4585	597	4197	596	2	13	13	3	4	2665	2664	0	4	49	2660	0	2	0	1472	111	851	1	1
46456	47161	101125	Colicin D immunity protein	132	272	92	0	3	3	3	1	4	53	53	0	0	0	53	0	0	0	52	0	0	0	0
46456	47363	101148	Plant invertase/pectin methylesterase inhibitor	5115	670	2221	648	19	25	25	11	8	87	87	0	0	0	0	0	87	0	0	0	0	0	0
46456	47363	101152	Mob1/phocein	3498	573	2748	27	5	10	10	24	23	809	808	0	0	0	0	0	74	287	0	0	0	38	366
46456	47379	101156	Nonstructural protein ns2, Nep, M1-binding domain	4588	1255	4554	183	2	2	2	3	6	4519	0	4519	0	0	0	0	0	0	0	0	0	0	0
46456	47379	101160	Dimerisation domain of CENP-B	104	104	104	0	4	4	4	7	6	83	83	0	0	0	0	0	0	83	0	0	0	0	0
46456	47405	101166	Docking domain A of the erythromycin polyketide synthase (DEBS)	8	8	8	0	2	2	2	4	18	5	4	0	0	0	4	0	0	0	0	4	0	0	0
46456	47458	101173	Docking domain B of the erythromycin polyketide synthase (DEBS)	13	14	1	0	8	8	8	1	4	1	1	0	0	0	1	0	0	0	0	1	0	0	0
46456	101214	101215	KaiA/RbsU domain	828	796	684	504	22	22	22	11	10	483	483	0	0	0	476	7	0	0	4	6	293	0	0
46456	101223	101224	HAND domain of the nucleosome remodeling ATPase ISWI	1322	917	1187	14	1	5	5	25	21	639	639	0	0	0	0	0	50	258	0	0	0	0	325
46456	101232	101233	PWI domain	2493	685	1179	684	1	7	7	13	10	729	729	0	0	0	0	0	68	252	0	0	0	68	324
46456	101237	101238	XPC-binding domain	1463	988	1450	980	13	13	13	31	22	752	751	0	0	0	0	0	76	269	0	0	0	51	322
46456	101256	101257	Flavivirus capsid protein C	5341	1544	5341	48	10	2	10	42	17	70	0	65	0	0	0	0	0	0	0	0	0	0	0
46456	101261	101262	Methenyltetrahydrofolate cyclohydrolase-like	2003	1308	1584	1179	2	10	10	10	7	1176	1174	0	17	123	1001	27	0	143	93	156	486	1	0
46456	101277	101278	N-terminal domain of adenylylcyclase associated protein, CAP	1354	597	1194	22	4	4	4	11	12	744	743	0	0	0	0	0	75	260	0	0	0	23	362
46456	101282	101283	GRIP domain	534	512	533	1	8	8	8	6	6	221	221	0	0	0	0	0	0	221	0	0	0	0	0
46456	101287	101288	L27 domain	5228	1037	4764	974	3	29	29	123	57	287	284	0	0	0	0	0	1	282	0	0	0	0	0
46456	101306	101307	YutG-like	5000	679	1253	674	8	9	9	1	4	745	741	4	0	4	713	28	0	0	0	0	699	0	0
46456	101311	101312	Invasion protein A (SipA) , C-terminal actin binding domain	231	233	215	0	1	1	1	1	6	85	85	0	0	0	85	0	0	0	85	0	0	0	0
46456	101321	101322	YcfC-like	1922	678	1799	646	2	2	2	4	6	1084	1083	0	3	4	1080	0	0	2	1077	0	1	0	1
46456	101326	101327	YgfB-like	4100	819	1948	817	1	3	3	1	4	1191	1190	0	4	4	1190	0	0	0	1187	0	2	0	0
46456	101331	101332	Hypothetical protein MTH393	39	39	39	0	2	2	2	1	4	28	28	0	0	0	0	28	0	0	0	0	0	0	0
46456	101343	101344	Superantigen MAM	9	9	7	0	8	8	8	1	4	1	1	0	0	0	1	0	0	0	0	0	0	0	0
46456	101352	101353	Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)	5000	948	5000	945	8	20	21	7	27	2532	2532	0	1	54	2529	0	0	3	1344	20	880	0	0
46456	101385	101386	all-alpha NTP pyrophosphatases	19039	832	10815	832	4	59	59	32	23	5607	5605	1	18	210	5210	154	65	119	2110	545	1370	18	13
46456	101390	101391	Hsp90 co-chaperone CDC37	1084	710	369	317	3	3	3	13	9	243	242	0	0	0	0	0	5	226	0	0	0	7	0
46456	101398	101399	P40 nucleoprotein	238	239	79	0	2	2	2	1	4	23	18	5	0	0	0	0	0	18	0	0	0	0	0
46456	48370	101420	C-terminal domain of Ku80	854	634	444	0	2	3	3	11	8	307	307	0	0	0	0	0	56	184	0	0	0	18	36
46456	48370	101424	Hypothetical protein ST1625	17	17	17	0	1	1	1	1	4	11	11	0	0	0	0	11	0	0	0	0	0	0	0
46456	101446	101447	Formin homology 2 domain (FH2 domain)	8986	1492	6770	1408	20	25	25	95	36	889	888	0	0	0	0	0	71	275	0	0	0	59	441
46456	101472	101473	DhaL-like	5682	1361	5632	18	6	12	12	12	13	3045	3044	0	4	33	2520	30	32	135	884	720	730	13	306
46456	101477	101478	ADP-ribosylglycohydrolase	5000	2784	2136	1798	15	21	21	23	13	1442	1435	7	4	49	1222	100	2	89	422	116	347	3	16
46456	101488	101489	Eukaryotic initiation factor 4f subunit eIF4g, eIF4e-binding domain	536	518	131	0	1	1	1	2	6	97	97	0	0	0	0	0	0	0	0	0	0	0	97
46456	48661	101494	Stathmin	819	647	0	644	37	0	37	6	9	167	166	0	0	0	0	0	0	166	0	0	0	0	0
46456	48661	101498	Anti-sigma factor FlgM	1	787	1	267	5	5	5	1	4	193	193	0	0	1	193	0	0	0	15	0	175	0	0
48724	48725	101542	Fungal immunomodulatory protein, FIP	43	53	30	0	5	5	5	4	6	21	21	0	0	0	3	0	0	0	0	0	3	0	18
48724	48725	101546	ASF1-like	1033	658	949	625	35	35	35	3	6	741	740	0	0	0	0	0	70	224	0	0	0	56	350
48724	101575	101576	Supernatant protein factor (SPF), C-terminal domain	3453	565	1256	564	9	9	9	26	17	288	288	0	0	0	0	0	15	246	0	0	0	21	0
48724	101595	101596	Dextranase, N-terminal domain	103	561	97	0	12	12	12	5	8	85	85	0	0	0	29	0	0	0	2	27	0	0	56
48724	101600	101601	Smp-1-like	411	412	360	0	2	2	2	10	9	26	26	0	0	0	0	0	0	0	0	0	0	0	0
48724	101605	101606	Superantigen (mitogen) Ypm	7	7	6	0	4	4	4	1	4	2	2	0	0	0	2	0	0	0	2	0	0	0	0
48724	50036	101690	PAZ domain	5050	635	2628	634	6	48	48	75	14	510	510	0	0	0	2	2	80	300	0	0	0	21	104
48724	50036	101697	Hypothetical protein YfhH	518	506	503	0	2	2	2	2	4	326	326	0	0	0	326	0	0	0	0	0	326	0	0
48724	101737	101738	SspB-like	3652	1373	3591	13	28	33	33	3	5	2506	2503	2	3	14	2502	0	1	0	2488	1	5	0	0
48724	101743	101744	Rof/RNase P subunit-like	2201	902	1315	11	8	10	10	4	7	956	955	0	15	22	398	210	33	241	389	0	0	24	37
48724	101750	101751	Hydrophobin II, HfbII	282	310	274	266	26	26	26	7	8	149	148	0	0	0	0	0	0	0	0	0	0	0	148
48724	50198	101756	Hypothetical protein YgiW	2272	573	2084	0	1	1	1	1	4	856	855	0	0	11	854	0	0	1	841	2	5	0	0
48724	50464	101790	Aminomethyltransferase beta-barrel domain	12618	584	12253	582	4	37	37	33	31	5740	5734	0	22	92	5102	137	31	213	2381	994	733	17	219
48724	101800	101801	Surface presentation of antigens (SPOA)	5348	2486	5327	2463	8	4	8	12	8	3298	3297	0	5	57	3290	1	1	3	2043	109	870	0	2
48724	101815	101816	Replicase NSP9	1258	867	1243	0	10	10	10	53	20	230	0	228	0	0	0	0	0	0	0	0	0	0	0
48724	50614	101821	Aminopeptidase/glucanase lid domain	12871	1387	3700	105	7	142	142	7	13	1934	1934	0	6	141	1825	107	0	1	332	76	1219	0	0
48724	101851	101852	Bacterial fluorinating enzyme, C-terminal domain	2469	646	1105	641	48	70	70	4	5	412	412	0	0	8	404	8	0	0	77	25	244	0	0

48724	50875	101874	YceI-like	5569	1432	5564	1431	5	6	6	4	8	3099	3099	0	7	9	3094	5	0	0	1615	909	227	0	0
48724	50933	101887	Apyrase	734	632	533	0	8	8	8	9	9	301	300	0	0	0	7	0	0	249	7	0	0	29	0
48724	50938	101898	NHL repeat	24149	2812	2733	1031	25	67	67	302	64	954	953	0	10	12	639	27	1	265	178	193	63	15	1
48724	50938	101904	GyrA/ParC C-terminal domain-like	6267	3492	6265	3251	2	3	4	22	17	4365	4364	0	10	154	4270	90	0	3	1830	768	1374	0	1
48724	50964	101908	Putative isomerase YbhE	5000	606	3659	585	1	8	8	2	7	1660	1659	0	1	20	1640	8	0	2	729	188	431	5	3
48724	50964	101912	Sema domain	8009	1248	6773	932	23	37	37	78	34	263	262	0	0	0	0	0	0	262	0	0	0	0	0
48724	51044	101931	Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain	250	640	247	383	1	1	1	3	6	287	287	0	0	0	0	0	20	190	0	0	0	22	52
48724	101935	101936	DNA-binding pseudobarrel domain	7089	999	5678	886	1	15	15	52	24	258	257	0	1	5	119	0	138	0	86	0	14	0	0
48724	101940	101941	NAC domain	5000	799	4996	34	15	15	15	11	13	164	164	0	0	0	0	0	164	0	0	0	0	0	0
48724	51125	101960	Stabilizer of iron transporter SufD	5000	611	3035	610	4	4	4	2	5	1932	1932	0	5	23	1886	0	43	1	1257	27	2	0	1
48724	51160	101967	Adhesin YadA, collagen-binding domain	5000	1460	4157	89	1	10	10	1327	19	1010	1007	3	1	9	1004	2	0	1	891	1	58	0	0
48724	101998	101999	Trimeric adhesin	182	212	55	0	9	9	9	38	12	18	18	0	0	0	18	0	0	0	17	0	1	0	0
48724	102030	102031	AXH domain	5000	696	842	679	18	23	23	8	8	227	227	0	0	0	2	0	0	225	0	0	0	0	0
51349	51350	102110	(2r)-phospho-3-sulfolactate synthase ComA	832	624	699	7	2	2	2	3	5	577	577	0	5	8	408	54	11	0	54	42	178	0	100
51349	51350	102114	Radical SAM enzymes	30000	739	21148	718	8	11	11	32	21	7945	7940	0	42	120	6933	277	72	241	3753	1138	1076	29	374
51349	52008	102198	Putative cyclase	5392	1849	4260	1823	19	33	33	13	13	2599	2597	0	27	68	2231	234	65	16	786	403	670	0	48
51349	102214	102215	Creatininase	5000	1793	2982	1469	75	87	87	7	7	1837	1836	0	14	30	1707	124	2	0	906	237	271	1	0
51349	102219	102220	DNA polymerase III psi subunit	984	576	849	553	3	3	3	2	4	411	411	0	0	0	410	0	0	1	409	0	0	0	0
51349	102323	102324	F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)	107	108	103	0	54	54	54	1	4	92	92	0	3	4	0	92	0	0	0	0	0	0	0
51349	102399	102400	DNA polymerase III chi subunit	3631	726	2584	694	3	3	3	3	6	1692	1691	0	5	8	1690	0	0	0	1679	2	1	1	0
51349	102404	102405	MCP/YpsA-like	12801	859	11613	856	8	25	27	21	20	5866	5861	2	15	86	5548	23	79	3	2259	1084	1072	22	160
51349	102413	102414	Alpha-2,3/8-sialyltransferase CstII	4952	2345	197	197	15	15	15	1	6	41	41	0	0	0	41	0	0	0	41	0	0	0	0
51349	102461	102462	Peptidyl-tRNA hydrolase II	4587	1866	2629	1808	24	24	24	17	11	1955	1946	9	33	42	811	343	77	262	329	411	47	54	358
51349	102521	102522	Bacterial fluorinating enzyme, N-terminal domain	2573	1145	119	0	60	70	70	2	5	94	94	0	1	2	85	9	0	0	7	34	6	0	0
51349	102545	102546	RbsD-like	4678	2398	4476	3	48	86	86	3	7	2395	2394	0	4	51	2276	2	0	98	1056	354	742	8	8
51349	102587	102588	LmbE-like	13167	1891	5639	1	12	29	29	15	7	2718	2716	0	14	34	2644	71	0	1	299	1125	522	0	0
51349	53612	102645	CoaB-like	6255	1351	6128	617	12	12	12	11	11	3879	3873	4	11	158	3276	0	61	169	1528	50	1135	20	315
51349	102704	102705	NIF3 (NGG1p interacting factor 3)-like	9365	774	9137	754	3	24	24	11	10	5938	5938	0	6	198	5342	124	0	232	1776	1058	1476	1	214
51349	53926	102712	JAB1/MPN domain	5000	1492	164	13	7	8	8	2	4	164	164	0	23	29	0	164	0	0	0	0	0	0	0
53931	100965	102735	Trigger factor ribosome-binding domain	5000	624	4920	618	14	14	14	8	10	3192	3190	0	6	71	3185	0	0	4	1508	797	868	0	1
53931	102740	102741	Obg GTP-binding protein C-terminal domain	4739	719	2272	709	1	1	1	4	7	1730	1730	0	1	129	1722	0	5	0	4	844	768	1	0
53931	54402	102816	Putative dsDNA mimic	688	512	666	0	1	1	1	1	4	400	400	0	0	0	400	0	0	0	399	0	1	0	0
53931	102823	102824	Colicin D/E5 nuclease domain	479	504	380	0	13	13	13	46	8	165	164	0	0	0	157	7	0	0	127	11	16	0	0
53931	102828	102829	Cell division protein ZapA-like	1738	778	1326	0	8	8	8	1	4	957	956	0	4	6	955	1	0	0	951	0	0	0	0
53931	102847	102848	NSFL1 (p97 ATPase) cofactor p47, SEP domain	2196	612	1835	583	2	2	2	19	15	805	805	0	0	0	0	0	72	269	0	0	0	58	380
53931	102859	102860	mRNA decapping enzyme DcpS N-terminal domain	764	696	465	0	30	30	30	10	9	376	376	0	0	0	0	0	1	230	0	0	0	12	132
53931	102874	102875	Chromosomal protein MC1	194	218	182	6	2	2	2	3	4	138	125	13	9	9	0	125	0	0	0	0	0	0	0
53931	102885	102886	Coproporphyrinogen III oxidase	5161	2379	5140	2338	24	24	24	8	9	3318	3316	0	7	9	2583	0	72	245	2047	5	4	30	356
53931	102890	102891	Hypothetical protein Ta1206	543	537	214	0	1	1	1	1	4	184	184	0	2	8	134	50	0	0	4	1	124	0	0
53931	54861	103007	Hypothetical protein TT1725	1724	903	448	0	1	1	1	1	4	403	403	0	1	1	402	1	0	0	26	168	104	0	0
53931	103024	103025	Folate-binding domain	19388	930	17441	921	4	49	49	41	47	6802	6798	0	24	274	6308	94	19	245	2585	720	1693	9	116
53931	103031	103032	Hypothetical protein YwqG	2797	846	842	718	1	1	1	6	8	396	396	0	1	12	389	0	0	0	72	18	221	0	2
53931	103038	103039	CheC-like	6214	1943	3018	942	14	19	19	20	13	1609	1609	0	2	47	1470	139	0	0	415	8	861	0	0
53931	55185	103054	General secretion pathway protein M, EpsM	996	626	809	622	2	2	2	1	4	362	361	0	0	0	361	0	0	0	359	0	1	0	0
53931	103062	103063	Hypothetical protein YoaG	238	239	235	0	2	2	2	4	6	102	102	0	0	0	101	0	0	0	100	0	1	0	1
53931	103067	103068	Nucleocapsid protein dimerization domain	2331	548	2255	516	12	30	30	3	6	232	3	227	0	0	3	0	0	0	3	0	0	0	0
53931	55297	103084	Holliday junction resolvase RusA	4755	867	1983	824	7	7	7	2	4	422	406	16	2	3	406	0	0	0	349	5	23	0	0
53931	55297	103088	OmpA-like	8290	1698	8243	1416	24	30	30	72	28	3335	3333	0	9	19	3331	0	0	1	2870	9	13	0	1
53931	55382	103107	Hypothetical protein c14orf129, hspc210	1506	931	321	0	1	1	1	2	5	216	216	0	0	0	0	0	0	215	0	0	0	0	0
53931	55393	103111	Activator of Hsp90 ATPase, Aha1	1402	815	671	599	5	7	7	8	9	526	526	0	0	0	0	0	4	138	0	0	0	1	363
53931	103144	103145	Tombusvirus P19 core protein, VP19	53	53	53	0	13	13	13	1	4	21	0	20	0	0	0	0	0	0	0	0	0	0	0
53931	103164	103165	Ta1353-like	599	559	586	0	23	26	27	2	6	487	487	0	6	12	368	108	2	0	160	61	4	0	6
53931	55769	103190	Sensory domain-like	11755	848	7157	303	6	44	44	108	34	2256	2254	0	0	2	2254	0	0	0	1012	590	614	0	0
53931	55769	103196	Roadblock/LC7 domain	6635	1514	3258	899	14	48	48	26	17	1327	1326	0	5	5	852	49	11	272	182	539	0	55	51
53931	55944	103239	MoaD-related protein, C-terminal domain	24	145	24	16	4	4	4	2	5	21	21	0	0	0	18	3	0	0	0	0	1	0	0
53931	55944	103243	KA1-like	4873	598	3981	597	2	41	41	32	13	573	572	0	0	0	1	0	71	278	1	0	0	19	188
53931	55944	103247	TT1751-like	3789	1373	2259	1316	4	4	4	11	7	1513	1512	0	9	15	1364	141	0	0	559	350	177	0	6
53931	103255	103256	Hypothetical protein TM0160	2771	891	2528	891	4	4	4	6	8	2002	2002	0	11	55	1780	154	67	0	137	668	53	0	0
53931	103262	103263	Chorismate synthase, AroC	9100	745	9083	741	5	36	36	5	11	5941	5939	1	14	111	5435	72	73	7	2433	1139	898	9	335
53931	103276	103277	Hypothetical protein HI1480	3	3	3	0	2	2	2	0	5	2	2	0	0	0	2	0	0	0	2	0	0	0	0
53931	103358	103359	Suppressor of Fused, N-terminal domain	2818	635	743	564	28	29	29	7	6	477	477	0	0	8	267	0	0	210	42	30	134	0	0
53931	103364	103365	Hypothetical protein PH1602	5000	1120	2543	0	15	15	15	10	13	1697	1691	2	43	51	1042	336	10	224	436	233	148	34	17
53931	103369	103370	NinB	1900	699	896	659	2	2	2	1	4	296	268	28	0	0	268	0	0	0	268	0	0	0	0
56572	103377	103378	2-methylcitrate dehydratase PrpD	5000	599	3261	599	2	2	2	11	10	1873	1871	0	9	10	1503	49	4	4	810	446	168	0	306
56572	103382	103383	Antivirulence factor	101	104	42	0	4	4	4	1	4	22	22	0	0	0	22	0	0	0	22	0	0	0	0
56572	103387	103388	Virulence-associated V antigen	409	410	308	0	2	2	2	3	6	65	64	0	0	0	64	0	0	0	64	0	0	0	0
56572	103408	103409	39 kda initiator binding protein, IBP39, C-terminal domains	8	8	5	0	5	5	5	2	5	2	2	0	0	0	0	0	0	0	0	0	0	0	0
56572	103416	103417	Major capsid protein VP5	237	237	142	0	2	2	2	1	4	61	0	60	0	0	0	0	0	0	0	0	0	0	0
56835	81407	103431	Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor	1213	594	1203	0	1	15	15	4	7	1077	1077	0	2	2	191	0	818	0	2	0	2	39	0
56835	81407	103436	PetL subunit of the cytochrome b6f complex	0	6	0	6	12	0	12	1	4	5	5	0	0	0	1	0	4	0	0	0	0	0	0
56835	81407	103441	PetM subunit of the cytochrome b6f complex	0	37	0	37	15	0	15	1	4	33	33	0	0	0	30	0	3	0	0	0	0	0	0
56835	81407	103446	PetG subunit of the cytochrome b6f complex	0	348	0	348	4	0	4	4	6	322	322	0	1	1	97	0	186	0	0	0	0	11	0
56835	81407	103451	PetN subunit of the cytochrome b6f complex	2	14	2	14	1	0	1	1	4	12	12	0	0	0	0	0	12	0	0	0	0	0	0
56835	81407	103456	Preprotein translocase SecE subunit	659	745	334	108	15	17	17	3	5	380	380	0	8	8	2	127	48	67	2	0	0	23	106
56835	81407	103460	Sec-beta subunit	1	9	1	8	9	1	9	1	4	9	9	0	0	0	0	8	0	1	0	0	0	0	0
56835	81407	103464	Oligosaccharyltransferase subunit ost4p	0	22	0	22	1	0	1	1	5	21	21	0	0	0	0	0	0	0	0	0	0	0	21
56835	103472	103473	MFS general substrate transporter	10000	1308	6803	1274	13	13	13	7	14	1831	1829	0	3	38	1708	0	8	106	1024	141	356	4	1
56835	103480	103481	Multidrug resistance efflux transporter EmrE	5000	754	4986	732	16	16	16	1	4	2792	2789	0	3	23	2711	74	0	0	1720	314	444	0	1
56835	103485	103486	V-type ATP synthase subunit C	2939	706	392	377	5	8	8	1	5	334	334	0	8	14	130	204	0	0	1	1	66	0	0
56835	103490	103491	Preprotein translocase SecY subunit	5000	1760	1180	95	22	19	23	16	11	932	931	0	14	17	15	202	70	237	15	0	0	54	313
56835	81344	103501	Respiratory nitrate reductase 1 gamma chain	5000	639	2842	634	10	10	10	6	4	1605	1603	0	6	12	1593	10	0	0	778	546	239	0	0
56835	103505	103506	Mitochondrial carrier	5000	636	4478	633	2	9	9	82	43	933	933	0	0	0	2	0	90	333	2	0	0	66	401
56835	103510	103511	Chlorophyll a-b binding protein	3356	603	2171	576	17	42	42	15	9	274	274	0	0	0	3	0	245	3	2	0	1	13	0
56835	56924	103515	Autotransporter	5000	1224	108	118	2	4	4	3	5	28	28	0	0	0	28	0	0	0	28	0	0	0	0
56992	57015	103565	Bubble protein	10	10	10	0	1	1	1	1	4	9	9	0	0	0	0	0	0	0	0	0	0	0	9
56992	57491	103575	Plexin repeat	7487	726	3583	683	3	118	118	123	58	246	245	0	0	0	0	0	0	244	0	0	0	0	0
56992	103579	103580	Necrosis inducing protein 1, NIP1	24	24	24	0	1	1	1	1	4	2	2	0	0	0	0	0	0	0	0	0	0	0	2
56992	103588	103589	Mini-collagen I, C-terminal domain	0	4	0	3	2	0	2	1	4	2	1	0	0	0	0	0	0	1	0	0	0	0	0
56992	103611	103612	SBT domain	1904	1233	1838	1214	2	3	3	9	8	104	104	0	0	0	0	0	104	0	0	0	0	0	0
56992	57769	103623	Hypothetical protein Ta0289 C-terminal domain	7	7	7	0	4	4	4	1	5	5	5	0	0	1	0	5	0	0	0	0	0	0	0
56992	103636	103637	CCHHC domain	2534	681	1360	680	1	5	5	32	12	233	233	0	0	0	0	0	0	233	0	0	0	0	0
56992	103641	103642	Sec-C motif	12	799	12	31	1	1	1	14	28	512	512	0	1	68	511	0	1	0	207	2	263	0	0
56992	103646	103647	TSP type-3 repeat	3704	625	1775	618	1	6	6	176	64	389	388	0	7	7	132	9	0	247	79	0	1	0	0
46456	116747	103657	BAR/IMD domain-like	25247	733	12279	730	10	117	117	193	73	723	722	0	0	0	0	0	39	302	0	0	0	0	371
46456	109603	109604	HD-domain/PDEase-like	42838	577	33543	539	38	672	672	114	65	8718	8691	22	62	278	7463	365	76	292	3103	1105	2054	52	401
46456	46556	109631	Transcriptional repressor TraM	70	135	68	82	12	10	12	1	4	47	47	0	0	0	47	0	0	0	47	0	0	0	0
46456	46556	109635	DnaK suppressor protein DksA, alpha-hairpin domain	3531	639	3444	638	10	15	15	3	6	2376	2374	0	21	32	2372	0	0	2	2332	0	2	0	0
46456	109639	109640	KRAB domain (Kruppel-associated box)	5000	661	1467	659	1	0	1	543	132	85	84	0	0	0	0	0	0	84	0	0	0	0	0
46456	46688	109709	KorB DNA-binding domain-like	6406	4073	6406	3938	12	12	12	12	10	5110	5107	0	12	233	5103	0	0	4	1805	1172	1299	0	0
46456	81602	109715	DEK C-terminal domain	2643	743	464	12	1	1	1	16	12	305	304	0	0	0	0	0	6	214	0	0	0	1	83
46456	46928	109728	Hypothetical protein AF0491, middle domain	1277	842	784	22	6	6	6	7	8	695	694	0	40	45	2	339	42	174	1	0	0	8	105
46456	46928	109732	HBS1-like domain	740	594	347	4	1	2	2	10	9	194	194	0	0	0	0	0	0	194	0	0	0	0	0
46456	46928	109736	FGAM synthase PurL, linker domain	5000	750	4999	749	8	8	8	11	36	2423	2423	0	4	7	2191	0	1	6	2142	32	5	0	224
46456	46965	109747	Glycogen synthesis protein GlgS	222	912	197	198	8	1	8	1	4	111	111	0	0	0	111	0	0	0	111	0	0	0	0
46456	46965	109751	Alpha-hemoglobin stabilizing protein AHSP	103	103	101	0	10	10	10	1	4	78	78	0	0	0	0	0	0	78	0	0	0	0	0
46456	46965	109755	PhoU-like	5617	1530	5617	1509	6	17	17	17	14	4066	4065	0	17	148	3838	224	1	2	2071	303	1145	0	0
46456	47161	109770	Nickel-containing superoxide dismutase, NiSOD	677	538	603	0	81	81	81	1	4	474	473	0	4	4	472	1	0	0	47	312	0	0	0
46456	47161	109775	Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain	1225	732	1020	0	1	1	1	12	9	178	177	0	0	0	0	0	0	177	0	0	0	0	0
46456	47161	109779	Domain from hypothetical 2610208m17rik protein	236	234	140	0	1	1	1	4	4	96	96	0	0	0	0	0	1	86	0	0	0	7	0
46456	47363	109797	Bacteriocin immunity protein-like	468	193	211	110	4	6	6	1	4	106	106	0	0	0	106	0	0	0	0	0	106	0	0
46456	47379	109801	Hypothetical protein D-63	2	7	2	5	4	4	4	0	4	6	1	5	0	0	0	1	0	0	0	0	0	0	0
46456	47405	109805	Phenylalanine zipper	812	554	750	532	3	3	3	8	7	186	186	0	0	0	0	0	0	186	0	0	0	0	0
46456	47654	109839	Cag-Z	124	124	114	0	1	1	1	1	4	5	5	0	0	0	5	0	0	0	5	0	0	0	0
46456	47654	109843	CAPPD, an extracellular domain of amyloid beta A4 protein	2454	632	0	632	5	0	5	13	19	137	136	0	0	0	0	0	0	136	0	0	0	0	0
46456	109853	109854	DinB/YfiT-like putative metalloenzymes	21439	595	10584	589	4	31	31	24	11	3258	3255	0	7	8	3090	3	3	1	1002	934	590	0	157
46456	109858	109859	NblA-like	97	181	97	149	12	12	12	1	4	105	105	0	2	2	105	0	0	0	0	0	0	0	0
46456	109879	109880	A middle domain of Talin 1	782	640	747	0	4	4	4	38	42	260	260	0	0	0	0	0	0	256	0	0	0	0	1
46456	109884	109885	I/LWEQ domain	22189	728	2105	726	1	11	11	89	77	692	692	0	0	0	0	0	0	273	0	0	0	0	401
46456	109904	109905	Surp module (SWAP domain)	4132	677	3829	676	1	7	7	76	32	837	837	0	0	0	0	0	73	278	0	0	0	81	365
46456	109909	109910	YgfY-like	3486	730	1879	713	5	6	6	3	6	1368	1367	0	1	2	1346	0	0	0	1341	0	1	11	9
46456	109914	109915	Hypothetical protein YhaI	234	234	234	0	3	3	3	1	4	150	150	0	0	0	150	0	0	0	0	0	150	0	0
46456	109919	109920	Hypothetical protein At3g22680	111	111	105	0	3	3	3	1	4	53	53	0	0	0	0	0	53	0	0	0	0	0	0
46456	109924	109925	Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain	657	553	598	0	14	14	14	21	7	472	472	0	0	0	0	0	0	155	0	0	0	14	293
46456	109992	109993	VPS9 domain	5000	873	1236	0	5	14	14	36	16	759	758	0	0	0	0	0	64	250	0	0	0	59	365
46456	109997	109998	Triger factor/SurA peptide-binding domain-like	10000	1283	6906	1270	14	14	14	26	15	2999	2996	0	9	24	2989	0	1	5	2706	2	236	0	1
46456	110003	110004	Glycolipid transfer protein, GLTP	2369	951	1661	888	33	78	78	9	6	695	695	0	0	0	0	0	104	269	0	0	0	10	302
46456	110008	110009	Hypothetical protein MG354	8	8	8	0	1	1	1	1	4	7	7	0	0	0	7	0	0	0	0	0	0	0	0
46456	110013	110014	Her-1	21	21	17	0	2	2	2	1	4	13	13	0	0	0	0	0	0	13	0	0	0	0	0
46456	110018	110019	ERO1-like	1408	996	995	0	6	6	6	8	9	651	651	0	0	0	0	0	65	242	0	0	0	16	309
46456	110034	110035	GDNF receptor-like	1430	647	1103	629	6	8	8	9	6	187	186	0	0	0	0	0	0	186	0	0	0	0	0
48724	48725	110069	ApaG-like	3830	1631	3693	8	6	9	9	16	8	2540	2539	0	8	12	2154	0	70	265	1771	1	1	23	1
48724	49379	110083	Peptidylarginine deiminase Pad4, middle domain	891	818	554	0	33	33	33	10	15	171	170	0	0	0	10	0	0	160	2	0	0	0	0
48724	49379	110087	DR1885-like metal-binding protein	5000	1371	3628	0	6	8	8	4	6	2187	2186	0	5	5	2185	0	0	1	1651	465	3	0	0
48724	110110	110111	Ctag/Cox11	3438	1410	3307	2	2	2	2	19	10	2453	2452	0	1	1	1714	0	63	234	1705	1	0	51	350
48724	110131	110132	BTV NS2-like ssRNA-binding domain	241	241	238	0	2	2	2	1	4	72	0	72	0	0	0	0	0	0	0	0	0	0	0
48724	50352	110217	DNA-binding protein LAG-1 (CSL)	1047	609	824	13	12	12	12	8	12	334	334	0	0	0	0	0	0	276	0	0	0	0	55
48724	50352	110221	AbfB domain	1871	722	540	503	8	16	16	21	13	364	364	0	0	0	245	0	0	0	11	227	7	0	118

48724	50964	110296	Oligoxyloglucan reducing end-specific cellobiohydrolase	5669	1261	1088	938	12	17	17	56	32	639	637	0	2	17	508	0	1	0	100	246	107	0	127
48724	110303	110304	Coronavirus RNA-binding domain	1250	1419	813	529	1739	19	1739	1	5	174	2	172	0	0	2	0	0	0	2	0	0	0	0
48724	51229	110324	Ribosomal L27 protein-like	6727	1357	6276	1357	195	328	328	25	17	4779	4775	0	34	258	3847	148	78	227	1640	238	1101	76	367
51349	51350	110391	GlpP-like	1754	1100	1675	0	12	12	12	1	4	996	996	0	0	33	996	0	0	0	101	45	782	0	0
51349	51350	110395	CutC-like	5000	803	4815	793	6	22	22	10	9	2738	2736	0	2	101	2422	0	4	210	847	289	704	5	82
51349	51350	110399	ThiG-like	5000	1214	5000	1197	8	8	8	7	12	3340	3339	0	5	39	3284	2	0	4	1625	685	333	28	0
51349	110454	110455	Toprim domain	8261	2053	2426	762	8	16	18	10	7	1415	1415	0	15	51	1267	148	0	0	1	1	1173	0	0
51349	110580	110581	Indigoidine synthase A-like	3294	968	3060	968	15	20	20	14	14	2156	2156	0	3	34	1561	0	64	163	647	477	284	24	327
51349	110709	110710	TTHA0583/YokD-like	3942	1583	3179	664	29	33	33	5	5	1745	1740	0	3	72	1683	37	0	1	120	300	1176	0	18
51349	110737	110738	Glycerate kinase I	4171	1730	4141	50	4	4	4	2	8	1435	1434	1	0	39	1434	0	0	0	759	19	617	0	0
53931	110782	110783	Hypothetical protein MTH677	42	36	32	0	7	7	7	1	4	27	27	0	0	0	0	27	0	0	0	0	0	0	0
53931	54235	110814	TmoB-like	111	112	99	0	39	39	39	1	4	83	83	0	0	0	83	0	0	0	53	25	2	0	0
53931	110835	110836	Hypothetical protein SAV1430	3444	1347	968	714	5	7	7	14	6	511	511	0	2	3	497	1	0	10	30	1	456	0	1
53931	110848	110849	ParB/Sulfiredoxin	8967	659	8299	556	6	28	28	11	16	5238	5236	0	9	273	5034	18	3	174	1857	979	1519	0	0
53931	110856	110857	Gamma-glutamyl cyclotransferase-like	10418	571	2955	504	5	10	10	17	10	1881	1862	18	6	11	1468	69	54	241	808	137	292	16	7
53931	54767	110916	Peptidyl-tRNA hydrolase domain-like	5000	1272	4578	1200	4	8	8	6	6	3529	3527	0	12	15	2968	0	62	248	1905	625	2	33	202
53931	110920	110921	2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain	5000	845	4843	840	10	10	10	13	15	3278	3278	0	4	126	2914	0	0	5	1148	1185	496	0	359
53931	110941	110942	HSP90 C-terminal domain	5000	621	4996	617	14	14	14	5	11	2759	2759	0	12	34	2725	0	0	6	2079	409	147	0	13
53931	54861	110993	eIF-2-alpha, C-terminal domain	1221	1138	1034	2	14	14	14	12	14	890	889	0	20	23	0	183	70	196	0	0	0	53	344
53931	54861	110997	Sporulation related repeat	211	751	201	637	1	0	1	2	7	332	332	0	0	0	331	0	0	0	331	0	0	0	1
53931	111005	111006	Dystroglycan, domain 2	446	451	326	0	2	2	2	4	5	209	209	0	0	0	0	0	0	209	0	0	0	0	0
53931	111037	111038	YjbQ-like	5177	1157	5138	14	16	22	22	9	11	3512	3509	0	24	79	2818	262	71	62	1512	76	477	17	266
53931	111056	111057	Hypothetical protein PF0899	41	41	39	0	1	1	1	1	4	22	22	0	0	0	0	22	0	0	0	0	0	0	0
53931	111063	111064	Hut operon positive regulatory protein HutP	275	518	215	0	40	40	40	1	4	156	156	0	0	0	156	0	0	0	0	1	142	0	0
53931	111068	111069	Hypothetical protein yfbM	962	637	336	0	2	2	2	1	4	171	171	0	0	3	171	0	0	0	40	6	96	0	0
53931	111073	111074	Bacillus phage protein	71	177	25	1	2	2	2	0	4	15	14	1	0	0	14	0	0	0	0	0	14	0	0
53931	111125	111126	Ligand-binding domain in the NO signalling and Golgi transport	7473	674	2741	673	12	109	109	38	19	1325	1324	0	1	1	479	27	73	273	245	2	114	58	369
53931	111147	111148	YggX-like	1865	850	1835	2	2	4	4	4	6	1359	1359	0	3	8	1359	0	0	0	1314	0	2	0	0
53931	55944	111171	Rbstp2229 protein	227	228	223	0	1	1	1	1	5	143	143	0	0	0	143	0	0	0	0	0	143	0	0
53931	111248	111249	Sulfolobus fructose-1,6-bisphosphatase-like	380	382	357	0	8	8	8	1	4	310	309	0	18	22	130	179	0	0	26	11	31	0	0
53931	111264	111265	Hemolytic lectin CEL-III, C-terminal domain	9	53	9	8	13	13	13	1	6	4	4	0	0	0	0	0	0	2	0	0	0	2	0
53931	111277	111278	SSo0622-like	953	674	339	0	11	11	11	34	8	267	267	0	6	6	0	99	39	113	0	0	0	10	5
53931	111282	111283	Putative modulator of DNA gyrase, PmbA/TldD	5585	2388	5207	2367	4	8	8	4	7	2995	2993	0	8	51	2974	15	0	4	2489	10	201	0	0
56572	111303	111304	Recombination protein RecR	5000	1301	4994	1299	23	23	23	6	7	3715	3714	0	11	188	3711	1	0	2	1086	910	1268	0	0
56572	111320	111321	AF1104-like	2720	871	1151	17	6	7	7	7	13	809	807	0	8	22	359	142	71	227	119	0	160	0	4
56572	111325	111326	Urocanase	5000	586	4911	579	10	16	16	2	7	2852	2852	0	10	16	2764	82	1	4	1585	703	321	0	1
56572	111330	111331	NAD kinase/diacylglycerol kinase-like	10988	2430	10871	2422	18	60	60	14	13	6023	6021	0	24	261	5828	135	52	4	2031	1100	1682	0	2
56572	111336	111337	QueA-like	5000	2332	2955	1491	2	4	4	1	7	2051	2050	0	2	133	2047	2	0	1	517	0	1155	0	0
56572	111341	111342	CbiD-like	3842	1269	1460	592	1	1	1	3	6	871	871	0	15	28	750	121	0	0	353	107	159	0	0
56572	111346	111347	Rap/Ran-GAP	5000	745	2941	743	7	7	7	34	20	286	286	0	0	0	0	0	0	267	0	0	0	0	4
56835	111351	111352	Ammonium transporter	5000	588	4995	587	31	31	31	9	25	2885	2885	0	8	29	2434	25	2	4	1658	288	260	10	409
56835	111356	111357	Mitochondrial ATP synthase coupling factor 6	415	435	406	3	7	7	7	4	5	251	250	0	0	0	0	0	0	250	0	0	0	0	0
56835	56924	111364	Tsx-like channel	2551	707	865	602	6	6	6	1	4	430	430	0	0	0	430	0	0	0	428	0	1	0	0
56835	111368	111369	HlyD-like secretion proteins	5000	810	5000	800	39	43	43	13	7	1971	1969	0	3	11	1967	0	0	1	1941	1	2	0	1
56835	111378	111379	VP4 membrane interaction domain	3533	619	1615	96	9	14	14	1	5	237	0	237	0	0	0	0	0	0	0	0	0	0	0
56835	111383	111384	OmpH-like	2003	968	187	211	6	6	6	1	4	135	135	0	0	0	135	0	0	0	131	0	4	0	0
56992	57006	111388	Pollen allergen ole e 6	12	34	12	22	1	1	1	1	4	18	18	0	0	0	0	0	18	0	0	0	0	0	0
56992	111417	111418	Hormone receptor domain	5081	1437	1703	545	19	52	52	8	6	213	212	0	0	0	0	0	0	212	0	0	0	0	0
56992	111422	111423	Resistin	218	227	180	0	12	12	12	2	5	87	87	0	0	0	0	0	0	87	0	0	0	0	0
56992	111429	111430	YAP1 redox domain	932	850	87	2	2	1	2	3	5	81	81	0	0	0	1	0	0	0	1	0	0	0	80
53931	116725	116726	TrkA C-terminal domain-like	5902	939	4089	646	4	72	72	25	26	2486	2486	0	9	89	2253	230	1	1	623	277	742	0	1
53931	116733	116734	DNA methylase specificity domain	9657	852	8594	851	2	27	27	27	12	3574	3573	1	11	72	3469	102	0	1	1460	206	950	0	0
56992	57769	116738	NADH pyrophosphatase intervening domain	263	520	263	257	3	3	3	3	7	225	225	0	0	0	224	0	0	1	223	0	1	0	0
46456	47768	116742	eIF2alpha middle domain-like	1214	876	966	684	13	15	15	13	14	823	822	0	6	8	0	137	71	198	0	0	0	60	331
46456	63450	116768	DNA-binding domain of EIN3-like	548	535	507	0	1	1	1	1	4	94	94	0	0	0	0	0	94	0	0	0	0	0	0
46456	46688	116820	Rps17e-like	1314	892	1259	40	71	73	73	20	15	954	953	0	25	31	2	283	76	217	2	0	0	45	288
46456	46965	116842	XseB-like	4329	656	4066	0	6	6	6	4	6	3246	3245	0	7	94	3223	20	0	1	2073	195	786	0	1
46456	46965	116846	MIT domain	3801	1102	2855	1049	21	25	25	62	37	827	826	0	1	1	4	13	74	277	1	0	0	55	363
46456	46996	116854	Avirulence protein AvrPto	22	22	22	0	2	2	2	2	4	18	17	0	0	0	17	0	0	0	17	0	0	0	0
46456	47013	116858	Hypothetical membrane protein Ta0354, soluble domain	12	16	12	4	1	1	1	1	4	15	15	0	2	7	0	15	0	0	0	0	0	0	0
46456	47161	116878	TrmE connector domain	5000	1203	2126	927	2	2	2	9	12	1205	1205	0	6	21	1198	0	2	4	432	1	715	0	1
46456	47575	116907	Hook domain	2493	758	1882	729	1	1	1	10	12	448	447	0	0	0	0	0	1	255	0	0	0	16	167
46456	116914	116915	Hypothetical protein YqbG	161	1003	142	1	2	2	2	1	4	49	49	0	0	1	49	0	0	0	0	0	48	0	0
46456	116921	116922	YugE-like	383	600	287	4	2	2	2	1	4	194	194	0	0	0	194	0	0	0	0	0	192	0	0
46456	116926	116927	EspA/CesA-like	144	145	77	0	6	6	6	2	4	28	28	0	0	0	28	0	0	0	28	0	0	0	0
46456	116941	116942	RNA-binding protein She2p	42	42	41	0	2	2	2	2	5	36	35	0	0	0	0	0	0	0	0	0	0	0	35
46456	116959	116960	YfbU-like	871	547	704	0	32	32	32	3	5	434	434	0	1	2	431	2	0	0	387	10	20	0	1
46456	116964	116965	Hypothetical protein MPN330	3798	0	12	0	0	1	1	1	4	9	9	0	0	0	9	0	0	0	0	0	0	0	0
46456	117017	117018	ATP-dependent DNA ligase DNA-binding domain	5000	985	1389	927	1	15	15	23	13	802	795	6	1	1	3	50	68	198	0	0	0	31	410
46456	117022	117023	DNA primase DnaG, C-terminal domain	2489	662	1707	653	3	6	6	10	6	821	821	0	1	1	821	0	0	0	819	0	0	0	0
48724	48725	117066	Accessory protein X4 (ORF8, ORF7a)	23	23	22	0	2	2	2	1	4	16	0	16	0	0	0	0	0	0	0	0	0	0	0
48724	48725	117070	LEA14-like	5567	1039	361	352	2	2	2	2	5	126	126	0	0	0	34	0	92	0	21	0	0	0	0
48724	49451	117074	Hypothetical protein PA1324	267	1842	83	82	353	2	353	0	4	58	57	0	0	0	57	0	0	0	54	0	0	0	0
48724	117099	117100	Beta-galactosidase LacA, domain 3	903	633	383	0	7	7	7	21	18	213	213	0	0	0	5	0	0	0	0	4	1	0	208
48724	117124	117125	Putative glucosidase YicI, C-terminal domain	1685	713	1155	1	30	30	30	4	8	374	374	0	1	15	372	0	0	1	193	13	154	0	1
48724	117129	117130	CsrA-like	3058	617	3019	616	6	31	31	8	10	1956	1952	3	5	46	1948	0	0	3	954	107	687	0	0
48724	117142	117143	Flagellar hook protein flgE	5000	595	3810	583	5	5	5	11	5	2092	2092	0	5	25	2090	0	0	1	1697	69	160	0	0
48724	50938	117281	Kelch motif	5000	3365	1716	212	38	42	42	51	26	286	284	0	0	0	6	0	11	264	3	0	3	1	0
48724	50964	117289	Nucleoporin domain	20000	1568	0	247	1	130	131	3	6	179	179	0	0	0	0	0	0	179	0	0	0	0	0
51349	51350	117396	TM1631-like	6063	2932	4296	2579	4	4	4	3	6	2505	2503	0	8	13	2461	37	1	2	951	521	621	0	0
51349	52008	117457	FumA C-terminal domain-like	5000	993	5000	993	1	0	1	5	7	2874	2873	0	12	156	2703	147	1	12	1555	324	587	0	1
53931	117772	117773	GTF2I-like repeat	1254	993	1234	959	7	10	10	28	19	176	175	0	0	0	0	0	0	175	0	0	0	0	0
53931	88797	117778	D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain	325	328	325	0	1	1	1	2	5	273	273	0	1	14	273	0	0	0	21	99	93	0	0
53931	88797	117782	YbjQ-like	4542	699	4013	696	5	15	15	8	7	2756	2754	1	17	85	2551	152	0	1	966	418	656	14	30
53931	117838	117839	WWE domain	4117	862	2583	811	6	9	9	85	48	317	317	0	0	0	0	0	0	281	0	0	0	14	0
53931	117855	117856	AF0104/ALDC/Ptd012-like	7630	1526	4568	1477	4	23	23	15	11	2564	2563	0	20	83	1932	220	39	248	717	176	722	7	109
53931	54712	117892	Band 7/SPFH domain	5000	860	1478	40	1	1	1	11	11	751	750	0	1	3	510	1	0	234	21	23	397	1	0
53931	54805	117916	Fe-S cluster assembly (FSCA) domain-like	11066	909	11036	901	3	26	26	41	29	6207	6203	1	40	146	5235	154	78	263	2188	983	867	61	376
53931	54861	117987	CRISPR-associated protein	1593	909	843	0	22	22	22	2	5	556	555	0	2	8	548	7	0	0	152	258	75	0	0
53931	54861	117991	YbeD/HP0495-like	2769	1557	2472	1537	3	3	3	5	10	1734	1733	0	8	14	1711	0	14	2	1461	0	3	3	1
53931	118000	118001	YehU-like	992	772	609	0	1	1	1	1	4	416	415	0	0	0	415	0	0	0	414	0	1	0	0
53931	55158	118010	TM1457-like	2121	832	2060	784	4	16	16	1	4	1500	1497	2	1	183	1497	0	0	0	1	0	1315	0	0
53931	55944	118104	RalF, C-terminal domain	46	46	44	0	5	5	5	1	5	15	15	0	0	0	15	0	0	0	15	0	0	0	0
53931	118115	118116	DNA mismatch repair protein MutL	5000	661	1428	660	2	4	4	4	6	369	369	0	2	3	368	0	0	1	366	0	0	0	0
53931	118172	118173	Phosphoprotein M1, C-terminal domain	818	546	604	0	3	4	4	1	4	28	0	28	0	0	0	0	0	0	0	0	0	0	0
56572	118195	118196	YaeB-like	5000	685	1676	683	2	6	6	2	6	896	894	0	2	33	877	2	0	14	783	2	69	0	0
56572	118202	118203	Vacuolar ATP synthase subunit C	1329	975	1082	0	7	7	7	6	6	718	717	0	0	0	0	0	72	247	0	0	0	43	319
56572	118207	118208	Viral ssDNA binding protein	271	275	189	0	2	2	2	1	4	82	0	81	0	0	0	0	0	0	0	0	0	0	0
56835	118214	118215	Proton glutamate symport protein	5000	2310	5000	2303	69	69	69	1	5	2664	2663	0	2	42	2579	80	0	4	1632	109	682	0	0
56835	118219	118220	Connexin43	197	199	182	0	1	1	1	3	4	146	145	0	0	0	0	0	0	145	0	0	0	0	0
56992	57491	118251	Variant surface glycoprotein MITAT 1.2, VSG 221, C-terminal domain	101	262	71	129	1	1	1	5	4	7	7	0	0	0	0	0	0	0	0	0	0	0	0
56992	118289	118290	WRKY DNA-binding domain	5000	767	4999	754	2	3	3	32	17	179	179	0	0	0	0	0	174	0	0	0	0	0	0
56992	118309	118310	AN1-like Zinc finger	3849	1894	2385	570	7	7	8	17	10	468	468	0	0	0	0	0	91	274	0	0	0	41	46
56992	118351	118352	HSP33 redox switch-like	5110	1523	5109	1518	4	4	4	3	6	3284	3281	0	4	173	3275	0	2	0	1524	4	1469	2	1
56992	118358	118359	Expressed protein At2g23090/F21P24.15	418	684	375	19	1	1	1	8	7	283	283	0	0	0	0	0	67	3	0	0	0	39	159
46456	46556	140102	ISY1 domain-like	862	664	794	0	1	1	1	12	8	708	707	0	0	0	1	0	68	228	0	0	1	51	340
46456	46556	140106	Calcyclin-binding protein-like	121	222	121	98	4	0	4	6	5	133	133	0	0	0	0	0	0	133	0	0	0	0	0
46456	46556	140111	Endosomal sorting complex assembly domain	2972	628	1541	620	7	19	19	18	14	768	767	0	0	0	0	0	68	263	0	0	0	16	387
46456	46556	140121	SPy1572-like	213	213	211	0	1	1	1	2	5	84	84	0	0	0	84	0	0	0	0	0	83	0	0
46456	46556	140125	Rabenosyn-5 Rab-binding domain-like	425	726	350	3	21	21	21	11	9	246	246	0	0	0	0	0	0	244	0	0	0	0	2
46456	46556	140129	MxiH-like	297	328	240	12	103	103	103	1	5	142	142	0	0	0	142	0	0	0	141	0	1	0	0
46456	81602	140319	IscX-like	1279	811	1275	0	2	2	2	3	6	897	896	0	2	6	877	0	1	0	806	2	2	17	1
46456	46965	140356	PPK N-terminal domain-like	6644	2104	4898	1753	6	6	6	8	15	3202	3201	0	6	91	3172	29	0	0	1462	715	520	0	0
46456	46965	140361	MIT domain-like	3664	1128	220	242	2	23	24	1	4	184	183	0	0	0	0	0	0	182	0	0	0	0	1
46456	46996	140367	Coronavirus NSP7-like	1170	667	1170	83	10	10	10	51	21	214	0	212	0	0	0	0	0	0	0	0	0	0	0
46456	46996	140371	Vng1086c-like	295	308	239	2	2	2	2	1	4	148	148	0	8	8	0	148	0	0	0	0	0	0	0
46456	140375	140376	ChaB-like	718	584	595	2	1	1	1	1	5	389	376	12	0	0	358	15	0	1	289	4	13	0	1
46456	140382	140383	BSD domain-like	2190	1292	1070	530	2	2	2	13	9	439	438	0	0	0	0	0	55	275	0	0	0	42	57
46456	47143	140404	EF2458-like	559	542	545	0	4	4	4	1	4	420	420	0	0	0	420	0	0	0	0	0	419	0	0
46456	47161	140415	YppE-like	530	513	518	0	5	5	5	1	4	335	335	0	0	0	335	0	0	0	0	0	334	0	0
46456	47161	140423	MW0975(SA0943)-like	2410	2248	0	328	1	0	1	1	4	157	157	0	0	0	157	0	0	0	0	0	156	0	0
46456	47161	140427	VPS28 C-terminal domain-like	794	707	745	0	12	12	12	11	10	633	632	0	0	0	0	0	68	199	0	0	0	24	310
46456	47239	140453	EsxAB dimer-like	3688	1495	1488	688	37	59	59	3	5	795	794	0	0	6	794	0	0	0	1	747	44	0	0
46456	47239	140459	PE/PPE dimer-like	5016	1420	5015	1400	12	6	12	63	6	654	654	0	0	0	654	0	0	0	0	654	0	0	0
46456	47363	140478	LemA-like	5000	2405	5000	50	1	1	1	2	5	3436	3435	0	9	138	3389	45	0	1	1458	310	675	0	0
46456	47363	140482	MAST3 pre-PK domain-like	1886	1014	1842	7	2	2	2	14	11	260	259	0	0	0	0	0	0	259	0	0	0	0	0
46456	47363	140486	PA2201 N-terminal domain-like	92	92	91	0	3	3	3	1	5	12	11	0	0	0	11	0	0	0	11	0	0	0	0
46456	47363	140490	Nqo1C-terminal domain-like	5000	1164	4999	1163	17	17	17	43	32	3660	3658	0	5	15	3018	0	67	233	1828	785	79	22	290
46456	47379	140496	HP1531-like	71	72	70	0	6	6	6	1	4	29	29	0	0	0	29	0	0	0	29	0	0	0	0
46456	47379	140500	BAS1536-like	45	790	45	385	3	1	3	2	5	163	163	0	0	0	163	0	0	0	0	0	163	0	0
46456	47379	140506	FHV B2 protein-like	7	7	7	0	6	6	6	1	4	4	0	4	0	0	0	0	0	0	0	0	0	0	0
46456	47643	140560	TM0693-like	6	9	6	3	4	4	4	0	4	7	7	0	0	0	7	0	0	0	0	0	0	0	0
46456	47654	140566	FlgN-like	1245	795	425	0	1	3	3	1	4	229	228	0	0	0	228	0	0	0	228	0	0	0	0
46456	47654	140570	MukF C-terminal domain-like	1078	611	1021	389	7	7	7	2	5	469	469	0	0	1	467	0	0	1	466	0	1	0	1
46456	47667	140576	HIV integrase-binding domain	671	530	610	0	29	29	29	5	7	211	210	0	0	0	0	0	0	210	0	0	0	0	0
46456	140580	140581	TraM-like	336	436	312	29	14	10	14	1	5	75	74	0	0	0	73	0	0	1	73	0	0	0	0
46456	140585	140586	Dcp2 domain-like	1042	698	876	695	7	7	7	10	8	707	707	0	0	0	0	0	63	184	0	0	0	53	394
46456	140590	140591	Type III secretion system domain	3746	877	398	237	14	13	17	4	5	92	91	0	0	0	91	0	0	0	86	0	1	0	0
46456	140606	140607	EF2947-like	9	9	9	0	1	1	1	1	4	6	6	0	0	0	6	0	0	0	0	0	6	0	0
46456	140611	140612	EB1 dimerisation domain-like	1694	717	1535	0	23	23	23	19	18	616	615	0	0	0	0	0	70	266	0	0	0	21	247
46456	47768	140652	YozE-like	823	782	818	0	3	3	3	1	4	557	557	0	0	1	557	0	0	0	1	0	555	0	0
46456	140656	140657	Hyaluronidase post-catalytic domain-like	1285	756	250	216	34	54	54	14	13	128	128	0	0	26	126	0	0	0	0	11	28	0	2
46456	140656	140663	TTHA0068-like	2400	1310	922	169	5	5	5	3	7	683	683	0	5	5	569	110	3	0	26	211	187	1	0
46456	140669	140670	YoaC-like	268	294	194	0	2	2	2	1	4	96	96	0	0	0	96	0	0	0	95	0	1	0	0
46456	140682	140683	SP0561-like	848	627	609	1	1	1	1	16	6	422	422	0	1	4	419	3	0	0	5	11	331	0	0
46456	140687	140688	YfmB-like	83	83	82	0	2	2	2	1	4	47	47	0	0	0	47	0	0	0	0	0	47	0	0
46456	140692	140693	IpaD-like	465	1303	366	43	34	34	34	2	5	126	126	0	0	0	126	0	0	0	126	0	0	0	0
46456	140712	140713	Phage replication organizer domain	6	8	6	2	10	10	10	1	4	6	0	6	0	0	0	0	0	0	0	0	0	0	0
46456	140717	140718	Mediator hinge subcomplex-like	1565	1398	1049	1	6	6	6	14	12	666	665	0	0	0	0	0	62	252	0	0	0	13	324
46456	140725	140726	AF0941-like	5	4	5	0	2	2	2	1	4	4	4	0	0	0	0	4	0	0	0	0	0	0	0

46456	140730	140731	PA2201 C-terminal domain-like	939	659	250	0	3	3	3	2	5	71	70	0	0	1	70	0	0	0	46	0	20	0	0
46456	140735	140736	Rv1873-like	1222	866	1185	849	1	1	1	9	7	854	854	0	1	28	837	6	0	0	508	150	50	0	6
46456	140740	140741	RUN domain-like	5000	772	1999	768	5	6	6	14	13	257	256	0	0	0	0	0	0	250	0	0	0	0	0
46456	140745	140746	SipA N-terminal domain-like	256	254	242	0	2	2	2	1	6	94	94	0	0	0	94	0	0	0	94	0	0	0	0
46456	140752	140753	PG0816-like	662	547	625	0	1	1	1	1	4	240	240	0	1	8	240	0	0	0	0	2	0	0	0
46456	140803	140804	YidB-like	1708	727	1002	0	1	1	1	5	6	585	584	0	1	1	582	0	0	1	551	12	2	0	1
46456	140808	140809	Rhabdovirus nucleoprotein-like	3378	1161	1747	888	82	82	82	1	4	164	2	162	0	0	0	0	0	2	0	0	0	0	0
46456	48370	140856	USP8 N-terminal domain-like	1533	1017	364	0	4	4	4	13	9	207	207	0	0	0	0	0	0	205	0	0	0	0	2
46456	48370	140860	Pseudo ankyrin repeat-like	5000	2548	0	33	27	2	29	0	4	8	8	0	0	0	8	0	0	0	8	0	0	0	0
46456	48370	140864	TROVE domain-like	1602	743	453	426	6	6	6	2	8	323	310	13	1	1	92	0	1	215	7	15	3	0	0
46456	140868	140869	GUN4-like	1480	863	1103	0	5	5	5	25	12	342	342	0	0	0	247	0	70	0	1	1	0	5	0
46456	140913	140914	PriB N-terminal domain-like	336	893	97	96	13	5	13	1	4	87	87	0	10	11	0	87	0	0	0	0	0	0	0
46456	140918	140919	DNA terminal protein	7	7	6	0	6	6	6	1	4	5	0	5	0	0	0	0	0	0	0	0	0	0	0
46456	140923	140924	Duffy binding domain-like	5209	840	2532	800	8	32	32	153	11	38	37	0	0	0	0	0	0	0	0	0	0	37	0
46456	140930	140931	Fic-like	12378	738	945	736	25	70	70	6	4	498	498	0	3	51	496	2	0	0	137	9	200	0	0
46456	140958	140959	Indolic compounds 2,3-dioxygenase-like	5570	1050	4114	949	8	73	73	21	18	2456	2455	0	11	11	1761	12	3	259	871	613	194	7	400
46456	140978	140979	Topoisomerase V catalytic domain-like	6	6	6	0	11	11	11	2	7	2	2	0	0	0	0	2	0	0	0	0	0	0	0
46456	140983	140984	PTPA-like	1640	829	1466	20	21	23	23	10	8	828	827	0	0	0	0	0	64	255	0	0	0	54	413
46456	140989	140990	FtsH protease domain-like	5000	1178	5000	1176	15	15	15	6	33	3681	3679	0	8	76	3652	1	25	1	1643	936	730	0	0
46456	140995	140996	Hermes dimerisation domain	1465	1141	12	4	6	6	6	3	7	8	8	0	0	0	0	0	0	8	0	0	0	0	0
46456	48661	141000	Glu-tRNAGln amidotransferase C subunit	5000	773	4936	767	6	34	34	6	11	3933	3932	0	11	111	3865	66	0	0	1473	812	991	0	0
46456	48661	141004	RelB-like	1	6	1	5	2	2	2	0	4	6	6	0	0	0	0	6	0	0	0	0	0	0	0
48724	48725	141066	ICP-like	1179	552	880	0	17	17	17	14	10	544	543	0	1	2	460	52	0	1	276	98	43	7	0
48724	48725	141072	CalX-like	5413	1237	4726	0	10	32	32	447	109	1042	1041	0	3	3	225	2	3	792	88	7	32	13	1
48724	141085	141086	Agglutinin HPA-like	463	541	228	0	32	32	32	5	6	166	166	0	0	0	129	0	0	5	119	0	2	0	25
48724	141090	141091	L21p-like	5000	1008	5000	1008	192	304	304	4	10	4142	4140	0	10	209	4116	0	15	3	1753	414	1186	1	0
48724	141098	141099	Atu1913-like	461	571	200	0	1	1	1	3	5	149	149	0	0	4	148	0	0	0	104	18	18	0	1
48724	49853	141130	Acetamidase/Formamidase-like	4648	964	2026	877	12	24	24	6	8	1259	1257	0	7	19	1081	92	0	0	408	237	281	0	84
48724	50036	141251	Kinase-associated protein B-like	496	499	440	0	2	2	2	1	5	270	270	0	0	0	270	0	0	0	0	0	270	0	0
48724	50036	141255	YccV-like	1861	756	306	277	1	1	1	2	6	230	230	0	0	0	229	0	0	0	225	3	0	0	1
48724	50036	141259	CarD-like	5000	797	5000	795	2	2	2	5	18	2400	2400	0	5	12	2400	0	0	0	2097	1	300	0	0
48724	50181	141300	GatD N-terminal domain-like	309	361	162	3	4	4	4	1	5	142	142	0	20	21	1	141	0	0	1	0	0	0	0
48724	50198	141318	TM0957-like	835	672	25	0	4	4	4	1	4	21	21	0	0	0	21	0	0	0	0	0	0	0	0
48724	50198	141322	NfeD domain-like	5000	1040	268	212	2	4	4	3	4	164	164	0	0	3	118	46	0	0	62	0	33	0	0
48724	50474	141371	PilZ domain-like	7362	596	1234	594	2	18	18	4	5	650	650	0	1	1	650	0	0	0	642	0	2	0	0
48724	50728	141447	PA2021-like	209	210	182	0	1	1	1	1	4	81	81	0	0	0	80	0	0	0	80	0	0	0	1
48724	141451	141452	Hcp1-like	5000	758	1879	739	15	31	31	4	5	838	837	0	2	2	834	2	0	0	773	18	2	0	1
48724	141456	141457	BH3618-like	2096	732	1614	728	2	2	2	3	6	1263	1263	0	2	48	1263	0	0	0	205	74	787	0	0
48724	50875	141480	Extracellular hemoglobin linker subunit, receptor domain	20	0	18	0	0	39	39	2	5	9	9	0	0	0	0	0	0	9	0	0	0	0	0
48724	50875	141488	YdhA-like	2097	520	967	507	1	10	10	6	4	566	565	0	0	1	564	0	0	0	547	0	1	0	1
48724	141492	141493	Allene oxide cyclase-like	438	987	234	213	61	61	61	2	4	85	85	0	0	0	0	0	85	0	0	0	0	0	0
48724	141522	141523	L,D-transpeptidase catalytic domain-like	20118	1570	10093	1557	22	52	52	72	25	4143	4141	0	9	138	4141	0	0	0	992	1228	1457	0	0
48724	141529	141530	PTSIIA/GutA-like	1285	925	686	0	2	2	2	1	4	400	400	0	0	4	400	0	0	0	78	16	303	0	0
48724	141561	141562	At5g01610-like	1902	752	265	0	1	1	1	2	5	64	64	0	0	0	0	0	64	0	0	0	0	0	0
48724	51125	141571	Pentapeptide repeat-like	6608	716	5445	714	2	12	12	457	41	1690	1674	16	31	36	1312	92	67	186	613	258	114	4	0
48724	141657	141658	Bacteriophage trimeric proteins domain	196	90	106	0	69	82	82	3	8	92	14	78	1	1	14	0	0	0	9	0	3	0	0
48724	141665	141666	'SARS ORF9b-like	25	25	25	0	8	8	8	1	4	21	0	21	0	0	0	0	0	0	0	0	0	0	0
48724	141672	141673	MOSC N-terminal domain-like	5000	675	1459	653	1	1	1	8	7	791	790	0	2	2	547	0	57	182	406	122	0	1	0
48724	141677	141678	MAL13P1.257-like	981	651	652	0	2	2	2	10	9	568	568	0	0	0	0	0	66	199	0	0	0	48	244
48724	89446	141694	AF2212/PG0164-like	1842	834	608	495	3	3	3	7	7	421	421	0	2	6	409	11	0	1	8	167	166	0	0
48724	141728	141729	FimD N-terminal domain-like	5000	764	4995	764	5	7	7	8	9	1044	1044	0	0	1	1043	0	0	0	1041	1	1	0	1
48724	141733	141734	HisI-like	5000	1539	5000	36	2	2	2	7	13	3759	3756	0	18	145	3571	182	0	0	1672	644	894	0	0
48724	141738	141739	MFPT repeat-like	171	174	134	0	3	3	3	2	6	18	18	0	0	0	0	0	0	18	0	0	0	0	0
51349	51350	141868	EAL domain-like	5000	2020	497	1053	8	6	10	102	48	869	868	0	3	3	868	0	0	0	491	8	302	0	0
51349	52008	141986	LD-carboxypeptidase A C-terminal domain-like	5000	2381	4477	2352	8	42	42	6	9	2578	2576	0	8	53	2575	1	0	0	1056	400	415	0	0
51349	142018	142019	Nqo1 FMN-binding domain-like	5000	2899	4999	2888	17	17	17	57	31	3807	3804	0	8	65	3205	14	66	185	1728	632	341	21	280
51349	142337	142338	CofD-like	6420	2470	6347	2357	17	21	21	7	7	3803	3803	0	27	107	3557	234	0	0	610	1144	1219	11	1
51349	52953	142433	CinA-like	5000	934	4579	930	2	2	2	6	10	2968	2966	0	7	93	2951	12	0	3	1991	123	373	0	0
51349	53162	142535	AF0625-like	527	519	449	0	4	4	4	4	7	379	377	0	27	33	16	305	54	0	8	0	7	1	0
51349	142694	142695	RibA-like	5000	734	5000	734	3	5	5	6	15	3409	3408	0	7	130	3337	5	64	1	1015	616	896	0	0
51349	142753	142754	NadA-like	5000	1011	5000	1010	3	2	3	4	9	3381	3381	0	22	135	3238	139	0	2	1939	173	366	0	1
51349	142763	142764	YgbK-like	5000	767	3370	767	4	9	9	11	10	1469	1468	0	3	20	1463	5	0	0	1018	135	261	0	0
51349	142794	142795	CAC2185-like	5000	2875	15	14	4	4	4	1	4	11	11	0	0	2	11	0	0	0	0	0	11	0	0
51349	142822	142823	ComB-like	2060	988	1075	0	7	15	15	2	5	833	833	0	7	12	794	31	0	1	18	5	308	1	0
53931	142876	142877	EndoU-like	1991	1457	1700	0	16	16	16	47	19	602	362	238	0	0	25	0	60	258	8	0	7	14	1
53931	54116	142887	PhtA domain-like	2660	857	2430	845	3	3	3	31	14	241	240	0	0	0	240	0	0	0	1	0	238	0	0
53931	142896	142897	TFB5-like	381	515	334	32	6	3	6	4	6	311	311	0	0	0	0	0	44	132	0	0	0	3	126
53931	69634	142906	YjbR-like	5376	1309	4055	1275	2	7	7	8	8	2454	2454	0	3	106	2454	0	0	0	883	514	479	0	0
53931	142912	142913	YktB/PF0168-like	951	741	875	0	2	3	3	2	4	542	542	0	1	1	521	21	0	0	0	3	517	0	0
53931	142920	142921	WGR domain-like	2368	802	1377	753	9	10	10	86	55	567	566	0	0	0	0	0	61	265	0	0	0	28	186
53931	54235	142984	Nqo1 middle domain-like	5000	751	5000	750	17	17	17	84	31	3409	3406	0	12	119	2961	27	63	55	1605	390	495	6	261
53931	143010	143011	RelE-like	10850	1250	7566	1197	9	74	74	11	5	3199	3192	6	15	102	3122	68	0	1	1299	482	621	0	1
53931	143020	143021	Ns1 effector domain-like	5000	671	5000	665	22	29	29	1	6	4931	0	4929	0	0	0	0	0	0	0	0	0	0	0
53931	143025	143026	Kinetochore globular domain	258	324	201	0	8	8	8	2	6	186	186	0	0	0	0	0	0	0	0	0	0	0	186
53931	143033	143034	L35p-like	3944	2414	3919	223	302	262	302	3	6	3496	3494	0	15	162	3349	0	67	2	1390	493	703	35	34
53931	143075	143076	Coronavirus NSP8-like	1210	927	1197	0	4	6	6	53	22	231	1	228	0	0	1	0	0	0	1	0	0	0	0
53931	143080	143081	BB1717-like	7026	746	6798	704	3	9	9	11	8	3683	3677	4	14	20	3093	101	55	148	1480	933	342	8	269
53931	143099	143100	TTHA1013/TTHA0281-like	5155	1987	542	76	5	11	11	4	5	417	417	0	6	18	388	29	0	0	115	8	94	0	0
53931	143112	143113	NAP-like	4582	1943	3438	1065	7	31	31	22	14	843	842	0	0	0	0	0	76	293	0	0	0	61	375
53931	143119	143120	YefM-like	4084	1477	3240	880	8	27	27	3	5	1961	1961	0	9	42	1960	0	0	0	962	443	230	0	1
53931	54767	143212	Rv2632c-like	794	706	730	5	3	3	3	2	5	408	408	0	1	1	408	0	0	0	1	407	0	0	0
53931	143242	143243	Nqo5-like	5000	1529	224	107	17	17	17	2	5	182	182	0	1	2	179	0	0	0	68	54	4	0	3
53931	54861	143410	DOPA-like	1297	656	1227	653	8	8	8	4	5	809	809	0	2	2	567	0	2	0	519	1	0	2	236
53931	54861	143414	CcmK-like	4807	1387	4595	1384	79	197	197	8	7	1262	1260	0	9	36	1259	0	0	0	380	58	510	1	0
53931	54861	143422	Transposase IS200-like	5454	1533	5433	58	40	40	40	8	6	2006	2002	4	6	40	1893	109	0	1	710	147	803	0	0
53931	54861	143430	TTP0101/SSO1404-like	3132	1002	2984	994	12	17	17	2	5	1949	1949	0	9	75	1750	199	0	0	447	139	652	0	0
53931	143436	143437	THUMP domain-like	6018	698	5625	543	1	12	12	11	9	3499	3498	0	8	196	2770	249	56	229	917	148	1453	7	176
53931	143446	143447	AMMECR1-like	2707	665	1325	652	7	7	7	7	6	1160	1159	0	23	46	766	284	16	3	332	39	221	7	76
53931	143455	143456	VC0467-like	5192	744	5088	743	2	8	8	4	8	3766	3765	0	14	50	3761	0	4	0	2443	765	2	0	0
53931	143468	143469	ImmE5-like	53	54	45	0	2	2	2	1	4	33	33	0	0	0	33	0	0	0	31	0	0	0	0
53931	143476	143477	TM1622-like	21	21	21	0	1	1	1	1	4	16	16	0	0	0	16	0	0	0	0	0	0	0	0
53931	143491	143492	Prenyltransferase-like	157	160	121	0	14	14	14	1	4	68	68	0	1	1	67	0	0	0	2	63	1	0	1
53931	143502	143503	PUG domain-like	1788	880	334	276	5	27	27	23	16	221	221	0	0	0	0	0	18	176	0	0	0	15	2
53931	143516	143517	TRCF domain-like	5000	794	4963	790	2	2	2	6	13	2434	2434	0	5	12	2434	0	0	0	2423	1	4	0	0
53931	55346	143548	Serine metabolism enzymes domain	11980	2362	9567	2311	11	11	11	15	20	4758	4756	0	13	87	4505	184	1	16	2055	994	1023	12	37
53931	55346	143555	FwdE-like	974	915	187	0	4	4	4	5	5	160	159	0	2	4	106	53	0	0	33	0	55	0	0
53931	143559	143560	MK0786-like	239	239	231	0	14	14	14	1	4	212	212	0	6	10	0	212	0	0	0	0	0	0	0
53931	143566	143567	YkuJ-like	386	397	288	0	2	2	2	1	4	212	212	0	0	0	212	0	0	0	0	0	212	0	0
53931	55382	143575	GAS2 domain-like	3201	833	1457	6	1	1	1	99	73	293	293	0	0	0	0	0	0	258	0	0	0	2	30
53931	55382	143579	GK1464-like	55	55	55	0	2	2	2	0	4	40	40	0	0	0	40	0	0	0	0	0	40	0	0
53931	143586	143587	SARS receptor-binding domain-like	627	584	171	0	31	31	31	3	4	110	2	104	0	0	1	0	0	1	1	0	0	0	0
53931	143591	143592	TTHA1528-like	50	50	50	0	4	4	4	1	4	43	43	0	0	0	43	0	0	0	0	0	0	0	0
53931	143596	143597	YojJ-like	5000	1275	311	275	3	7	7	2	4	186	185	0	1	7	185	0	0	0	4	0	170	0	0
53931	143601	143602	STIV B116-like	17998	96	80	77	8	8	8	2	6	70	54	16	0	1	48	6	0	0	8	0	27	0	0
53931	55619	143631	ApbE-like	5662	2685	5082	1736	3	11	11	5	9	2742	2742	0	4	147	2665	77	0	0	1289	6	849	0	0
53931	143723	143724	PHP14-like	6054	994	4990	978	6	13	13	14	17	2643	2642	0	5	27	2402	8	9	198	1414	526	38	20	1
53931	55769	143737	YeeU-like	2215	609	1544	1	4	6	6	3	4	357	357	0	1	1	357	0	0	0	355	0	0	0	0
53931	55769	143744	GlcG-like	5000	746	4791	4	4	4	4	14	10	2494	2493	0	7	21	2379	44	1	1	1512	398	253	3	65
53931	143748	143749	Phage tail protein-like	1309	1504	979	1	29	29	29	2	4	204	198	6	0	0	198	0	0	0	196	0	0	0	0
53931	143790	143791	DUSP-like	3103	669	1245	649	12	16	16	20	18	434	434	0	0	0	0	0	56	196	0	0	0	13	165
53931	143799	143800	L28p-like	11427	1586	10264	1579	227	438	438	10	9	6078	6075	0	27	275	5823	0	76	1	2206	1076	1102	32	112
53931	55944	143842	YwmB-like	589	602	361	0	1	1	1	1	4	201	201	0	0	0	201	0	0	0	0	0	201	0	0
53931	143846	143847	XisI-like	913	652	849	0	7	7	7	3	5	145	145	0	0	0	145	0	0	0	8	0	0	0	0
53931	143855	143856	DeoB insert domain-like	4995	1047	4032	1027	63	64	64	5	11	2181	2180	0	2	98	2177	0	1	2	881	19	1140	0	0
53931	143864	143865	CorA soluble domain-like	5000	823	3380	815	42	42	42	3	8	2316	2314	0	7	23	2162	78	1	1	848	666	123	0	71
53931	143869	143870	PF0523-like	1070	918	38	38	12	12	12	1	4	36	36	0	0	0	0	32	4	0	0	0	0	0	0
53931	143874	143875	ERH-like	456	460	424	3	7	7	7	7	8	272	271	0	0	0	0	0	59	157	0	0	0	33	12
53931	143879	143880	NE0471 N-terminal domain-like	1344	0	217	0	0	2	2	4	6	145	145	0	1	1	145	0	0	0	130	3	3	0	0
53931	143884	143885	RGC domain-like	1664	669	1231	651	1	6	6	34	16	539	539	0	0	0	1	0	0	221	1	0	0	0	304
53931	143967	143968	UbiD C-terminal domain-like	5000	694	4755	682	3	3	3	3	10	2639	2638	0	22	30	2545	87	0	5	1914	265	92	1	0
53931	143974	143975	IlvD/EDD N-terminal domain-like	20000	878	10140	878	2	2	2	6	12	4864	4864	0	24	134	4734	95	5	5	2495	759	881	1	20
53931	143984	143985	L,D-transpeptidase pre-catalytic domain-like	1672	808	1276	0	4	4	4	4	5	632	632	0	0	74	632	0	0	0	0	14	616	0	0
53931	143989	143990	YbiA-like	3521	1265	2547	4	1	1	1	32	21	1595	1571	23	1	23	1321	1	66	24	420	417	204	21	113
53931	143994	143995	AF2331-like	5	5	5	0	2	2	2	1	4	5	5	0	0	0	0	5	0	0	0	0	0	0	0
53931	143999	144000	Oxysterol-binding protein-like	5000	1422	2691	611	18	18	18	17	14	633	632	0	0	0	0	0	0	255	0	0	0	0	371
53931	144004	144005	ORC1-binding domain	103	192	62	61	4	4	4	3	4	53	53	0	0	0	0	0	0	0	0	0	0	0	53
53931	144009	144010	CofE-like	2540	1063	1595	934	4	4	4	7	7	1171	1170	0	41	42	910	260	0	0	126	704	27	0	0
53931	144014	144015	Peptidoglycan deacetylase N-terminal noncatalytic region	644	557	303	0	2	2	2	1	5	115	115	0	0	0	115	0	0	0	0	0	114	0	0
56572	144019	144020	FdhE-like	2097	792	1589	773	2	2	2	2	5	805	805	0	0	0	804	0	0	0	800	1	0	0	1
56572	144051	144052	Thermophilic metalloprotease-like	5045	2439	3930	0	12	12	12	1	4	1967	1965	0	10	97	1870	94	0	0	389	58	1171	0	0
56572	144058	144059	ImpE-like	20000	870	181	846	4	68	68	5	4	391	390	0	1	1	390	0	0	0	384	0	0	0	0
56572	144063	144064	Heme iron utilization protein-like	3210	1412	2729	672	11	19	19	11	7	1337	1337	0	0	6	1334	1	0	1	1226	3	1	0	1
56572	144073	144074	E2F-DP heterodimerization region	3673	1299	3094	664	2	2	2	16	9	404	403	0	0	0	0	0	77	275	0	0	0	16	20
56835	81334	144083	Magnesium transport protein CorA, transmembrane region	5000	735	329	89	40	40	40	1	7	212	212	0	2	5	198	14	0	0	60	0	65	0	0
56835	144090	144091	Rhomboid-like	5406	1111	5167	1091	27	27	27	43	13	2927	2926	0	2	99	2569	20	88	2	1033	677	647	32	206
56992	144121	144122	Tim10-like	1653	1424	1170	9	8	8	8	14	10	642	642	0	0	0	0	0	62	215	0	0	0	45	309
56992	144128	144129	Vanabin-like	764	566	0	3	1	0	1	1	4	1	1	0	0	0	0	0	0	1	0	0	0	0	0
56992	57769	144206	NOB1 zinc finger-like	953	622	839	0	1	1	1	9	8	703	703	0	0	0	0	0	51	250	0	0	0	42	319
56992	57769	144210	Nop10-like SnoRNP	922	909	892	1	22	22	22	5	4	848	848	0	26	28	0	270	62	157	0	0	0	42	283
56992	57769	144217	CSL zinc finger	1352	761	1128	0	14	15	15	18	13	723	723	0	0	0	0	0	65	239	0	0	0	43	347
56992	144231	144232	HIT/MYND zinc finger-like	6265	1011	4504	989	2	1	3	127	68	669	668	0	0	0	2	0	64	264	1	0	0	47	273
56992	144245	144246	Coronavirus NSP10-like	1204	789	1203	70	53	53	53	52	21	229	0	227	0	0	0	0	0	0	0	0	0	0	0
56992	144250	144251	Viral leader polypeptide zinc finger	59	59	59	0	6	6	6	4	8	7	0	7	0	0	0	0	0	0	0	0	0	0	0
56992	144255	144256	TSP9-like	66	87	64	13	1	1	1	1	4	51	51	0	0	0	0	0	51	0	0	0	0	0	0
56835	81334	158212	Htr2 transmembrane domain-like	8	9	8	1	4	4	4	2	4	4	4	0	0	0	0	4	0	0	0	0	0	0	0
46456	46556	158221	YnzC-like	691	751	690	145	5	5	5	3	5	604	604	0	0	50	604	0	0	0	1	0	599	0	0
46456	63450	158230	PRP4-like	394	1072	296	291	1	1	1	4	6	204	203	0	0	0	0	0	2	180	0	0	0	18	3
46456	158234	158235	SOCS box-like	1809	1044	1158	0	3	3	3	9	11	231	230	0	0	0	0	0	0	230	0	0	0	0	0
46456	46965	158366	Efb C-domain-like	57	110	55	53	12	8	12	1	5	13	13	0	0	0	13	0	0	0	0	0	13	0	0
46456	46996	158372	AF1782-like	362	367	196	2	6	6	6	5	7	186	185	0	23	28	1	184	0	0	0	0	0	0	0

46456	158378	158379	YqgQ-like	900	683	885	0	3	3	3	2	5	592	592	0	0	1	592	0	0	0	0	0	591	0	0
46456	47143	158388	YvfG-like	37	45	37	6	4	4	4	1	4	31	31	0	0	0	31	0	0	0	0	0	31	0	0
46456	47161	158397	TM1646-like	1061	783	921	655	2	2	2	2	4	727	727	0	1	39	727	0	0	0	12	0	631	0	0
46456	47239	158414	HP0062-like	266	290	241	9	3	3	3	1	4	57	57	0	0	0	57	0	0	0	31	0	5	0	0
46456	47239	158418	SO2669-like	2	3	2	1	8	8	8	0	4	3	3	0	0	0	3	0	0	0	3	0	0	0	0
46456	47363	158430	Bacillus cereus metalloprotein-like	1146	787	1018	0	26	26	26	3	7	480	477	3	1	5	477	0	0	0	4	0	470	0	0
46456	47363	158436	Ta0600-like	222	224	220	0	5	5	5	1	4	206	206	0	17	23	0	206	0	0	0	0	0	0	0
46456	47363	158442	DsbB-like	4810	675	2195	665	11	11	11	2	5	1249	1248	0	1	4	1248	0	0	0	1225	4	13	0	0
46456	47363	158446	IVS-encoded protein-like	4569	1623	4029	1535	10	10	10	7	6	1553	1552	0	10	57	1546	6	0	0	411	0	119	0	0
46456	47363	158452	YqcC-like	1705	926	1552	0	1	1	1	4	7	860	859	0	0	1	858	0	0	0	854	0	2	0	1
46456	158456	158457	Orange domain-like	1371	540	1239	539	2	2	2	6	7	256	255	0	0	0	0	0	0	255	0	0	0	0	0
46456	158471	158472	HAMP domain-like	5000	895	1665	694	60	58	60	69	35	916	916	0	1	15	903	13	0	0	401	33	383	0	0
46456	47667	158494	PG0775 C-terminal domain-like	328	541	318	7	2	2	2	5	7	239	239	0	1	54	239	0	0	0	1	0	0	0	0
46456	158498	158499	DnaD domain-like	3565	687	353	330	1	3	3	6	4	124	120	4	0	0	120	0	0	0	0	0	120	0	0
46456	158503	158504	BH2638-like	1042	0	1021	0	0	2	2	1	5	620	620	0	0	5	620	0	0	0	0	0	617	0	0
46456	47768	158544	GspK insert domain-like	3484	784	1827	752	1	1	1	4	5	891	889	0	6	7	886	0	1	2	877	0	2	0	0
46456	140656	158548	FLJ32549 domain-like	366	319	260	1	1	1	1	3	5	182	181	0	0	0	0	0	0	179	0	0	0	0	0
46456	158552	158553	TAFH domain-like	1907	1375	1787	1332	2	4	4	14	11	254	253	0	0	0	0	0	0	253	0	0	0	0	0
46456	47916	158560	BH3980-like	833	726	818	0	4	4	4	1	4	443	443	0	1	1	443	0	0	0	3	195	241	0	0
46456	47927	158568	AF1862-like	304	336	51	0	11	11	11	1	5	46	46	0	1	1	33	13	0	0	8	1	11	0	0
46456	158572	158573	GINS helical bundle-like	3505	720	2368	15	7	28	28	26	20	765	765	0	0	0	0	0	75	275	0	0	0	26	352
46456	158586	158587	Jann4075-like	505	505	496	0	4	4	4	2	5	416	416	0	1	1	416	0	0	0	258	15	0	0	0
46456	158614	158615	RbcX-like	674	566	488	0	79	81	81	1	4	421	421	0	0	0	372	0	49	0	0	0	0	0	0
46456	158621	158622	YheA/YmcA-like	3106	922	2569	807	2	8	8	2	5	1107	1107	0	4	48	1040	67	0	0	2	0	1026	0	0
46456	158633	158634	RPA2825-like	650	601	607	566	1	1	1	5	5	411	410	0	2	3	404	0	0	1	395	0	0	0	5
46456	158638	158639	ENT-like	1636	1037	883	0	5	5	5	5	7	260	260	0	0	0	0	0	19	239	0	0	0	0	0
46456	158650	158651	YejL-like	581	553	571	0	13	13	13	2	4	407	407	0	0	1	407	0	0	0	407	0	0	0	0
46456	158667	158668	MtlR-like	1303	923	1006	0	8	8	8	3	5	470	470	0	0	0	469	0	0	0	469	0	0	0	1
46456	158674	158675	Sama2622-like	32	179	32	47	1	1	1	1	4	57	57	0	0	0	57	0	0	0	57	0	0	0	0
46456	158681	158682	TerB-like	7202	1403	113	0	4	6	6	4	6	104	104	0	0	4	104	0	0	0	30	7	2	0	0
46456	158693	158694	UraD-Like	4865	670	4149	668	1	26	26	18	19	2626	2625	0	3	4	2351	15	60	112	1390	746	130	14	63
46456	158701	158702	Sec63 N-terminal domain-like	9694	2045	2266	1131	14	343	343	59	58	1227	1227	0	38	43	0	319	69	269	0	0	0	81	447
46456	158709	158710	PSPTO4464-like	2571	759	2422	756	1	1	1	1	4	1589	1588	0	1	8	1588	0	0	0	1580	2	3	0	0
46456	158714	158715	MG296-like	4	12	4	7	3	3	3	1	4	7	7	0	0	0	7	0	0	0	0	0	0	0	0
46456	48207	158745	LanC-like	5000	1414	366	1	8	9	9	2	4	209	209	0	0	1	209	0	0	0	3	77	111	0	0
46456	158751	158752	HP0242-like	154	220	130	10	9	8	9	2	5	50	50	0	0	0	50	0	0	0	50	0	0	0	0
46456	158756	158757	SMc04008-like	1459	772	1450	771	2	4	4	5	7	1045	1044	0	1	1	1039	0	3	0	1036	0	1	1	1
46456	48370	158791	MgtE N-terminal domain-like	5753	1674	4620	1663	11	11	11	11	9	3486	3485	0	11	161	3469	14	0	1	857	972	928	1	0
46456	158831	158832	Tex N-terminal region-like	5000	595	4999	594	3	3	3	7	18	2660	2660	0	3	6	2657	0	0	3	1951	701	1	0	0
46456	158836	158837	AGR C 984p-like	814	624	692	572	2	2	2	5	5	402	402	0	0	0	401	0	1	0	400	0	0	0	0
46456	158841	158842	PMT central region-like	602	753	17	15	26	22	30	1	6	2	2	0	1	1	2	0	0	0	2	0	0	0	0
46456	48661	158851	Lag-3 N-terminal region	10	10	10	0	1	1	1	1	4	4	4	0	0	0	0	0	0	4	0	0	0	0	0
46456	48661	158855	Lipase chaperone-like	1008	674	749	3	2	2	2	1	4	302	301	0	2	3	301	0	0	0	295	2	2	0	0
48724	48725	158911	NEAT domain-like	2674	1145	2045	1111	39	72	72	63	14	347	346	0	0	2	346	0	0	0	0	0	346	0	0
48724	49561	158949	Smr-associated domain-like	384	488	376	0	1	1	1	2	4	263	263	0	0	57	263	0	0	0	0	0	0	0	0
48724	158973	158974	WSSV envelope protein-like	24	31	24	22	13	13	13	1	4	2	0	2	0	0	0	0	0	0	0	0	0	0	0
48724	158996	158997	Trm112p-like	2579	874	2476	868	5	7	7	5	6	1990	1989	0	6	10	1874	0	11	94	1735	103	1	9	0
48724	159005	159006	YopX-like	1927	869	813	564	6	9	9	1	4	311	274	37	2	4	272	2	0	0	14	2	233	0	0
48724	50036	159034	Mib/herc2 domain-like	2136	638	1956	628	2	5	5	305	68	291	290	0	0	0	0	0	1	266	0	0	0	16	0
48724	50036	159038	YorP-like	24	24	20	0	1	1	1	1	4	10	10	0	0	0	10	0	0	0	0	0	10	0	0
48724	50036	159042	Plus3-like	1610	730	1164	720	12	12	12	15	16	696	696	0	0	0	0	0	69	237	0	0	0	18	359
48724	50181	159065	Dom34/Pelota N-terminal domain-like	1328	991	923	0	15	15	15	7	7	764	764	0	21	27	1	287	67	191	0	0	0	59	124
48724	50181	159071	TrmB C-terminal domain-like	355	367	42	0	2	2	2	2	5	38	38	0	1	1	0	38	0	0	0	0	0	0	0
48724	50198	159121	BC4932-like	1720	872	1268	732	4	4	4	1	4	398	398	0	0	5	398	0	0	0	5	8	384	0	0
48724	50198	159127	HupF/HypC-like	3190	859	3136	854	7	10	10	9	8	1991	1990	0	9	38	1844	144	1	1	873	371	301	0	0
48724	50198	159133	EutN/CcmL-like	1631	863	1537	0	78	83	83	4	6	902	901	0	8	27	899	0	0	0	213	50	373	1	1
48724	50198	159141	HIN-2000 domain-like	426	426	422	0	36	36	36	12	9	82	81	0	0	0	0	0	0	81	0	0	0	0	0
48724	50474	159173	YkvR-like	157	157	153	0	1	1	1	1	4	105	105	0	0	0	105	0	0	0	0	0	105	0	0
48724	159202	159203	NifT/FixU-like	485	485	428	0	1	1	1	3	4	338	338	0	0	0	338	0	0	0	246	0	0	0	0
48724	159221	159222	YopT-like	15	15	15	0	2	2	2	1	4	9	9	0	0	0	9	0	0	0	0	0	9	0	0
48724	159233	159234	FomD-like	2347	673	513	0	3	4	4	1	4	350	350	0	0	0	350	0	0	0	0	325	0	0	0
48724	141492	159238	SO1590-like	866	819	797	0	4	4	4	2	4	533	533	0	0	0	530	0	0	0	187	288	23	0	3
48724	159244	159245	AttH-like	3386	921	1931	1	2	2	2	4	6	1123	1123	0	2	2	1123	0	0	0	964	18	2	0	0
48724	159269	159270	YmcC-like	1446	702	1105	3	2	2	2	2	4	452	452	0	0	0	451	0	0	0	451	0	0	0	1
48724	159274	159275	PA1994-like	1162	859	849	0	2	2	2	2	4	575	574	0	1	1	566	7	0	1	270	221	52	0	0
48724	51160	159283	Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain	5000	1390	2634	1198	1	0	1	5	12	1540	1540	0	5	9	1503	34	0	1	1098	50	134	1	1
51349	159467	159468	AtpF-like	1950	1188	631	485	22	31	31	1	4	551	550	0	28	83	317	229	1	2	13	2	212	1	0
51349	159500	159501	EreA/ChaN-like	7112	1071	2802	938	4	9	9	34	16	1515	1514	0	2	7	1403	17	1	0	623	357	270	0	92
51349	52953	159594	XCC0632-like	5863	1201	2221	632	11	11	11	4	5	916	913	0	3	3	913	0	0	0	906	1	0	0	0
51349	52979	159612	TBP-interacting protein-like	22	22	22	0	1	1	1	1	4	22	22	0	0	0	0	22	0	0	0	0	0	0	0
51349	53162	159659	Cgl1923-like	3554	747	2561	746	6	22	22	1	5	1280	1280	0	0	2	1276	4	0	0	2	1260	2	0	0
51349	159663	159664	CobE/GbiG C-terminal domain-like	4456	1160	4330	1145	3	5	5	28	17	3030	3029	0	21	115	2816	213	0	0	1184	399	732	0	0
51349	159671	159672	CbiG N-terminal domain-like	4053	1490	176	168	2	2	2	5	6	126	126	0	7	9	37	89	0	0	2	0	21	0	0
51349	53382	159709	PhnH-like	1789	768	1495	734	1	1	1	2	5	837	836	0	5	5	836	0	0	0	774	9	24	0	0
51349	53382	159713	Dhaf3308-like	1058	702	305	0	6	6	6	4	4	253	253	0	2	5	220	33	0	0	68	69	47	0	0
51349	159773	159774	YerB-like	1850	564	1158	0	1	1	1	4	5	880	880	0	1	101	880	0	0	0	0	42	653	0	0
51349	159778	159779	CdCA1 repeat-like	13	11	11	0	8	8	8	0	6	8	8	0	0	0	3	0	2	0	1	0	0	3	0
51349	53799	159800	PrpR receptor domain-like	2678	590	1812	575	4	6	6	24	7	726	726	0	0	5	725	0	0	1	481	10	225	0	0
53931	64209	159865	XkdW-like	121	168	107	9	1	1	1	1	4	51	50	1	1	1	50	0	0	0	1	0	49	0	0
53931	88797	159871	YdgH-like	3748	1129	2453	2	6	7	7	3	5	456	456	0	1	1	454	0	0	1	452	0	1	0	1
53931	69634	159888	YdhG-like	2240	850	572	542	5	5	5	3	4	356	356	0	0	0	356	0	0	0	1	36	312	0	0
53931	69634	159894	YgaC/TfoX-N like	2906	1450	1799	0	3	3	3	5	5	855	854	0	2	3	852	0	0	0	810	5	7	0	2
53931	159901	159902	PH1570-like	23	23	21	0	2	2	2	1	4	19	19	0	0	0	0	19	0	0	0	0	0	0	0
53931	54235	159936	NSP3A-like	950	556	567	3	3	3	3	27	13	143	1	141	0	0	1	0	0	0	1	0	0	0	0
53931	159940	159941	MM3350-like	3065	746	1784	737	2	2	2	13	11	1158	1158	0	8	29	1115	25	1	2	441	219	244	1	14
53931	160058	160059	PriA/YqbF domain	1917	648	1190	566	7	23	23	12	13	699	699	0	0	0	69	0	65	263	45	0	24	20	246
53931	160087	160088	NRDP1 C-terminal domain-like	230	230	220	0	6	6	6	8	7	143	143	0	0	0	0	0	0	143	0	0	0	0	0
53931	160098	160099	SARS Nsp1-like	181	350	171	0	2	2	2	7	7	66	0	66	0	0	0	0	0	0	0	0	0	0	0
53931	160103	160104	Acetoacetate decarboxylase-like	3299	933	1084	782	20	28	28	7	8	701	701	0	3	3	577	16	0	0	343	144	73	1	103
53931	160112	160113	YegP-like	1903	950	1831	13	3	12	12	12	10	1179	1175	2	3	12	1072	102	0	0	675	147	41	0	1
53931	160147	160148	CPE0013-like	959	678	705	608	1	1	1	2	5	475	475	0	2	62	456	19	0	0	4	12	359	0	0
53931	160190	160191	YcgL-like	1766	755	1393	713	1	1	1	1	4	889	889	0	0	1	889	0	0	0	887	0	2	0	0
53931	160206	160207	NMB0488-like	317	395	192	0	2	2	2	2	4	88	88	0	0	0	88	0	0	0	88	0	0	0	0
53931	160213	160214	FlaG-like	2883	696	554	282	1	1	1	1	4	416	416	0	2	22	416	0	0	0	121	0	265	0	0
53931	160218	160219	AMPKBI-like	1549	878	1314	27	26	38	38	6	8	671	670	0	0	0	1	0	81	256	1	0	0	16	306
53931	54805	160240	Cation efflux protein cytoplasmic domain-like	5325	1411	5260	1404	9	11	11	6	10	3177	3177	0	8	74	3057	70	43	6	2094	145	473	0	1
53931	54805	160246	EspE N-terminal domain-like	7252	1751	2351	809	7	7	7	13	9	1518	1517	0	6	23	1517	0	0	0	888	33	415	0	0
53931	160271	160272	Shew3726-like	1241	696	659	643	1	1	1	2	5	333	333	0	1	1	333	0	0	0	332	0	1	0	0
53931	54861	160350	Rnp2-like	1373	687	387	341	7	7	7	2	5	356	356	0	8	8	0	249	23	15	0	0	0	6	59
53931	54861	160355	Bacterial polysaccharide co-polymerase-like	3557	546	2749	542	40	73	73	5	4	710	709	0	0	1	709	0	0	0	708	0	1	0	0
53931	54861	160363	MTH889-like	240	243	240	2	29	29	29	1	4	225	225	0	1	5	51	174	0	0	30	18	0	0	0
53931	54861	160369	Ribosomal protein L10-like	5000	1324	5000	1322	3	33	33	3	6	4068	4067	0	21	194	4041	1	21	4	1427	872	1353	0	0
53931	160373	160374	RplX-like	1399	1022	164	25	58	66	66	1	4	175	175	0	12	12	0	159	0	0	0	0	0	7	9
53931	160378	160379	SP0830-like	3314	1093	923	0	4	4	4	1	4	578	578	0	2	15	575	2	0	0	24	99	319	0	0
53931	160386	160387	NosL/MerB-like	3156	1208	864	561	15	15	15	12	9	646	646	0	6	8	624	9	1	1	469	106	26	0	11
53931	160418	160419	YdfO-like	923	809	308	0	1	1	1	1	4	79	78	1	0	0	78	0	0	0	74	0	2	0	0
53931	160423	160424	BH3703-like	2592	997	1574	0	4	4	4	4	5	265	265	0	0	6	265	0	0	0	0	2	262	0	0
53931	55199	160443	SMR domain-like	5000	721	1191	584	6	6	6	48	18	712	711	0	1	2	32	0	70	221	26	0	0	14	337
53931	160447	160448	PG1857-like	301	301	295	0	2	2	2	1	4	238	238	0	0	39	235	3	0	0	29	0	4	0	0
53931	160452	160453	PB2 C-terminal domain-like	5000	1377	5000	1353	6	1	6	1	4	5419	0	5419	0	0	0	0	0	0	0	0	0	0	0
53931	160458	160459	BLRF2-like	45	46	26	1	6	0	6	1	4	14	0	14	0	0	0	0	0	0	0	0	0	0	0
53931	55247	160467	PH0987 N-terminal domain-like	5000	901	1227	682	2	3	3	9	12	835	832	0	4	24	803	22	0	1	296	27	401	1	5
53931	160471	160472	NMB0513-like	355	383	138	0	2	2	2	1	4	61	61	0	0	1	61	0	0	0	61	0	0	0	0
53931	160476	160477	PA1123-like	225	225	222	0	1	1	1	1	4	113	113	0	0	0	113	0	0	0	113	0	0	0	0
53931	55276	160481	BRK domain-like	2259	994	1251	784	5	5	5	34	20	235	234	0	0	0	0	0	0	234	0	0	0	0	0
53931	55297	160515	YueI-like	1131	629	978	45	2	2	2	1	4	526	525	1	0	2	525	0	0	0	0	0	502	0	0
53931	55297	160519	BB2672-like	1306	1099	1278	0	4	4	4	2	5	678	677	0	3	3	673	2	1	1	552	87	28	0	0
53931	55346	160527	V-type ATPase subunit E-like	2036	961	756	535	6	24	24	5	7	670	669	0	9	11	40	209	3	158	21	0	15	5	236
53931	160531	160532	Ava3019-like	220	222	185	0	3	3	3	1	4	147	147	0	2	2	145	0	2	0	0	0	0	0	0
53931	160536	160537	SpoVG-like	1462	697	1359	692	10	10	10	2	5	997	996	0	2	140	989	7	0	0	23	0	830	0	0
53931	160543	160544	EscU C-terminal domain-like	5277	2207	5277	2145	24	0	24	2	5	3220	3220	0	4	64	3217	0	0	2	2124	52	831	0	1
53931	160569	160570	YonK-like	13	14	13	1	4	4	4	1	4	10	10	0	0	0	10	0	0	0	0	0	10	0	0
53931	55647	160574	BT0923-like	1027	719	707	0	9	9	9	5	6	319	319	0	1	55	319	0	0	0	14	0	0	0	0
53931	55657	160582	MbtH-like	3390	642	3330	642	2	13	13	15	12	1419	1418	0	15	15	1418	0	0	0	581	680	84	0	0
53931	160630	160631	SMI1/KNR4-like	6064	1026	1332	584	3	6	6	5	6	632	631	0	1	5	628	2	0	0	320	21	225	1	0
53931	55752	160651	FLJ32549 C-terminal domain-like	359	368	282	0	1	1	1	2	5	204	203	0	0	0	0	0	0	189	0	0	0	5	7
53931	55769	160683	YNR034W-A-like	38	39	20	1	1	1	1	1	4	20	20	0	0	0	0	0	0	0	0	0	0	0	20
53931	160695	160696	BTG domain-like	1513	820	1240	659	8	8	8	6	6	311	310	0	0	0	0	0	0	275	0	0	0	0	26
53931	160703	160704	YehR-like	808	582	570	0	1	1	1	4	5	208	208	0	0	0	207	0	0	1	91	2	114	0	0
53931	160712	160713	YqaI-like	101	175	71	11	2	2	2	1	4	27	27	0	0	0	27	0	0	0	0	0	27	0	0
53931	160718	160719	gpW/gp25-like	5000	578	1792	578	1	3	3	1	4	1108	1053	55	2	15	1032	21	0	0	494	273	64	0	0
53931	55944	160755	YugN-like	890	650	568	0	3	3	3	2	5	331	331	0	0	0	331	0	0	0	0	0	330	0	0
53931	160760	160761	TTHC002-like	9	9	9	0	2	2	2	0	4	7	7	0	0	0	7	0	0	0	0	0	0	0	0
53931	160765	160766	NE1680-like	206	209	203	1	1	1	1	1	4	147	146	0	13	13	114	32	0	0	59	0	0	0	0
53931	160799	160800	Lp2179-like	498	501	486	0	1	1	1	2	5	276	276	0	0	0	276	0	0	0	0	0	275	0	0
53931	160886	160887	Rv2827c C-terminal domain-like	56	798	42	0	2	2	2	1	5	16	16	0	0	0	16	0	0	0	0	16	0	0	0
53931	160891	160892	Phosphoprotein oligomerization domain-like	215	215	215	0	6	6	6	1	4	15	0	15	0	0	0	0	0	0	0	0	0	0	0
53931	160896	160897	Taf5 N-terminal domain-like	1351	718	1251	15	13	14	14	28	17	757	757	0	0	0	0	0	66	263	0	0	0	29	383
53931	160903	160904	Jann2411-like	5000	1027	909	573	1	1	1	4	4	498	498	0	0	0	498	0	0	0	32	460	5	0	0
53931	160908	160909	ATP12-like	2043	941	1738	933	7	7	7	12	12	1364	1363	0	2	3	781	0	63	253	777	0	0	18	215
53931	160919	160920	PSTPO5379-like	2489	738	2326	738	3	3	3	7	7	1562	1561	0	1	23	1275	0	0	141	596	365	274	11	130
53931	160924	160925	PG1388-like	328	330	174	0	2	2	2	1	4	112	112	0	0	34	112	0	0	0	0	0	0	0	0
56572	160929	160930	FlhC-like	1278	603	1084	591	2	2	2	3	5	609	609	0	0	0	608	0	0	0	606	1	0	0	1
56572	160934	160935	VPA0735-like	5000	786	1248	739	6	9	9	7	6	496	496	0	3	3	487	3	0	0	307	84	16	0	6
56572	160939	160940	Api92-like	1493	720	869	0	1	1	1	2	4	222	222	0	0	0	222	0	0	0	222	0	0	0	0
56572	160944	160945	PH0156-like	24	27	22	0	2	2	2	1	4	18	18	0	0	0	0	18	0	0	0	0	0	0	0
56572	160949	160950	YacF-like	1652	1097	1599	1085	2	2	2	1	4	1031	1031	0	3	6	1031	0	0	0	1026	1	0	0	0
56572	160956	160957	Poly(A) polymerase catalytic subunit-like	82	83	73	0	9	9	9	1	5	43	0	43	0	0	0	0	0	0	0	0	0	0	0
56572	160963	160964	MalF N-terminal region-like	1714	597	1255	1	14	14	14	3	6	564	564	0	0	1	563	0	0	0	514	42	1	0	1

56572	160974	160975	AF1531-like	9478	1030	349	349	1	2	2	1	5	321	321	0	19	25	1	320	0	0	0	0	0	0	0
56572	160979	160980	SSO1389-like	153	152	12	0	3	3	3	1	5	12	12	0	0	0	0	12	0	0	0	0	0	0	0
56572	160990	160991	CV3147-like	1961	871	401	354	2	2	2	2	4	280	280	0	0	1	261	16	0	0	105	88	51	0	2
56572	160995	160996	HI0933 insert domain-like	7936	2012	7903	1345	2	9	9	4	13	4538	4536	0	7	194	4517	6	8	4	2475	8	1420	0	1
56572	161002	161003	flu NP-like	5000	652	5000	652	60	2	62	1	4	5016	0	5016	0	0	0	0	0	0	0	0	0	0	0
56572	161007	161008	Viral glycoprotein ectodomain-like	4624	1792	1388	381	36	38	38	5	7	284	0	282	0	0	0	0	0	0	0	0	0	0	0
56835	81407	161017	Photosystem II reaction center protein L, PsbL	5	306	5	304	41	0	41	3	5	287	287	0	2	2	83	0	164	0	0	0	0	19	0
56835	81407	161021	Photosystem II reaction center protein J, PsbJ	0	468	0	468	41	0	41	1	4	438	438	0	2	2	102	0	274	0	0	0	0	34	0
56835	81407	161025	Photosystem II 10 kDa phosphoprotein PsbH	871	721	849	0	41	41	41	3	6	790	790	0	1	1	131	0	593	0	1	0	2	36	0
56835	81407	161029	Photosystem II reaction center protein T, PsbT	0	12	0	12	41	0	41	1	4	11	10	0	0	0	9	0	0	0	0	0	0	1	0
56835	81407	161033	Photosystem II reaction center protein M, PsbM	0	345	0	344	41	0	41	1	4	318	318	0	0	0	108	0	206	0	0	0	0	3	0
56835	81407	161037	Photosystem II reaction center protein K, PsbK	9	772	9	771	43	0	43	3	6	734	734	0	2	2	93	0	577	0	1	0	0	30	0
56835	81407	161041	Photosystem II reaction center protein I, PsbI	1	381	1	379	41	29	41	2	5	359	359	0	1	1	96	0	215	0	0	0	0	25	0
56835	81407	161045	Cytochrome b559 subunits	1054	994	1007	0	90	84	90	7	6	742	742	0	2	2	185	0	491	0	2	0	2	38	0
56835	81334	161055	PsbZ-like	542	627	542	96	41	41	41	1	5	609	609	0	0	0	116	0	479	0	2	0	1	0	0
56835	161059	161060	ATP synthase B chain-like	427	635	376	14	6	6	6	2	4	265	265	0	0	0	0	0	0	263	0	0	0	0	0
56835	161064	161065	ATP synthase D chain-like	988	683	697	0	5	5	5	6	6	482	482	0	0	0	1	0	52	244	1	0	0	4	179
56835	161069	161070	SNF-like	5000	3009	1834	2538	65	77	79	9	11	1836	1835	0	3	126	1555	20	0	259	517	250	528	1	0
56835	161076	161077	Photosystem II antenna protein-like	5089	1637	4162	49	86	90	90	4	6	2520	2520	0	4	4	202	0	1765	0	2	0	1	500	0
56835	161083	161084	MAPEG domain-like	5732	0	1914	0	0	46	46	4	5	700	699	0	0	0	404	0	12	271	351	0	0	4	6
56835	161092	161093	MgtE membrane domain-like	5000	1391	5000	1390	12	6	12	8	10	3088	3088	0	8	101	3069	18	0	0	1722	135	801	0	1
56835	161097	161098	MetI-like	35000	1602	34953	1598	6	44	48	21	22	6777	6774	0	20	184	6576	177	15	4	2714	1438	1810	0	2
56835	161110	161111	Cation efflux protein transmembrane domain-like	5000	638	4990	638	6	8	8	7	13	2682	2681	0	4	170	2596	65	10	5	1010	56	1211	2	1
56992	57006	161148	VhTI-like	0	0	0	0	1	1	0	1	3	1	1	0	0	0	0	0	1	0	0	0	0	0	0
56992	57769	161187	YfgJ-like	742	602	703	0	2	2	2	1	4	331	331	0	0	0	331	0	0	0	329	0	0	0	0
56992	161218	161219	CHY zinc finger-like	5000	1071	508	1015	2	0	2	29	10	455	454	0	0	0	0	0	70	135	0	0	0	21	215
56992	161228	161229	E6 C-terminal domain-like	927	586	876	536	5	6	6	3	6	214	1	212	0	0	1	0	0	0	0	0	0	0	0
56992	161233	161234	E7 C-terminal domain-like	433	576	433	508	5	5	5	3	6	233	2	229	0	0	1	0	0	1	0	0	0	0	0
56992	161239	161240	T-antigen specific domain-like	292	298	276	0	6	6	6	2	6	83	1	82	0	0	0	0	0	1	0	0	0	0	0
56992	161244	161245	Zinc hairpin stack	1412	757	1404	716	2	2	2	38	13	538	537	0	0	0	1	0	77	181	1	0	0	41	223

Supplementary Table 5: A comparison of the number of validated hits by our procedure compared to the other databases for the 12 superfamilies in the dataset has been provided. Corresponding Pfam families were identified from the Pfam HMM searches and the list of the families is provided below. Interpro families were identified from the links in Pfam site. Superfamily database has a list of SCOP superfamily homologues identified in complete genomes.

SCOP superfamily code	**Superfamily description**	**Total TP**	**Number of members in Superfamily**	**Number of members in Pfam**	**Number of members in InterPro**
47336	ACP-like	22,882	21,857	47,239	1,19,098
47565	Insect Pheromone-OBPs	2362	1373	1338	7136
48345	A virus capsid protein alpha helical domain	1693	3184	2	3016
50203	Bacterial Enterotoxins	2907	925	18	625
51069	Carbonic anhydrase	7427	3859	5155	10,143
51101	Mannose-binding lectins	1932	1970	3063	4616
51351	Triosephosphate isomerase	7598	3939	6289	23,265
51679	Bacterial-luciferase like	21,998	11046	20579	78,487
51971	Nucleotide-binding domain	17,918	8765		68585
55031	Bacterial exopeptidase dimerisation	28,405	15,894	31,615	1,06,058
55239	RuBisCo-small subunit	1979	697	1064	3478
55307	Tubulin-CTD-like	15,953	9307	13,920	60,676

Supplementary Table 6: Percentage of the total Refseq proteome of 13 selected model organisms covered by the sequence search approach. We have identified 13-45% of the total sequences except for *Arabidopsis thaliana* (2.72%) and Mouse (72%).

Taxid	**Organism**	**Common name**	**Proteins identified in GenDiS+**	**Total proteins (Refseq)**	**% of total proteins covered by GenDiS+**	**Proteins in PDB**	**% of total proteins covered by PDB**	**Proteins in Superfamily**	**% of total proteins covered by Superfamily**
9606	*Homo sapiens*	Human	107273	662155	16.20	42971	6.48	60672	9.16
140831	*Escherichia coli*	Escherichia coli	269176	2014886	13.35	7997	0.39	3003	0.14
3702	*Arabidopsis thaliana*	Thale cress	14294	525318	2.72	1157	0.22	16735	3.18
4932	*Saccharomyces cerevisiae*	Baker's yeast	27059	130595	20.71	3811	2.91	3654	2.79
3218	*Physcomitrella patens*	Spreading earthmoss	5085	35982	14.13	15	0.04	18313	50.89
7955	*Danio rerio*	Zebrafish	21368	46860	45.59	281	0.59	31400	67.00
8355	*Xenopus laevis*	African clawed frog	7760	57279	13.54	518	0.90	15386	26.86
10090	*Mus musculus*	Mouse	55898	77385	72.23	6358	8.21	16482	21.29
6239	*Caenorhabditis elegans*	Caenorhabditis elegans	5115	36597	13.97	368	1.00	10383	28.37
7227	*Drosophila melanogaster*	Fruitfly	11878	61447	19.33	910	1.48	8404	13.67
7070	*Tribolium castaneum*	Flour beetle	6612	23392	28.26	7	0.02	8930	38.17
4577	*Zea mays*	Maize	19301	58492	32.9	175	0.29	31014	53.02
9031	*Gallus gallus*	Chicken	13725	47175	29.09	1550	3.28	11686	24.77

Supplementary Table 7: The statistics for the fold prediction studies carried out for the 20 hits with the least sequence identity with the superfamily members. Hits from each member with varying percentage identity were used.

Superfamily	**Superfamily description**	**Number of members in PASS2.4**	**Number of hits for which fold prediction was done**	**Range of percentage identities for the hits selected (%)**
47336	ACP-like	8	160	11.69-19.75
47565	Insect Pheromone-OBPs	5	100	7.69-10.62
48345	A virus capsid protein alpha helical domain	3	60	10.89-24.22
50203	Bacterial Enterotoxins	17	340	15.79-19
51069	Mannose-binding lectins	4	80	30.58-33.58
51101	Carbonic anhydrase	4	80	13.33-17.42
51351	Triosephosphate isomerase	3	60	15.69-17.06
51679	Bacterial-luciferase like	6	120	15.34-18.29
51971	Nucleotide-binding domain	9	180	17.41-32.69
55031	Bacterial exopeptidase dimerisation	8	160	22.32-25.89
55239	RuBisCo-small subunit	4	80	24.79-27.50
55307	Tubulin-CTD-like	6	120	29.32-35.08

Supplementary Table 8: The number of members identified for each SCOP class normalised with the number of superfamilies, families, SCOP domains and PDB entries for the class. Class α/β shows a higher representation of hits even after normalisation. The numbers have been rounded-off to nearest integers.

SCOP description	**Number of members normalised with number of superfamilies (SCOP v1.75)**	**Number of members normalised with number of families (SCOP v1.75)**	**Number of members normalised with number of superfamilies (SCOPe v2.06)**	**Number of members normalised with number of families(SCOPe v2.06)**
All alpha	5676	3304	5610	2743
All beta	8106	3867	7861	3014
Alpha and beta (α/β)	25583	7774	25375	6344
Alpha and beta (α+β)	7905	4129	7751	3302
Multi-domain proteins	6679	4953	6389	3971
Membrane and cell-surface proteins and peptides	307	275	287	200
Small proteins	4003	2358	3825	1934

SCOP description	**Number of members normalised with number of PDB entries (SCOP v1.75)**	**Number of members normalised with number of domains (SCOP v1.75)**	**Number of members normalised with number of PDB entries (SCOPe v2.06)**	**Number of members normalised with number of domains (SCOPe v2.06)**
All alpha	375	169	203	89
All beta	268	108	136	54
Alpha and beta (α/β)	519	221	248	101
Alpha and beta (α+β)	392	171	193	81
Multi-domain proteins	367	201	167	83
Membrane and cell-surface proteins and peptides	55	18	25	8
Small proteins	226	122	156	85

Supplementary Table 9: The increase in the range of organisms covered in SCOP1.75 to the sequences obtained in GenDiS for the test superfamilies. Many taxa not sampled by PDB have been identified in these superfamily.

SCOP sf code	**#organisms identified in this study**	**No. of organisms in SCOP (v2.06)**	**Organisms in PDB**
47336	29026	34	*Streptomyces coelicolor*, *A3(2)* [TaxId: 1902], *Bacillus subtilis* [TaxId: 1423], *Escherichia coli* [TaxId: 562], *Mycobacterium tuberculosis* [TaxId: 1773], *Shigella flexneri* [TaxId: 373384], *Thermotoga maritima* [TaxId: 2336], *Streptomyces roseofulvus* [TaxId: 33902], *Agrobacterium tumefaciens* [TaxId: 358], *Streptomyces rimosus* [TaxId: 1927], Norway rat (*Rattus norvegicus*) [TaxId: 10116], *A. tumefaciens* [TaxId: 176299], *Aquifex aeolicus* [TaxId: 224324], *B. subtilis* [TaxId: 224308], *E. coli* [TaxId: 885275], Human (*Homo sapiens*) [TaxId: 9606], *Thermus thermophilus HB8* [TaxId: 300852], *Vibrio harveyi* [TaxId: 673519], Bacillus brevis [TaxId: 1393], *Lactobacillus casei* [TaxId: 1582], *Actinoplanes teichomyceticus* [TaxId: 1867], *Anaplasma phagocytophilum* [TaxId: 212042], *Brucella melitensis* [TaxId: 520466], *Enterococcus faecalis* [TaxId: 226185], *Leishmania major* [TaxId: 5664], Lyme disease spirochete (*Borrelia burgdorferi*) [TaxId: 139], *Plasmodium falciparum* [TaxId: 5833], *M. tuberculosis* [TaxId: 83332], *P. falciparum* [TaxId: 36329], *Rickettsia prowazekii* [TaxId: 272947], Spinach (*Spinacia oleracea*) [TaxId: 3562], *S. aureus* [TaxId: 93062], *S. coelicolor* [TaxId: 100226], *Streptomyces sp.* [TaxId: 1001349]
47565	244	13	Polyphemus moth (*Antheraea polyphemus*) [TaxId: 7120], Fruit fly (*Drosophila melanogaster*) [TaxId: 7227], Madeira cockroach (*Leucophaea maderae*) [TaxId: 36963], Honeybee (*Apis mellifera*) [TaxId: 7460], Yellow mealworm (*Tenebrio molitor*) [TaxId: 7067], *Amyelois transitella* [TaxId: 680683], Silkworm (*Bombyx mori*) [TaxId: 7091], African malaria mosquito (*Anopheles gambiae*) [TaxId: 7165], *A. gambiae* [TaxId: 180454], *Culex quinquefasciatus* [TaxId: 7176], Yellow fever mosquito (*Aedes aegypti*) [TaxId: 7159], Fungus (*Caldariomyces fumago*) [TaxId: 5474]
48345	304	4	Bluetongue virus [TaxId: 40051], Bovine rotavirus strain uk/g6 [TaxId: 10934], Bovine rotavirus [TaxId: 10927], Rice dwarf virus [TaxId: 10991]
50203	5132	16	*Vibrio cholerae* [TaxId: 666], *E. coli, type IB* [TaxId: 562], *Bordetella pertussis* [TaxId: 520], Enterobacteria phage [TaxId: 10730], *Shigella dysenteriae*, toxin I [TaxId: 622], *Citrobacter freundii* [TaxId: 546], *E. coli O157:H7* [TaxId: 83334], *V. cholerae* [TaxId: 37965], *S. aureus* [TaxId: 1280], *Streptococcus pyogenes* [TaxId: 1314], *S. aureus* [TaxId: 158879], *S. aureus* [TaxId: 426430], *S. aureus* [TaxId: 93061], *S. aureus* [TaxId: 93062]
51101	472	24	Jackfruit (*Artocarpus heterophyllus*) [TaxId: 3489], Hedge bindweed (*Calystegia sepium*) [TaxId: 47519], *Griffithsia sp. Q66D336* [TaxId: 373036], Red alga (*Griffithsia*) [TaxId: 35158], Jerusalem artishoke (*Helianthus tuberosus*) [TaxId: 4233], *Artocarpus hirsuta* [TaxId: 291940], Osage orange (*Maclura pomifera*) [TaxId: 3496], *Artocarpus integer* [TaxId: 3490], *Griffithsia sp.* [TaxId: 373036], *Musa acuminata* [TaxId: 4641], Sweet potato (*Ipomoea batatas*) [TaxId: 4120], Bluebell (*Scilla campanulata*) [TaxId: 81759], *Gastrodia elata* [TaxId: 91201], Daffodil (*Narcissus pseudonarcissus*) [TaxId: 39639], Garlic (*Allium sativum*) [TaxId: 4682], Snowdrop (*Galanthus nivalis*) [TaxId: 4670], *Colocasia esculenta* [TaxId: 4460],

			Crocus vernus [TaxId: 87752], *Curculigo latifolia* [TaxId: 4676], Fairy-ring mushroom (*Marasmius oreades*) [TaxId: 181124], *Mycobacterium smegmatis* [TaxId: 246196], *Polygonatum cyrtonema* [TaxId: 195526], *Remusatia vivipara* [TaxId: 189456]
51069	2555	15	Cow (*Bos taurus*) [TaxId: 9913], Human (*H. sapiens*) [TaxId: 9606], Mouse (*Mus musculus*) [TaxId: 10090], *Neisseria gonorrhoeae* [TaxId: 485], Norway rat (*R. norvegicus*) [TaxId: 10116], *Dioscorea japonica* [TaxId: 4673], *Dunaliella salina* [TaxId: 3046], Fungus (*Aspergillus oryzae*) [TaxId: 5062], Green alga (*Chlamydomonas reinhardtii*) [TaxId: 3055], *Helicobacter pylori* [TaxId: 563041], *Helicobacter pylori* [TaxId: 85962], *Thermovibrio ammonificans* [TaxId: 228745], *Thiomicrospira crunogena* [TaxId: 317025], *T. ammonificans* [TaxId: 648996], *Vaccinia virus* [TaxId: 10245]
55031	22247	11	*E. coli* [TaxId: 562], *Lactobacillus delbrueckii* [TaxId: 1584], *Pseudomonas sp., strain rs-16* [TaxId: 306], Thale cress (*Arabidopsis thaliana*) [TaxId: 3702], *Salmonella typhimurium* [TaxId: 90371], Yeast (*Saccharomyces kluyveri*) [TaxId: 4934], *B. subtilis* [TaxId: 1423], *Neisseria meningitidis* [TaxId: 487], Human (*H. sapiens*) [TaxId: 9606], *Pseudomonas mevalonii* [TaxId: 32044]
55239	1337	14	*Alcaligenes eutrophus* [TaxId: 106590], *Galdieria partita* [TaxId: 83374], Green alga (*Chlamydomonas reinhardtii*) [TaxId: 3055], *Halothiobacillus neapolitanus* [TaxId: 927], Rice (*Oryza sativa*) [TaxId: 4530], Spinach (*S. oleracea*) [TaxId: 3562], *Synechococcus sp., strain pcc 6301* [TaxId: 1131], Tobacco (*Nicotiana tabacum*), variant turkish samsun [TaxId: 4097], *Oryza sativa* [TaxId: 39947], Pea (*Pisum sativum*) [TaxId: 3888], Red algae (*Galdieria sulphuraria*) [TaxId: 130081], *Thermosynechococcus elongatus* [TaxId: 197221]
55307	21380	19	*A. aeolicus* [TaxId: 224324], *A. aeolicus* [TaxId: 63363], *B. subtilis* [TaxId: 1423], *Methanococcus jannaschii* [TaxId: 2190], *M. tuberculosis* [TaxId: 1773], *Pseudomonas aeruginosa* [TaxId: 287], *S. aureus* [TaxId: 1280], *S. aureus* [TaxId: 158878], *T. maritima* [TaxId: 2336], Cow (*Bos taurus*) [TaxId: 9913], Pig (*Sus scrofa*) [TaxId: 9823], *Prosthecobacter dejongeii* [TaxId: 48465], Chicken (*Gallus gallus*) [TaxId: 9031], Sheep (*Ovis aries*) [TaxId: 9940], *Sus barbatus* [TaxId: 41807], *B. subtilis* [TaxId: 1423], Baker's yeast (*Saccharomyces cerevisiae*) [TaxId: 4932], Baker's yeast (*S. cerevisiae*) [TaxId: 559292], *Staphylococcus epidermidis* [TaxId: 176279]
51351	19143	38	*Bacillus stearothermophilus* [TaxId: 1422], Baker's yeast (*S. cerevisiae*) [TaxId: 4932], Chicken (*Gallus gallus*) [TaxId: 9031], Entamoeba (*Entamoeba histolytica*) [TaxId: 5759], *E. coli* [TaxId: 562], Human (*H. sapiens*) [TaxId: 9606], Malaria parasite (*P. falciparum*) [TaxId: 5833], *Methanocaldococcus jannaschii* [TaxId: 243232], Nematode (*Caenorhabditis elegans*) [TaxId: 6239], *Pyrococcus woesei* [TaxId: 2262], Rabbit (*Oryctolagus cuniculus*) [TaxId: 9986], *S. aureus* [TaxId: 282458], *Thermoproteus tenax* [TaxId: 2271], *T. maritima* [TaxId: 2336], Trypanosoma cruzi [TaxId: 5693], Trypanosome (*Leishmania mexicana*) [TaxId: 5665], Trypanosome (*Trypanosoma brucei*) [TaxId: 5691], *Vibrio marinus* [TaxId: 90736], Yellow mealworm (*Tenebrio molitor*) [TaxId: 7067], *Gemmata obscuriglobus* [TaxId: 114], *Rhipicephalus microplus* [TaxId: 6941], *Trypanosoma brucei* [TaxId: 5702], *Bartonella henselae* [TaxId: 38323], *B. melitensis* [TaxId: 546272], *Burkholderia thailandensis* [TaxId: 271848], *Clostridium perfringens* [TaxId: 195102], *Cryptosporidium parvum* [TaxId: 353152], *Deinococcus radiodurans* [TaxId: 243230], *E. coli* [TaxId: 316385], *Giardia intestinalis* [TaxId: 5741], Green alga (*Chlamydomonas reinhardtii*) [TaxId: 3055], *Helicobacter pylori* [TaxId: 85962], *Leishmania sp.* [TaxId: 438838], *M. tuberculosis* [TaxId: 1773], *M.*

			tuberculosis [TaxId: 83332], *S. coelicolor* [TaxId: 100226], Thale cress (*A. thaliana*) [TaxId: 3702], *Trichomonas vaginalis* [TaxId: 5722]
51679	16109	13	*V. harveyi* [TaxId: 669], *Photobacterium leiognathi* [TaxId: 553611], *Photobacterium phosphoreum* [TaxId: 659], *Methanoculleus thermophilicus* [TaxId: 2200], *Methanobacterium thermoautotrophicum* [TaxId: 145262], *Methanopyrus kandleri* [TaxId: 2320], *E. coli* [TaxId: 562], *B. subtilis* [TaxId: 1423], *Bacillus cereus* [TaxId: 222523], *Burkholderia pseudomallei* [TaxId: 320372], *Geobacillus thermodenitrificans* [TaxId: 33940], *Methanosarcina barkeri* [TaxId: 2208], *M. tuberculosis* [TaxId: 83332]
51971	20745	8	*E. coli* [TaxId: 562], Cow (*Bos taurus*) [TaxId: 9913], Pig (*Sus scrofa*) [TaxId: 9823], *M. tuberculosis* [TaxId: 1773], *Methylophilus methylotrophus*, w3a1 [TaxId: 17], *Rhodotorula gracilis* [TaxId: 5286], *Klebsiella pneumoniae* [TaxId: 573]

Supplementary Table 10: The superfamilies which show instances of lateral gene transfer from viruses to cellular organisms. In most cases, the cellular host of the virus showed presence of the superfamilies which had been reported only in Viruses. Most of these are retroviral transfer events.

Class	Fold	Super-family	Description	GIs	Taxids	Cellular host	Viruses
46456	47076	47077	T4 endonuclease V	207	138	*Proteobacteria*	Caudovirales, Phycodnaviridae
46456	47835	47836	Retroviral matrix proteins	8265	295	*Amniota, Chlamydia trachomatis, Trypanosoma congolense*	Retroviridae, Poxviridae
46456	47942	47943	Retrovirus capsid protein, N-terminal core domain	22440	305	*Amniota, Trypanosoma congolense*	Retroviridae, Poxviridae
46456	48492	48493	gene 59 helicase assembly protein	129	102	*Proteobacteria, Actinobacteria*	Caudovirales
48724	88632	49749	Group II dsDNA viruses VP	1209	350	*Ectocarpus siliculosus, Verrucomicrobia, Acanthamoeba castellanii str. Neff, Hydra vulgaris*	Adenoviridae, Iridoviridae, Phycodnaviridae, Mimiviridae, Tectiviridae
48724	49829	49830	ENV polyprotein, receptor-binding domain	104	30	*Amniota*	Retroviridae
48724	49834	49835	Virus attachment protein globular domain	602	217	*Lactococcus lactis, E. Coli, Chlamydia trachomatis, Rhodococcus sp., Porphyromonas macacae, Ensifer sp.*	Caudovirales, Adenoviridae, Reoviridae
48724	50016	50017	gp9	63	63	*Streptomyces ahygroscopicus*	Caudovirales
48724	50036	50122	DNA-binding domain of retroviral integrase	5701	103	*Amniota, Brugia malayi, Nuttalliella namaqua*	Retroviridae
48724	50938	50939	Sialidases	16625	11206	*Bacteria, Metazoa, Fungi, Euglenozoa, Choanoflagellida, Trichomonas vaginalis, Karenia brevis*	Orthomyxoviridae, Mononegavirales, Phycodnaviridae, Caudovirales, Adenoviridae
48724	51224	51225	Fibre shaft of virus attachment proteins	122	40	*Xenorhabdus cabanillasii*	Adenoviridae, Reoviridae, Claudovirales
48724	51331	51332	E2 regulatory, transactivation domain	723	337	*Chlamydia trachomatis*	Papillomaviridae
53931	54861	54957	Viral DNA-binding domain	802	346	*Chlamydia trachomatis*	Papillomaviridae, Herpesvirales
53931	54861	55056	Killer toxin KP6 alpha-subunit	6	3	*Ustilago maydis*	Ustilago maydis virus P6, Ustilago maydis dsRNA virus
53931	54861	55064	Translational regulator protein regA	124	108	*Streptomyces ahygroscopicus, Proteobacteria bacterium JGI 0000113-L05, Proteobacteria bacterium JGI 0000113-L07*	Caudovirales
53931	55670	55671	Regulatory factor Nef	6177	24	*Mus musculus*	Retroviridae
53931	56501	56502	gp120 core	4994	17	*Homo sapiens*	Retroviridae
53931	56547	56548	Conserved core of transcriptional regulatory protein vp16	88	41	*Gallus gallus*	Herpesvirales
53931	56557	56558	Baseplate structural protein gp11	60	60	*Streptomyces ahygroscopicus*	Caudovirales
56572	56825	56826	Upper collar protein gp10 (connector protein)	27	20	*Enterococcus faecium, Enterococcus faecalis, Chlamydia trachomatis, Trichuris trichiura, Eggerthella sp. CAG:1427, Bacteroides sp. CAG:1076*	Caudovirales
56992	57755	57756	Retrovirus zinc finger-like domains	6605	154	*Metazoa, Brugia malayi, Echinococcus multilocularis*	Retroviridae
48724	69348	69349	Phage fibre proteins	379	139	*Proteobacteria, Firmicutes, Streptomyces ahygroscopicus*	Caudovirales
56835	69921	69922	Head and neck region of the ectodomain of NDV fusion glycoprotein	2161	130	*Clostridium tetani*	Mononegavirales
56572	82855	82856	L-A virus major coat protein	13	7	*Saccharomycetes*	Totivirus
48724	88632	88633	Positive stranded ssRNA viruses	15700	2255	*Propionibacterium acnes J165*	Caliciviridae, Picornavirales, Bromoviridae, Tombusviridae, Tymovirales, Birnaviridae, Nodaviridae, Sobemovirus, Alphatetraviridae, Primate T-lymphotropic virus 1, Polemovirus, Alphacarmotetravirus
48724	88632	88645	ssDNA viruses	2578	319	*Saitoella complicata NRRL Y-17804, Zygosaccharomyces bailii ISA1307, Xanthophyllomyces dendrorhous, Proteobacteria, Firmicutes, Actinobacteria, Capnocytophaga sp., Bacteroidetes, Chlamydia psittaci*	Parvoviridae, Microviridae
48724	88632	88648	Group I dsDNA viruses	1451	460	*Chlamydia trachomatis, Homo sapiens*	Papillomaviridae, Polyomaviridae
48724	88632	88650	Satellite viruses	76	13	*Wuchereria bancrofti*	Satellite Viruses, Necrovirus
53931	88873	88874	Receptor-binding domain of short tail fibre protein gp12	88	69	*Proteobacteria, firmicutes, Bacteroidetes, Streptomyces ahygroscopicus*	Caudovirales
48724	89432	89433	Baseplate structural protein gp8	66	63	*Streptomyces ahygroscopicus*	Caudovirales

53931	103067	103068	Nucleocapsid protein dimerization domain	2255	232	*Escherichia coli 1-176-05_S1_C1,Escherichia coli 1-110-08_S3_C2*	Nidovirales
46456	47379	109801	Hypothetical protein D-63	7	6	*Sulfolobus islandicus*	Sulfolobus spindle-shaped virus
48724	110303	110304	Coronavirus RNA-binding domain	813	174	*Escherichia coli 1-176-05_S1_C1,Escherichia coli 1-110-08_S3_C2*	Nidovirales
46456	140808	140809	Rhabdovirus nucleoprotein-like	1747	164	*Aedes aegypti, Brugia malayi*	Mononegavirales
48724	141657	141658	Bacteriophage trimeric proteins domain	106	92	*Proteobacteria, Firmicutes, Porphyromonas macacae, Chlamydia trachomatis*	Caudovirales
53931	143075	143076	Coronavirus NSP8-like	1197	231	*Escherichia coli*	Nidovirales
53931	143586	143587	SARS receptor-binding domain-like	171	112	*Escherichia coli 1-110-08_S3_C3, Homo sapiens*	Nidovirales
53931	54235	159936	NSP3A-like	567	143	*E. coli*	Nidovirales
56992	161228	161229	E6 C-terminal domain-like	876	215	*Chlamydia trachomatis*	Papillomaviridae
56992	161233	161234	E7 C-terminal domain-like	574	233	*Chlamydia trachomatis, Homo sapiens*	Papillomaviridae
56992	161239	161240	T-antigen specific domain-like	276	83	*Mus musculus*	Polyomaviridae

Supplementary Table 11: Trends in some superfamilies with a narrow taxonomic distribution. The taxonomic and DA details of the superfamilies with only multi-domain architectures. Either these domains do not occur singly or the single domain forms might emerge after taxonomic sampling of a wider range of genomes.

Super-family	**Super-family description**	**Number of True positive hits**	**Number of Taxid**	**SCOP domain architectures**	**Phyletic distribution**
103623	Rubredoxin-like	7	5	56712~103623, 54631~103623	Euryarchaeota
64043	Cell-division inhibitor MinC, N-terminal domain	24	20	64043~63848	Thermotogae
68930	Protein-L-isoaspartyl O-methyltransferase, C-terminal domain	6	1	53335~68930	Thermotogae
69008	RecG, N-terminal domain	26	24	169008~50249~52540~52540	Thermotogae
69075	Glutamyl tRNA-reductase dimerization domain	49	37	69742~51984~69075, 69742~69075, 69742~51735~69075	Euryarchaeota, Proteobacteria
69322	Tricorn protease domain 2	364	253	69304~69322~52096, 69304~69304~69322~52096, 69322~52096~50156~52096, 69304~69322~50156~52096, 69304~69322~52096~52096, 69322~52096, 69304~69304~69322~52096~52096, 69304~69304~69322, 69304~69322~52096~50156~52096, 69304~69322, 69322~52096~52096	Actinobacteria, Thermoprotei, Chlorobi, Thermotogae, Thermoplasmata, Armatimonadetes, Proteobacteria, Firmicutes
81665	Metal cation-transporting ATPase, transmembrane domain	5	1	81653~81665~81660~81665, 81653~81665~81660~56784~81665, 81665~81660~81665, 81653~81660~81665	Fusobacteria, Fungi, Metazoa, Apicomplexa
81878	BRCA2 tower domain	30	6	81872~50249~81878, 50249~81878,50249~81878~50249~50249~50249, 50249~81878~50249~50249, 81872~50249~81878~50249, 81878~50249~50249, 81872~50249~81878~50249~50249, 50249~81878~50249	Superfamily:Muroidea
82220	Tp47 lipoprotein, N-terminal domain	8	2	82220~81986~81986	Genus: Treponema Family: Spirochaetes

Supplementary Table 12: The most frequently occuring SCOP and Pfam DA have been listed for all the superfamilies. The Pfam family and SCOP superfamily codes have been used for the Pfam DA and SCOP DA respectively. In both the cases, we see that the single domain forms are more common, even though other multi-domain forms may exist in the superfamily. The superfamilies in red do not have any matches in Pfam.

SCOP	SUPERFAMILY DESCRIPTION	MOST COMMON SCOP DA	MOST COMMON Pfam DA
46458	Globin-like	46458	Globin
46548	alpha-helical ferredoxin	54292~46548	Fer2_3~Fer4_17
46557	GreA transcript cleavage protein, N-terminal domain	46557~54534	GreA_GreB_N~GreA_GreB
46561	Ribosomal protein L29 (L29p)	46561	Ribosomal_L29
46565	Chaperone J-domain	46565~57938~49493	DnaJ~DnaJ_C
46575	DNA polymerase III theta subunit-like	46575	DNA_pol3_theta
46579	Prefoldin	46579	Prefoldin
46585	HR1 repeat	46585~46585~46585~56112	HR1~HR1~HR1~Pkinase~Pkinase_C
46589	tRNA-binding arm	46589~55681	Phe_tRNA-synt_N~tRNA-synt_2d
46596	Eukaryotic DNA topoisomerase I, dispensable insert domain	46596	Topo_C_assoc
46600	C-terminal UvrC-binding domain of UvrB	52540~52540~52540~46600	Helicase_C~UvrB~UVR
46604	Epsilon subunit of F1F0-ATP synthase C-terminal domain	51344~46604	ATP-synt_DE_N~ATP-synt_DE
46609	Fe,Mn superoxide dismutase (SOD), N-terminal domain	46609~54719	Sod_Fe_N~Sod_Fe_C
46626	Cytochrome c	46626	Cytochrom_C
46689	Homeodomain-like	46689	TetR_N
46767	Methylated DNA-protein cysteine methyltransferase, C-terminal domain	46767	Methyltransf_1N~DNA_binding_1
46774	ARID-like	46774	ARID
46785	Winged helix DNA-binding domain	46785	MarR
46894	C-terminal effector domain of the bipartite response regulators	52172~46894	Response_reg~GerE
46906	Ribosomal protein L11, C-terminal domain	54747~46906	Ribosomal_L11_N~Ribosomal_L11
46911	Ribosomal protein S18	46911	Ribosomal_S18
46915	Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3	54211~55666~46915~54211~55666~50249	RNase_PH~RNase_PH_C~PNPase~RNase_PH~RNase_PH_C~KH_1~S1
46919	N-terminal Zn binding domain of HIV integrase	50630~56672~53098~46919~53098~50122	RVP~RVT_1~RVT_thumb~RVT_connect~RNase_H~Integrase_Zn~rve~IN_DBD_C
46924	RNA polymerase subunit RPB10	46924	RNA_pol_N
46929	DNA helicase RuvA subunit, C-terminal domain	50249~47781~46929	RuvA_N~HHH_5~RuvA_C
46934	UBA-like	46934~54713~54713	EF_TS
46938	CRAL/TRIO N-terminal domain	46938~52087	CRAL_TRIO

46942	Elongation factor TFIIS domain 2	47676~46942~57783	Med26~TFIIS_M~TFIIS_C
46946	S13-like H2TH domain	81624~46946~57716	Fapy_DNA_glyco~H2TH~zf-FPG_IleRS
46950	Double-stranded DNA-binding domain	46950	dsDNA_bind
46955	Putative DNA-binding domain	46955	tRNA_bind~B3_4~B5~FDX-ACB
46966	Spectrin repeat	47576~47576~46966~46966~46966~46966~47473	CH~CH~Spectrin~Spectrin~Spectrin~Spectrin~EFhand_Ca_insen
46973	Enzyme IIa from lactose specific PTS, IIa-lac	46973	PTS_IIA
46977	Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain	51905~56425~46977	FAD_binding_2~Succ_DH_flav_C
46984	Smac/diablo	46984	Smac_DIABLO
46988	Tubulin chaperone cofactor A	46988	TBCA
46992	Ribosomal protein S20	46992	Ribosomal_S20p
46997	Bacterial immunoglobulin/albumin-binding domains	46997~46997~46997~46997~46997	YSIRK_signal~B~B~B~B~LysM~Gram_pos_anchor
47005	Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex	51230~47005~52777	Biotin_lipoyl~E3_binding~2-oxoacid_dh
47014	Protozoan pheromone proteins	47014	E_raikovi_mat
47027	Acyl-CoA binding protein	47027	ACBP
47031	Second domain of FERM	54236~47031~50729	FERM_N~FERM_M~FERM_C~FA~SAB~4_1_CTD
47040	Kix domain of CBP (creb binding protein)	57933~47040~47370~57850~57933~69125	zf-TAZ~KIX~Bromodomain~DUF902~HAT_KAT11~ZZ~zf-TAZ~Creb_binding
47045	RAP domain-like	47045~47045	Alpha-2-MRAP_N~Alpha-2-MRAP_C
47050	VHP, Villin headpiece domain	57716~57716~57716~57716~57716~47050	LIM~LIM~LIM~LIM~VHP
47055	TAF(II)230 TBP-binding fragment	47055~47370~47370	TBP-binding~DUF3591~zf-CCHC_6~Bromodomain~Bromodomain
47060	S15/NS1 RNA-binding domain	47060~143021	Flu_NS1
47072	Cysteine alpha-hairpin motif	47072	COX17
47077	T4 endonuclease V	47077	Pyr_excise
47082	Fertilization protein	47082	Egg_lysin
47090	PGBD-like	47090	Amidase_2~PG_binding_1
47095	HMG-box	47095	HMG_box
47113	Histone-fold	47113	CBFD_NFYB_HMF
47144	HSC20 (HSCB), C-terminal oligomerisation domain	47144	DnaJ~HSCB_C
47148	Diol dehydratase, gamma subunit	47148	Dehydratase_SU
47152	Methane monooxygenase hydrolase, gamma subunit	47152	MeMO_Hyd_G
47157	Mitochondrial import receptor subunit Tom20	47157	MAS20
47162	Apolipoprotein	47162	Apolipoprotein
47170	Aspartate receptor, ligand-binding domain	47170	TarH~HAMP~MCPsignal
47175	Cytochromes	47175	Cytochrom_C_2
47188	Hemerythrin-like	47188	Hemerythrin
47195	TMV-like viral coat proteins	47195	TMV_coat

47203	Acyl-CoA dehydrogenase C-terminal domain-like	56645~47203	Acyl-CoA_dh_N~Acyl-CoA_dh_M~Acyl-CoA_dh_1
47212	FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)	47212	DUF3385~FAT~Rapamycin_bind~PI3_PI4_kinase~FATC
47216	Proteasome activator	47216	PA28_alpha~PA28_beta
47220	alpha-catenin/vinculin-like	47220~47220	Vinculin
47226	Histidine-containing phosphotransfer domain, HPT domain	47226	Hpt
47233	Bacterial GAP domain	47233	YopE~ADPrib_exo_Tox
47240	Ferritin-like	47240	Ferritin
47266	4-helical cytokines	47266	Interferon
47323	Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases	52374~47323	tRNA-synt_1~Anticodon_1
47336	ACP-like	47336	PP-binding
47345	Colicin E immunity proteins	47345	Colicin_Pyocin
47353	Retrovirus capsid dimerization domain-like	47836~47943~47353~57756	Gag_p17~Gag_p24~zf-CCHC~zf-CCHC~Gag_p6
47364	Domain of the SRP/SRP receptor G-proteins	47364~52540~47446	SRP54_N~SRP54~SRP_SPB
47370	Bromodomain	57903~47370	Bromodomain~Bromodomain~BET
47380	ROP protein	47380	Rop
47384	Homodimeric domain of signal transducing histidine kinase	47384~55874	HAMP~HisKA~HATPase_c
47391	Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit	47391~51206~51206	RIIa~cNMP_binding~cNMP_binding
47396	Transcription factor IIA (TFIIA), alpha-helical domain	47396~50784	TFIIA_gamma_N~TFIIA_gamma_C
47401	Ectatomin subunits	47401	Ectatomin
47406	SinR repressor dimerisation domain-like	47413~47406	HTH_3~SinI
47413	lambda repressor-like DNA-binding domains	47413	HTH_3
47446	Signal peptide-binding domain	47364~52540~47446	SRP54_N~SRP54~SRP_SPB
47454	A DNA-binding domain in eukaryotic transcription factors	47454	bZIP_Maf
47459	HLH, helix-loop-helix DNA-binding domain	47459	HLH
47473	EF-hand	47473	EF-hand_7
47565	Insect pheromone/odorant-binding proteins	47565	PBP_GOBP
47571	Cloroperoxidase	47571	Peroxidase_2
47576	Calponin-homology domain, CH-domain	47576	CH
47587	Domain of poly(ADP-ribose) polymerase	142921~47587~56399	WGR~PARP_reg~PARP
47592	SWIB/MDM2 domain	47592	SWIB
47598	Ribbon-helix-helix	47598	Pro_dh-DNA_bdg~Pro_dh~Aldedh
47616	GST C-terminal domain-like	52833~47616	GST_N~GST_C
47644	Methionine synthase domain	82282~51717~47644~52242~56507	S-methyl_trans~Pterin_bind~B12-binding_2~B12-binding~Met_synt_B12
47648	Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain	47648~52418	Glycos_trans_3N~Glycos_transf_3

47655	STAT	48092~47655~49417~55550	STAT_int~STAT_alpha~STAT_bind~SH2
47661	t-snare proteins	47661	Syntaxin~SNARE
47668	N-terminal domain of cbl (N-cbl)	47668~47473~55550	Cbl_N~Cbl_N2~Cbl_N3~zf-C3HC4_3
47672	Transferrin receptor-like dimerisation domain	52025~53187~47672	PA~Peptidase_M28~TFR_dimer
47676	Conserved domain common to transcription factors TFIIS, elongin A, CRSP70	47676	Med26~TFIIS_M~TFIIS_C
47681	C-terminal domain of B transposition protein	47681	AAA_22~Phage-MuB_C
47686	Anaphylotoxins (complement system)	47686~48239~50242	A2M_N~A2M_N_2~ANATO~A2M~Thiol-ester_cl~A2M_comp~A2M_recep~NTR
47694	Cytochrome c oxidase subunit h	47694	COX6B
47699	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin	47699	Tryp_alpha_amyl
47719	p53 tetramerization domain	49417~47719	P53_TAD~P53~P53_tetramer
47724	Domain of early E2A DNA-binding protein, ADDBP	47724~57917~57917	Viral_DNA_bi~Viral_DNA_Zn_bi~Viral_DNA_Zn_bi
47729	IHF-like DNA-binding proteins	47729	Bac_DNA_binding
47741	CO dehydrogenase ISP C-domain like	54292~47741	Fer2_2
47752	Protein HNS-dependent expression A; HdeA	47752	HdeA
47757	Chemotaxis receptor methyltransferase CheR, N-terminal domain	47757~53335	CheR_N~CheR
47762	PAH2 domain	47762	PAH~PAH~PAH~Sin3_corepress~Sin3a_C
47769	SAM/Pointed domain	47769	SAM_1
47781	RuvA domain 2-like	47781	DNA_ligase_aden~DNA_ligase_OB~DNA_ligase_ZBD~HHH_2~BRCT
47789	C-terminal domain of RNA polymerase alpha subunit	56553~47789	RNA_pol_A_bac~RNA_pol_A_CTD
47794	Rad51 N-terminal domain-like	69705~54814~54814~47794~47794	NusA_N~S1~KH_5~HHH_5
47798	Barrier-to-autointegration factor, BAF	47798	BAF
47802	DNA polymerase beta, N-terminal domain-like	47802~81585~81301	HHH_8~DNA_pol_lambd_f~DNA_pol_B_palm~DNA_pol_B_thumb
47807	5' to 3' exonuclease, C-terminal subdomain	88723~47807~53098~56672	5_3_exonuc_N~5_3_exonuc~DNA_pol_A
47819	HRDC-like	52540~52540~46785~47819	DEAD~Helicase_C~RecQ_Zn_bind~RQC~HRDC
47823	lambda integrase-like, N-terminal domain	47823~56349	Phage_int_SAM_1~Phage_integrase
47831	Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain	47831~52009	PEP-utilisers_N~PEP-utilizers~PEP-utilizers_C
47836	Retroviral matrix proteins	47836~47943~47353~57756	Gag_p17~Gag_p24~zf-CCHC~zf-CCHC~Gag_p6
47852	Hepatitis B viral capsid (hbcag)	47852	Hep_core_N
47857	Apolipophorin-III	47857	ApoLp-III

47862	Saposin	47862	SapA~SapB_1~SapB_2~SapB_1~SapB_2~SapB_1~SapB_2~SapB_1~SapB_2~SapA
47869	Bacteriocin AS-48	47869	Bacteriocin_IId
47874	Annexin	47874	Annexin~Annexin~Annexin~Annexin
47895	Transducin (alpha subunit), insertion domain	47895~52540	G-alpha
47912	Wiscott-Aldrich syndrome protein, WASP, C-terminal domain	50729~47912~47912	WH1~PBD~WH2
47917	C-terminal domain of alpha and beta subunits of F1 ATP synthase	50615~52540~47917	ATP-synt_ab_N~ATP-synt_ab~ATP-synt_ab_C
47923	Ypt/Rab-GAP domain of gyp1p	47923	RabGAP-TBC
47928	N-terminal domain of the delta subunit of the F1F0-ATP synthase	47928	OSCP
47933	ERP29 C domain-like	52833~52833~47933	Thioredoxin~Thioredoxin~ERp29
47938	Functional domain of the splicing factor Prp18	47938	Prp18
47943	Retrovirus capsid protein, N-terminal core domain	47836~47943~47353~57756	Gag_p17~Gag_p24~zf-CCHC~zf-CCHC~Gag_p6
47954	Cyclin-like	47954~47954	Cyclin_N~Cyclin_C
47973	Ribosomal protein S7	47973	Ribosomal_S7
47979	Iron-dependent repressor protein, dimerization domain	46785~47979	Fe_dep_repress~Fe_dep_repr_C~FeoA
47986	DEATH domain	47986	I-set~TSP_1~TSP_1~ZU5~Death
48008	GntR ligand-binding domain-like	46785~48008	GntR~FCD
48013	NusB-like	48013	NusB
48019	post-AAA+ oligomerization domain-like	52540~48019	AAA~AAA_assoc_2~MgsA_C
48024	N-terminal domain of DnaB helicase	48024	DnaB~DnaB_C
48029	FliG	48029	FliG_N~FliG_M~FliG_C
48034	Guanido kinase N-terminal domain	48034~55931	ATP-gua_PtransN~ATP-gua_Ptrans
48045	Scaffolding protein gpD of bacteriophage procapsid	48045	gpD
48050	Hemocyanin, N-terminal domain	48050~48056~81296	Hemocyanin_N~Hemocyanin_M~Hemocyanin_C
48056	Di-copper centre-containing domain	48056	Hemocyanin_N~Hemocyanin_M~Hemocyanin_C
48065	DBL homology domain (DH-domain)	48065~50729	RhoGEF
48076	LigA subunit of an aromatic-ring-opening dioxygenase LigAB	48076	LigA
48081	Methyl-coenzyme M reductase alpha and beta chain C-terminal domain	48081	MCR_alpha
48092	Transcription factor STAT-4 N-domain	48092~47655~49417~55550	STAT_int~STAT_alpha~STAT_bind~SH2
48097	Regulator of G-protein signaling, RGS	48097	RGS
48108	Carbamoyl phosphate synthetase, large subunit connection domain	52440~56059~48108~52440~56059~52335	CPSase_L_D2~CPSase_L_D3~CPSase_L_D2~MGS
48113	Heme-dependent peroxidases	48113	peroxidase
48140	Ribosomal protein L19 (L19e)	48140	Ribosomal_L19e
48145	Influenza virus matrix protein M1	48145	Flu_M1~Flu_M1_C
48150	DNA-glycosylase	48150	Adenine_glyco
48163	An anticodon-binding domain of class I aminoacyl-tRNA synthetases	52374~48163	tRNA-synt_1c

48168	R1 subunit of ribonucleotide reductase, N-terminal domain	48168~51998	RNR_N~Ribonuc_red_lgN~Ribonuc_red_lgC
48173	Cryptochrome/photolyase FAD-binding domain	52425~48173	DNA_photolyase~FAD_binding_7
48179	6-phosphogluconate dehydrogenase C-terminal domain-like	51735~48179	NAD_binding_2~NAD_binding_11
48201	Uteroglobin-like	48201	Uteroglobin
48208	Six-hairpin glycosidases	48208	Glyco_hydro_9
48225	Seven-hairpin glycosidases	48225	Glyco_hydro_47
48230	Chondroitin AC/alginate lyase	48230~74650~49863	Lyase_8_N~Lyase_8~Lyase_8_C
48239	Terpenoid cyclases/Protein prenyltransferases	48239	SQHop_cyclase_N~SQHop_cyclase_C
48256	Citrate synthase	48256	Citrate_synt
48264	Cytochrome P450	48264~52218~63380~52343	p450
48295	TrpR-like	52540~48295	DnaA_N~Bac_DnaA~Bac_DnaA_C
48300	Ribosomal protein L7/12, oligomerisation (N-terminal) domain	48300~54736	Ribosomal_L12_N~Ribosomal_L12
48305	Class II MHC-associated invariant chain ectoplasmic trimerization domain	48305~57610	MHC2-interact~MHCassoc_trimer~Thyroglobulin_1
48310	Aldehyde ferredoxin oxidoreductase, C-terminal domains	56228~48310	AFOR_N~AFOR_C
48317	Acid phosphatase/Vanadium-dependent haloperoxidase	48317	
48334	DNA repair protein MutS, domain III	55271~53150~48334~52540	MutS_I~MutS_II~MutS_III~MutS_V
48340	Interferon-induced guanylate-binding protein 1 (GBP1), C-terminal domain	52540~48340	GBP~GBP_C
48345	A virus capsid protein alpha-helical domain	48345~48345	Rota_Capsid_VP6
48350	GTPase activation domain, GAP	48350	RhoGAP
48366	Ras GEF	47113~48065~50729~48366	Histone~RhoGEF~PH~RasGEF_N~RasGEF
48371	ARM repeat	48371	B56
48403	Ankyrin repeat	48403	Ank_2~Ank_5~Ank_2~Ank_2~Ank_4~Ank_3~Ank_2~Ank_5~Ank_4~Ank~Ank_5~Ank_2~ZU5~ZU5~Death
48425	Sec7 domain	48425	Sec7~IQ_SEC7_PH
48431	Lipovitellin-phosvitin complex, superhelical domain	56968~48431~56968~56968	Vitellogenin_N~DUF1943~DUF1944~VWD
48435	Bacterial muramidases	48435~53955	SLT_L~SLT
48439	Protein prenylyltransferase	48439	PPTA~PPTA~PPTA~PPTA
48445	14-3-3 protein	48445	14-03-2003
48452	TPR-like	48452	DUF924
48464	ENTH/VHS domain	48464	ANTH
48479	Cytochrome c oxidase subunit E	48479	COX5A
48484	Lipoxigenase	49723~48484	PLAT~Lipoxygenase
48493	gene 59 helicase assembly protein	48493	T4_Gp59_N~T4_Gp59_C
48498	Tetracyclin repressor-like, C-terminal domain	46689~48498	TetR_N
48508	Nuclear receptor ligand-binding domain	57716~48508	zf-C4~Hormone_recep
48537	Phospholipase C/P1 nuclease	48537	S1-P1_nuclease

48552	Serum albumin-like	48552~48552~48552	Serum_albumin~Serum_albumin~Serum_albumin
48557	L-aspartase-like	48557	Lyase_aromatic
48576	Terpenoid synthases	48576	polyprenyl_synt
48592	GroEL equatorial domain-like	48592~52029~48592	Cpn60_TCP1
48600	Chorismate mutase II	48600	CM_2
48608	Peridinin-chlorophyll protein	48608~48608	PCP~PCP
48613	Heme oxygenase-like	48613	TENA_THI-4
48619	Phospholipase A2, PLA2	48619	Phospholip_A2_1
48647	Fungal elicitin	48647	Elicitin
48652	Tetraspanin	48652	Tetraspannin
48657	FinO-like	48657	ProQ
48662	Ribosomal protein L39e	48662	Ribosomal_L39
48666	Methanol dehydrogenase subunit	48666	MDH
48670	Transducin (heterotrimeric G protein), gamma chain	48670	G-gamma
48674	Fe-only hydrogenase smaller subunit	48674	Fe_hyd_SSU
48678	Moesin tail domain	54236~47031~50729~48678	FERM_N~FERM_M~FERM_C~ERM
48686	Proteinase A inhibitor IA3	48686	Inhibitor_I34
48690	Epsilon subunit of mitochondrial F1F0-ATP synthase	48690	ATP-synt_Eps
48695	Multiheme cytochromes	48695	Cytochrom_C552
48726	Immunoglobulin	48726	V-set
49265	Fibronectin type III	49265	fn3
49299	PKD domain	49299	Sortilin-Vps10~Sortilin_C~PKD
49303	beta-Galactosidase/glucuronidase domain	49785~49303~51445~49303~74650	Glyco_hydro_2_N~Glyco_hydro_2~Glyco_hydro_2_C~DUF4981~Bgal_small_N
49309	Transglutaminase, two C-terminal domains	81296~54001~49309~49309	Transglut_N~Transglut_C~Transglut_C
49313	Cadherin-like	49313~49313	Cadherin_2~Cadherin~Cadherin~Cadherin~Cadherin~Cadherin~Cadherin_C_2
49319	Actinoxanthin-like	49319	Neocarzinostat
49329	Cu,Zn superoxide dismutase-like	49329	Sod_Cu
49344	CBD9-like	49344	CDH-cyt
49348	Clathrin adaptor appendage domain	48371~49348~55711	Adaptin_N~Alpha_adaptinC2
49354	PapD-like	49354~49584	PapD_N~PapD_C
49363	Purple acid phosphatase, N-terminal domain	49363~56300	Pur_ac_phosph_N~Metallophos~Metallophos_C
49367	Superoxide reductase-like	49367	Desulfoferrod_N~Desulfoferrodox
49373	Invasin/intimin cell-adhesion fragments	49373	Invasin_beta~Invasin_D3~Big_1~Big_1~Big_1
49380	Diphtheria toxin, C-terminal domain	56399~56845~49380	Diphtheria_C~Diphtheria_T~Diphtheria_R
49384	Carbohydrate-binding domain	49384	CBM_2
49401	Bacterial adhesins	49401	Fimbrial
49410	Alpha-macroglobulin receptor domain	48239~49410	A2M_N~A2M_N_2~A2M~Thiol-ester_cl~A2M_comp~A2M_recep
49417	p53-like transcription factors	49417	T-box
49441	Cytochrome f, large domain	49441~51246~103431	Apocytochr_F_N~Apocytochr_F_C
49447	Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor	64356~49447	Clat_adaptor_s~Adap_comp_sub
49452	Starch-binding domain-like	49452	PUD~CBM_48

49464	Carboxypeptidase regulatory domain-like	49464	CarbopepD_reg_2~Plug
49468	VHL	49468	VHL
49472	Transthyretin (synonym: prealbumin)	49472	Transthyretin
49478	Cna protein B-type domain	49478	Collagen_bind~Cna_B
49482	Aromatic compound dioxygenase	49482	Dioxygenase_N~Dioxygenase_C
49493	HSP40/DnaJ peptide-binding domain	46565~57938~49493	DnaJ~DnaJ_C
49498	alpha-Amylase inhibitor tendamistat	49498	A_amylase_inhib
49503	Cupredoxins	49503	Cu-oxidase_3~Cu-oxidase~Cu-oxidase_2
49562	C2 domain (Calcium/lipid-binding domain, CaLB)	49562	C2~C2
49584	Periplasmic chaperone C-domain	49354~49584	PapD_N~PapD_C
49590	PHL pollen allergen	50685~49590	DPBB_1~Pollen_allerg_1
49594	Rab geranylgeranyltransferase alpha-subunit, insert domain	48439~49594~52058	PPTA~PPTA~PPTA~PPTA~RabGGT_insert
49599	TRAF domain-like	49599	Sina
49606	Neurophysin II	49606	Hormone_4~Hormone_5
49695	gamma-Crystallin-like	49695~49695	Crystall~Crystall
49723	Lipase/lipooxygenase domain (PLAT/LH2 domain)	49723~48484	PLAT~Lipoxygenase
49742	PHM/PNGase F	49742~49742	DOMON~Cu2_monooxygen~Cu2_monoox_C
49749	Group II dsDNA viruses VP	49749	Adeno_hexon~Adeno_hexon_C
49758	Calpain large subunit, middle domain (domain III)	54001~49758~47473	Peptidase_C2~Calpain_III~EF-hand_8
49764	HSP20-like chaperones	49764	HSP20
49772	Ecotin, trypsin inhibitor	49772	Ecotin
49777	PEBP-like	49777	PBP
49785	Galactose-binding domain-like	49785	Glyco_hydro_2_N~Glyco_hydro_2~Glyco_hydro_2_C~DUF4981~Bgal_small_N
49818	Viral protein domain	49818	Hemagglutinin
49830	ENV polyprotein, receptor-binding domain	49830	TLV_coat
49835	Virus attachment protein globular domain	49835	Adeno_knob
49842	TNF-like	49842	TNF
49854	Spermadhesin, CUB domain	49854~57196~49854~57535~57535~50494	CUB~CUB~F5_F8_type_C~F5_F8_type_C~MAM~DUF3481
49863	Hyaluronate lyase-like, C-terminal domain	48230~74650~49863	Lyase_8_N~Lyase_8~Lyase_8_C
49870	Osmotin, thaumatin-like protein	49870	Thaumatin
49879	SMAD/FHA domain	49879	FHA
49889	Soluble secreted chemokine inhibitor, VCCI	49889	Orthopox_35kD
49894	Baculovirus p35 protein	49894	P35
49899	Concanavalin A-like lectins/glucanases	49899	Glyco_hydro_16~XET_C
49998	Amine oxidase catalytic domain	54416~49998	Cu_amine_oxidN2~Cu_amine_oxidN3~Cu_amine_oxid
50012	EV matrix protein	50012~50012	VP40
50017	gp9	50017	T4_gp9_10
50022	ISP domain	50022	Rieske
50037	C-terminal domain of transcriptional repressors	46785~55681~50037	HTH_11~BPL_LplA_LipB~BPL_C

50044	SH3-domain	50044	SH3_1~SH2~Pkinase_Tyr
50084	Myosin S1 fragment, N-terminal domain	50084~52540	Myosin_N~Myosin_head~Myosin_tail_1
50090	Electron transport accessory proteins	50090	NHase_beta
50104	Translation proteins SH3-like domain	50104	Ribosomal_L2~Ribosomal_L2_C
50118	Cell growth inhibitor/plasmid maintenance toxic component	50118	PemK_toxin
50122	DNA-binding domain of retroviral integrase	50630~56672~53098~46919~53098~50122	Integrase_Zn~rve~IN_DBD_C
50129	GroES-like	50129~51735	ADH_N~ADH_zinc_N
50151	SacY-like RNA-binding domain	50151~63520~63520	CAT_RBD~PRD~PRD
50156	PDZ domain-like	50156	Trypsin_2~PDZ_2
50176	N-terminal domains of the minor coat protein g3p	50176	Phage_Coat_A~Phage_Coat_A
50182	Sm-like ribonucleoproteins	50182	LSM
50193	Ribosomal protein L14	50193	Ribosomal_L14
50199	Staphylococcal nuclease	50199	SNase
50203	Bacterial enterotoxins	50203~54334	SSL_OB
50242	TIMP-like	50242	TIMP
50249	Nucleic acid-binding proteins	50249	tRNA_anti-codon~tRNA-synt_2
50324	Inorganic pyrophosphatase	50324	Pyrophosphatase
50331	MOP-like	52540~50331	ABC_tran~TOBE_2
50341	CheW-like	50341	CheW
50346	PRC-barrel domain	50447~50346	RimM~PRC
50353	Cytokine	50353	FGF
50370	Ricin B-like lectins	50370	Glycos_transf_2~Ricin_B_lectin
50382	Agglutinin	50382	Agglutinin
50386	STI-like	50386	Kunitz_legume
50405	Actin-crosslinking proteins	50405~50405~50405~50405	Fascin~Fascin~Fascin~Fascin
50443	FucI/AraA C-terminal domain-like	53743~50443	Arabinose_Isome~Arabinose_Iso_C
50447	Translation proteins	52540~50447~50465	GTP_EFTU~GTP_EFTU_D2~GTP_EFTU_D3
50465	EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain	52540~50447~50465	GTP_EFTU~GTP_EFTU_D2~GTP_EFTU_D3
50475	FMN-binding split barrel	50475	Flavin_Reduct
50486	FMT C-terminal domain-like	53328~50486	Formyl_trans_N~Formyl_trans_C
50494	Trypsin-like serine proteases	50494	Trypsin
50610	mu transposase, C-terminal domain	46955~46689~46689~53098~50610	HTH_Tnp_Mu_1~HTH_Tnp_Mu_2~DDE_2~Mu-transpos_C
50615	N-terminal domain of alpha and beta subunits of F1 ATP synthase	50615~52540~47917	ATP-synt_ab_N~ATP-synt_ab~ATP-synt_ab_C
50621	Alanine racemase C-terminal domain-like	51419~50621	Ala_racemase_N~Ala_racemase_C
50630	Acid proteases	50630	Asp
50677	ValRS/IleRS/LeuRS editing domain	50677~47323	tRNA-synt_1_2~Anticodon_1
50685	Barwin-like endoglucanases	50685	MltA~3D
50692	ADC-like	53706~50692	Molybdopterin~Molydop_binding
50715	Ribosomal protein L25-like	50715	Ribosomal_L25p~Ribosomal_TL5_C
50723	Core binding factor beta, CBF	50723	CBF_beta
50729	PH domain-like	50729	PH
50784	Transcription factor IIA (TFIIA), beta-barrel domain	47396~50784	TFIIA

50789	Herpes virus serine proteinase, assemblin	50789	Peptidase_S21
50800	PK beta-barrel domain-like	50800~52935	PK~PK_C
50809	XRCC4, N-terminal domain	50809	XRCC4
50814	Lipocalins	50814	Lipocalin
50876	Avidin/streptavidin	50876	Avidin
50882	beta-Barrel protease inhibitors	50882	Inh
50886	D-aminopeptidase, middle and C-terminal domains	56601~50886~50886	Beta-lactamase~DAP_B
50891	Cyclophilin-like	50891	Pro_isomerase
50904	Oncogene products	50904	TCL1_MTCP1
50911	Mannose 6-phosphate receptor domain	50911	Man-6-P_recep
50916	Rap30/74 interaction domains	50916~46785	TFIIF_alpha
50923	Hemopexin-like domain	47090~55486~50923	PG_binding_1~Peptidase_M10~Hemopexin~Hemopexin~Hemopexin~Hemopexin
50934	Tachylectin-2	50934	Tachylectin
50939	Sialidases	50939	Neur
50952	Soluble quinoprotein glucose dehydrogenase	50952	GSDH
50956	Thermostable phytase (3-phytase)	50956	Phytase
50960	TolB, C-terminal domain	52964~50960	TolB_N~PD40~PD40~PD40
50965	Galactose oxidase, central domain	50965~81296	Glyoxal_oxid_N~Kelch_6~DUF1929
50969	YVTN repeat-like/Quinoprotein amine dehydrogenase	50969	Me-amine-dh_H
50974	Nitrous oxide reductase, N-terminal domain	50974~49503	Cupredoxin_1
50978	WD40 repeat-like	50978	WD40~WD40~WD40~WD40~WD40~WD40
50985	RCC1/BLIP-II	50985	RCC1~RCC1_2~RCC1~RCC1_2~RCC1~RCC1_2~RCC1~RCC1_2~RCC1~RCC1~HECT
50989	Clathrin heavy-chain terminal domain	50989~48371~48371~48371	Clathrin_propel~Clathrin_propel~Clathrin_propel~Clathrin_propel~Clathrin_propel~Clathrin-link~Clathrin_H_link~Clathrin~Clathrin~Clathrin~Clathrin~Clathrin~Clathrin~Clathrin
50993	Peptidase/esterase 'gauge' domain	50993~53474	Peptidase_S9_N~Peptidase_S9
50998	Quinoprotein alcohol dehydrogenase-like	50998	PQQ_2~PQQ_3~PQQ
51004	C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase	46626~51004	Cytochrome_CBB3~Cytochrom_D1
51011	Glycosyl hydrolase domain	51445~51011	CBM_48~Alpha-amylase_C
51045	WW domain	51045~50729	WW
51055	Carbohydrate binding domain	51055	CBM_5_12
51064	Head domain of nucleotide exchange factor GrpE	51064	GrpE
51069	Carbonic anhydrase	51069	Carb_anhydrase
51081	Bacteriochlorophyll A protein	51081	BChl_A
51087	Outer surface protein	51087	Lipoprotein_1
51092	Vitelline membrane outer protein-I (VMO-I)	51092	VOMI

51096	delta-Endotoxin (insectocide), middle domain	56849~51096~49785	Endotoxin_N~Endotoxin_M~Endotoxin_C
51101	Mannose-binding lectins	51101	Jacalin
51110	alpha-D-mannose-specific plant lectins	51110	B_lectin
51120	beta-Roll	55486~51120	Peptidase_M10_C
51126	Pectin lyase-like	51126	Glyco_hydro_28
51156	Insect cysteine-rich antifreeze protein	51156	AFP~AFP~AFP~AFP~AFP~AFP
51161	Trimeric LpxA-like enzymes	51161	Hexapep
51177	An insect antifreeze protein	51177	CfAFP
51182	RmlC-like cupins	51182	Cupin_2
51197	Clavaminate synthase-like	51197	DIOX_N~2OG-FeII_Oxy
51206	cAMP-binding domain-like	51206	cNMP_binding~HTH_Crp_2
51215	Regulatory protein AraC	51215	AraC_binding~HTH_18
51219	TRAP-like	51219	AIM24
51225	Fibre shaft of virus attachment proteins	51225~49835	Reo_sigma1
51230	Single hybrid motif	51230~47005~52777	Biotin_lipoyl~E3_binding~2-oxoacid_dh
51246	Rudiment single hybrid motif	52440~56059~51246	ATP-grasp
51261	Duplicated hybrid motif	55604~51261	PTS_EIIC~PTS_EIIB~PTS_EIIA_1
51269	AFP III-like domain	51569~51269	NeuB~SAF
51274	Head decoration protein D (gpD, major capsid protein D)	51274	HDPD
51278	Urease, beta-subunit	51278	Urease_beta
51283	dUTPase-like	51283	dUTPase
51289	Tlp20, baculovirus telokin-like protein	51289	TLP-20
51294	Hedgehog/intein (Hint) domain	51294	PT-HINT
51306	LexA/Signal peptidase	51306	Peptidase_S24
51316	Mss4-like	51316	PMSR~SelR
51322	Cyanovirin-N	51322	CVNH
51327	Head-binding domain of phage P22 tailspike protein	51327	Head_binding
51332	E2 regulatory, transactivation domain	51332~54957	PPV_E2_N~PPV_E2_C
51338	Composite domain of metallo-dependent hydrolases	51338~51556	Amidohydro_1
51344	Epsilon subunit of F1F0-ATP synthase N-terminal domain	51344	ATP-synt_DE_N~ATP-synt_DE
51351	Triosephosphate isomerase (TIM)	51351	TIM
51366	Ribulose-phoshate binding barrel	51366	His_biosynth
51391	Thiamin phosphate synthase	51391	TMP-TENI
51395	FMN-linked oxidoreductases	51395	Oxidored_FMN
51412	Inosine monophosphate dehydrogenase (IMPDH)	54631~51412	IMPDH
51419	PLP-binding barrel	51419~50621	Ala_racemase_N~Ala_racemase_C
51430	NAD(P)-linked oxidoreductase	51430	Aldo_ket_red
51445	(Trans)glycosidases	51445	Glyco_hydro_1
51556	Metallo-dependent hydrolases	51556	Amidohydro_1
51569	Aldolase	51569	DAHP_synth_1
51604	Enolase C-terminal domain-like	54826~51604	MR_MLE_N~MR_MLE_C
51621	Phosphoenolpyruvate/pyruvate domain	51621	HpcH_HpaI
51645	Malate synthase G	51645	Malate_synthase

51649	RuBisCo, C-terminal domain	54966~51649	RuBisCO_large_N~RuBisCO_large
51658	Xylose isomerase-like	51658	AP_endonuc_2
51679	Bacterial luciferase-like	51679	Bac_luciferase
51690	Nicotinate/Quinolinate PRTase C-terminal domain-like	54675~51690	NAPRTase
51695	PLC-like phosphodiesterases	51695	GDPD
51703	Cobalamin (vitamin B12)-dependent enzymes	51703~52242	MM_CoA_mutase~B12-binding
51713	tRNA-guanine transglycosylase	51713	TGT
51717	Dihydropteroate synthetase-like	51717	Pterin_bind
51726	UROD/MetE-like	51726	URO-D
51730	FAD-linked oxidoreductase	51730	MTHFR
51735	NAD(P)-binding Rossmann-fold domains	51735	adh_short
51905	FAD/NAD(P)-binding domain	51905	Pyr_redox_2~Pyr_redox_dim
51971	Nucleotide-binding domain	51971	NAD_binding_8~GLF
51984	MurCD N-terminal domain	51984~53623~53244	Mur_ligase~Mur_ligase_M~Mur_ligase_C
51989	Glycosyl hydrolases family 6, cellulases	51989	Glyco_hydro_6
51998	PFL-like glycyl radical enzymes	51998	PFL-like~Gly_radical
52009	Phosphohistidine domain	56059~52009~51621	PEP-utilisers_N~PEP-utilizers~PEP-utilizers_C
52016	LeuD/IlvD-like	53732~52016	Aconitase~Aconitase_C
52021	Carbamoyl phosphate synthetase, small subunit N-terminal domain	52021~52317	CPSase_sm_chain~GATase
52025	PA domain	52025~53187~47672	PA~Peptidase_M28~TFR_dimer
52029	GroEL apical domain-like	52029	Cpn60_TCP1
52038	Barstar-related	52038	Barstar
52042	Ribosomal protein L32e	52042	Ribosomal_L32e
52047	RNI-like	52047	Tropomodulin
52058	L domain-like	52058	LRR_9
52075	Outer arm dynein light chain 1	52075	LRR_4
52080	Ribosomal proteins L15p and L18e	52080	Ribosomal_L18e
52087	CRAL/TRIO domain	46938~52087	CRAL_TRIO
52091	SpoIIaa-like	52091	STAS
52096	ClpP/crotonase	52096	ECH_1
52113	BRCT domain	56091~50249~47781~52113	DNA_ligase_aden~DNA_ligase_OB~DNA_ligase_ZBD~HHH_2~BRCT
52121	Lumazine synthase	52121	DMRL_synthase
52129	Caspase-like	52129	Peptidase_C14
52141	Uracil-DNA glycosylase-like	52141	UDG
52151	FabD/lysophospholipase-like	52151	Acyl_transf_1
52156	Initiation factor IF2/eIF5b, domain 3	52540~52156~50447	IF2_N~IF2_N~GTP_EFTU~IF-2
52161	Ribosomal protein L13	52161	Ribosomal_L13
52166	Ribosomal protein L4	52166	Ribosomal_L4
52172	CheY-like	52172~46894	Response_reg~Trans_reg_C
52200	Toll/Interleukin receptor TIR domain	52058~52200	LRR_8~LRR_8~TIR
52206	Hypothetical protein MTH538	52206	TIR_2
52210	Succinyl-CoA synthetase domains	51735~52210	CoA_binding~Ligase_CoA
52218	Flavoproteins	52218	FMN_red
52242	Cobalamin (vitamin B12)-binding domain	51703~52242	S-methyl_trans~Pterin_bind~B12-binding_2~B12-binding~Met_synt_B12

52255	N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)	52255	AIRC
52266	SGNH hydrolase	52266	Lipase_GDSL_2
52279	Beta-D-glucan exohydrolase, C-terminal domain	51445~52279	Glyco_hydro_3~Glyco_hydro_3_C
52283	Formate/glycerate dehydrogenase catalytic domain-like	52283~51735	2-Hacid_dh_C
52304	Type II 3-dehydroquinate dehydratase	52304	DHquinase_II
52309	N-(deoxy)ribosyltransferase-like	52309	Nuc_deoxyrib_tr
52313	Ribosomal protein S2	52313	Ribosomal_S2
52317	Class I glutamine amidotransferase-like	52317	DJ-1_PfpI
52335	Methylglyoxal synthase-like	52440~56059~48108~52440~56059~52335	CPSase_L_D2~CPSase_L_D3~CPSase_L_D2~MGS
52343	Ferredoxin reductase-like, C-terminal NADP-linked domain	63380~52343	FAD_binding_6~NAD_binding_1
52374	Nucleotidylyl transferase	52374	CTP_transf_like
52402	Adenine nucleotide alpha hydrolases-like	52402	Usp
52413	UDP-glucose/GDP-mannose dehydrogenase C-terminal domain	51735~48179~52413	UDPG_MGDP_dh_N~UDPG_MGDP_dh~UDPG_MGDP_dh_C
52418	Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain	47648~52418	Glycos_trans_3N~Glycos_transf_3
52425	Cryptochrome/photolyase, N-terminal domain	52425~48173	DNA_photolyase~FAD_binding_7
52440	PreATP-grasp domain	52440~56059~51246	Dala_Dala_lig_N~Dala_Dala_lig_C
52467	DHS-like NAD/FAD-binding domain	52518~52467~52518	TPP_enzyme_N~TPP_enzyme_M~TPP_enzyme_C
52490	Tubulin nucleotide-binding domain-like	52490~55307	Tubulin~Tubulin_C
52499	Isochorismatase-like hydrolases	52499	Isochorismatase
52507	Homo-oligomeric flavin-containing Cys decarboxylases, HFCD	52507~102645	Flavoprotein
52518	Thiamin diphosphate-binding fold (THDP-binding)	52518~52467~52518	TPP_enzyme_N~TPP_enzyme_M~TPP_enzyme_C
52540	P-loop containing nucleoside triphosphate hydrolases	52540	ABC_tran
52728	PTS IIb component	52728	PTSIIB_sorb
52733	Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)	52733	DBI_PRT
52738	Methylesterase CheB, C-terminal domain	52172~52738	Response_reg~CheB_methylest
52743	Subtilisin-like	52743	Peptidase_S8
52768	Arginase/deacetylase	52768	Arginase
52777	CoA-dependent acyltransferases	51230~47005~52777	Biotin_lipoyl~E3_binding~2-oxoacid_dh
52788	Phosphotyrosine protein phosphatases I	52788	LMWPc
52794	PTS system IIB component-like	52794	PTS_IIB
52799	(Phosphotyrosine protein) phosphatases II	52799	DSPc
52821	Rhodanese/Cell cycle control phosphatase	52821	Rhodanese
52833	Thioredoxin-like	52833~47616	Thioredoxin

52913	RNA 3'-terminal phosphate cyclase, RPTC, insert domain	52913	RTC
52922	TK C-terminal domain-like	52518~52922	Transket_pyr~Transketolase_C
52935	PK C-terminal domain-like	50800~52935	PK~PK_C
52943	ATP synthase (F1-ATPase), gamma subunit	52943	ATP-synt
52949	Macro domain-like	52949	Macro
52954	Class II aaRS ABD-related	55681~52954	tRNA-synt_His~HGTP_anticodon
52964	TolB, N-terminal domain	52964~50960	TolB_N~PD40~PD40~PD40
52968	B12-dependent dehydatase associated subunit	52968	Dehydratase_MU
52972	ITPase-like	52972	Ham1p_like
52980	Restriction endonuclease-like	52980	UvrD-helicase~UvrD_C
53032	tRNA-intron endonuclease catalytic domain-like	53032	tRNA_int_endo
53036	Eukaryotic RPB5 N-terminal domain	53036~55287	RNA_pol_Rpb5_N~RNA_pol_Rpb5_C
53041	Resolvase-like	53041	Resolvase~HTH_7
53056	beta-carbonic anhydrase, cab	53056	Pro_CA
53062	PTS system fructose IIA component-like	53062	EIIA-man
53067	Actin-like ATPase domain	53067~53067	ROK
53092	Creatinase/prolidase N-terminal domain	53092~55920	Creatinase_N~Peptidase_M24
53098	Ribonuclease H-like	53098	RNase_T
53137	Translational machinery components	53137	Ribosomal_L18p
53146	Nitrogenase accessory factor-like	53146	Nitro_FeMo-Co
53150	DNA repair protein MutS, domain II	55271~53150~48334~52540	MutS_I~MutS_II~MutS_III~MutS_V
53155	Methylated DNA-protein cysteine methyltransferase domain	57884~53155~46767	Ada_Zn_binding~HTH_18~Methyltransf_1N~DNA_binding_1
53163	HybD-like	53163	HycI
53167	Purine and uridine phosphorylases	53167	PNP_UDP_1
53178	Peptidyl-tRNA hydrolase-like	53178	Pept_tRNA_hydro
53182	Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)	53182	Peptidase_C15
53187	Zn-dependent exopeptidases	53187	Peptidase_M20
53213	LigB-like	53213	LigB
53218	Molybdenum cofactor biosynthesis proteins	53218	MoCF_biosynth
53223	Aminoacid dehydrogenase-like, N-terminal domain	53223~51735	ELFV_dehydrog_N~ELFV_dehydrog
53244	MurD-like peptide ligases, peptide-binding domain	51984~53623~53244	Mur_ligase~Mur_ligase_M~Mur_ligase_C
53254	Phosphoglycerate mutase-like	53254	His_Phos_1
53271	PRTase-like	53271	Pribosyltran
53300	vWA-like	53300	VWA_2
53323	Pyruvate-ferredoxin oxidoreductase, PFOR, domain III	52518~52922~53323~54862~52518	POR_N~POR~EKR~Fer4_6~Fer4_7
53328	Formyltransferase	53328~50486	Formyl_trans_N~Formyl_trans_C
53335	S-adenosyl-L-methionine-dependent methyltransferases	53335	Methyltransf_31
53383	PLP-dependent transferases	53383	Aminotran_1_2
53448	Nucleotide-diphospho-sugar transferases	53448	NTP_transferase

53474	alpha/beta-Hydrolases	53474	Abhydrolase_1
53590	Nucleoside hydrolase	53590	IU_nuc_hydro
53597	Dihydrofolate reductase-like	53597	DHFR_1
53613	Ribokinase-like	53613	PfkB
53623	MurD-like peptide ligases, catalytic domain	51984~53623~53244	Mur_ligase~Mur_ligase_M~Mur_ligase_C
53633	Carbamate kinase-like	53633	AA_kinase
53639	AraD/HMP-PK domain-like	53639	Aldolase_II
53649	Alkaline phosphatase-like	53649	Sulfatase
53659	Isocitrate/Isopropylmalate dehydrogenase-like	53659	Iso_dh
53671	Aspartate/ornithine carbamoyltransferase	53671~53671	OTCace_N~OTCace
53681	Aspartate/glutamate racemase	53681~53681	Asp_Glu_race
53686	Tryptophan synthase beta subunit-like PLP-dependent enzymes	53686	PALP
53697	SIS domain	53697	SIS_2
53706	Formate dehydrogenase/DMSO reductase, domains 1-3	53706~50692	Molybdopterin~Molydop_binding
53720	ALDH-like	53720	Aldedh
53732	Aconitase iron-sulfur domain	53732~52016	Aconitase~Aconitase_C
53738	Phosphoglucomutase, first 3 domains	53738~53738~53738~55957	PGM_PMM_I~PGM_PMM_II~PGM_PMM_III~PGM_PMM_IV
53743	FucI/AraA N-terminal and middle domains	53743~50443	Arabinose_Isome~Arabinose_Iso_C
53748	Phosphoglycerate kinase	53748	PGK
53756	UDP-Glycosyltransferase/glycogen phosphorylase	53756	Glyco_transf_5~Glycos_transf_1
53774	Glutaminase/Asparaginase	53774	Asparaginase
53784	Phosphofructokinase	53784	PFK
53790	Tetrapyrrole methylase	53790	TP_methylase
53795	PEP carboxykinase-like	68923~53795	PEPCK
53800	Chelatase	53800	Ferrochelatase
53807	Helical backbone metal receptor	53807	Peripla_BP_2
53822	Periplasmic binding protein-like I	53822	Peripla_BP_4
53850	Periplasmic binding protein-like II	53850	HTH_1~LysR_substrate
53901	Thiolase-like	53901~53901	Thiolase_N~Thiolase_C
53920	Fe-only hydrogenase	54292~54862~53920	Fe_hyd_lg_C~Fe_hyd_SSU
53927	Cytidine deaminase-like	53927	dCMP_cyt_deam_1
53933	Microbial ribonucleases	53933	Ribonuclease
53955	Lysozyme-like	53955	Phage_lysozyme
54001	Cysteine proteinases	54001	UCH
54060	His-Me finger endonucleases	54060	Endonuclease_NS
54076	RNase A-like	54076	RnaseA
54098	Prion-like	54098	Prion_bPrPp~Prion
54106	LysM domain	54106	SLT~LysM~LysM
54111	Urease, gamma-subunit	54111	Urease_gamma
54117	Interleukin 8-like chemokines	54117	IL8
54160	Chromo domain-like	54160	Chromo
54171	DNA-binding domain	54171	AP2
54184	Penicillin-binding protein 2x (pbp-2x), c-terminal domain	56601~54184~54184	PBP_dimer~Transpeptidase~PASTA
54189	Ribosomal proteins S24e, L23 and L15e	54189	Ribosomal_L23

54197	HIT-like	54197	HIT
54211	Ribosomal protein S5 domain 2-like	54211	HATPase_c~DNA_gyraseB~Toprim ~DNA_gyraseB_C
54236	Ubiquitin-like	54236	ubiquitin
54277	CAD & PB1 domains	54277	PB1~Pkinase
54285	MoaD/ThiS	54285	ThiS
54292	2Fe-2S ferredoxin-like	54292	Fer2
54328	Staphylokinase/streptokinase	54328	Staphylokinase
54334	Superantigen toxins, C-terminal domain	50203~54334	SSL_OB
54358	Immunoglobulin-binding domains	54358	IgG_binding_B
54364	Translation initiation factor IF3, N-terminal domain	54364~55200	IF3_N~IF3_C
54368	Glutamine synthetase, N-terminal domain	54368~55931	Gln-synt_N~Gln-synt_C
54373	FAD-linked reductases, C-terminal domain	54373	DAO
54403	Cystatin/monellin	54403	Cystatin
54416	Amine oxidase N-terminal region	54416~49998	Cu_amine_oxidN2~Cu_amine_oxid N3~Cu_amine_oxid
54423	DsbC/DsbG N-terminal domain-like	54423~52833	DsbC_N~Thioredoxin_2
54427	NTF2-like	54427	SnoaL_2
54441	Uracil-DNA glycosylase inhibitor protein	54441	
54447	ssDNA-binding transcriptional regulator domain	54447	PC4
54452	MHC antigen-recognition domain	54452~48726	MHC_I
54495	UBC-like	54495	UQ_con
54506	Diaminopimelate epimerase-like	54506	PhzC-PhzF
54511	GFP-like	54511	GFP
54518	Tubby C-terminal domain-like	54518	Tub
54523	Pili subunits	54523	N_methyl_2~T2SSG
54529	Mitochondrial glycoprotein MAM33-like	54529	MAM33
54534	FKBP-like	54534	FKBP_C
54552	Colicin E3 immunity protein	54552	Cloacin_immun
54556	Chitinase insertion domain	51445~54556	Glyco_hydro_18
54565	Ribosomal protein S16	54565	Ribosomal_S16
54570	Ribosomal protein S19	54570	Ribosomal_S19
54575	Ribosomal protein L31e	54575	Ribosomal_L31e
54580	Allophycocyanin linker chain (domain)	54580	CpcD
54585	Cdc48 domain 2-like	50692~54585~52540~ 52540	CDC48_N~CDC48_2~AAA~AAA
54593	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	54593	Glyoxalase
54611	SecB-like	54611	SecB
54616	DNA-binding domain of Mlu1-box binding protein MBP1	54616	Ank_4
54621	Heme-binding protein A (HasA)	54621	HasA
54626	Chalcone isomerase	54626	Chalcone
54631	CBS-domain pair	54631	CBS~CBS
54637	Thioesterase/thiol ester dehydrase-isomerase	54637	4HBT

54648	DLC	54648	Dynein_light
54654	CI-2 family of serine protease inhibitors	54654	potato_inhibit
54665	CO dehydrogenase molybdoprotein N-domain-like	54665~56003	Ald_Xan_dh_C~Ald_Xan_dh_C2
54675	Nicotinate/Quinolinate PRTase N-terminal domain-like	54675~51690	NAPRTase
54680	Pyrimidine nucleoside phosphorylase C-terminal domain	47648~52418~54680	Glycos_trans_3N~Glycos_transf_3~PYNP_C
54686	Ribosomal protein L16p/L10e	54686	Ribosomal_L16
54690	Molybdopterin synthase subunit MoaE	54690	MoaE
54695	POZ domain	54695~81324	BTB_2~Ion_trans
54713	Elongation factor Ts (EF-Ts), dimerisation domain	46934~54713~54713	EF_TS
54719	Fe,Mn superoxide dismutase (SOD), C-terminal domain	46609~54719	Sod_Fe_N~Sod_Fe_C
54736	ClpS-like	54736	Ribosomal_L12_N~Ribosomal_L12
54747	Ribosomal L11/L12e N-terminal domain	54747~46906	Ribosomal_L11_N~Ribosomal_L11
54752	RecA protein, C-terminal domain	52540~54752	RecA
54762	Signal recognition particle alu RNA binding heterodimer, SRP9/14	54762	SRP14
54768	dsRNA-binding domain-like	69065~54768	Ribonucleas_3_3~dsrm
54782	Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain	53850~54782	Porphobil_deam~Porphobil_deamC
54786	YcfA/nrd intein domain	54786	HicA_toxin
54791	Eukaryotic type KH-domain (KH-domain type I)	54791	KH_1~KH_1~KH_1
54806	Alpha-lytic protease prodomain	54806~50494	Pro_Al_protease
54810	GMP synthetase C-terminal dimerisation domain	52317~52402~54810	GATase~GMP_synt_C
54814	Prokaryotic type KH domain (KH-domain type II)	52540~54814	MMR_HSR1~KH_2
54821	Ribosomal protein S3 C-terminal domain	54814~54821	KH_2~Ribosomal_S3_C
54826	Enolase N-terminal domain-like	54826~51604	MR_MLE_N~MR_MLE_C
54843	Ribosomal protein L22	54843	Ribosomal_L22
54849	GroEL-intermediate domain like	54849~52029	Cpn60_TCP1
54857	DNA damage-inducible protein DinI	54857	DinI
54862	4Fe-4S ferredoxins	54862	ETF_QO
54893	Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain	54893~57825	PyrI~PyrI_C
54897	Protease propeptides/inhibitors	54897~53187	Propep_M14~Peptidase_M14
54909	Dimeric alpha+beta barrel	54909	ABM
54913	GlnB-like	54913	P-II
54919	Nucleoside diphosphate kinase, NDK	54919	NDK
54928	RNA-binding domain, RBD	54928	RRM_1
54957	Viral DNA-binding domain	51332~54957	PPV_E2_N~PPV_E2_C
54966	RuBisCO, large subunit, small (N-terminal) domain	54966~51649	RuBisCO_large_N~RuBisCO_large
54975	Acylphosphatase/BLUF domain-like	54975	Acylphosphatase
54980	EF-G C-terminal domain-like	52540~50447~54980~54211~54980	GTP_EFTU~GTP_EFTU_D2~EFG_II~EFG_IV~EFG_C
54984	eEF-1beta-like	54984	EF-1_beta_acid~EF1_GNE

54991	Anticodon-binding domain of PheRS	50249~56037~46955~55681~54991	tRNA_bind~B3_4~B5~FDX-ACB
54995	Ribosomal protein S6	54995	Ribosomal_S6
54999	Ribosomal protein S10	54999	Ribosomal_S10
55003	PAP/Archaeal CCA-adding enzyme, C-terminal domain	81301~81631~55003	PAP_central
55008	HMA, heavy metal-associated domain	55008	HMA~HMA~E1-E2_ATPase~Hydrolase
55021	ACT-like	55021~55021	ABC_tran~NIL
55031	Bacterial exopeptidase dimerisation domain	55031	Peptidase_M20
55035	NAD-binding domain of HMG-CoA reductase	55035	HMG-CoA_red
55040	Molybdenum cofactor biosynthesis protein C, MoaC	55040	MoaC
55044	TRADD, N-terminal domain	55044	TRADD_N~Death
55048	Probable ACP-binding domain of malonyl-CoA ACP transacylase	55048	Acyl_transf_1
55052	CheY-binding domain of CheA	47226~55052~47384~55874~50341	Hpt~CheY-binding~H-kinase_dim~HATPase_c~CheW
55056	Killer toxin KP6 alpha-subunit	55056	
55060	GHMP Kinase, C-terminal domain	54211~55060	GHMP_kinases_N~GHMP_kinases_C
55064	Translational regulator protein regA	55064	Translat_reg
55068	Peptide methionine sulfoxide reductase	55068	PMSR
55073	Nucleotide cyclase	55073	Guanylate_cyc
55083	6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK	55083	HPPK
55088	Methyl-coenzyme M reductase subunits	55088~48081	MCR_alpha_N~MCR_alpha
55103	FAD-linked oxidases, C-terminal domain	56176~55103	FAD_binding_4~Lact-deh-memb
55112	Formylmethanofuran:tetrahydromethanopterin formyltransferase	55112~55112	FTR~FTR_C
55116	Formiminotransferase domain of formiminotransferase-cyclodeaminase.	55116~55116	FTCD_N~FTCD
55120	Pseudouridine synthase	55120	S4~PseudoU_synth_2
55124	Nitrite/Sulfite reductase N-terminal domain-like	55124~56014~55124~56014	NIR_SIR_ferr~NIR_SIR~NIR_SIR_ferr~NIR_SIR
55129	Ribosomal protein L30p/L7e	55129	Ribosomal_L30
55136	Probable bacterial effector-binding domain	55136	HTH_18~GyrI-like
55144	LigT-like	55144	2_5_RNA_ligase2
55149	Pepsin inhibitor-3	55149	Pepsin-I3
55154	CYTH-like phosphatases	55154	CYTH
55159	eIF1-like	55159	SUI1
55166	Hedgehog/DD-peptidase	55166	Peptidase_M74
55174	Alpha-L RNA-binding motif	55174	Ribosomal_S4~S4
55186	ThrRS/AlaRS common domain	55681~101353~55186	tRNA-synt_2c~tRNA_SAD~DHHA1
55190	Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain	55190~52374~47323	Arg_tRNA_synt_N~tRNA-synt_1d~DALR_1
55194	Ribosome recycling factor, RRF	55194	RRF
55200	Translation initiation factor IF3, C-terminal domain	54364~55200	IF3_N~IF3_C

55205	EPT/RTPC-like	55205	EPSP_synthase
55221	Yeast killer toxins	55221	Kp4
55229	Cell division protein MinE topological specificity domain	55229	MinE
55234	Cyanase C-terminal domain	47413~55234	Cyanate_lyase
55239	RuBisCO, small subunit	55239	RuBisCO_small
55248	PCD-like	55248	Pterin_4a
55252	C-terminal domain of arginine repressor	46785~55252	Arg_repressor~Arg_repressor_C
55257	RBP11-like subunits of RNA polymerase	55257	RNA_pol_L_2
55261	GAD domain-like	50249~55681~55261~55681	tRNA_anti-codon~tRNA-synt_2
55267	tRNA-intron endonuclease N-terminal domain-like	55267~53032	tRNA_int_endo_N~tRNA_int_endo
55271	DNA repair protein MutS, domain I	55271~53150~48334~52540	MutS_I~MutS_II~MutS_III~MutS_V
55277	GYF domain	55277	GYF
55282	RL5-like	55282	Ribosomal_L5~Ribosomal_L5_C
55287	RPB5-like RNA polymerase subunit	53036~55287	RNA_pol_Rpb5_N~RNA_pol_Rpb5_C
55298	YjgF-like	55298	Ribonuc_L-PSP
55307	Tubulin C-terminal domain-like	52490~55307	Tubulin~Tubulin_C
55315	L30e-like	55315	Ribosomal_L7Ae
55326	PurM N-terminal domain-like	55326~56042	AIRS~AIRS_C
55331	Tautomerase/MIF	55331	Tautomerase
55347	Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain	51735~55347	Semialdhyde_dh~Semialdhyde_dhC
55383	Copper amine oxidase, domain N	55383~54416~54416~49998	Cu_amine_oxidN1~Cu_amine_oxidN2~Cu_amine_oxidN3~Cu_amine_oxid
55387	Frataxin/Nqo15-like	55387	Frataxin_Cyay
55394	Bactericidal permeability-increasing protein, BPI	55394	LBP_BPI_CETP~LBP_BPI_CETP_C
55399	Subtilisin inhibitor	55399	SSI
55405	RNA bacteriophage capsid protein	55405	Levi_coat
55418	eIF4e-like	55418	IF4E
55424	FAD/NAD-linked reductases, dimerisation (C-terminal) domain	51905~55424	Pyr_redox_2~Pyr_redox_dim
55447	CO dehydrogenase flavoprotein C-terminal domain-like	56176~55447	FAD_binding_5~CO_deh_flav_C
55455	SRF-like	55455	SRF-TF~K-box
55464	Origin of replication-binding domain, RBD-like	55464	Gemini_AL1~Gemini_AL1_M
55469	FMN-dependent nitroreductase-like	55469	Nitroreductase
55481	N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1	55481~53137~55315	eRF1_1~eRF1_2~eRF1_3
55486	Metalloproteases ("zincins"), catalytic domain	55486	Peptidase_M3
55545	beta-N-acetylhexosaminidase-like domain	55545~51445	Glyco_hydro_20b~Glyco_hydro_20
55550	SH2 domain	55550	SH2
55594	HPr-like	55594	PTS-HPr
55604	Glucose permease domain IIB	55604~51261	PTS_EIIC~PTS_EIIB

55608	Homing endonucleases	55608	LAGLIDADG_1~LAGLIDADG_1
55620	Tetrahydrobiopterin biosynthesis enzymes-like	55620	GTP_cyclohydroI
55637	Cell cycle regulatory proteins	55637	CKS
55648	beta-lactamase-inhibitor protein, BLIP	55648	BLIP
55653	Ribosomal protein L9 C-domain	55658~55653	Ribosomal_L9_N~Ribosomal_L9_C
55658	L9 N-domain-like	55658~55653	Ribosomal_L9_N~Ribosomal_L9_C
55666	Ribonuclease PH domain 2-like	54211~55666	RNase_PH~RNase_PH_C
55671	Regulatory factor Nef	55671	F-protein
55676	CytB endotoxin-like	55676	Bac_thur_toxin
55681	Class II aaRS and biotin synthetases	55681	tRNA_anti-codon~tRNA-synt_2
55711	Subdomain of clathrin and coatomer appendage domain	48371~49348~55711	Adaptin_N~Alpha_adaptinC2~Alpha_adaptin_C
55718	SCP-like	55718	SCP2
55724	Mog1p/PsbP-like	55724	DUF1795
55729	Acyl-CoA N-acyltransferases (Nat)	55729	Acetyltransf_1
55753	Actin depolymerizing proteins	55753	Cofilin_ADF
55770	Profilin (actin-binding protein)	55770	Profilin
55781	GAF domain-like	55781	HTH_IclR~IclR
55785	PYP-like sensor domain (PAS domain)	55785	PAS_9~GGDEF~EAL
55797	PR-1-like	55797	CAP
55804	Phoshotransferase/anion transport protein	55804	PTS_EIIA_2
55811	Nudix	55811	NUDIX
55816	5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain	56300~55816	Metallophos~5_nucleotid_C
55821	YrdC/RibB	55821	Sua5_yciO_yrdC
55826	YbaK/ProRS associated domain	55826	tRNA_edit
55831	Thymidylate synthase/dCMP hydroxymethylase	55831	Thymidylat_synt
55846	N-acetylmuramoyl-L-alanine amidase-like	55846	Amidase_2
55856	Cytochrome b5-like heme/steroid binding domain	55856	Cyt-b5
55869	DNA topoisomerase I domain	55869~56349	VirDNA-topo-I_N~Topoisom_I
55874	ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase	55874~54211	HATPase_c~DNA_gyraseB~Toprim~DNA_gyraseB_C
55890	Sporulation response regulatory protein Spo0B	55890	SPOB_a~SPOB_ab
55895	Ribonuclease Rh-like	55895	Ribonuclease_T2
55904	Ornithine decarboxylase C-terminal domain	53383~55904	OKR_DC_1_N~OKR_DC_1~OKR_DC_1_C
55909	Pentein	55909	Amidinotransf
55920	Creatinase/aminopeptidase	55920	Peptidase_M24
55931	Glutamine synthetase/guanido kinase	55931	GatB_N~GatB_Yqey
55945	TATA-box binding protein-like	55945~55945	TBP~TBP
55957	Phosphoglucomutase, C-terminal domain	53738~53738~53738~55957	PGM_PMM_I~PGM_PMM_II~PGM_PMM_III~PGM_PMM_IV
55961	Bet v1-like	55961	AHSA1
55973	S-adenosylmethionine synthetase	55973~55973~55973	S-AdoMet_synt_N~S-AdoMet_synt_M~S-AdoMet_synt_C

55979	DNA clamp	55979~55979~55979	DNA_pol3_beta~DNA_pol3_beta_2~DNA_pol3_beta_3
56003	Molybdenum cofactor-binding domain	54665~56003	Ald_Xan_dh_C~Ald_Xan_dh_C2
56014	Nitrite and sulphite reductase 4Fe-4S domain-like	55124~56014~55124~56014	NIR_SIR_ferr~NIR_SIR~NIR_SIR_ferr~NIR_SIR
56019	The spindle assembly checkpoint protein mad2	56019	HORMA
56024	Phospholipase D/nuclease	56024	PP_kinase_N~PP_kinase~PP_kinase_C
56029	Monooxygenase (hydroxylase) regulatory protein	56029	MmoB_DmpM
56037	PheT/TilS domain	50249~56037~46955~55681~54991	tRNA_bind~B3_4~B5~FDX-ACB
56042	PurM C-terminal domain-like	55326~56042	AIRS~AIRS_C
56047	Ribosomal protein S8	56047	Ribosomal_S8
56053	Ribosomal protein L6	56053~56053	Ribosomal_L6~Ribosomal_L6
56059	Glutathione synthetase ATP-binding domain-like	52440~56059~51246	CPSase_L_D2~CPSase_L_D3~CPSase_L_D2~MGS
56091	DNA ligase/mRNA capping enzyme, catalytic domain	56091~50249~47781~52113	DNA_ligase_A_M~DNA_ligase_A_C
56104	SAICAR synthase-like	56104	SAICAR_synt
56112	Protein kinase-like (PK-like)	56112	Pkinase
56176	FAD-binding/transporter-associated domain-like	56176	FAD_binding_4~MurB_C
56194	Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain	56176~56194	FAD_binding_4~MurB_C
56199	Methenyltetrahydromethanopterin cyclohydrolase	56199	MCH
56204	Hect, E3 ligase catalytic domain	56204	C2~WW~WW~WW~HECT
56209	Nitrile hydratase alpha chain	56209	NHase_alpha
56214	4'-phosphopantetheinyl transferase	56214	ACPS
56219	DNase I-like	56219	Exo_endo_phos
56228	Aldehyde ferredoxin oxidoreductase, N-terminal domain	56228~48310	AFOR_N~AFOR_C
56235	N-terminal nucleophile aminohydrolases (Ntn hydrolases)	56235	Proteasome
56266	DmpA/ArgJ-like	56266	ArgJ
56271	Pyruvoyl-dependent histidine and arginine decarboxylases	56271	PvlArgDC
56276	S-adenosylmethionine decarboxylase	56276	AdoMet_dc
56281	Metallo-hydrolase/oxidoreductase	56281	Lactamase_B
56300	Metallo-dependent phosphatases	56300	Metallophos
56317	Carbon-nitrogen hydrolase	56317	CN_hydrolase
56322	ADC synthase	56322	Anth_synt_I_N~Chorismate_bind
56327	LDH C-terminal domain-like	51735~56327	Ldh_1_N~Ldh_1_C
56349	DNA breaking-rejoining enzymes	56349	Phage_int_SAM_1~Phage_integrase
56366	SMAD MH1 domain	56366~49879	MH1~MH2
56371	Ribosome inactivating proteins (RIP)	56371	RIP
56399	ADP-ribosylation	56399	PTS_2-RNA
56420	Peptide deformylase	56420	Pep_deformylase
56425	Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain	51905~56425~46977	FAD_binding_2~Succ_DH_flav_C
56436	C-type lectin-like	56436	Lectin_C

56487	SRCR-like	56487	SRCR~SRCR~SRCR~SRCR~Lysyl_oxidase
56491	A heparin-binding domain	56491~89811~57362~109843	APP_N~APP_Cu_bd~APP_E2~APP_amyloid
56496	Fibrinogen C-terminal domain-like	56496	Fibrinogen_C
56502	gp120 core	56502~56502	GP120~GP41
56507	Methionine synthase activation domain-like	82282~51717~47644~52242~56507	S-methyl_trans~Pterin_bind~B12-binding_2~B12-binding~Met_synt_B12
56512	Nitric oxide (NO) synthase oxygenase domain	56512	NO_synthase
56519	Penicillin binding protein dimerisation domain	56519~56601	PBP_dimer~Transpeptidase
56524	Oxidoreductase molybdopterin-binding domain	56524	Oxidored_molyb
56529	FAH	56529	FAA_hydrolase
56534	Aromatic aminoacid monoxygenases, catalytic and oligomerization domains	56534	Biopterin_H
56542	Substrate-binding domain of HMG-CoA reductase	56542~55035~56542	HMG-CoA_red
56548	Conserved core of transcriptional regulatory protein vp16	56548	Alpha_TIF
56553	Insert subdomain of RNA polymerase alpha subunit	56553~47789	RNA_pol_A_bac~RNA_pol_A_CTD
56558	Baseplate structural protein gp11	56558	GP11
56563	Major capsid protein gp5	56563	Phage_capsid
56568	Non-globular alpha+beta subunits of globular proteins	56568~47233~52799	SicP-binding~YopE~Y_phosphatase
56574	Serpins	56574	Serpin
56596	Replication terminator protein (Tus)	56596	Ter
56601	beta-lactamase/transpeptidase-like	56601	Beta-lactamase
56634	Heme-dependent catalase-like	56634	Catalase~Catalase-rel
56645	Acyl-CoA dehydrogenase NM domain-like	56645~47203	Acyl-CoA_dh_N~Acyl-CoA_dh_M~Acyl-CoA_dh_1
56655	Carbohydrate phosphatase	56655	Inositol_P
56672	DNA/RNA polymerases	50630~56672	IMS~IMS_HHH~IMS_C
56712	Prokaryotic type I DNA topoisomerase	56712	Toprim~Topoisom_bac
56719	Type II DNA topoisomerase	56719~101904	DNA_topoisoIV~DNA_gyraseA_C~DNA_gyraseA_C~DNA_gyraseA_C~DNA_gyraseA_C~DNA_gyraseA_C~DNA_gyraseA_C
56726	DNA topoisomerase IV, alpha subunit	56726	TP6A_N
56731	DNA primase core	57783~56731	zf-CHC2~Toprim_N~Toprim_4~DnaB_bind~DnaG_DnaB_bind
56741	Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment	56741~56349	Topoisom_I_N~Topoisom_I~Topo_C_assoc
56747	Prim-pol domain	56747	DNA_primase_S
56752	D-aminoacid aminotransferase-like PLP-dependent enzymes	56752	Aminotran_4
56762	HydB/Nqo4-like	56762	Complex1_49kDa
56770	HydA/Nqo6-like	56770	Oxidored_q6
56784	HAD-like	56784	HAD_2
56796	Dehydroquinate synthase-like	56796	Fe-ADH

56801	Acetyl-CoA synthetase-like	56801	AMP-binding~AMP-binding_C
56808	Ribosomal protein L1	56808	Ribosomal_L1
56815	Sec1/munc18-like (SM) proteins	56815	Sec1
56821	Prismane protein-like	56821	Prismane
56826	Upper collar protein gp10 (connector protein)	56826	Phage_connector
56831	Reovirus inner layer core protein p3	56831	Orbi_VP3
56837	Colicin	56837	Colicin
56845	Diphtheria toxin, middle domain	56399~56845~49380	Diphtheria_C~Diphtheria_T~Diphtheria_R
56849	delta-Endotoxin (insectocide), N-terminal domain	56849~51096~49785	Endotoxin_N~Endotoxin_M~Endotoxin_C
56854	Bcl-2 inhibitors of programmed cell death	56854	Bcl-2
56864	Exotoxin A, middle domain	49899~56864~56399	Exotox-A_bind~Exotox-A_target~Exotox-A_cataly
56918	Light-harvesting complex subunits	56918	LHC
56925	OMPA-like	56925	Ail_Lom
56931	Outer membrane phospholipase A (OMPLA)	56931	PLA1
56935	Porins	56935	Plug~TonB_dep_Rec
56954	Outer membrane efflux proteins (OEP)	56954	OEP~OEP
56959	Leukocidin-like	56959	Leukocidin
56968	Lipovitellin-phosvitin complex; beta-sheet shell regions	56968~48431~56968~56968	Vitellogenin_N~DUF1943~DUF1944~VWD
56973	Aerolisin/ETX pore-forming domain	56436~56973	APT~Aerolysin
56978	Perfringolysin	56978	Thiol_cytolysin
56983	Viral glycoprotein, central and dimerisation domains	101257~56983~81296~50494~52540~52540~53335	Flavi_glycoprot~Flavi_glycop_C
56988	Anthrax protective antigen	56988	PA14~Binary_toxB
56994	Insulin-like	56994	Insulin
57007	Heat-stable enterotoxin B	57007	STb_secrete
57011	Neurotoxin B-IV	57011	Toxin_13
57016	Plant lectins/antimicrobial peptides	57016~53955	Chitin_bind_1~Glyco_hydro_19
57027	Plant inhibitors of proteinases and amylases	57027	Squash
57038	Cyclotides	57038	Cyclotide
57048	Gurmarin-like	57048	Antifungal_pept
57055	Agouti-related protein	57055	Agouti
57059	omega toxin-like	57059	Toxin_12
57095	Scorpion toxin-like	57095	Toxin_3
57180	Cellulose-binding domain	57180	CBM_1
57184	Growth factor receptor domain	52058~57184~52058~57184~56112	Recep_L_domain~Furin-like~Recep_L_domain~GF_recep_IV~Pkinase_Tyr
57190	Colipase-like	57190~57190	Prokineticin
57196	EGF/Laminin	57196	Laminin_G_2~Laminin_G_2~Laminin_G_2~EGF~Laminin_G_2~Laminin_G_2~Laminin_G_2
57243	Bromelain inhibitor VI (cysteine protease inhibitor)	57243~57243~57243~57243~57243,57243	Inhibitor_I67~Inhibitor_I67~Inhibitor_I67
57247	Bowman-Birk inhibitor, BBI	57247	Bowman-Birk_leg~Bowman-Birk_leg

57256	Elafin-like	57256	WAP~WAP
57262	Leech antihemostatic proteins	57262	Hirudin
57277	Granulin repeat	57277	Granulin
57283	PMP inhibitors	57283~54001	Pacifastin_I
57288	Midkine	57288~57288	PTN_MK_N~PTN_MK_C
57296	Amb V allergen	57296	Amb_V_allergen
57302	Snake toxin-like	57302~56112	Activin_recp~Pkinase
57362	BPTI-like	57362	Kunitz_BPTI
57392	Defensin-like	57392	Defensin_beta
57414	Hairpin loop containing domain-like	57414~57440~57440~57440~57440~50494	PAN_1~Kringle~Kringle~Kringle~Kringle~Trypsin
57419	Neurotoxin III (ATX III)	57419	ATX_III
57424	LDL receptor-like module	57424	Ldl_recept_a~Lectin_C
57429	Crambin-like	57429	Thionin
57440	Kringle-like	57440	fn2~Lectin_C~Lectin_C~Lectin_C~Lectin_C~Lectin_C~Lectin_C~Lectin_C~Lectin_C
57492	Trefoil	57492	Trefoil
57501	Cystine-knot cytokines	57501	TGFb_propeptide~TGF_beta
57535	Complement control module/SCR domain	57535~57535~57535~57535	Sushi~Sushi~Sushi~Sushi
57546	Crisp domain-like	55797~57546	CAP~Crisp
57552	Blood coagulation inhibitor (disintegrin)	55486~57552	Pep_M12B_propep~Reprolysin~Disintegrin~ADAM_CR
57561	Methylamine dehydrogenase, L chain	57561	Me-amine-dh_L
57567	Serine protease inhibitors	57567	TIL
57581	TB module/8-cys domain	57581~57196~57581~57196~57196~57196~57196~57196~57196~57196~57581~57581	TB~EGF_CA~TB~EGF_CA~cEGF~EGF_CA~cEGF~EGF_CA~EGF_CA~EGF_CA~cEGF~EGF_CA~cEGF~EGF_CA~EGF_CA~cEGF~EGF_CA~cEGF~EGF_CA~cEGF~EGF_CA~TB~EGF_CA~EGF_CA~TB~EGF_CA
57586	TNF receptor-like	57586	TNFR_c6~TNFR_c6
57593	Heparin-binding domain from vascular endothelial growth factor	57501~57593	PDGF~VEGF_C
57598	Antifungal protein (AGAFP)	57598	Antifungal_prot
57603	FnI-like domain	57603	VWC~VWC~VWC
57610	Thyroglobulin type-1 domain	57610	IGFBP~Thyroglobulin_1
57615	Type X cellulose binding domain, CBDX	57615	Glyco_hydro_11~CBM60~Polysacc_deac_1~CBM_10
57620	Carboxypeptidase inhibitor	57620	
57625	Invertebrate chitin-binding proteins	57625	CBM_14
57630	GLA-domain	57630~57440~57440~50494	Gla
57642	Cholecystokinin A receptor, N-domain	57642~81321~81321	CholecysA-Rec_N~7tm_1
57647	HIV-1 VPU cytoplasmic domain	57647	Vpu
57652	HIPIP (high potential iron protein)	57652	HIPIP
57662	Ferredoxin thioredoxin reductase (FTR), catalytic beta chain	57662	FeThRed_B
57667	beta-beta-alpha zinc fingers	57667~57667~57667	zf-C2H2
57701	Zn2/Cys6 DNA-binding domain	57701	Zn_clus
57716	Glucocorticoid receptor-like (DNA-binding domain)	57716	zf-C4~Hormone_recep

57756	Retrovirus zinc finger-like domains	47836~47943~47353~57756	Gag_p17~Gag_p24~zf-CCHC~zf-CCHC~Gag_p6
57770	Methionyl-tRNA synthetase (MetRS), Zn-domain	52374~57770~52374~47323~50249	tRNA-synt_1g~tRNA_bind
57774	Microbial and mitochondrial ADK, insert "zinc finger" domain	57774	ADK
57783	Zinc beta-ribbon	57783~56731	PhnA_Zn_Ribbon~PhnA
57798	Casein kinase II beta subunit	57798	CK_II_beta
57802	Rubredoxin-like	57802	Rubredoxin
57821	Hypothetical protein MTH1184	57821	DUF1922
57825	Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain	54893~57825	PyrI~PyrI_C
57829	Zn-binding ribosomal proteins	57829	Ribosomal_L33
57840	Ribosomal protein L36	57840	Ribosomal_L36
57845	B-box zinc-binding domain	57850~57845~49899	zf-C3HC4_4~zf-B_box~PRY~SPRY
57850	RING/U-box	57850	zf-RING_2
57863	ArfGap/RecO-like zinc finger	57863	BAR_3~PH~ArfGap~Ank_2
57868	Metallothionein	57868	Metallothio
57879	Zinc domain conserved in yeast copper-regulated transcription factors	57879	Copper-fist
57884	Ada DNA repair protein, N-terminal domain (N-Ada 10)	57884~53155~46767	Ada_Zn_binding~HTH_18~Methyltransf_1N~DNA_binding_1
57889	Cysteine-rich domain	57889	RBD~C1_1~Pkinase_Tyr
57903	FYVE/PHD zinc finger	57903	PHD
57917	Zn-binding domains of ADDBP	47724~57917~57917	Viral_DNA_bi~Viral_DNA_Zn_bi~Viral_DNA_Zn_bi
57924	Inhibitor of apoptosis (IAP) repeat	57924	BIR
57933	TAZ domain	57933~47040~47370~57850~57933~69125	zf-TAZ~KIX~Bromodomain~DUF902~HAT_KAT11~ZZ~zf-TAZ~Creb_binding
57938	DnaJ/Hsp40 cysteine-rich domain	46565~57938~49493	DnaJ~DnaJ_C
63380	Riboflavin synthase domain-like	63380~52343	Lum_binding~Lum_binding
63393	RNA polymerase subunits	63393	DNA_RNApol_7kD
63411	LuxS/MPP-like metallohydrolase	63411	Peptidase_M16~Peptidase_M16_C
63418	MurE/MurF N-terminal domain	63418~53623~53244	Mur_ligase~Mur_ligase_M~Mur_ligase_C
63433	Fumarylacetoacetate hydrolase, FAH, N-terminal domain	63433~56529	FAA_hydrolase_N~FAA_hydrolase
63446	Type I dockerin domain	63446	Dockerin_1~Dockerin_1
63451	LEM domain	63451	LEM
63491	BAG domain	63491	BAG
63501	Frizzled cysteine-rich domain	63501	Fz~Frizzled
63515	Outer surface protein C (OspC)	63515	Lipoprotein_6
63520	PTS-regulatory domain, PRD	50151~63520~63520	CAT_RBD~PRD~PRD
63562	RPB6/omega subunit-like	63562	RNA_pol_Rpb6
63570	PABC (PABP) domain	54928~54928~54928~54928~63570	RRM_1~RRM_1~RRM_1~RRM_1~PABP
63592	Flagellar transcriptional activator FlhD	63592	FlhD
63600	Telomeric repeat binding factor (TRF) dimerisation domain	63600~46689	TRF~Myb_DNA-binding
63697	Olfactory marker protein	63697	Olfactory_mark
63707	Ganglioside M2 (gm2) activator	63707	E1_DerP2_DerF2

63712	Nicotinic receptor ligand binding domain-like	63712~90112	Neur_chan_LBD~Neur_chan_memb
63724	Cytolysin/lectin	63724	FB_lectin
63737	Leukotriene A4 hydrolase N-terminal domain	63737~55486	Peptidase_M1~Leuk-A4-hydro_C
63748	Tudor/PWWP/MBT	63748	PWWP
63763	SAND domain-like	46955~63763	Ski_Sno~c-SKI_SMAD_bind
63817	Sortase	63817	Sortase
63825	YWTD domain	57424~57424~57424~57424~57424~57424~57424~57424~57196~57196~63825~57196	Ldl_recept_a~Ldl_recept_a~Ldl_recept_a~Ldl_recept_a~Ldl_recept_a~Ldl_recept_a~Ldl_recept_a~Ldl_recept_a~FXa_inhibition~EGF_CA~Ldl_recept_b~Ldl_recept_b~Ldl_recept_b~Ldl_recept_b~Ldl_recept_b~FXa_inhibition
63829	Calcium-dependent phosphotriesterase	63829	SGL
63840	Ribonuclease domain of colicin E3	63840	Pyocin_S~Cytotoxic
63848	Cell-division inhibitor MinC, C-terminal domain	63848	MinC_C
63862	Thiamin pyrophosphokinase, substrate-binding domain	63999~63862	TPK_catalytic~TPK_B1_binding
63867	MoeA C-terminal domain-like	63882~53218~63867	MoeA_N~MoCF_biosynth~MoeA_C
63877	Methuselah ectodomain	63877	Methuselah_N~7tm_2
63882	MoeA N-terminal region -like	63882~53218~63867	MoeA_N~MoCF_biosynth~MoeA_C
63887	P-domain of calnexin/calreticulin	49899~63887	Calreticulin
63892	Pyridoxine 5'-phosphate synthase	63892	PdxJ
63965	Precorrin-8X methylmutase CbiC/CobH	63965	CbiC
63992	Dipeptide transport protein	63992	Peptidase_M55
63999	Thiamin pyrophosphokinase, catalytic domain	63999~63862	TPK_catalytic~TPK_B1_binding
64005	Undecaprenyl diphosphate synthase	64005	Prenyltransf
64043	Cell-division inhibitor MinC, N-terminal domain	64043~63848	MinC_C
64076	MTH938-like	64076	DUF498
64153	YjeF N-terminal domain-like	64153~53613	YjeF_N~Carb_kinase
64158	2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain	64158~53649	iPGM_N
64167	SurE-like	64167	SurE
64182	DHH phosphoesterases	64182	DHH~DHHA1
64210	Head-to-tail joining protein W, gpW	64210	gpW
64234	Photosystem I subunit PsaD	64234	PsaD
64263	Prokaryotic ribosomal protein L17	64263	Ribosomal_L17
64268	PX domain	64268	PX
64288	Chorismate lyase-like	64288	GntR~UTRA
64307	SirA-like	64307	TusA
64356	SNARE-like	64356	Clat_adaptor_s
64376	YlxR-like	64376	DUF448
64383	Cell-division protein ZipA, C-terminal domain	64383	ZipA_C
64397	Hsp33 domain	64397~118352	HSP33

64438	CNF1/YfiH-like putative cysteine hydrolases	64438	Cu-oxidase_4
64449	YopH tyrosine phosphatase N-terminal domain	64449~52799	YopH_N~Y_phosphatase
64465	Outer capsid protein sigma 3	64465	Reovirus_cap
64484	beta and beta-prime subunits of DNA dependent RNA-polymerase	64484	RNA_pol_Rpb2_2~RNA_pol_Rpb2_3~RNA_pol_Rpb2_45~RNA_pol_Rpb2_6~RNA_pol_Rpb2_7
64496	DNA-binding domain of intron-encoded endonucleases	54060~64496	NUMOD4~HNH_3
64518	Phase 1 flagellin	64518	Flagellin_N~Flagellin_C
64546	Satiety factor CART (cocaine and amphetamine regulated transcript)	64546	CART
64571	Cellulose docking domain, dockering	64571~64571~51989	CBM_10~CBM_10~Glyco_hydro_6
64586	C-terminal domain of ProRS	55681~64586	tRNA-synt_2b~HGTP_anticodon~ProRS-C_1
68906	SAP domain	68906	PINIT~zf-MIZ
68912	Rho N-terminal domain-like	68912~50249~52540	Rho_N~Rho_RNA_bind~ATP-synt_ab
68918	Recombination endonuclease VII, C-terminal and dimerization domains	54060~68918	Endonuclease_7~Endonuc-dimeris
68923	PEP carboxykinase N-terminal domain	68923~53795	PEPCK_ATP
68930	Protein-L-isoaspartyl O-methyltransferase, C-terminal domain	53335~68930	PCMT
68989	Hemolysin expression modulating protein HHA	68989	HHA
68993	FAT domain of focal adhesion kinase	54236~47031~50729~56112~68993	FERM_M~Pkinase_Tyr~Focal_AT
69000	FAD-dependent thiol oxidase	69000	Evr1_Alr
69008	RecG, N-terminal domain	69008~50249~52540~52540	DEAD~Helicase_C
69012	alpha-ketoacid dehydrogenase kinase, N-terminal domain	69012~55874	BCDHK_Adom3~HATPase_c
69025	Hypothetical protein MTH865	69025	MTH865
69036	Bcr-Abl oncoprotein oligomerization domain	69036~48065~48350	Bcr-Abl_Oligo~RhoGEF~C2~RhoGAP
69047	Hypothetical protein YjbJ	69047	CsbD
69055	1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain	51735~55347~51735~69055	DXP_reductoisom~DXP_redisom_C~DXPR_C
69060	Arp2/3 complex 21 kDa subunit ARPC3	69060	P21-Arc
69065	RNase III domain-like	69065~54768	Ribonucleas_3_3~dsrm
69070	Anti-sigma factor AsiA	69070	AsiA
69075	Glutamyl tRNA-reductase dimerization domain	69742~51735~69075	GlutR_N~Shikimate_DH~GlutR_dimer
69099	Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain	52047~69099~69099~52058~52058 52047~69099~52058~52058~52058~52058	RanGAP1_C
69103	Arp2/3 complex 16 kDa subunit ARPC5	69103	P16-Arc
69118	AhpD-like	69118	CMD
69125	Nuclear receptor coactivator interlocking domain	55785~69125	zf-TAZ~KIX~Bromodomain~DUF902

			~HAT_KAT11~ZZ~zf-TAZ~Creb_binding
69131	Quinohemoprotein amine dehydrogenase C chain	69131	QH-AmDH_gamma
69179	Integrin domains	69318~69179~69179~69179	FG-GAP~FG-GAP~Integrin_alpha2
69189	Penicillin-binding protein associated domain	56601~69189	Peptidase_S11~PBP5_C
69203	Nucleoplasmin-like core domain	69203	Nucleoplasmin
69255	gp5 N-terminal domain-like	69279~69279~69255	Phage_GPD~T6SS_Vgr~DUF2345
69279	Phage tail proteins	69279	Phage_GPD
69287	Urease metallochaperone UreE, N-terminal domain	69287~69737	UreE_N~UreE_C
69298	Quinohemoprotein amine dehydrogenase A chain, domain 3	46626~46626~69298~81296~81296	Dehyd-heme_bind~Qn_am_d_aII~Qn_am_d_aIII~Qn_am_d_aIV
69304	Tricorn protease N-terminal domain	69304~52096 69304	
69318	Integrin alpha N-terminal domain	69318	FG-GAP~FG-GAP~Integrin_alpha2
69322	Tricorn protease domain 2	69304~69322~52096	Tricorn_C1~Tricorn_PDZ~Peptidase_S41
69336	Alpha subunit of glutamate synthase, C-terminal domain	56235~51395~69336	GATase_2~Glu_syn_central~Glu_synthase~GXGXG
69340	C-terminal domain of adenylylcyclase associated protein	101278~69340	CAP_N~CAP_C
69349	Phage fibre proteins	69349	Hyaluronidase_1
69360	Cell wall binding repeat	69360	CW_binding_1~CW_binding_1~CW_binding_1~CW_binding_1~CW_binding_1
69369	Cloacin translocation domain	69369	Cloacin
69500	DTD-like	69500	Tyr_Deacylase
69572	Activating enzymes of the ubiquitin-like proteins	69572	ThiF
69593	Glycerol-3-phosphate (1)-acyltransferase	69593	GPAT_N~Acyltransferase
69618	HemD-like	69618	HEM4
69635	Type III secretory system chaperone-like	69635	CesT
69645	Arp2/3 complex subunits	69645	P34-Arc
69652	DNA-binding C-terminal domain of the transcription factor MotA	46785~69652	MotA_activ~MotCF
69687	Integrin beta tail domain	103575~53300~57196~57196~69687	Integrin_beta~EGF_2~Integrin_B_tail~Integrin_b_cyt
69695	SRP19	69695	SRP19
69705	Transcription factor NusA, N-terminal domain	69705~50249~54814~54814	NusA_N~S1~KH_5
69721	DsrC, the gamma subunit of dissimilatory sulfite reductase	69721	DsrC
69737	Urease metallochaperone UreE, C-terminal domain	69287~69737	UreE_N~UreE_C
69742	Glutamyl tRNA-reductase catalytic, N-terminal domain	69742~51735	GlutR_N~Shikimate_DH~GlutR_dimer
69754	Ribosome binding protein Y (YfiA homologue)	69754	Ribosomal_S30AE~Ribosom_S30AE_C
69761	GTP cyclohydrolase I feedback regulatory protein, GFRP	69761	GFRP
69765	IpsF-like	69765	YgbB

69786	YggU-like	69786	DUF167
69796	Thymidylate synthase-complementing protein Thy1	69796	Thy1
69819	MTH1598-like	69819	Archease
69848	LCCL domain	69848~53300~53300	LCCL~VWA~VWA
69864	Argininosuccinate synthetase, C-terminal domain	52402~69864	Arginosuc_synth
69903	NSP3 homodimer	69903	Rota_NSP3
69908	Membrane penetration protein mu1	69908	Reovirus_M2
69917	OMPT-like	69917	Omptin
69922	Head and neck region of the ectodomain of NDV fusion glycoprotein	69922	Fusion_gly
69964	Pheromone ER-23	69964	
74650	Galactose mutarotase-like	74650	Aldose_epim
74653	TolA/TonB C-terminal domain	74653	TonB_C
74731	Ribosomal protein L20	74731	Ribosomal_L20
74748	Variable surface antigen VlsE	74748	Lipoprotein_2
74778	Aconitase B, N-terminal domain	74778~52016~53732	Aconitase_B_N~Aconitase_2_N~Aconitase
74784	Translin	74784	Translin
74788	Cullin repeat-like	74788~75632~46785	Cullin~Cullin_Nedd8
74853	Lamin A/C globular tail domain	74853	Filament~LTD
74863	Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha)	74863~52833	DsbC~DsbD~Thioredoxin_7
74877	Major surface antigen p30, SAG1	74877~74877	SAG~SAG
74914	V-region of surface antigen I/II (SA I/II, PAC)	74914	Strep_SA_rep~Strep_SA_rep~Strep_SA_rep~Strep_SA_rep~Strep_SA_rep~Strep_SA_rep~Strep_SA_rep~GbpC~Antigen_C~Antigen_C~Antigen_C~Gram_pos_anchor
74924	Cap-Gly domain	74924	CAP_GLY
74942	YhbC-like, C-terminal domain	75420~74942	DUF150
74982	Small protein B (SmpB)	74982	SmpB
75001	Dipeptidyl peptidase I (cathepsin C), exclusion domain	75001~54001	CathepsinC_exc~Peptidase_C1
75005	Arabinanase/levansucrase/invertase	75005	Glyco_hydro_43
75011	3-carboxy-cis,cis-mucoante lactonizing enzyme	75011	Lactonase
75098	Monomethylamine methyltransferase MtmB	75098	MtmB
75138	HprK N-terminal domain-like	75138~53795	Hpr_kinase_N~Hpr_kinase_C
75169	DsrEFH-like	75169	DrsE
75181	Hypothetical protein MTH777 (MT0777)	75181	DUF1890
75217	alpha/beta knot	75217	Methyltrans_RNA
75304	Amidase signature (AS) enzymes	75304	Amidase
75347	Rotavirus NSP2 fragment, C-terminal domain	75574~75347	Rota_NS35
75399	Plakin repeat	47576~47576~75399~75399~75399~75399~75399~75399	Plectin~Plectin~Plectin~Plectin~Plectin~Plectin~Plectin~Plectin
75404	VSV matrix protein	75404	Vesiculo_matrix
75412	Hypothetical protein MTH1880	75412	DUF749

75420	YhbC-like, N-terminal domain	75420	DUF150
75445	D-ribose-5-phosphate isomerase (RpiA), lid domain	100950~75445	Rib_5-P_isom_A
75471	YhbY-like	75471	CRS1_YhbY
75500	Putative transcriptional regulator TM1602, C-terminal domain	46785~75500	HTH_11~3H
75516	Pheromone-binding domain of LuxR-like quorum-sensing transcription factors	75516~46894	Autoind_bind~GerE
75553	Smc hinge domain	52540~75553~52540	SMC_N
75569	Archaeal IMP cyclohydrolase PurO	75569	IMP_cyclohyd
75574	Rotavirus NSP2 fragment, N-terminal domain	75574~75347	Rota_NS35
75615	Siroheme synthase middle domains-like	51735~75615~53790	NAD_binding_7~Sirohm_synth_M~CysG_dimeriser~TP_methylase
75620	Release factor	75620	PCRF~RF-1
75625	YebC-like	75625	Transcrip_reg
75632	Cullin homology domain	74788~75632~46785	Cullin~Cullin_Nedd8
75689	Zinc-binding domain of translation initiation factor 2 beta	100966~75689	eIF-5_eIF-2B
81271	TGS-like	52540~81271	TGS~tRNA_SAD~tRNA-synt_2b~HGTP_anticodon
81273	H-NS histone-like proteins	81273~81273	Histone_HNS
81277	C-terminal domain of mollusc hemocyanin	48056~81277~81277~48056~81277~81277~48056~81277~81277~48056~81277~81277	Tyrosinase~Haemocyan_bet_s~Tyrosinase~Haemocyan_bet_s~Tyrosinase~Haemocyan_bet_s~Tyrosinase~Haemocyan_bet_s~Tyrosinase~Haemocyan_bet_s~Tyrosinase~Haemocyan_bet_s~Tyrosinase~Haemocyan_bet_s~Tyrosinase~Haemocyan_bet_s
81296	E set domains	81296	CBM_48~Alpha-amylase_C
81298	Adenylylcyclase toxin (the edema factor)	55486~81298	ATLF~Anthrax_toxA
81301	Nucleotidyltransferase	81301	RsfS
81321	Family A G protein-coupled receptor-like	81321	7tm_1
81324	Voltage-gated potassium channels	54695~81324	BTB_2~Ion_trans
81327	Small-conductance potassium channel	81327	SK_channel~Ion_trans_2~CaMBD
81330	Gated mechanosensitive channel	81330	MscL
81333	F1F0 ATP synthase subunit C	81333	ATP-synt_C
81336	F1F0 ATP synthase subunit A	81336	ATP-synt_A
81338	Aquaporin-like	81338	MIP
81340	Clc chloride channel	81340	Voltage_CLC
81342	Transmembrane di-heme cytochromes	81342~81648	Cytochrom_B_N_2~Cytochrom_B_C
81343	Fumarate reductase respiratory complex transmembrane subunits	81343	Sdh_cyt
81345	ABC transporter involved in vitamin B12 uptake, BtuC	81345	FecCD
81382	Skp1 dimerisation domain-like	81382	Skp1_POZ~Skp1
81383	F-box domain	81383	F-box-like
81406	Mitochondrial cytochrome c oxidase subunit IV	81406	COX4
81411	Mitochondrial cytochrome c oxidase subunit VIa	81411	COX6A

81415	Mitochondrial cytochrome c oxidase subunit VIc	81415	COX6C
81419	Mitochondrial cytochrome c oxidase subunit VIIa	81419	COX7a
81423	Mitochondrial cytochrome c oxidase subunit VIIb	81423	COX7B
81427	Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa)	81427	COX7C
81431	Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)	81431	COX8
81442	Cytochrome c oxidase subunit I-like	81442	COX1
81452	Cytochrome c oxidase subunit III-like	81452	COX3
81464	Cytochrome c oxidase subunit II-like, transmembrane region	81464~49503	COX2_TM~COX2
81469	Bacterial aa3 type cytochrome c oxidase subunit IV	81469	COX4_pro_2
81473	Bacterial ba3 type cytochrome c oxidase subunit IIa	81473	CoxIIa
81483	Bacterial photosystem II reaction centre, L and M subunits	81483	Photo_RC
81490	Photosystem II reaction centre subunit H, transmembrane region	81490~50346	PRCH~PRC
81496	Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor	46626~81496	Cytochrom_C1
81502	ISP transmembrane anchor	81502~50022	UCR_TM
81508	Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	81508	UcrQ
81514	Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	81514	UCR_UQCRX_QCR9
81518	Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	81518	UCR_6-4kD
81524	14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	81524	UCR_14kD
81531	Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	81531	UCR_hinge
81536	Subunit III of photosystem I reaction centre, PsaF	81536	PSI_PsaF
81540	Subunit VIII of photosystem I reaction centre, PsaI	81540	PSI_8
81544	Subunit IX of photosystem I reaction centre, PsaJ	81544	PSI_PsaJ
81548	Subunit XII of photosystem I reaction centre, PsaM	81548	PsaM
81552	Subunit PsaX of photosystem I reaction centre	81552	PsaX
81558	Photosystem I subunits PsaA/PsaB	81558	PsaA_PsaB
81563	Photosystem I reaction center subunit X, PsaK	81563	PSI_PSAK
81568	Photosystem I reaction center subunit XI, PsaL	81568	PsaL

81573	F1F0 ATP synthase subunit B, membrane domain	81573	ATP-synt_B
81585	PsbU/PolX domain-like	47802~81585~81301	HHH_8~DNA_pol_lambd_f~DNA_pol_B_palm~DNA_pol_B_thumb
81593	Nucleotidyltransferase substrate binding subunit/domain	81301~81593	GlnE~GlnD_UR_UTase~GlnE
81597	Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor	54862~81597	Fer4_4~Fer4_11~Form-deh_trans
81601	Protein serine/threonine phosphatase 2C, C-terminal domain	81606~81601	PP2C~PP2C_C
81606	PP2C-like	81606	PP2C_2
81624	N-terminal domain of MutM-like DNA repair proteins	81624~46946~57716	Fapy_DNA_glyco~H2TH~zf-FPG_IleRS
81631	PAP/OAS1 substrate-binding domain	81631	PAP_central
81648	a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)	81342~81648	Cytochrom_B_N_2~Cytochrom_B_C
81653	Calcium ATPase, transduction domain A	81653~81660~56784	Cation_ATPase_N~E1-E2_ATPase~Hydrolase~Cation_ATPase_C
81660	Metal cation-transporting ATPase, ATP-binding domain N	81653~81660~56784	E1-E2_ATPase~Hydrolase
81665	Calcium ATPase, transmembrane domain M	81653~81665~81660~56784~81665	Cation_ATPase_N~E1-E2_ATPase~Hydrolase~Cation_ATPase_C
81698	FF domain	51045~51045~81698~81698	WW~WW~FF~FF~FF~FF~FF
81710	Plasmid maintenance system epsilon/zeta, antidote epsilon subunit	81710	Epsilon_antitox
81730	beta-catenin-interacting protein ICAT	81730	ICAT
81736	Group V grass pollen allergen	81736~81736	Pollen_allerg_2
81761	X-Prolyl dipeptidyl aminopeptidase PepX, N-terminal domain	81761~53474~49785	PepX_N~Peptidase_S15~PepX_C
81767	Pre-protein crosslinking domain of SecA	52540~81767~52540~81886	SecA_DEAD~SecA_SW~SEC-C
81778	Crustacean CHH/MIH/GIH neurohormone	81778	Crust_neurohorm
81783	C-terminal domain of DFF45/ICAD (DFF-C domain)	54277~81783	CIDE-N~DFF-C
81790	Myosin phosphatase inhibitor 17kDa protein, CPI-17	81790	PP1_inhibitor
81799	Putative methyltransferase TM0872, insert domain	81799	Methyltransf_5
81811	Helical domain of Sec23/24	81995~82919~53300~81995~81811~82754	zf-Sec23_Sec24~Sec23_trunk~Sec23_BS~Sec23_helical~Gelsolin
81822	RuBisCo LSMT C-terminal, substrate-binding domain	82199~81822	SET~Rubis-subs-bind
81832	SopE-like GEF domain	81832	SecIII_SopE_N~SopE_GEF
81837	BEACH domain	81837	Beach
81853	Family 10 polysaccharide lyase	81853	Pec_lyase
81872	BRCA2 helical domain	81872~50249~81878~50249~50249	BRCA2~BRCA2~BRCA2~BRCA2~BRCA2~BRCA2~BRCA2~BRCA-2_helical~BRCA-2_OB1~Tower~BRCA-2_OB3

81878	BRCA2 tower domain	81872~50249~81878~50249~50249	BRCA2~BRCA2~BRCA2~BRCA2~BRCA2~BRCA2~BRCA2~BRCA-2_helical~BRCA-2_OB1~Tower~BRCA-2_OB3
81886	Helical scaffold and wing domains of SecA	52540~81767~52540~81886	SecA_DEAD~SecA_SW~SEC-C
81891	Poly A polymerase C-terminal region-like	81301~81891	PolyA_pol~PolyA_pol_RNAbd~tRNA_NucTran2_2
81901	HCP-like	81901	Sel1~Sel1~Sel1~Sel1~Sel1~Sel1
81923	Double Clp-N motif	81923~52540~52540	Clp_N~Clp_N~AAA~AAA_2~ClpB_D2-small
81930	Orange carotenoid protein, N-terminal domain	81930	Carot_N
81935	N-terminal domain of bifunctional PutA protein	47598~81935~51730~53720	Pro_dh-DNA_bdg~Pro_dh~Aldedh
81982	Antigen MPT63/MPB63 (immunoprotective extracellular protein)	81982	DUF1942
81986	Tp47 lipoprotein, middle and C-terminal domains	82220~81986~81986	PBP-Tp47_a~PBP-Tp47_c
81995	beta-sandwich domain of Sec23/24	81995~82919~53300~81995~81811~82754	zf-Sec23_Sec24~Sec23_trunk~Sec23_BS~Sec23_helical~Gelsolin
82004	N-utilization substance G protein NusG, insert domain	82004	NusG_II
82026	Calcium-mediated lectin	82026	PA-IIL
82046	Viral chemokine binding protein m3	82046	M3
82051	Obg GTP-binding protein N-terminal domain	82051~52540	GTP1_OBG~MMR_HSR1
82057	Prokaryotic SH3-related domain	57783~82057	PhnA_Zn_Ribbon~PhnA
82061	BAH domain	82061	BAH
82093	Heme chaperone CcmE	82093	CcmE
82109	MIR domain	82109	PMT~MIR~PMT_4TMC
82114	Riboflavin kinase-like	52374~82114	FAD_syn~Flavokinase
82153	FAS1 domain	82153	Fasciclin
82171	DPP6 N-terminal domain-like	82171~53474	DPPIV_N~Peptidase_S9
82185	Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain	82185~82199	MORN~MORN~MORN
82199	SET domain	82199	SET
82215	C-terminal autoproteolytic domain of nucleoporin nup98	82215	Nucleoporin2~Nup96
82220	Tp47 lipoprotein, N-terminal domain	82220~81986~81986	PBP-Tp47_a~PBP-Tp47_c
82282	Homocysteine S-methyltransferase	82282~51717~47644~52242~56507	S-methyl_trans~Pterin_bind~B12-binding_2~B12-binding~Met_synt_B12
82317	Swiveling domain of dehydratase reactivase alpha subunit	82317~53067	DDR
82544	GckA/TtuD-like	82544	DUF4147~MOFRL
82549	DAK1/DegV-like	82549	DegV
82602	Nuclease A inhibitor (NuiA)	82602	NuiA
82607	YbaB-like	82607	YbaB_DNA_bd
82615	Polo-box domain	56112~82615~82615	Pkinase~POLO_box~POLO_box
82649	SufE/NifU	82649	NifU_N
82653	Probable GTPase Der, C-terminal domain	52540~52540~82653	MMR_HSR1~MMR_HSR1~KH_dom-like

82657	BolA-like	82657	BolA
82671	SEA domain	82671	SEA
82679	N-utilization substance G protein NusG, N-terminal domain	82679~50104	NusG~KOW
82689	Mechanosensitive channel protein MscS (YggB), C-terminal domain	82861~50182~82689	MS_channel
82693	Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains	82693~82714~82866~82693~82714~82866	ACR_tran
82697	PurS-like	82697~109736~55326~56042~55326~56042~52317	AIRS_C~AIRS_C~GATase_5
82704	AlbA-like	82704	Alba
82708	R3H domain	82708	R3H~SUZ
82714	Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains	82693~82714~82866~82693~82714~82866	ACR_tran
82754	C-terminal, gelsolin-like domain of Sec23/24	81995~82919~53300~81995~81811~82754	zf-Sec23_Sec24~Sec23_trunk~Sec23_BS~Sec23_helical~Gelsolin
82771	GIY-YIG endonuclease	82771	GIY-YIG
82784	OsmC-like	82784	OsmC
82808	Replication modulator SeqA, C-terminal DNA-binding domain	47598~82808	SeqA
82829	MesJ substrate recognition domain-like	52402~82829~56037	ATP_bind_3~TilS~TilS_C
82856	L-A virus major coat protein	82856	LA-virus_coat
82861	Mechanosensitive channel protein MscS (YggB), transmembrane region	82861~50182~82689	MS_channel
82866	Multidrug efflux transporter AcrB transmembrane domain	82693~82714~82866~82693~82714~82866	ACR_tran
82895	TSP-1 type 1 repeat	55486~82895	I-set~TSP_1~TSP_1~ZU5~Death
82910	Apical membrane antigen 1	82910	AMA-1
82919	Zn-finger domain of Sec23/24	81995~82919~53300~81995~81811~82754	zf-Sec23_Sec24~Sec23_trunk~Sec23_BS~Sec23_helical~Gelsolin
82927	Cysteine-rich DNA binding domain, (DM domain)	82927	DM
88633	Positive stranded ssRNA viruses	88633	Rhv
88645	ssDNA viruses	88645	Parvo_coat
88648	Group I dsDNA viruses	88648	Late_protein_L1
88650	Satellite viruses	88650	Potex_coat
88659	Sigma3 and sigma4 domains of RNA polymerase sigma factors	88946~88659	Sigma70_r2~Sigma70_r3~Sigma70_r4
88688	Families 57/38 glycoside transferase middle domain	88713~88688	Glyco_hydro_38~Alpha-mann_mid~Glyco_hydro_38C
88697	PUA domain-like	88697	LON_substr_bdg~AAA~Lon_C
88713	Glycoside hydrolase/deacetylase	88713	Polysacc_deac_1
88723	PIN domain-like	88723~47807~53098~56672	5_3_exonuc_N~5_3_exonuc~DNA_pol_A_exo1~DNA_pol_A
88798	N-terminal, heterodimerisation domain of RBP7 (RpoE)	88798	SHS2_Rpb7-N~S1
88802	Pre-PUA domain	88802~88697	UPF0113
88874	Receptor-binding domain of short tail fibre protein gp12	88874	gp12-short_mid~Collar~S_tail_recep_bd
88946	Sigma2 domain of RNA polymerase sigma factors	88946~88659	Sigma70_r2~Sigma70_r4_2

89000	post-HMGL domain-like	51569~89000	HMGL-like~PYC_OADA~Biotin_lipoyl
89009	GAT-like domain	48464~89009	ANTH
89028	Cobalamin adenosyltransferase-like	89028	Cob_adeno_trans
89043	Soluble domain of poliovirus core protein 3a	88633~88633~88633~50494~89043~50494~56672	Pico_P1A~Rhv~Rhv~Rhv~Pico_P2A~Pico_P2B~RNA_helicase~P3A~Peptidase_C3~RdRP_1
89064	Replisome organizer (g39p helicase loader/inhibitor protein)	89064	Inhibitor_G39P
89069	N-terminal, cytoplasmic domain of anti-sigmaE factor RseA	89069	RseA_N~RseA_C
89082	Antibiotic binding domain of TipA-like multidrug resistance regulators	46955~89082	MerR_1~TipAS
89095	GatB/YqeY motif	55931~89095	YqeY
89124	Nop domain	89124	NOP5NT~Nop
89155	TorD-like	89155	Nitrate_red_del
89162	Gametocyte protein Pfg27	89162	Pfg27
89232	Hypothetical protein TM1070	89232	ASRT
89260	Collagen-binding domain	89260	Peptidase_M9_N~Peptidase_M9~PPC
89360	HesB-like domain	89360	Fe-S_biosyn
89372	Fucose-specific lectin	89372	Fungal_lectin
89392	Prokaryotic lipoproteins and lipoprotein localization factors	89392	LolA
89428	Adsorption protein p2	89428	Prd1-P2
89433	Baseplate structural protein gp8	89433	Phage-Gp8
89442	Hypothetical protein YojF	89442	DUF1806
89447	AbrB/MazE/MraZ-like	89447	MraZ~MraZ
89550	PHP domain-like	89550	PHP
89562	RraA-like	89562	Methyltransf_6
89623	Ribose/Galactose isomerase RpiB/AlsB	89623	LacAB_rpiB
89733	L-sulfolactate dehydrogenase-like	89733	Ldh_2
89796	CoA-transferase family III (CaiB/BaiF)	89796	CoA_transf_3
89807	Dodecin-like	89807	Dodecin
89811	Amyloid beta a4 protein copper binding domain (domain 2)	56491~89811~57362~109843	APP_N~APP_Cu_bd~APP_E2~APP_amyloid
89817	Mago nashi protein	89817	Mago_nashi
89837	Doublecortin (DC)	89837	DCX~DCX
89872	Inhibitor of vertebrate lysozyme, Ivy	89872	Ivy
89890	Proguanylin	89890	Guanylin
89895	FYSH domain	89895	SBDS~SBDS_C
89915	DNA-binding protein Tfx	89915	Sigma70_r4~TFX_C
89919	Ribosome-binding factor A, RbfA	89919	RBFA
89942	eEF1-gamma domain	47616~89942	GST_N~GST_C~EF1G
89946	Hypothetical protein VC0424	89946	RraB
89957	MTH1187/YkoF-like	89957	Thiamine_BP
89963	YajQ-like	89963~89963	DUF520
89975	Hypothetical protein Yml108w	89975	DUF1892
90002	Hypothetical protein YjiA, C-terminal domain	52540~90002	cobW~CobW_C
90064	Hypothetical protein TM0875	90064	DUF3855
90073	GCM domain	90073	GCM

90096	Subunits of heterodimeric actin filament capping protein Capz	90096	F-actin_cap_A
90112	Neurotransmitter-gated ion-channel transmembrane pore	63712~90112	Neur_chan_LBD~Neur_chan_memb
90123	ABC transporter transmembrane region	90123~52540	ABC_membrane~ABC_tran
90148	DPY module	90148~90148	EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA~EGF_CA
90183	Mollusk pheromone	90183	Attractin
90188	Somatomedin B domain	90188	Somatomedin_B~Hemopexin~Hemopexin~Hemopexin~Hemopexin
90193	Notch domain	57196~90193~48403	EGF~EGF~hEGF~EGF~EGF_CA~EGF~hEGF~EGF~EGF_CA~EGF~hEGF~EGF_CA~EGF~hEGF~EGF~EGF~EGF~EGF~EGF~EGF~EGF~hEGF~EGF~EGF~EGF~EGF_CA~EGF~hEGF~EGF~hEGF~EGF~hEGF~EGF~hEGF~EGF~EGF~EGF~EGF~hEGF~EGF~Notch~Notch~Notch~NOD~NODP~Ank_5~Ank_5~Ank~Ank_2~DUF3454
90209	Ran binding protein zinc finger-like	54928~90209	RRM_1~zf-RanBP
90229	CCCH zinc finger	90229~90229	zf-CCCH
90234	Zinc finger domain of DNA polymerase-alpha	56672~90234	DNA_pol_alpha_N~DNA_pol_B_exo1~DNA_pol_B~zf-DNA_Pol
100879	Lesion bypass DNA polymerase (Y-family), little finger domain	56672~100879	IMS~IMS_HHH~IMS_C
100895	Kazal-type serine protease inhibitors	100895	Kazal_1
100897	Plant proteinase inhibitors	100897~100897	Prot_inhib_II~Prot_inhib_II
100909	IP3 receptor type 1 binding core, domain 2	82109~100909	Ins145_P3_rec~MIR~RYDR_ITPR~RYDR_ITPR~RIH_assoc~Ion_trans
100910	Chemosensory protein Csp2	100910	OS-D
100920	Heat shock protein 70kD (HSP70), peptide-binding domain	53067~53067~100920~100934	HSP70
100934	Heat shock protein 70kD (HSP70), C-terminal subdomain	53067~53067~100920~100934	HSP70
100939	SPOC domain-like	54928~54928~54928~100939	Ku_N~Ku~Ku_C~SAP

100950	NagB/RpiA/CoA transferase-like	100950	CoA_trans
100957	Dimerization cofactor of HNF-1 alpha	100957~47413~46689	HNF-1_N~Homeobox~HNF-1B_C~HNF-1A_C
100966	Translation initiation factor 2 beta, aIF2beta, N-terminal domain	100966~75689	eIF-5_eIF-2B
100985	Sporulation inhibitor Sda	100985	Sda
101059	B-form DNA mimic Ocr	101059	ocr
101082	Typo IV secretion system protein TraC	101082	T4SS
101089	Phosphoprotein XD domain	101089	Paramyxo_PNT~Paramyx_P_V_C
101094	Staphylocoagulase	101094~101094	Coagulase
101112	Oxygen-evolving enhancer protein 3,	101112	PsbQ
101116	Flagellar export chaperone FliS	101116	FliS
101125	Colicin D immunity protein	101125	Colicin_immun
101148	Plant invertase/pectin methylesterase inhibitor	101148	PMEI
101152	Mob1/phocein	101152	Mob1_phocein
101156	Nonstructural protein ns2, Nep, M1-binding domain	101156	Flu_NS2
101160	Dimerisation domain of CENP-B	46689~46689~101160	CENP-B_N~HTH_Tnp_Tc5~DDE_1~CENP-B_dimeris
101166	Docking domain A of the erythromycin polyketide synthase (DEBS)	53901~53901~51735~51735~47336~53901~51735~51735~47336~101166	Docking~ketoacyl-synt~Ketoacyl-synt_C~KAsynt_C_assoc~Acyl_transf_1~KR~PP-binding~ketoacyl-synt~Ketoacyl-synt_C~KAsynt_C_assoc~Acyl_transf_1~PS-DH~ADH_zinc_N~KR~PP-binding~Erythro-docking
101173	Docking domain B of the erythromycin polyketide synthase (DEBS)	101173	Docking
101215	KaiA/RbsU domain	101215	RsbU_N~SpoIIE
101224	HAND domain of the nucleosome remodeling ATPase ISWI	52540~52540~101224~46689~46689	SNF2_N~Helicase_C~HAND~SLIDE
101233	PWI domain	101233	PWI
101238	XPC-binding domain	54236~46934~101238~46934	ubiquitin~UBA~XPC-binding~UBA
101257	Flavivirus capsid protein C	101257~56983~81296~50494~52540~52540~53335	Flavi_capsid~Flavi_propep~Flavi_M~Flavi_glycoprot~Flavi_glycop_C~Flavi_NS1~Flavi_NS2A~Flavi_NS2B~Peptidase_S7~Flavi_DEAD~Flavi_NS4A~Flavi_NS4B~FtsJ~Flavi_NS5
101262	Methenyltetrahydrofolate cyclohydrolase-like	101262	FTCD_C
101278	N-terminal domain of adenylylcyclase associated protein, CAP	101278~69340	CAP_N~CAP_C
101283	GRIP domain	101283	GRIP
101288	L27 domain	101288~50156~50044~52540	L27~L27~PDZ~SH3_2~Guanylate_kin
101307	YutG-like	101307	PgpA
101312	Invasion protein A (SipA) , C-terminal actin binding domain	140746~101312	SipA
101322	YcfC-like	101322	DUF489
101327	YgfB-like	101327	UPF0149

101332	Hypothetical protein MTH393	101332	DUF1959
101344	Superantigen MAM	101344	MA-Mit
101353	Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)	55681~101353~55186	tRNA-synt_2c~tRNA_SAD~DHHA1
101386	all-alpha NTP pyrophosphatases	101386	PRA-CH~PRA-PH
101391	Hsp90 co-chaperone CDC37	101391	CDC37_N~CDC37_M~CDC37_C
101399	P40 nucleoprotein	101399	BDV_P40
101420	C-terminal domain of Ku80	53300~100939~101420	Ku_N~Ku~Ku_C~Ku_PK_bind
101424	Hypothetical protein ST1625	101424	DUF1955
101447	Formin homology 2 domain (FH2 domain)	101447	FH2
101473	DhaL-like	101473	Dak2
101478	ADP-ribosylglycohydrolase	101478	ADP_ribosyl_GH
101489	Eukaryotic initiation factor 4f subunit eIF4g, eIF4e-binding domain	101489	eIF_4G1~MIF4G
101494	Stathmin	101494	Stathmin
101498	Anti-sigma factor FlgM	101498	FlgM
101542	Fungal immunomodulatory protein, FIP	101542	Fve
101546	ASF1-like	101546	ASF1_hist_chap
101576	Supernatant protein factor (SPF), C-terminal domain	46938~52087~101576	CRAL_TRIO
101596	Dextranase, N-terminal domain	101596~51126	Glyco_hydro_49
101601	Smp-1-like	101601	DUF1935~Peptidase_C2
101606	Superantigen (mitogen) Ypm	101606	YpM
101690	PAZ domain	101690	ArgoN~ArgoL1~PAZ~ArgoL2~ArgoMid~Piwi
101697	Hypothetical protein YfhH	101697	DUF1811
101738	SspB-like	101738	SspB
101744	Rof/RNase P subunit-like	101744	UPF0086
101751	Hydrophobin II, HfbII	101751	Hydrophobin_2
101756	Hypothetical protein YgiW	101756	BOF
101790	Aminomethyltransferase beta-barrel domain	103025~101790	GCV_T~GCV_T_C
101801	Surface presentation of antigens (SPOA)	101801	FliMN_C
101816	Replicase NSP9	52949~50494~140367~143076~101816~144246~53335~142877	Macro~Viral_protease~Corona_NSP4_C~Peptidase_C30~nsp7~nsp8~nsp9~NSP10~Corona_RPol_N~Viral_helicase1~NSP11~NSP13
101821	Aminopeptidase/glucanase lid domain	101821	Peptidase_M42
101852	Bacterial fluorinating enzyme, C-terminal domain	101852	SAM_adeno_trans
101874	YceI-like	101874	YceI
101887	Apyrase	101887	Apyrase
101898	NHL repeat	101898	zf-RING_UBOX~zf-B_box~Filamin~NHL~NHL~NHL~NHL~NHL~NHL
101904	GyrA/ParC C-terminal domain-like	56719~101904	DNA_topoisoIV~DNA_gyraseA_C~DNA_gyraseA_C~DNA_gyraseA_C~DNA_gyraseA_C~DNA_gyraseA_C~DNA_gyraseA_C
101908	Putative isomerase YbhE	101908	Lactonase
101912	Sema domain	101912	Sema

101931	Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain	101931	Mago-bind
101936	DNA-binding pseudobarrel domain	101936	B3~Auxin_resp
101941	NAC domain	101941	NAM
101960	Stabilizer of iron transporter SufD	101960	UPF0051
101967	Adhesin YadA, collagen-binding domain	101967	ESPR~YadA_head~YadA_head~YadA_head~YadA_head~YadA_head~YadA_head~YadA_head~YadA_head~YadA_head~YadA_stalk~YadA_stalk~YadA_stalk~YadA_stalk~YadA_stalk~YadA_stalk~YadA_head~YadA_stalk~YadA_stalk~YadA_head~YadA_head~YadA_stalk~YadA_anchor
101999	Trimeric adhesin	101999~54523	YadA_head~YadA_stalk~TAA-Trp-ring~YadA_stalk~YadA_anchor
102031	AXH domain	102031	AXH
102110	(2r)-phospho-3-sulfolactate synthase ComA	102110	ComA
102114	Radical SAM enzymes	102114	Radical_SAM~Mob_synth_C
102198	Putative cyclase	102198	Cyclase
102215	Creatininase	102215	Creatininase
102220	DNA polymerase III psi subunit	102220	DNA_III_psi
102324	F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)	102324	MTD
102400	DNA polymerase III chi subunit	102400	DNA_pol3_chi
102405	MCP/YpsA-like	102405	Lysine_decarbox
102414	Alpha-2,3/8-sialyltransferase CstII	102414	CST-I
102462	Peptidyl-tRNA hydrolase II	102462	PTH2
102522	Bacterial fluorinating enzyme, N-terminal domain	102522	SAM_adeno_trans
102546	RbsD-like	102546	RbsD_FucU
102588	LmbE-like	102588	PIG-L
102645	CoaB-like	52507~102645	Flavoprotein~DFP
102705	NIF3 (NGG1p interacting factor 3)-like	102705	NIF3
102712	JAB1/MPN domain	102712	Prok-JAB
102735	Trigger factor ribosome-binding domain	102735~54534~109998	Trigger_N~FKBP_C~Trigger_C
102741	Obg GTP-binding protein C-terminal domain	82051~52540~102741	GTP1_OBG~MMR_HSR1~DUF1967
102816	Putative dsDNA mimic	102816	DUF440
102824	Colicin D/E5 nuclease domain	102824	Colicin_D
102829	Cell division protein ZapA-like	102829	ZapA
102848	NSFL1 (p97 ATPase) cofactor p47, SEP domain	102848~54236	SEP~UBX
102860	mRNA decapping enzyme DcpS N-terminal domain	102860~54197	DcpS~DcpS_C
102875	Chromosomal protein MC1	102875	MC1
102886	Coproporphyrinogen III oxidase	102886	Coprogen_oxidas
102891	Hypothetical protein Ta1206	102891	DUF1805
103007	Hypothetical protein TT1725	103007	DUF503
103025	Folate-binding domain	103025~101790	GCV_T~GCV_T_C
103032	Hypothetical protein YwqG	103032	DUF1963

103039	CheC-like	103039	CheX
103054	General secretion pathway protein M, EpsM	103054	T2SSM
103063	Hypothetical protein YoaG	103063	DUF1869
103068	Nucleocapsid protein dimerization domain	103068	Corona_nucleoca
103084	Holliday junction resolvase RusA	103084	RusA
103088	OmpA-like	103088	OmpA
103107	Hypothetical protein c14orf129, hspc210	103107	DUF727
103111	Activator of Hsp90 ATPase, Aha1	103111~55961	Aha1_N~AHSA1
103145	Tombusvirus P19 core protein, VP19	103145	Tombus_P19
103165	Ta1353-like	103165	Adenosine_kin
103190	Sensory domain-like	103190	Cache_3~SPOB_a~HATPase_c
103196	Roadblock/LC7 domain	103196	Robl_LC7
103239	MoaD-related protein, C-terminal domain	54285~103239	ThiS~DUF1952
103243	KA1-like	56112~103243	Pkinase~UBA~KA1
103247	TT1751-like	103247	DUF302
103256	Hypothetical protein TM0160	103256	DNase-RNase
103263	Chorismate synthase, AroC	103263	Chorismate_synt
103277	Hypothetical protein HI1480	52540~103277	
103359	Suppressor of Fused, N-terminal domain	103359	SUFU
103365	Hypothetical protein PH1602	103365	RtcB
103370	NinB	103370	NinB
103378	2-methylcitrate dehydratase PrpD	103378	MmgE_PrpD
103383	Antivirulence factor	103383	AvrB_AvrC
103388	Virulence-associated V antigen	103388	LcrV
103409	39 kda initiator binding protein, IBP39, C-terminal domains	46785~103409	IBD~IBP39
103417	Major capsid protein VP5	103417	Herpes_MCP
103431	Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor	49441~51246~103431	Apocytochr_F_N~Apocytochr_F_C
103436	PetL subunit of the cytochrome b6f complex	103436	PetL
103441	PetM subunit of the cytochrome b6f complex	103441	PetM
103446	PetG subunit of the cytochrome b6f complex	103446	PetG
103451	PetN subunit of the cytochrome b6f complex	103451	PetN
103456	Preprotein translocase SecE subunit	103456	SecE
103460	Sec-beta subunit	103460	Sec61_beta
103464	Oligosaccharyltransferase subunit ost4p	103464	Ost4
103473	MFS general substrate transporter	103473	MFS_1
103481	Multidrug resistance efflux transporter EmrE	103481	Multi_Drug_Res
103486	V-type ATP synthase subunit C	103486	vATP-synt_AC39
103491	Preprotein translocase SecY subunit	103491~103491	Plug_translocon~SecY
103501	Respiratory nitrate reductase 1 gamma chain	103501	Nitrate_red_gam
103506	Mitochondrial carrier	103506	Mito_carr~Mito_carr~Mito_carr

103511	Chlorophyll a-b binding protein	103511	Chloroa_b-bind
103515	Autotransporter	103515	Peptidase_S8~Autotransporter
103565	Bubble protein	103565	DUF1962
103575	Plexin repeat	101912~103575	Sema
103580	Necrosis inducing protein 1, NIP1	103580	NIP_1
103589	Mini-collagen I, C-terminal domain	103589	Collagen
103612	SBT domain	103612	SBP
103623	Hypothetical protein Ta0289 C-terminal domain	54631~103623	CBS~CBS~DUF1936
103637	CCHHC domain	103637	zf-C2HC~zf-C2HC~zf-C2HC~MYT1~zf-C2HC~zf-C2HC~zf-C2HC
103642	Sec-C motif	54427~103642	SEC-C
103647	TSP type-3 repeat	103647~49899	COMP~EGF_CA~EGF_CA~TSP_3~TSP_3~TSP_3~TSP_3~TSP_3~TSP_C
103657	BAR/IMD domain-like	103657~50044	BAR~SH3_9
109604	HD-domain/PDEase-like	109604	HD
109631	Transcriptional repressor TraM	109631	Prok-TraM
109635	DnaK suppressor protein DksA, alpha-hairpin domain	109635~57716	zf-dskA_traR
109640	KRAB domain (Kruppel-associated box)	109640~57667~57667~57667~57667~57667~57667~57667~57667~57667~57667	KRAB
109709	KorB DNA-binding domain-like	110849~109709	ParBc
109715	DEK C-terminal domain	109715	DEK_C
109728	Hypothetical protein AF0491, middle domain	89895~109728	SBDS~SBDS_C
109732	HBS1-like domain	109732~52540~50447~50465	HBS1_N~GTP_EFTU~GTP_EFTU_D3
109736	FGAM synthase PurL, linker domain	82697~109736~55326~56042~55326~56042~52317	AIRS_C~AIRS_C~GATase_5
109747	Glycogen synthesis protein GlgS	109747	GlgS
109751	Alpha-hemoglobin stabilizing protein AHSP	109751	AHSP
109755	PhoU-like	109755	PhoU~PhoU
109770	Nickel-containing superoxide dismutase, NiSOD	109770	Sod_Ni
109775	Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain	109775	Perilipin
109779	Domain from hypothetical 2610208m17rik protein	109779	Aida_N~Aida_C2
109797	Bacteriocin immunity protein-like	109797	EntA_Immun
109801	Hypothetical protein D-63	109801	
109805	Phenylalanine zipper	109805~50729~55550	Phe_ZIP~PH~SH2
109839	Cag-Z	109839	CagZ
109843	CAPPD, an extracellular domain of amyloid beta A4 protein	56491~89811~57362~109843	APP_N~APP_Cu_bd~Kunitz_BPTI~APP_E2~Beta-APP~APP_amyloid
109854	DinB/YfiT-like putative metalloenzymes	109854	DinB_2
109859	NblA-like	109859	NblA

109880	A middle domain of Talin 1	47031~50729~109880~109885~109885~47220~109885	FERM_f0~FERM_N~FERM_M~Talin_middle~VBS~I_LWEQ
109885	I/LWEQ domain	109885	ANTH~I_LWEQ
109905	Surp module (SWAP domain)	109905~109905	DRY_EERY~Surp~Surp
109910	YgfY-like	109910	Sdh5
109915	Hypothetical protein YhaI	109915	DUF1878
109920	Hypothetical protein At3g22680	109920	DUF1950
109925	Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain	109925~50978	WD40~WD40~WD40~WD40~WD40~WD40
109993	VPS9 domain	109993	VPS9
109998	Triger factor/SurA peptide-binding domain-like	102735~54534~109998	Trigger_N~FKBP_C~Trigger_C
110004	Glycolipid transfer protein, GLTP	110004	GLTP
110009	Hypothetical protein MG354	110009	DUF1951
110014	Her-1	110014	Caenor_Her-1
110019	ERO1-like	110019	ERO1
110035	GDNF receptor-like	110035	GDNF~GDNF~GDNF
110069	ApaG-like	110069	DUF525
110083	Peptidylarginine deiminase Pad4, middle domain	49503~110083~55909	PAD_N~PAD_M~PAD
110087	DR1885-like metal-binding protein	110087	DUF461
110111	Ctag/Cox11	110111	CtaG_Cox11
110132	BTV NS2-like ssRNA-binding domain	110132	BTV_NS2
110217	DNA-binding protein LAG-1 (CSL)	49417~110217~81296	LAG1-DNAbind~BTD
110221	AbfB domain	49899~110221	ArabFuran-catal~AbfB
110296	Oligoxyloglucan reducing end-specific cellobiohydrolase	110296~110296	CBM_2
110304	Coronavirus RNA-binding domain	110304~103068	Corona_nucleoca
110324	Ribosomal L27 protein-like	110324	Ribosomal_L27
110391	GlpP-like	110391	G3P_antiterm
110395	CutC-like	110395	CutC
110399	ThiG-like	110399	ThiG
110455	Toprim domain	110455	Toprim~DUF4093
110581	Indigoidine synthase A-like	110581	Indigoidine_A
110710	TTHA0583/YokD-like	110710	DUF436
110738	Glycerate kinase I	110738	Gly_kinase
110783	Hypothetical protein MTH677	110783	DUF3194
110814	TmoB-like	110814	TmoB
110836	Hypothetical protein SAV1430	110836	Nfu_N~Virulence_fact~HEAT_2~HEAT_2
110849	ParB/Sulfiredoxin	110849~109709	ParBc
110857	Gamma-glutamyl cyclotransferase-like	110857	GGACT
110916	Peptidyl-tRNA hydrolase domain-like	110916	RF-1
110921	2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain	51569~110921	HMGL-like~LeuA_dimer
110942	HSP90 C-terminal domain	55874~54211~110942	HATPase_c~HSP90
110993	eIF-2-alpha, C-terminal domain	50249~116742~110993	S1~EIF_2_alpha
110997	Sporulation related repeat	110997	SPOR
111006	Dystroglycan, domain 2	49313~111006	DAG1

111038	YjbQ-like	111038	UPF0047
111057	Hypothetical protein PF0899	111057	DUF1884
111064	Hut operon positive regulatory protein HutP	111064	HutP
111069	Hypothetical protein yfbM	111069	DUF1877
111074	Bacillus phage protein	111074	
111126	Ligand-binding domain in the NO signalling and Golgi transport	111126	TRAPP
111148	YggX-like	111148	Iron_traffic
111171	Rbstp2229 protein	111171	DUF1885
111249	Sulfolobus fructose-1,6-bisphosphatase-like	111249	FBPase_3
111265	Hemolytic lectin CEL-III, C-terminal domain	50370~50370~111265	Ricin_B_lectin
111278	SSo0622-like	111278	TYW3
111283	Putative modulator of DNA gyrase, PmbA/TldD	111283	PmbA_TldD
111304	Recombination protein RecR	111304	RecR~Toprim_4
111321	AF1104-like	111321	DUF89
111326	Urocanase	111326	Urocanase
111331	NAD kinase/diacylglycerol kinase-like	111331	NAD_kinase
111337	QueA-like	111337~111337	Queuosine_synth
111342	CbiD-like	111342	CbiD
111347	Rap/Ran-GAP	111347	Rap_GAP
111352	Ammonium transporter	111352	Ammonium_transp
111357	Mitochondrial ATP synthase coupling factor 6	111357	ATP-synt_F6
111364	Tsx-like channel	111364	Channel_Tsx
111369	HlyD-like secretion proteins	111369	Biotin_lipoyl_2~HlyD_3
111379	VP4 membrane interaction domain	49899~111379	VP4_haemagglut
111384	OmpH-like	111384	OmpH
111388	Pollen allergen ole e 6	111388	Ole-e-6
111418	Hormone receptor domain	111418	HRM~7tm_2
111423	Resistin	111423	Resistin
111430	YAP1 redox domain	111430	PAP1
116726	TrkA C-terminal domain-like	116726	TrkA_N~TrkA_C
116734	DNA methylase specificity domain	116734	Methylase_S~Methylase_S
116738	NADH pyrophosphatase intervening domain	55811~116738~55811	zf-NADH-PPase~NUDIX
116742	eIF2alpha middle domain-like	50249~116742~110993	S1~EIF_2_alpha
116768	DNA-binding domain of EIN3-like	116768	EIN3
116820	Rps17e-like	116820	Ribosomal_S17e
116842	XseB-like	116842	Exonuc_VII_S
116846	MIT domain	116846~52540	MIT~AAA~Vps4_C
116854	Avirulence protein AvrPto	116854	AvrPto
116858	Hypothetical membrane protein Ta0354, soluble domain	116858	DUF3198
116878	TrmE connector domain	103025~116878	TrmE_N~MnmE_helical
116907	Hook domain	116907	HOOK
116915	Hypothetical protein YqbG	116915	DUF3199
116922	YugE-like	116922	DUF1871
116927	EspA/CesA-like	116927	EspA

116942	RNA-binding protein She2p	116942	She2p
116960	YfbU-like	116960	YfbU
116965	Hypothetical protein MPN330	116965	DUF3196
117018	ATP-dependent DNA ligase DNA-binding domain	117018~56091~50249	DNA_ligase_A_N~DNA_ligase_A_M~DNA_ligase_A_C
117023	DNA primase DnaG, C-terminal domain	57783~56731~117023	zf-CHC2~Toprim_N~Toprim_4~DnaB_bind~DnaG_DnaB_bind
117066	Accessory protein X4 (ORF8, ORF7a)	117066	SARS_X4
117070	LEA14-like	117070	LEA_2
117074	Hypothetical protein PA1324	117074	
117100	Beta-galactosidase LacA, domain 3	51445~51011~117100~49785~49785	Glyco_hydro_35~BetaGal_dom2~BetaGal_dom3~BetaGal_dom4_5~BetaGal_dom4_5
117125	Putative glucosidase YicI, C-terminal domain	74650~51445~51011~117125	Gal_mutarotas_2~Glyco_hydro_31
117130	CsrA-like	117130	CsrA
117143	Flagellar hook protein flgE	117143	Flg_bb_rod~FlaE~Flg_bbr_C
117281	Kelch motif	54695~117281	BTB~BACK~Kelch_1~Kelch_1~Kelch_1~Kelch_1~Kelch_1
117289	Nucleoporin domain	117289	Nucleoporin_C
117396	TM1631-like	117396	DUF72
117457	FumA C-terminal domain-like	117457	Fumerase~Fumerase_C
117773	GTF2I-like repeat	117773~117773~117773~117773~117773~117773	GTF2I~GTF2I~GTF2I~GTF2I~GTF2I~GTF2I
117778	D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain	117778~52242	OAM_dimer~B12-binding
117782	YbjQ-like	117782	YbjQ_1
117839	WWE domain	117839~56204	WWE~HECT
117856	AF0104/ALDC/Ptd012-like	117856	AAL_decarboxy
117892	Band 7/SPFH domain	117892	Band_7
117916	Fe-S cluster assembly (FSCA) domain-like	117916	DUF59
117987	CRISPR-associated protein	117987	CRISPR_assoc
117991	YbeD/HP0495-like	117991	DUF493
118001	YehU-like	118001	UPF0270
118010	TM1457-like	118010	Peptidase_C108
118104	RalF, C-terminal domain	48425~118104	Sec7
118116	DNA mismatch repair protein MutL	55874~54211~118116	HATPase_c_3~DNA_mis_repair~MutL_C
118173	Phosphoprotein M1, C-terminal domain	118173	PP_M1
118196	YaeB-like	118196	UPF0066
118203	Vacuolar ATP synthase subunit C	118203	V-ATPase_C
118208	Viral ssDNA binding protein	118208	Viral_DNA_bp
118215	Proton glutamate symport protein	118215	SDF
118220	Connexin43	118220	Connexin~Connexin43
118251	Variant surface glycoprotein MITAT 1.2, VSG 221, C-terminal domain	118251	Trypan_glycop
118290	WRKY DNA-binding domain	118290	WRKY
118310	AN1-like Zinc finger	118310	zf-A20~zf-AN1
118352	HSP33 redox switch-like	64397~118352	HSP33

118359	Expressed protein At2g23090/F21P24.15	118359	4F5~zf-met2
140102	ISY1 domain-like	140102	Isy1
140106	Calcyclin-binding protein-like	140106~49764	Siah-Interact_N~CS
140111	Endosomal sorting complex assembly domain	54495~140111	UEV~Vps23_core
140121	SPy1572-like	140121	DUF1912
140125	Rabenosyn-5 Rab-binding domain-like	140125~140125	FYVE~Rbsn~NPF~Rbsn
140129	MxiH-like	140129	T3SS_needle_F
140319	IscX-like	140319	Fe-S_assembly
140356	PPK N-terminal domain-like	140356~143724~56024~56024	PP_kinase_N~PP_kinase~PP_kinase_C
140361	MIT domain-like	140361	DUF1875
140367	Coronavirus NSP7-like	52949~50494~140367~143076~101816~144246~53335~142877	Macro~Viral_protease~Corona_NSP4_C~Peptidase_C30~nsp7~nsp8~nsp9~NSP10~Corona_RPol_N~Viral_helicase1~NSP11~NSP13
140371	Vng1086c-like	140371	UPF0058
140376	ChaB-like	140376	ChaB
140383	BSD domain-like	140383	BSD
140404	EF2458-like	140404	DUF1507
140415	YppE-like	140415	DUF1798
140423	MW0975(SA0943)-like	140423	YkyA
140427	VPS28 C-terminal domain-like	140111~140427	VPS28
140453	EsxAB dimer-like	140453	WXG100
140459	PE/PPE dimer-like	140459	PPE~PE_PPE_C
140478	LemA-like	140478	LemA
140482	MAST3 pre-PK domain-like	140482~56112~50156	DUF1908~Pkinase
140486	PA2201 N-terminal domain-like	140486~140731	DUF1911
140490	Nqo1C-terminal domain-like	142019~142984~140490	Complex1_51K~SLBB~NADH_4Fe-4S
140496	HP1531-like	140496	DUF2443
140500	BAS1536-like	140500	SpoOE-like
140506	FHV B2 protein-like	140506	B2
140560	TM0693-like	140560	
140566	FlgN-like	140566	FlgN
140570	MukF C-terminal domain-like	46785~140570	KicB
140576	HIV integrase-binding domain	63748~140576	PWWP~LEDGF
140581	TraM-like	47729~140581	Tra_M
140586	Dcp2 domain-like	140586~55811	DCP2~NUDIX
140591	Type III secretion system domain	140591	HrpJ
140607	EF2947-like	140607	DUF3206
140612	EB1 dimerisation domain-like	47576~140612	CH~EB1
140652	YozE-like	140652	YozE_SAM_like
140657	Hyaluronidase post-catalytic domain-like	55545~51445~140657	Glyco_hydro_20b~NAGidase
140663	TTHA0068-like	140663	DUF309
140670	YoaC-like	140670	DUF1889
140683	SP0561-like	140683	DUF1858
140688	YfmB-like	140688	DUF3212
140693	IpaD-like	140693	IpaD
140713	Phage replication organizer domain	140713	Phi-29_GP16_7

140718	Mediator hinge subcomplex-like	140718	Med7
140726	AF0941-like	140726	AF0941-like
140731	PA2201 C-terminal domain-like	140731	DUF1910~DUF1911
140736	Rv1873-like	140736	DUF1810
140741	RUN domain-like	140741	RUN
140746	SipA N-terminal domain-like	140746~101312	SipA
140753	PG0816-like	140753	DUF1896
140804	YidB-like	140804	DUF937
140809	Rhabdovirus nucleoprotein-like	140809	Rhabdo_ncap
140856	USP8 N-terminal domain-like	140856~52821~54001	USP8_dimer~Rhodanese~UCH
140860	Pseudo ankyrin repeat-like	140860	
140864	TROVE domain-like	140864~53300	TROVE
140869	GUN4-like	140869	GUN4
140914	PriB N-terminal domain-like	140914	DNA_primase_lrg
140919	DNA terminal protein	140919	Phi-29_GP3
140924	Duffy binding domain-like	140924	Duffy_binding
140931	Fic-like	140931	Fic
140959	Indolic compounds 2,3-dioxygenase-like	140959	IDO
140979	Topoisomerase V catalytic domain-like	140979~47781~47781~47781~47781	HHH_5~HHH_5
140984	PTPA-like	140984	PTPA
140990	FtsH protease domain-like	52540~140990	FtsH_ext~AAA~Peptidase_M41
140996	Hermes dimerisation domain	140996~53098	DBD_Tnp_Hermes~Dimer_Tnp_hAT
141000	Glu-tRNAGln amidotransferase C subunit	141000	Glu-tRNAGln
141004	RelB-like	141004	
141066	ICP-like	141066	Inhibitor_I42
141072	CalX-like	141072~141072	Na_Ca_ex~Na_Ca_ex_C~Calx-beta~Calx-beta~Na_Ca_ex
141086	Agglutinin HPA-like	141086	H_lectin
141091	L21p-like	141091	Ribosomal_L21p
141099	Atu1913-like	141099	DUF1883
141130	Acetamidase/Formamidase-like	141130	FmdA_AmdA
141251	Kinase-associated protein B-like	141251	KapB
141255	YccV-like	141255	YccV-like
141259	CarD-like	52540~52540~141259~52540~52540~143517	CarD_CdnL_TRCF~DEAD~Helicase_C~TRCF
141300	GatD N-terminal domain-like	141300~53774	Asparaginase
141318	TM0957-like	141318	DUF2291
141322	NfeD domain-like	141322	NfeD
141371	PilZ domain-like	141371	PilZ
141447	PA2021-like	141447	DUF3203
141452	Hcp1-like	141452	T6SS_HCP
141457	BH3618-like	141457	FliW
141480	Extracellular hemoglobin linker subunit, receptor domain	57424~141480	Ldl_recept_a~Eryth_link_C
141488	YdhA-like	141488	MliC
141493	Allene oxide cyclase-like	141493	Allene_ox_cyc
141523	L,D-transpeptidase catalytic domain-like	141523	YkuD

141530	PTSIIA/GutA-like	141530	PTSIIA_gutA
141562	At5g01610-like	141562	DUF538
141571	Pentapeptide repeat-like	141571	Pentapeptide~Pentapeptide~Pentapeptide~Pentapeptide
141658	Bacteriophage trimeric proteins domain	141658	Caudo_bapla_RBP
141666	'SARS ORF9b-like	141666	SARS_lipid_bind
141673	MOSC N-terminal domain-like	141673	MOSC_N~MOSC
141678	MAL13P1.257-like	141678	DUF866
141694	AF2212/PG0164-like	141694	DUF1905
141729	FimD N-terminal domain-like	141729	PapC_N~Usher~PapC_C
141734	HisI-like	141734~101386	PRA-CH
141739	MFPT repeat-like	141739~141739	MFP2b
141868	EAL domain-like	55785~55073~141868	EAL~YkuI_C
141986	LD-carboxypeptidase A C-terminal domain-like	52317~141986	Peptidase_S66
142019	Nqo1 FMN-binding domain-like	142019~142984~140490	Complex1_51K~SLBB~NADH_4Fe-4S
142338	CofD-like	142338	UPF0052
142433	CinA-like	142433	CinA
142535	AF0625-like	142535	tRNA_deacylase
142695	RibA-like	55821~142695	DHBP_synthase~GTP_cyclohydro2
142754	NadA-like	142754	NadA
142764	YgbK-like	142764	DUF1537~DUF1357_C
142795	CAC2185-like	142795	DUF1919
142823	ComB-like	142823	2-ph_phosp
142877	EndoU-like	142877	XendoU
142887	PhtA domain-like	142887~142887~142887	Strep_his_triad~PHtD_u1~Strep_his_triad~Strep_his_triad
142897	TFB5-like	142897	Tfb5
142906	YjbR-like	142906	YjbR
142913	YktB/PF0168-like	142913	DUF1054
142921	WGR domain-like	142921~47587~56399	WGR~PARP_reg~PARP
142984	Nqo1 middle domain-like	142019~142984~140490	Complex1_51K~SLBB~NADH_4Fe-4S
143011	RelE-like	143011	YoeB_toxin
143021	Ns1 effector domain-like	47060~143021	Flu_NS1
143026	Kinetochore globular domain	143026	Spc24
143034	L35p-like	143034	Ribosomal_L35p
143076	Coronavirus NSP8-like	52949~50494~140367~143076~101816~144246~53335~142877	Macro~Viral_protease~Corona_NSP4_C~Peptidase_C30~nsp7~nsp8~nsp9~NSP10~Corona_RPol_N~Viral_helicase1~NSP11~NSP13
143081	BB1717-like	143081	SRAP
143100	TTHA1013/TTHA0281-like	143100	DUF1902
143113	NAP-like	143113	NAP
143120	YefM-like	143120	PhdYeFM_antitox
143212	Rv2632c-like	143212	DUF1876
143243	Nqo5-like	143243	Complex1_30kDa
143410	DOPA-like	143410	DOPA_dioxygen
143414	CcmK-like	143414	BMC
143422	Transposase IS200-like	143422	Y1_Tnp
143430	TTP0101/SSO1404-like	143430	CRISPR_Cas2

143437	THUMP domain-like	143437~52402	THUMP~ThiI
143447	AMMECR1-like	143447	AMMECR1
143456	VC0467-like	143456	DUF179
143469	ImmE5-like	143469	ImmE5
143477	TM1622-like	143477	DUF3242
143492	Prenyltransferase-like	143492	PTase_Orf2
143503	PUG domain-like	143503~54001~49785	PUB~Transglut_core~PAW
143517	TRCF domain-like	52540~52540~141259~52540~52540~143517	CarD_CdnL_TRCF~DEAD~Helicase_C~TRCF
143548	Serine metabolism enzymes domain	143548	SDH_beta~SDH_alpha
143555	FwdE-like	143555	FmdE~zf-dskA_traR
143560	MK0786-like	143560	DHNA
143567	YkuJ-like	143567	DUF1797
143575	GAS2 domain-like	143575	CH~GAS2
143579	GK1464-like	143579	
143587	SARS receptor-binding domain-like	143587	Spike_rec_bind~Corona_S2
143592	TTHA1528-like	143592	DUF3197
143597	YojJ-like	143597	YojJ~DisA_N
143602	STIV B116-like	143602	DUF1874
143631	ApbE-like	143631	ApbE
143724	PHP14-like	140356~143724~56024~56024	PP_kinase_N~PP_kinase~PP_kinase_C
143737	YeeU-like	143737	CbeA_antitoxin
143744	GlcG-like	143744	Haem_degrading
143749	Phage tail protein-like	143749	Phage_tail_U
143791	DUSP-like	143791	DUSP~Ubiquitin_3~UCH
143800	L28p-like	143800	Ribosomal_L28
143842	YwmB-like	143842	DUF1779
143847	XisI-like	143847	XisI
143856	DeoB insert domain-like	143856	Metalloenzyme
143865	CorA soluble domain-like	143865	CorA
143870	PF0523-like	143870	CGI-121
143875	ERH-like	143875	ER
143880	NE0471 N-terminal domain-like	143880~47413	DUF2442
143885	RGC domain-like	47576~143885	CH~IQ~IQ~IQ~IQ~RasGAP~RasGAP_C
143968	UbiD C-terminal domain-like	143968	UbiD
143975	IlvD/EDD N-terminal domain-like	143975~52016	ILVD_EDD
143985	L,D-transpeptidase pre-catalytic domain-like	143985~141523	PG_binding_4~PG_binding_4~YkuD
143990	YbiA-like	143990	DUF1768
143995	AF2331-like	143995	AF2331-like
144000	Oxysterol-binding protein-like	144000	PH~Oxysterol_BP
144005	ORC1-binding domain	144005	Sir1~Sir1
144010	CofE-like	144010	F420_ligase
144015	Peptidoglycan deacetylase N-terminal noncatalytic region	144015~88713	Polysacc_deac_1
144020	FdhE-like	144020	FdhE
144052	Thermophilic metalloprotease-like	144052	Peptidase_M29
144059	ImpE-like	144059	ImpE
144064	Heme iron utilization protein-like	144064	HemS~HemS
144074	E2F-DP heterodimerization region	46785~144074	E2F_TDP~E2F_CC-MB

144083	Magnesium transport protein CorA, transmembrane region	144083	CorA
144091	Rhomboid-like	144091	Rhomboid
144122	Tim10-like	144122	zf-Tim10_DDP
144129	Vanabin-like	144129	Vanabin-2
144206	NOB1 zinc finger-like	144206	NOB1_Zn_bind
144210	Nop10-like SnoRNP	144210	Nop10p
144217	CSL zinc finger	144217	zf-CSL
144232	HIT/MYND zinc finger-like	144232	zf-MYND
144246	Coronavirus NSP10-like	52949~50494~140367~143076~101816~144246~53335~142877	Macro~Viral_protease~Corona_NSP4_C~Peptidase_C30~nsp7~nsp8~nsp9~NSP10~Corona_RPol_N~Viral_helicase1~NSP11~NSP13
144251	Viral leader polypeptide zinc finger	144251~88633~88633~88633~50494~56672	VP_N-CPKC~Rhv~Rhv~RNA_helicase~Peptidase_C3~RdRP_1
144256	TSP9-like	144256	TSP9
158212	Htr2 transmembrane domain-like	158212	HAMP~MCPsignal
158221	YnzC-like	158221	DUF896
158230	PRP4-like	158230	PRP4~Prp18
158235	SOCS box-like	55550~158235	SH2~SOCS_box
158366	Efb C-domain-like	158366	efb-c
158372	AF1782-like	158372	DUF357
158379	YqgQ-like	158379	DUF910
158388	YvfG-like	158388	YvfG
158397	TM1646-like	158397	DUF327
158414	HP0062-like	158414	WXG100
158418	SO2669-like	158418	
158430	Bacillus cereus metalloprotein-like	158430~158430	DUF2935~DUF2935
158436	Ta0600-like	158436	UPF0147
158442	DsbB-like	158442	DsbB
158446	IVS-encoded protein-like	158446	23S_rRNA_IVP
158452	YqcC-like	158452	DUF446
158457	Orange domain-like	158457	HLH~Hairy_orange
158472	HAMP domain-like	158472	HAMP~HisKA~HATPase_c
158494	PG0775 C-terminal domain-like	56645~47203~158494	Acyl-CoA_dh_N~Acyl-CoA_dh_M~Acyl-CoA_dh_1~AcylCoA_dehyd_C
158499	DnaD domain-like	158499	DnaB_2
158504	BH2638-like	158504	UPF0223
158544	GspK insert domain-like	158544	T2SSK
158548	FLJ32549 domain-like	158548~160651	DUF2003
158553	TAFH domain-like	158553~144232	TAFH~NHR2~zf-MYND
158560	BH3980-like	158560	DUF1048
158568	AF1862-like	158568	Cas_Cmr5
158573	GINS helical bundle-like	158573	Sld5
158587	Jann4075-like	158587	DUF2853
158615	RbcX-like	158615	RcbX
158622	YheA/YmcA-like	158622	Com_YlbF
158634	RPA2825-like	158634	DUF3597
158639	ENT-like	158639	ENT
158651	YejL-like	158651	DUF1414
158668	MtlR-like	158668	MtlR

158675	Sama2622-like	158675	DUF3069
158682	TerB-like	158682	TerB
158694	UraD-Like	158694	OHCU_decarbox
158702	Sec63 N-terminal domain-like	52540~52540~158702~158702~81296	DEAD~Helicase_C~Sec63~DEAD~Sec63
158710	PSPTO4464-like	158710	DUF615
158715	MG296-like	158715	Mg296
158745	LanC-like	158745	LANC_like
158752	HP0242-like	158752	DUF2018
158757	SMc04008-like	158757	DUF1244
158791	MgtE N-terminal domain-like	158791~54631~161093	MgtE_N~CBS~CBS~MgtE
158832	Tex N-terminal region-like	158832~53098~47781~47781~50249	Tex_N~Tex_YqgF~HHH_3~S1
158837	AGR C 984p-like	158837	DUF1217
158842	PMT central region-like	158842~159501~54001	PMT_C
158851	Lag-3 N-terminal region	158851	Activator_LAG-3
158855	Lipase chaperone-like	158855	Lipase_chap
158911	NEAT domain-like	158911	NEAT
158949	Smr-associated domain-like	158949	DUF2027~Smr
158974	WSSV envelope protein-like	158974	WSS_VP
158997	Trm112p-like	158997	Trm112p
159006	YopX-like	159006	YopX
159034	Mib/herc2 domain-like	159034~159034~48403	Ank_5~Sad1_UNC~MIB_HERC2~HECT
159038	YorP-like	159038	YorP
159042	Plus3-like	159042	Plus-3
159065	Dom34/Pelota N-terminal domain-like	159065~53137~55315	eRF1_1~eRF1_2~eRF1_3
159071	TrmB C-terminal domain-like	159071	TrmB~Regulator_TrmB
159121	BC4932-like	159121	DUF1093
159127	HupF/HypC-like	159127	HupF_HypC
159133	EutN/CcmL-like	159133	EutN_CcmL
159141	HIN-2000 domain-like	159141~159141	PYRIN~HIN
159173	YkvR-like	159173	DUF3219
159203	NifT/FixU-like	159203	NifT
159222	YopT-like	159222	Yopt
159234	FomD-like	159234	DUF402
159238	SO1590-like	159238	DUF3224
159245	AttH-like	159245	CrtC
159270	YmcC-like	159270	YjbF
159275	PA1994-like	159275	Glycolipid_bind
159283	Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain	53448~159283	NTP_transferase~MannoseP_isomer
159468	AtpF-like	159468	ATP-synt_F
159501	EreA/ChaN-like	159501	Erythro_esteras
159594	XCC0632-like	159594	ABC_trans_aux
159612	TBP-interacting protein-like	159612	TBPIP_N
159659	Cgl1923-like	159659	PAC2
159664	CobE/GbiG C-terminal domain-like	159664	CbiG_C
159672	CbiG N-terminal domain-like	159672~159664	CbiG_N~CbiG_C

159709	PhnH-like	159709	PhnH
159713	Dhaf3308-like	159713	DUF4213~DUF364
159774	YerB-like	159774	DUF3048
159779	CdCA1 repeat-like	159779	
159800	PrpR receptor domain-like	159800~52540	PrpR_N~Sigma54_activat
159865	XkdW-like	159865	XkdW
159871	YdgH-like	159871	DUF1471
159888	YdhG-like	159888	DUF1801
159894	YgaC/TfoX-N like	159894	TfoX_N~TfoX_C
159902	PH1570-like	159902	Ph1570
159936	NSP3A-like	159936~52949~50494~140367~143076~101816~144246~53335~142877	DUF3477~Peptidase_C16~Macro~Viral_protease~NAR~Corona_NSP4_C~Peptidase_C30~nsp7~nsp8~nsp9~NSP10~Corona_RPol_N~AAA_12~NSP11~NSP13
159941	MM3350-like	159941	PRiA4_ORF3
160059	PriA/YqbF domain	160059~158573	Sld5
160088	NRDP1 C-terminal domain-like	57850~160088	zf-C3HC4~USP8_interact
160099	SARS Nsp1-like	160099~159936~52949~50494~140367~143076~101816~144246~53335~142877	Nsp1~DUF3655~Macro~SUD-M~Nsp3_PL2pro~Viral_protease~NAR~Corona_NSP4_C~Peptidase_C30~nsp7~nsp8~nsp9~NSP10~Corona_RPol_N~Viral_helicase1~NSP11~NSP13
160104	Acetoacetate decarboxylase-like	160104	ADC
160113	YegP-like	160113~160113	DUF1508~DUF1508
160148	CPE0013-like	160148	DUF1667
160191	YcgL-like	160191	YcgL
160207	NMB0488-like	160207	DUF1436
160214	FlaG-like	160214	FlaG
160219	AMPKBI-like	81296~160219	AMPK1_CBM~AMPKBI
160240	Cation efflux protein cytoplasmic domain-like	161111~160240	Cation_efflux~ZT_dimer
160246	EspE N-terminal domain-like	160246~52540	T2SSE_N~T2SSE
160272	Shew3726-like	160272	DUF1488
160350	Rnp2-like	160350	RNase_P_Rpp14
160355	Bacterial polysaccharide co-polymerase-like	160355	Wzz
160363	MTH889-like	160363	DUF211
160369	Ribosomal protein L10-like	160369	Ribosomal_L10
160374	RplX-like	160374	Ribosomal_L18ae
160379	SP0830-like	160379	DUF1697
160387	NosL/MerB-like	160387	NosL
160419	YdfO-like	160419	DUF1398
160424	BH3703-like	160424	DUF600
160443	SMR domain-like	160443	DUF1771~Smr
160448	PG1857-like	160448	DUF2023
160453	PB2 C-terminal domain-like	160453	Flu_PB2
160459	BLRF2-like	160459	Herpes_BLRF2
160467	PH0987 N-terminal domain-like	160467~50891	AHS1
160472	NMB0513-like	160472	DUF596
160477	PA1123-like	160477	DUF2025
160481	BRK domain-like	52540~52540~160481~160481	Chromo~Chromo~SNF2_N~Helicase_C~BRK~BRK

160515	YueI-like	160515	DUF1694
160519	BB2672-like	160519	AA_synth
160527	V-type ATPase subunit E-like	160527	vATP-synt_E
160532	Ava3019-like	160532	DUF1824
160537	SpoVG-like	160537	SpoVG
160544	EscU C-terminal domain-like	160544	Bac_export_2
160570	YonK-like	160570	YonK
160574	BT0923-like	160574	PepSY_like
160582	MbtH-like	160582	MbtH
160631	SMI1/KNR4-like	160631	SUKH_6
160651	FLJ32549 C-terminal domain-like	158548~160651	DUF2003
160683	YNR034W-A-like	160683	DUF3215
160696	BTG domain-like	160696	BTG
160704	YehR-like	160704	DUF1307
160713	YqaI-like	160713	Yqai
160719	gpW/gp25-like	160719	GPW_gp25
160755	YugN-like	160755	YugN
160761	TTHC002-like	160761	
160766	NE1680-like	160766	DUF2024
160800	Lp2179-like	160800	DUF1831
160887	Rv2827c C-terminal domain-like	46785~160887	AbiEi_1
160892	Phosphoprotein oligomerization domain-like	160892	Phosphoprotein
160897	Taf5 N-terminal domain-like	160897~50978	TFIID_NTD2~WD40~WD40~WD40~WD40~WD40
160904	Jann2411-like	160904	ABATE~zf-CGNR
160909	ATP12-like	160909	ATP12
160920	PSTPO5379-like	160920	DUF1445
160925	PG1388-like	160925	DUF3256
160930	FlhC-like	160930	FlhC
160935	VPA0735-like	160935	DUF1254~DUF1214
160940	Api92-like	160940	DUF1281
160945	PH0156-like	160945	DUF3226
160950	YacF-like	160950	DUF1342
160957	Poly(A) polymerase catalytic subunit-like	160957	Pox_polyA_pol_N~Pox_polyA_pol~Pox_polyA_pol_C
160964	MalF N-terminal region-like	160964~161098	MalF_P2~BPD_transp_1
160975	AF1531-like	160975	DUF655
160980	SSO1389-like	160980	Cas_DxTHG
160991	CV3147-like	160991	DUF917
160996	HI0933 insert domain-like	51905~160996	HI0933_like
161003	flu NP-like	161003	Flu_NP
161008	Viral glycoprotein ectodomain-like	161008	Rhabdo_glycop
161017	Photosystem II reaction center protein L, PsbL	161017	PsbL
161021	Photosystem II reaction center protein J, PsbJ	161021	PsbJ
161025	Photosystem II 10 kDa phosphoprotein PsbH	161025	PsbH
161029	Photosystem II reaction center protein T, PsbT	161029	PsbT
161033	Photosystem II reaction center protein M, PsbM	161033	PsbM

161037	Photosystem II reaction center protein K, PsbK	161037	PsbK
161041	Photosystem II reaction center protein I, PsbI	161041	PsbI
161045	Cytochrome b559 subunits	161045	Cytochrom_B559~Cytochrom_B559a
161055	PsbZ-like	161055	Ycf9
161060	ATP synthase B chain-like	161060	Mt_ATP-synt_B
161065	ATP synthase D chain-like	161065	Mt_ATP-synt_D
161070	SNF-like	161070	SNF
161077	Photosystem II antenna protein-like	161077	PSII
161084	MAPEG domain-like	161084	MAPEG
161093	MgtE membrane domain-like	158791~54631~161093	MgtE_N~CBS~CBS~MgtE
161098	MetI-like	161098	BPD_transp_1
161111	Cation efflux protein transmembrane domain-like	161111~160240	Cation_efflux~ZT_dimer
161148	VhTI-like	161148	
161187	YfgJ-like	161187	zinc-ribbons_6
161219	CHY zinc finger-like	161219~161245	zf-CHY~zf-RING_2~zinc_ribbon_6
161229	E6 C-terminal domain-like	161229	E6
161234	E7 C-terminal domain-like	161234	E7
161240	T-antigen specific domain-like	46565~161240	Papo_T_antigen
161245	Zinc hairpin stack	161219~161245	zf-CHY~zf-RING_2~zinc_ribbon_6

Supplementary Table 13: A list of all the superfamilies which have more than 100 gene products with putatively discontinuous domains along with the class and fold details. The domains with more than 25 residue breaks have been referred to as discontinuous domains. The interrupted domains which have been listed in SCOP have been highlighted in a green background. Discontinuous domains refer to domain match instances with a break of 25 residues or more in the hmm matches. Instances of domain matches with breaks less than 25 residues are listed under the column SCOP hmm breaks. The column "Total interrupted domains" refers to number of sequences with hmm breaks in the superfamily.

SCOP Class	**SCOP Fold**	**SCOP Sf**	**Description**	**#GI**	**#discontinuous SCOP domains**	**#SCOP hmm breaks**	**Total interrupted domains**
46456	46457	46458	Globin-like	22203	114	17	121
46456	46625	46626	Cytochrome c	37850	9	353	32
46456	46688	46785	Winged helix DNA-binding domain	300000	14	272	59
46456	47363	47203	Acyl-CoA dehydrogenase C-terminal domain-like	34517	2	100	22
46456	47161	47216	Proteasome activator	764	149	216	168
46456	47239	47240	Ferritin-like	49804	619	826	892
46456	47265	47266	4-helical cytokines	9157	10	170	19
46456	47458	47459	HLH, helix-loop-helix DNA-binding domain	15534	3	164	109
46456	47472	47473	EF-hand	56632	503	580	575
46456	47575	47576	Calponin-homology domain, CH-domain	18473	4	148	5
46456	47615	47616	GST C-terminal domain-like	46546	3	102	5
46456	47768	47781	RuvA domain 2-like	36409	87	579	94
46456	47861	47862	Saposin	1936	2	399	25
46456	47911	47912	Wiscott-Aldrich syndrome protein, WASP, C-terminal domain	232	213	6	214
46456	47916	47923	Ypt/Rab-GAP domain of gyp1p	2255	28	158	34
46456	47953	47954	Cyclin-like	17027	1	228	38
46456	48007	48008	GntR ligand-binding domain-like	5048	3	111	12
46456	48112	48113	Heme-dependent peroxidases	16717	119	445	299
46456	48207	48208	Six-hairpin glycosidases	31846	68	232	72
46456	48207	48225	Seven-hairpin glycosidases	4216	94	119	97
46456	48207	48239	Terpenoid cyclases/Protein prenyltransferases	13588	331	254	344
46456	48263	48264	Cytochrome P450	43685	65	687	128
46456	48344	48345	A virus capsid protein alpha-helical domain	1055	989	0	989
46456	48349	48350	GTPase activation domain, GAP	15107	14	1019	183
46456	48370	48371	ARM repeat	46755	627	3967	724
53931	74651	48403	Ankyrin repeat	10411	38	2490	124
46456	48370	48452	TPR-like	31956	13	692	88
46456	48507	48508	Nuclear receptor ligand-binding domain	15326	91	171	116
46456	48591	48592	GroEL equatorial domain-like	3393	2909	2	2910
46456	48694	48695	Multiheme cytochromes	4852	0	112	2
48724	48725	48726	Immunoglobulin	200000	18	221	113
48724	48725	49265	Fibronectin type III	54163	523	81	531
48724	49379	49417	p53-like transcription factors	14329	23	129	25
48724	49492	49493	HSP40/DnaJ peptide-binding domain	17814	115	196	123
48724	49502	49503	Cupredoxins	55723	72	658	137
48724	49561	49562	C2 domain (Calcium/lipid-binding domain, CaLB)	37948	23	152	43
48724	49757	49758	Calpain large subunit, middle domain (domain III)	3698	4	108	7
48724	49784	49785	Galactose-binding domain-like	50161	45	299	90
48724	49878	49879	SMAD/FHA domain	21383	14	317	19
48724	49898	49899	Concanavalin A-like lectins/glucanases	55607	126	419	198

48724	50128	50129	GroES-like	87332	2002	21	2009
48724	50181	50182	Sm-like ribonucleoproteins	22421	4	198	10
48724	50198	50249	Nucleic acid-binding proteins	200000	46	390	80
48724	50493	50494	Trypsin-like serine proteases	69184	160	727	275
48724	50629	50630	Acid proteases	33784	442	332	488
48724	50728	50729	PH domain-like	94233	168	619	213
48724	50890	50891	Cyclophilin-like	22143	1	607	266
48724	50938	50939	Sialidases	16625	158	145	165
48724	50964	50978	WD40 repeat-like	18251	105	2466	144
48724	51125	51126	Pectin lyase-like	20582	135	548	171
48724	51160	51161	Trimeric LpxA-like enzymes	40854	1	570	17
48724	51181	51182	RmlC-like cupins	73150	48	324	68
48724	51181	51197	Clavaminate synthase-like	32860	137	1328	149
48724	51268	51283	dUTPase-like	15930	3	188	128
48724	51293	51294	Hedgehog/intein (Hint) domain	2845	246	58	291
48724	51337	51338	Composite domain of metallo-dependent hydrolases	10738	3266	4	3267
51349	51350	51366	Ribulose-phoshate binding barrel	55482	13	112	25
51349	51350	51395	FMN-linked oxidoreductases	50703	2773	4229	2806
51349	51350	51412	Inosine monophosphate dehydrogenase (IMPDH)	7136	854	93	855
51349	51350	51430	NAD(P)-linked oxidoreductase	32331	14	1925	93
51349	51350	51445	(Trans)glycosidases	200000	1333	5204	1852
51349	51350	51556	Metallo-dependent hydrolases	100000	1080	2710	1195
51349	51350	51569	Aldolase	98214	50	751	68
51349	51350	51621	Phosphoenolpyruvate/pyruvate domain	40158	1597	1081	1712
51349	51350	51658	Xylose isomerase-like	23988	484	1033	485
51349	51350	51679	Bacterial luciferase-like	22089	220	185	290
51349	51350	51690	Nicotinate/Quinolinate PRTase C-terminal domain-like	15789	127	99	131
51349	51350	51695	PLC-like phosphodiesterases	15637	811	728	836
51349	51734	51735	NAD(P)-binding Rossmann-fold domains	500000	695	5034	1217
51349	51904	51905	FAD/NAD(P)-binding domain	100000	39118	2883	39549
51349	51970	51971	Nucleotide-binding domain	12631	526	280	735
51349	51988	51989	Glycosyl hydrolases family 6, cellulases	2620	24	225	60
51349	52046	52047	RNI-like	4887	2	269	17
51349	52046	52058	L domain-like	33813	82	7565	347
51349	52095	52096	ClpP/crotonase	54126	643	1315	667
51349	52120	52121	Lumazine synthase	5809	41	202	47
51349	52128	52129	Caspase-like	5523	275	1385	679
51349	52150	52151	FabD/lysophospholipase-like	8265	381	6785	437
51349	52171	52218	Flavoproteins	48806	112	283	287
51349	52171	52266	SGNH hydrolase	30731	164	73	208
51349	52171	52283	Formate/glycerate dehydrogenase catalytic domain-like	28310	268	1656	277
51349	52171	52313	Ribosomal protein S2	6818	2470	1383	2777
51349	52171	52317	Class I glutamine amidotransferase-like	84154	19	144	44
51349	52334	52335	Methylglyoxal synthase-like	16664	21	358	114
51349	52373	52374	Nucleotidylyl transferase	99969	8093	8395	8350
51349	52373	52402	Adenine nucleotide alpha hydrolases-like	86310	402	279	474
51349	52439	52440	PreATP-grasp domain	44211	164	53	188
51349	52466	52467	DHS-like NAD/FAD-binding domain	43920	718	1509	812
51349	52498	52499	Isochorismatase-like hydrolases	30084	18	235	46
51349	52517	52518	Thiamin diphosphate-binding fold (THDP-binding)	66457	6	520	23
51349	52539	52540	P-loop containing nucleoside triphosphate hydrolases	700000	12866	21753	15695
51349	52742	52743	Subtilisin-like	19994	828	539	867
51349	52767	52768	Arginase/deacetylase	20491	16	141	23
51349	52776	52777	CoA-dependent acyltransferases	29848	62	225	70
51349	52798	52799	(Phosphotyrosine protein) phosphatases II	37820	267	1082	344
51349	52934	52943	ATP synthase (F1-ATPase), gamma subunit	6655	4	336	13
51349	52979	52980	Restriction endonuclease-like	23809	5	241	18

51349	53066	53067	Actin-like ATPase domain	100000	76	523	200
51349	53066	53098	Ribonuclease H-like	87336	59	1705	76
51349	53066	53137	Translational machinery components	13502	8	506	170
51349	53162	53167	Purine and uridine phosphorylases	27446	43	613	84
51349	53162	53187	Zn-dependent exopeptidases	65531	16265	4278	16921
51349	53253	53254	Phosphoglycerate mutase-like	22479	31	211	43
51349	53270	53271	PRTase-like	58777	205	64	214
51349	53299	53300	vWA-like	23899	22	283	42
51349	53334	53335	S-adenosyl-L-methionine-dependent methyltransferases	200000	454	2964	675
51349	53382	53383	PLP-dependent transferases	200000	4829	4827	4865
51349	53447	53448	Nucleotide-diphospho-sugar transferases	66877	258	633	288
51349	53473	53474	alpha/beta-Hydrolases	100000	693	1380	782
51349	53612	53613	Ribokinase-like	43195	18	236	34
51349	53648	53649	Alkaline phosphatase-like	23205	3543	225	3546
51349	53658	53659	Isocitrate/Isopropylmalate dehydrogenase-like	37932	115	1747	117
51349	53670	53671	Aspartate/ornithine carbamoyltransferase	20038	7	181	62
51349	53685	53686	Tryptophan synthase beta subunit-like PLP-dependent enzymes	28976	65	176	98
51349	53696	53697	SIS domain	25589	0	212	5
51349	53731	53732	Aconitase iron-sulfur domain	14131	850	1242	851
51349	53755	53756	UDP-Glycosyltransferase/glycogen phosphorylase	33769	50	459	88
51349	53783	53784	Phosphofructokinase	10736	50	2574	61
51349	53799	53807	Helical backbone metal receptor	30627	238	803	377
51349	53821	53822	Periplasmic binding protein-like I	44197	303	1030	316
51349	53849	53850	Periplasmic binding protein-like II	200000	6083	200	6104
51349	53900	53901	Thiolase-like	46678	215	1617	270
51349	53926	53927	Cytidine deaminase-like	30896	42	191	97
53931	54000	54001	Cysteine proteinases	46943	973	3598	1216
48724	50036	54160	Chromo domain-like	9047	32	266	42
53931	54196	54197	HIT-like	25573	26	140	43
53931	54210	54211	Ribosomal protein S5 domain 2-like	100000	25	672	94
53931	54494	54495	UBC-like	24481	18	183	51
53931	54528	54529	Mitochondrial glycoprotein MAM33-like	552	3	137	14
53931	54592	54593	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	61184	22	215	62
53931	54630	54631	CBS-domain pair	38306	86	206	198
53931	54694	54695	POZ domain	14517	443	234	459
53931	54712	54713	Elongation factor Ts (EF-Ts), dimerisation domain	7911	5	228	24
53931	54790	54791	Eukaryotic type KH-domain (KH-domain type I)	23938	2	488	15
53931	54842	54843	Ribosomal protein L22	6646	0	304	1
53931	54848	54849	GroEL-intermediate domain like	708	124	4	126
53931	54861	54862	4Fe-4S ferredoxins	55310	178	319	233
53931	54861	54928	RNA-binding domain, RBD	90213	116	234	137
53931	100877	55120	Pseudouridine synthase	28501	350	2371	365
53931	55165	55166	Hedgehog/DD-peptidase	6183	0	562	2
53931	55247	55257	RBP11-like subunits of RNA polymerase	2775	261	28	264
53931	55346	55347	Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain	56969	4	953	335
53931	55423	55424	FAD/NAD-linked reductases, dimerisation (C-terminal) domain	37694	0	317	8
53931	55485	55486	Metalloproteases ("zincins"), catalytic domain	55043	224	1059	272
53931	55680	55681	Class II aaRS and biotin synthetases	85386	3010	1303	3234
53931	55728	55729	Acyl-CoA N-acyltransferases (Nat)	100000	281	346	318
53931	55769	55781	GAF domain-like	21258	4	137	66
53931	55803	55804	Phoshotransferase/anion transport protein	16188	15	166	16
53931	55815	55816	5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain	7009	52	153	77
53931	55830	55831	Thymidylate synthase/dCMP hydroxymethylase	5735	16	106	17
53931	55873	55874	ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase	64445	215	4367	316
53931	55919	55920	Creatinase/aminopeptidase	19532	3	172	13

53931	56002	56003	Molybdenum cofactor-binding domain	12554	94	363	97
53931	56013	56014	Nitrite and sulphite reductase 4Fe-4S domain-like	10652	334	717	341
53931	56041	56042	PurM C-terminal domain-like	29399	0	414	3
53931	56058	56059	Glutathione synthetase ATP-binding domain-like	78679	1942	367	1958
53931	56103	56104	SAICAR synthase-like	11765	22	111	24
53931	56111	56112	Protein kinase-like (PK-like)	100000	1061	3237	1932
53931	56218	56219	DNase I-like	31507	533	527	695
53931	56234	56235	N-terminal nucleophile aminohydrolases (Ntn hydrolases)	69250	838	3278	1049
53931	56275	56276	S-adenosylmethionine decarboxylase	3217	62	128	63
53931	56280	56281	Metallo-hydrolase/oxidoreductase	58954	849	3373	1009
53931	56299	56300	Metallo-dependent phosphatases	49712	34	249	51
53931	56316	56317	Carbon-nitrogen hydrolase	10726	9	149	50
53931	56321	56322	ADC synthase	13593	727	5200	1148
53931	56326	56327	LDH C-terminal domain-like	20461	66	152	108
53931	56419	56420	Peptide deformylase	9313	17	382	51
53931	56435	56436	C-type lectin-like	31099	63	559	129
53931	56501	56502	gp120 core	4994	0	4957	1
53931	56533	56534	Aromatic aminoacid monoxygenases, catalytic and oligomerization domains	4073	254	244	258
53931	56541	56542	Substrate-binding domain of HMG-CoA reductase	2868	2509	556	2510
56572	56654	56655	Carbohydrate phosphatase	21399	3	230	91
56572	56671	56672	DNA/RNA polymerases	40060	595	393	649
56572	56711	56712	Prokaryotic type I DNA topoisomerase	11153	847	926	849
56572	56718	56719	Type II DNA topoisomerase	6527	820	526	821
56572	56761	56762	HydB/Nqo4-like	8303	123	638	124
56572	56769	56770	HydA/Nqo6-like	8362	11	441	31
51349	56783	56784	HAD-like	100000	110	1058	261
56572	56800	56801	Acetyl-CoA synthetase-like	39939	367	835	531
56572	56814	56815	Sec1/munc18-like (SM) proteins	3087	76	181	79
56835	56924	56925	OMPA-like	7364	1	164	61
56835	56924	56931	Outer membrane phospholipase A (OMPLA)	2905	4	406	5
56835	56924	56935	Porins	29682	10	230	25
56835	56967	56968	Lipovitellin-phosvitin complex; beta-sheet shell regions	578	7	112	11
56992	56993	56994	Insulin-like	1348	165	143	173
56992	57769	57798	Casein kinase II beta subunit	1627	9	156	11
56992	57902	57903	FYVE/PHD zinc finger	30442	2	355	6
53931	63410	63411	LuxS/MPP-like metallohydrolase	33281	71	154	100
48724	50036	63748	Tudor/PWWP/MBT	16111	0	146	28
48724	50938	63825	YWTD domain	5075	14	161	20
48724	63886	63887	P-domain of calnexin/calreticulin	2511	0	163	1
51349	51350	63892	Pyridoxine 5'-phosphate synthase	4992	1	216	2
51349	64181	64182	DHH phosphoesterases	9069	406	22	407
53931	64287	64288	Chorismate lyase-like	26262	0	143	59
53931	55769	64356	SNARE-like	9542	60	337	94
56572	64483	64484	beta and beta-prime subunits of DNA dependent RNA-polymerase	10444	1781	228	1790
46456	47363	69012	alpha-ketoacid dehydrogenase kinase, N-terminal domain	2585	315	70	326
48724	48725	69179	Integrin domains	1271	157	281	161
48724	51125	69336	Alpha subunit of glutamate synthase, C-terminal domain	11999	1	268	192
48724	69359	69360	Cell wall binding repeat	5215	0	1087	39
51349	69571	69572	Activating enzymes of the ubiquitin-like proteins	15902	302	49	311
53931	69704	69705	Transcription factor NusA, N-terminal domain	6731	5	432	170
48724	49993	74650	Galactose mutarotase-like	29513	8	153	24
51349	75216	75217	alpha/beta knot	37376	91	187	105
51349	75303	75304	Amidase signature (AS) enzymes	19575	12	807	22
56572	75631	75632	Cullin homology domain	4413	40	119	47
48724	48725	81296	E set domains	75728	13	434	29

53931	81302	81301	Nucleotidyltransferase	41539	88	262	147
56835	81337	81336	F1F0 ATP synthase subunit A	2014	2	1760	8
53931	81607	81606	PP2C-like	9873	225	166	232
46456	48370	81901	HCP-like	5673	10	586	33
48724	49379	81995	beta-sandwich domain of Sec23/24	2470	2170	1	2171
48724	50352	82109	MIR domain	3740	27	695	29
48724	50412	82114	Riboflavin kinase-like	7988	34	119	37
48724	51268	82199	SET domain	6673	32	168	39
51349	82543	82544	GckA/TtuD-like	2961	166	48	167
53931	54861	82693	Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains	7369	2300	91	2331
48724	88632	88633	Positive stranded ssRNA viruses	15700	1718	279	1769
51349	51988	88713	Glycoside hydrolase/deacetylase	27734	5	164	51
51349	88722	88723	PIN domain-like	27483	658	83	676
46456	88945	88946	Sigma2 domain of RNA polymerase sigma factors	15595	131	665	144
51349	89795	89796	CoA-transferase family III (CaiB/BaiF)	12338	5	100	39
56835	90122	90123	ABC transporter transmembrane region	8518	2	415	45
51349	100949	100950	NagB/RpiA/CoA transferase-like	58283	22	891	127
46456	101446	101447	Formin homology 2 domain (FH2 domain)	6770	11	687	196
48724	50614	101821	Aminopeptidase/glucanase lid domain	3704	10	396	106
48724	50938	101898	NHL repeat	2734	2	117	13
48724	50938	101904	GyrA/ParC C-terminal domain-like	7996	276	678	321
48724	51160	101967	Adhesin YadA, collagen-binding domain	4243	10	178	39
51349	102704	102705	NIF3 (NGG1p interacting factor 3)-like	9137	1448	29	1459
53931	102885	102886	Coproporphyrinogen III oxidase	5144	7	325	11
53931	103262	103263	Chorismate synthase, AroC	9090	124	1730	683
56835	103490	103491	Preprotein translocase SecY subunit	1271	771	219	772
46456	109603	109604	HD-domain/PDEase-like	33545	534	890	936
46456	47161	109775	Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain	1020	24	670	27
46456	110018	110019	ERO1-like	995	118	423	119
56572	111336	111337	QueA-like	3053	763	2290	764
56835	111351	111352	Ammonium transporter	5003	4	131	5
56992	111417	111418	Hormone receptor domain	1703	1	233	53
46456	47161	116878	TrmE connector domain	2173	193	5	195
48724	117142	117143	Flagellar hook protein flgE	3810	59	344	65
48724	50938	117281	Kelch motif	1891	0	262	1
51349	51350	117396	TM1631-like	4328	147	774	227
56572	118195	118196	YaeB-like	1676	1	1606	2
46456	140923	140924	Duffy binding domain-like	2532	87	539	215
46456	140958	140959	Indolic compounds 2,3-dioxygenase-like	4114	63	104	78
48724	48725	141072	CalX-like	4726	43	123	50
48724	50036	141255	YccV-like	306	0	184	1
48724	51125	141571	Pentapeptide repeat-like	6094	7	468	29
53931	143080	143081	BB1717-like	6802	7	134	9
53931	143112	143113	NAP-like	3438	88	131	115
53931	143974	143975	IlvD/EDD N-terminal domain-like	10140	5	4789	74
56835	81334	144083	Magnesium transport protein CorA, transmembrane region	329	0	100	37
46456	47363	158430	Bacillus cereus metalloprotein-like	1018	69	126	104
56572	161007	161008	Viral glycoprotein ectodomain-like	1388	85	102	86
56835	161069	161070	SNF-like	3767	7	109	8