Phyre^2

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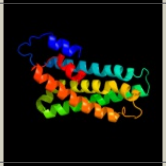
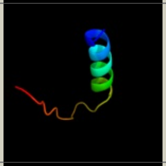
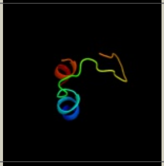
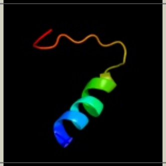
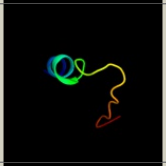
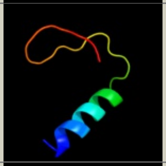
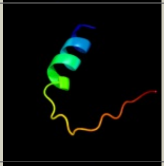
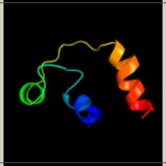
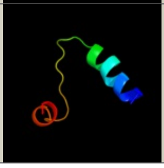
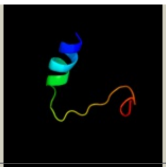
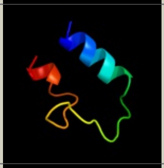
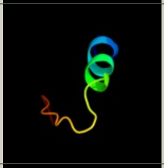
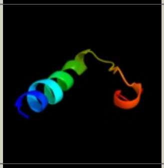
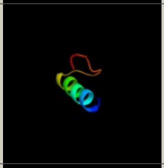
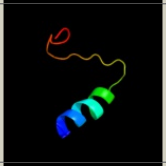
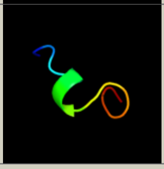
Description	P0ABG1
Date	Thu Jan 5 11:15:26 GMT 2012
Unique Job ID	ac14ab8a421bee90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b9yA_	Alignment		93.7	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
2	d1u7ga_	Alignment		82.0	17	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter
3	c3r2uC_	Alignment		53.6	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
4	d2p97a1	Alignment		52.1	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
5	c2xf4A_	Alignment		50.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
6	c2gcuD_	Alignment		47.1	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana2 at1g53580
7	d1mqoa_	Alignment		45.7	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
8	c3tp9B_	Alignment		38.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase and rhodanese domain protein; **PDBTitle:** crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
9	c3hd6A_	Alignment		38.4	13	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
10	d1nxca_	Alignment		36.2	19	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
11	d1xm8a_	Alignment		35.9	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)

12	d1qh5a_	Alignment		34.9	7	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
13	d1znba_	Alignment		34.8	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
14	c2zwrA_	Alignment		34.2	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase superfamily protein; **PDBTitle:** crystal structure of ttha1623 from thermus thermophilus hb8
15	d1dl2a_	Alignment		31.1	17	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
16	d2aioa1	Alignment		30.2	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
17	d1bh9b_	Alignment		28.7	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
18	c3hnnD_	Alignment		27.1	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative diflavin flavoprotein a 5; **PDBTitle:** crystal structure of putative diflavin flavoprotein a 5 (fragment 1-2 254) from nostoc sp. pcc 7120, northeast structural genomics3 consortium target nsr435a
19	d2qeda1	Alignment		25.1	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
20	c3bboU_	Alignment		24.8	14	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**ribosomal protein l22; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
21	c2zo4A_	Alignment	not modelled	24.6	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** crystal structure of metallo-beta-lactamase family protein ttha14292 from thermus thermophilus hb8
22	c1ze2B_	Alignment	not modelled	24.2	29	**PDB header:**lyase/rna **Chain:** B: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
23	d1m2xa_	Alignment	not modelled	23.6	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
24	d1bk8a_	Alignment	not modelled	21.8	57	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Plant defensins
25	d2gycq1	Alignment	not modelled	21.7	36	**Fold:**Ribosomal protein L22 **Superfamily:**Ribosomal protein L22 **Family:**Ribosomal protein L22
26	c1s1iN_	Alignment	not modelled	20.6	33	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l17-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
27	d2ey4a2	Alignment	not modelled	20.0	30	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
28	c3l6nA_	Alignment	not modelled	19.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of metallo-beta-lactamase ind-7

29	c1krfA_	Alignment	not modelled	19.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannosyl-oligosaccharide alpha-1,2-mannosidase; **PDBTitle:** structure of p. citrinum alpha 1,2-mannosidase reveals the basis for2 differences in specificity of the er and golgi class i enzymes
30	d2ri9a1	Alignment	not modelled	19.4	19	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
31	c1vmeB_	Alignment	not modelled	18.9	17	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
32	d1r3ea2	Alignment	not modelled	18.4	29	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
33	d1ycga2	Alignment	not modelled	18.0	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
34	d2gmna1	Alignment	not modelled	17.8	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
35	c2yz3B_	Alignment	not modelled	16.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
36	d1hcua_	Alignment	not modelled	16.7	21	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
37	c2b2hA_	Alignment	not modelled	16.0	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
38	c3pisA_	Alignment	not modelled	15.8	25	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kazal-type serine protease inhibitor spi-1; **PDBTitle:** crystal structure of carcinoscorpius rotundicauda serine protease2 inhibitor domain 1
39	c2p18A_	Alignment	not modelled	15.6	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glyoxalase ii; **PDBTitle:** crystal structure of the leishmania infantum glyoxalase ii
40	d1sgva2	Alignment	not modelled	15.5	26	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
41	d1k8wa5	Alignment	not modelled	15.5	30	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
42	d2nn6h2	Alignment	not modelled	15.4	33	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
43	c1g6iA_	Alignment	not modelled	15.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i alpha-1,2-mannosidase; **PDBTitle:** crystal structure of the yeast alpha-1,2-mannosidase with bound 1-2 deoxymannojirimycin at 1.59 a resolution
44	c1k8wA_	Alignment	not modelled	15.0	30	**PDB header:**lyase/rna **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
45	d1ko3a_	Alignment	not modelled	15.0	23	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
46	c1x9dA_	Alignment	not modelled	14.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum mannosyl-oligosaccharide 1, **PDBTitle:** crystal structure of human class i alpha-1,2-mannosidase in2 complex with thio-disaccharide substrate analogue
47	d1x9da1	Alignment	not modelled	14.8	14	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
48	d1jv1a_	Alignment	not modelled	14.7	25	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
49	d2foka4	Alignment	not modelled	14.6	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease FokI, C-terminal (catalytic) domain
50	d1pcfa_	Alignment	not modelled	14.5	42	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
51	d2icya2	Alignment	not modelled	14.3	40	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
52	d1ayja_	Alignment	not modelled	14.1	57	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Plant defensins
53	c3uaiA_	Alignment	not modelled	13.9	33	**PDB header:**isomerase/chaperone **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
						PDB header:hydrolase, metal binding protein

54	c2fhxB_	Alignment	not modelled	13.8	28	**Chain:** B: **PDB Molecule:**spm-1; **PDBTitle:** pseudomonas aeruginosa spm-1 metallo-beta-lactamase
55	d1f0la3	Alignment	not modelled	13.4	67	**Fold:**Toxins' membrane translocation domains **Superfamily:**Diphtheria toxin, middle domain **Family:**Diphtheria toxin, middle domain
56	c2q9uB_	Alignment	not modelled	13.3	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
57	c3oc9A_	Alignment	not modelled	13.3	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
58	d1gu2a_	Alignment	not modelled	13.1	46	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
59	d1b0aa2	Alignment	not modelled	12.9	30	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
60	d2apoa2	Alignment	not modelled	12.5	38	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
61	c3pesA_	Alignment	not modelled	12.4	67	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein gp49; **PDBTitle:** crystal structure of uncharacterized protein from pseudomonas phage2 yua
62	c3jywN_	Alignment	not modelled	11.7	33	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l17(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
63	d1vm8a_	Alignment	not modelled	11.4	25	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
64	c2e55D_	Alignment	not modelled	11.1	43	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
65	c3lvzA_	Alignment	not modelled	11.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr6230 protein; **PDBTitle:** new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
66	c2oefA_	Alignment	not modelled	11.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**utp-glucose-1-phosphate uridylyltransferase 2, **PDBTitle:** open and closed structures of the udp-glucose2 pyrophosphorylase from leishmania major
67	c3h0dB_	Alignment	not modelled	10.8	15	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**ctsr; **PDBTitle:** crystal structure of ctsr in complex with a 26bp dna duplex
68	d1e5da2	Alignment	not modelled	10.7	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
69	c1sgvA_	Alignment	not modelled	10.6	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
70	c2ey4A_	Alignment	not modelled	10.4	33	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
71	c4a17Q_	Alignment	not modelled	10.3	22	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**rpl17; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
72	d1jjta_	Alignment	not modelled	10.2	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
73	c3gueB_	Alignment	not modelled	9.9	42	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp-glucose-1-phosphate uridylyltransferase 2; **PDBTitle:** crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
74	d1vqor1	Alignment	not modelled	9.8	11	**Fold:**Ribosomal protein L22 **Superfamily:**Ribosomal protein L22 **Family:**Ribosomal protein L22
75	c3fvyA_	Alignment	not modelled	9.6	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl-peptidase 3; **PDBTitle:** crystal structure of human dipeptidyl peptidase iii
76	c2q4jB_	Alignment	not modelled	9.3	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable utp-glucose-1-phosphate uridylyltransferase 2; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
77	d1ecia_	Alignment	not modelled	9.3	50	**Fold:**Ectatomin subunits **Superfamily:**Ectatomin subunits **Family:**Ectatomin subunits
78	c3sd9B_	Alignment	not modelled	9.3	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of serratia fonticola sfh-i: source of the2 nucleophile in the catalytic mechanism of mono-zinc metallo-beta-3 lactamases

79	c2yqsA_	Alignment	not modelled	9.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
80	c3dmpD_	Alignment	not modelled	9.1	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
81	c3spuB_	Alignment	not modelled	9.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** apo ndm-1 crystal structure
82	d1i5ea_	Alignment	not modelled	8.9	33	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
83	c2i5kB_	Alignment	not modelled	8.9	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of ugp1p
84	c1ychD_	Alignment	not modelled	8.7	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
85	d1i4ja_	Alignment	not modelled	8.6	33	**Fold:**Ribosomal protein L22 **Superfamily:**Ribosomal protein L22 **Family:**Ribosomal protein L22
86	c2ftcM_	Alignment	not modelled	8.5	29	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**mitochondrial ribosomal protein l22 isoform a; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
87	c2apoA_	Alignment	not modelled	8.4	38	**PDB header:**isomerase/rna binding protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
88	c3cskA_	Alignment	not modelled	8.4	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidyl-peptidase 3; **PDBTitle:** structure of dpp iii from saccharomyces cerevisiae
89	d1a4ia2	Alignment	not modelled	8.4	30	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
90	c3mv2A_	Alignment	not modelled	8.3	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
91	c2fs1A_	Alignment	not modelled	8.3	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**psd-1; **PDBTitle:** solution structure of psd-1
92	d1gjsa_	Alignment	not modelled	8.3	33	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**GA module, an albumin-binding domain
93	c2zvrA_	Alignment	not modelled	8.1	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uncharacterized protein tm_0416; **PDBTitle:** crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
94	d2q0ia1	Alignment	not modelled	8.0	35	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like
95	c2zkrr_	Alignment	not modelled	8.0	22	**PDB header:**ribosomal protein/rna **Chain:** R: **PDB Molecule:**rna expansion segment es39 part i; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
96	c1e5dA_	Alignment	not modelled	7.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
97	d1edza2	Alignment	not modelled	7.9	30	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
98	c3adrA_	Alignment	not modelled	7.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein st1585; **PDBTitle:** the first crystal structure of an archaeal metallo-beta-lactamase2 superfamily protein; st1585 from sulfolobus tokodaii
99	c3iz5V_	Alignment	not modelled	7.7	22	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**60s ribosomal protein l17 (l22p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome