Phyre2

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Description	P76091
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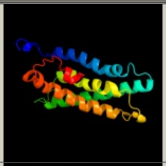
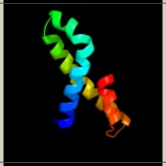
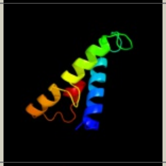
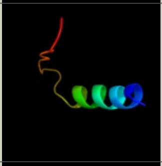
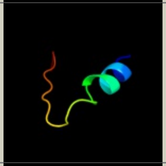
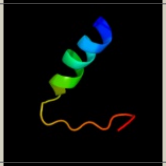
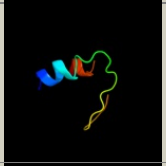
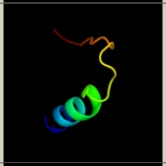
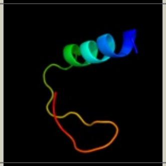
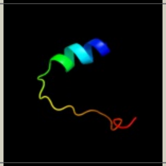
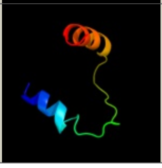
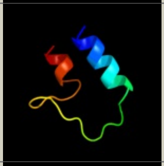
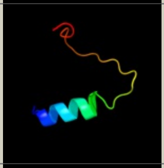
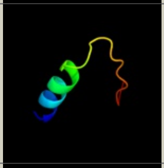
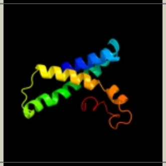
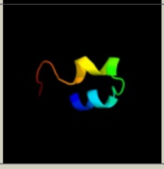
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hd6A_	Alignment		85.1	11	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
2	d1u7ga_	Alignment		69.3	24	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter
3	c2b2hA_	Alignment		57.0	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
4	c3r2uC_	Alignment		56.1	26	**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
5	c2gcuD_	Alignment		53.2	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana2 at1g53580
6	c2xf4A_	Alignment		52.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
7	d2p97a1	Alignment		52.6	30	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
8	c3tp9B_	Alignment		44.1	24	**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	d1mqoa_	Alignment		42.6	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
10	d1qh5a_	Alignment		41.3	7	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
11	d1xm8a_	Alignment		36.6	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)

12	c1vmeB_	Alignment		35.7	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
13	d1znba_	Alignment		33.3	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
14	c3hnnD_	Alignment		33.1	21	**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
15	d2aioa1	Alignment		31.7	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
16	c2q9uB_	Alignment		27.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
17	d2qeda1	Alignment		27.4	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
18	c2zwrA_	Alignment		27.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase superfamily protein; **PDBTitle:** crystal structure of ttha1623 from thermus thermophilus hb8
19	c3c1iA_	Alignment		26.7	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonia channel; **PDBTitle:** substrate binding, deprotonation and selectivity at the2 periplasmic entrance of the e. coli ammonia channel amtb
20	c1ze2B_	Alignment		26.7	33	**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
21	d1ycga2	Alignment	not modelled	26.0	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
22	c1k8wA_	Alignment	not modelled	24.4	33	**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
23	d1bh9b_	Alignment	not modelled	24.3	31	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
24	c2p18A_	Alignment	not modelled	23.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glyoxalase ii; **PDBTitle:** crystal structure of the leishmania infantum glyoxalase ii
25	d1m2xa_	Alignment	not modelled	22.7	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
26	c3l6nA_	Alignment	not modelled	22.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of metallo-beta-lactamase ind-7
27	d1nxca_	Alignment	not modelled	21.9	12	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
28	d2ey4a2	Alignment	not modelled	21.1	39	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
29	d2apoa2	Alignment	not modelled	21.0	38	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase

						Family: Pseudouridine synthase II TruB
30	c1kveA_	Alignment	not modelled	20.4	32	**PDB header:**toxin **Chain:** A: **PDB Molecule:**smk toxin; **PDBTitle:** killer toxin from halotolerant yeast
31	d2gmna1	Alignment	not modelled	20.3	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
32	c3bboU_	Alignment	not modelled	19.8	22	**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
33	c1sgvA_	Alignment	not modelled	19.5	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
34	d1r3ea2	Alignment	not modelled	19.2	30	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
35	d1dl2a_	Alignment	not modelled	19.0	19	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
36	c1s1iN_	Alignment	not modelled	18.8	44	**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.
37	c2yz3B_	Alignment	not modelled	18.0	17	**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
38	c2e55D_	Alignment	not modelled	17.8	38	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
39	c1ychD_	Alignment	not modelled	17.5	12	**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
40	d1e5da2	Alignment	not modelled	17.3	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
41	d1k8wa5	Alignment	not modelled	17.3	30	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
42	c3pisA_	Alignment	not modelled	16.6	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
43	c3sd9B_	Alignment	not modelled	16.6	15	**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
44	d1sgva2	Alignment	not modelled	16.3	30	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
45	c2fhxB_	Alignment	not modelled	16.1	28	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**spm-1; **PDBTitle:** pseudomonas aeruginosa spm-1 metallo-beta-lactamase
46	d2gycq1	Alignment	not modelled	15.8	14	**Fold:**Ribosomal protein L22 **Superfamily:**Ribosomal protein L22 **Family:**Ribosomal protein L22
47	d1jv1a_	Alignment	not modelled	15.7	33	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
48	d2icya2	Alignment	not modelled	15.7	40	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
49	c2zo4A_	Alignment	not modelled	15.7	21	**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
50	d1ko3a_	Alignment	not modelled	15.3	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
51	c1e5dA_	Alignment	not modelled	15.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
52	c3dmpD_	Alignment	not modelled	15.2	33	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
53	d1i5ea_	Alignment	not modelled	15.1	38	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
54	c3uaiA_	Alignment	not modelled	15.0	43	**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
55	c2zvrA_	Alignment	not modelled	15.0	40	**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
56	c3spuB_	Alignment	not modelled	14.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** apo ndm-1 crystal structure
57	c3pesA_	Alignment	not modelled	14.8	67	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein gp49; **PDBTitle:** crystal structure of uncharacterized protein from pseudomonas phage2 yua
58	c2ohiB_	Alignment	not modelled	14.7	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
59	d2nn6h2	Alignment	not modelled	14.4	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
60	c3oc9A_	Alignment	not modelled	14.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
61	c3lvzA_	Alignment	not modelled	14.0	16	**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
62	c2ehjA_	Alignment	not modelled	13.4	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
63	d1k07a_	Alignment	not modelled	13.1	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
64	d1bk8a_	Alignment	not modelled	13.1	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Plant defensins
65	d1jjta_	Alignment	not modelled	12.9	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
66	d1xtta1	Alignment	not modelled	12.7	38	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
67	c2oefA_	Alignment	not modelled	12.7	33	**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
68	d1vmea2	Alignment	not modelled	12.4	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
69	d1vm8a_	Alignment	not modelled	12.4	33	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
70	d2q0ia1	Alignment	not modelled	12.2	32	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like
71	c2ey4A_	Alignment	not modelled	12.1	42	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
72	c2zkru_	Alignment	not modelled	12.1	41	**PDB header:**ribosomal protein/rna **Chain:** U: **PDB Molecule:**rna expansion segment es41; **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
73	c1s1iS_	Alignment	not modelled	12.1	47	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l24-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.
74	c1krfA_	Alignment	not modelled	12.1	18	**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
75	d2ri9a1	Alignment	not modelled	12.1	18	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
76	c3jywN_	Alignment	not modelled	11.8	44	**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
77	d1vqou1	Alignment	not modelled	11.8	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Ribosomal protein L24e
78	d1f0la3	Alignment	not modelled	11.5	67	**Fold:**Toxins' membrane translocation domains **Superfamily:**Diphtheria toxin, middle domain **Family:**Diphtheria toxin, middle domain
						PDB header:isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel;

79	c2qw5B_	Alignment	not modelled	11.5	11	**PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
80	c3adrA_	Alignment	not modelled	11.4	29	**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
81	c3gueB_	Alignment	not modelled	11.1	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)
82	c2q4jB_	Alignment	not modelled	11.0	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
83	d1v9sa1	Alignment	not modelled	10.7	43	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
84	c2i5kB_	Alignment	not modelled	10.6	42	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of ugp1p
85	c3ccjU_	Alignment	not modelled	10.6	24	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**50s ribosomal protein l24e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
86	c4a17Q_	Alignment	not modelled	10.5	33	**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.
87	c2hk1D_	Alignment	not modelled	10.5	25	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**d-psicose 3-epimerase; **PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
88	d1x8ha_	Alignment	not modelled	10.5	8	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
89	d1gu2a_	Alignment	not modelled	10.4	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
90	d1b0aa2	Alignment	not modelled	10.4	36	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
91	c2yqsA_	Alignment	not modelled	10.3	33	**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
92	d1gjsa_	Alignment	not modelled	10.3	44	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**GA module, an albumin-binding domain
93	d1vqor1	Alignment	not modelled	10.1	11	**Fold:**Ribosomal protein L22 **Superfamily:**Ribosomal protein L22 **Family:**Ribosomal protein L22
94	c2apoA_	Alignment	not modelled	10.1	42	**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
95	c4a1eT_	Alignment	not modelled	10.1	24	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**rpl24; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
96	d2foka4	Alignment	not modelled	10.1	8	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease FokI, C-terminal (catalytic) domain
97	d1ztca1	Alignment	not modelled	10.0	23	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**TM0894-like
98	c1ckkB_	Alignment	not modelled	9.8	45	**PDB header:**calmodulin-peptide complex **Chain:** B: **PDB Molecule:**protein (rat ca2+/calmodulin dependent protein **PDBTitle:** calmodulin/rat ca2+/calmodulin dependent protein kinase2 fragment
99	d1ayja_	Alignment	not modelled	9.8	43	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Plant defensins