Phyre^2

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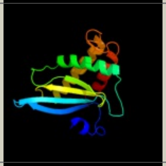
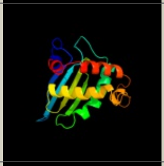
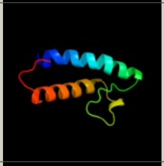
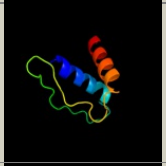
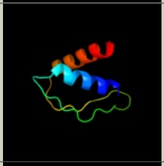
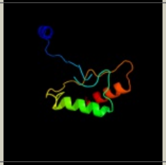
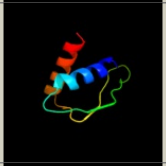
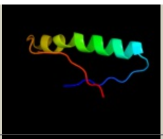
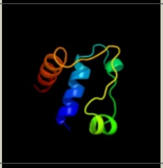
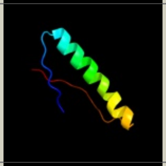
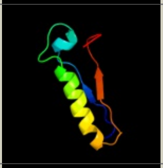
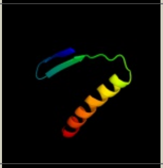
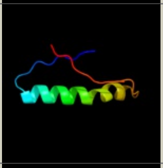
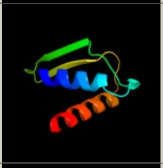
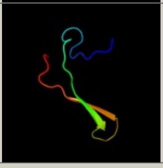
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1j6wa_	Alignment		100.0	66	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
2	d1j6xa_	Alignment		100.0	37	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
3	d1vjea_	Alignment		100.0	46	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
4	d1j98a_	Alignment		100.0	35	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
5	d1k1sa1	Alignment		76.4	19	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
6	c3gqeA_	Alignment		75.6	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of venezuelan equine encephalitis2 virus
7	d1nyra3	Alignment		69.1	21	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
8	d1tkea2	Alignment		63.5	25	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
9	c3k2gA_	Alignment		61.8	16	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
10	c1tkeA_	Alignment		56.7	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
11	d1m5ha2	Alignment		49.4	18	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase

12	d1m5sa2	Alignment		48.0	26	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
13	c1nyqA_	Alignment		44.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
14	d1ryp1_	Alignment		43.2	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
15	d1ftra2	Alignment		42.8	24	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
16	d1fcda2	Alignment		40.8	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
17	c2rp4C_	Alignment		40.2	30	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription factor p53; **PDBTitle:** solution structure of the oligomerization domain in dmp53
18	c1m5sC_	Alignment		39.4	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**formylmethanofuran--tetrahydromethanopterin **PDBTitle:** formylmethanofuran:tetrahydromethanopterin2 fromyltransferase from methanosarcina barkeri
19	c3kewA_	Alignment		38.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhha1 domain protein; **PDBTitle:** crystal structure of probable alanyl-trna-synthase from clostridium2 perfringens
20	c2kvoA_	Alignment		38.0	28	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii reaction center psb28 protein; **PDBTitle:** solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171
21	c1m5hF_	Alignment	not modelled	37.2	18	**PDB header:**transferase **Chain:** F: **PDB Molecule:**formylmethanofuran--tetrahydromethanopterin **PDBTitle:** formylmethanofuran:tetrahydromethanopterin2 formyltransferase from archaeoglobus fulgidus
22	c2fhjD_	Alignment	not modelled	37.0	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**formylmethanofuran--tetrahydromethanopterin **PDBTitle:** crystal structure of formylmethanofuran:2 tetrahydromethanopterin formyltransferase in complex with3 its coenzymes
23	d1hk8a_	Alignment	not modelled	34.1	67	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
24	c1hk8A_	Alignment	not modelled	34.1	67	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
25	c2kdnA_	Alignment	not modelled	32.1	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein pfe0790c; **PDBTitle:** solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
26	d3bvua1	Alignment	not modelled	31.8	12	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**alpha-mannosidase, domain 2
27	d1p42a1	Alignment	not modelled	31.3	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC

28	c3ol0C_	Alignment	not modelled	30.9	43	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
29	d1v9ja_	Alignment	not modelled	24.8	23	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
30	d1v4pa_	Alignment	not modelled	24.4	15	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**AlaX-like
31	c2go4A_	Alignment	not modelled	23.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** crystal structure of aquifex aeolicus lpxc complexed with tu-514
32	c3nzkB_	Alignment	not modelled	19.3	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** structure of lpxc from yersinia enterocolitica complexed with chir0902 inhibitor
33	c2vesA_	Alignment	not modelled	19.3	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** crystal structure of lpxc from pseudomonas aeruginosa2 complexed with the potent bb-78485 inhibitor
34	d1vlia1	Alignment	not modelled	18.8	6	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
35	d1qkia1	Alignment	not modelled	18.3	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
36	d2e1ba2	Alignment	not modelled	17.7	18	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**AlaX-like
37	c3jtzA_	Alignment	not modelled	17.4	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
38	d1r5pa_	Alignment	not modelled	16.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
39	c3p5rB_	Alignment	not modelled	16.5	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**taxadiene synthase; **PDBTitle:** crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
40	d1vg0a2	Alignment	not modelled	16.4	14	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GDI-like
41	d1ppja1	Alignment	not modelled	16.3	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
42	c3ju0A_	Alignment	not modelled	15.9	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
43	c2wyhA_	Alignment	not modelled	15.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase; **PDBTitle:** structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
44	c2dj9A_	Alignment	not modelled	15.3	83	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**growth-blocking peptide; **PDBTitle:** solution structure of growth-blocking peptide of the2 cabbage armyworm, mamestra brassicae
45	c3fwcO_	Alignment	not modelled	15.1	21	**PDB header:**cell cycle, transcription **Chain:** O: **PDB Molecule:**protein sus1; **PDBTitle:** sac3:sus1:cdc31 complex
46	c1qf6A_	Alignment	not modelled	15.0	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
47	d2zdra1	Alignment	not modelled	14.6	17	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
48	d1hr6b1	Alignment	not modelled	14.4	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
49	c2kvtA_	Alignment	not modelled	14.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yaia; **PDBTitle:** solution nmr structure of yaia from escherichia eoli. northeast2 structural genomics target er244
50	d3eeqa1	Alignment	not modelled	14.1	13	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
51	d2fgea4	Alignment	not modelled	14.1	23	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
52	d1xg0b_	Alignment	not modelled	14.0	38	**Fold:**Non-globular alpha+beta subunits of globular proteins **Superfamily:**Non-globular alpha+beta subunits of globular proteins **Family:**Phycoerythrin 545 alpha-subunits
						PDB header:de novo protein

53	c3ogfA_	Alignment	not modelled	14.0	33	**Chain:** A: **PDB Molecule:**de novo designed dimeric trefoil-fold sub-domain which **PDBTitle:** crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
54	d1q5qa_	Alignment	not modelled	13.0	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
55	d1vp8a_	Alignment	not modelled	12.7	23	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
56	d1xg0a_	Alignment	not modelled	12.5	38	**Fold:**Non-globular alpha+beta subunits of globular proteins **Superfamily:**Non-globular alpha+beta subunits of globular proteins **Family:**Phycoerythrin 545 alpha-subunits
57	d1bcca1	Alignment	not modelled	12.4	15	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
58	c2pmfA_	Alignment	not modelled	11.8	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant
59	d3by5a1	Alignment	not modelled	11.8	35	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
60	c3by5A_	Alignment	not modelled	11.8	35	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein; **PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
61	c3siiA_	Alignment	not modelled	11.8	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
62	c1irrA_	Alignment	not modelled	11.5	83	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**paralytic peptide; **PDBTitle:** solution structure of paralytic peptide of the silkworm,2 bombyx mori
63	c1wsuA_	Alignment	not modelled	11.4	10	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** c-terminal domain of elongation factor selb complexed with2 secis rna
64	c1v28A_	Alignment	not modelled	11.4	83	**PDB header:**toxin **Chain:** A: **PDB Molecule:**paralytic peptide; **PDBTitle:** solution structure of paralytic peptide of the wild2 silkmoth, antheraea yamamai
65	d1ivza_	Alignment	not modelled	11.3	15	**Fold:**Ferredoxin-like **Superfamily:**SEA domain **Family:**SEA domain
66	c2djcA_	Alignment	not modelled	11.3	67	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**growth-blocking peptide; **PDBTitle:** solution structure of growth-blocking peptide of the2 tobacco cutworm, spodoptera litura
67	c3hbwA_	Alignment	not modelled	11.0	25	**PDB header:**hormone **Chain:** A: **PDB Molecule:**fibroblast growth factor 13; **PDBTitle:** crystal structure of human fibroblast growth factor2 homologous factor 2a (fhf2a), also referred to as3 fibroblast growth factor 13a (fgf13a)
68	d2w6ka1	Alignment	not modelled	10.5	18	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
69	c1xuzA_	Alignment	not modelled	10.2	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
70	c1vliA_	Alignment	not modelled	10.1	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
71	d1q1ua_	Alignment	not modelled	10.0	8	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
72	c3o3nB_	Alignment	not modelled	9.7	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
73	d1qqla_	Alignment	not modelled	9.5	33	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
74	d1qqka_	Alignment	not modelled	9.3	33	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
75	c2q7aA_	Alignment	not modelled	8.9	33	**PDB header:**heme binding protein **Chain:** A: **PDB Molecule:**cell surface heme-binding protein; **PDBTitle:** crystal structure of the cell surface heme transfer protein shp
76	c1hrlA_	Alignment	not modelled	8.8	67	**PDB header:**toxin **Chain:** A: **PDB Molecule:**paralytic peptide i; **PDBTitle:** structure of a paralytic peptide from an insect, manduca sexta

77	d1osce_	Alignment	not modelled	8.7	29	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
78	d1su7a_	Alignment	not modelled	8.6	17	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
79	c2piaA_	Alignment	not modelled	8.4	43	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
80	d1musa_	Alignment	not modelled	8.4	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
81	c3h20A_	Alignment	not modelled	8.1	17	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein b; **PDBTitle:** crystal structure of primase repb'
82	c2yutA_	Alignment	not modelled	8.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative short-chain oxidoreductase; **PDBTitle:** crystal structure of putative short-chain oxidoreductase tthb094 from2 thermus thermophilus hb8
83	d1kr4a_	Alignment	not modelled	7.6	29	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
84	c3lmaC_	Alignment	not modelled	7.6	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**stage v sporulation protein ad (spovad); **PDBTitle:** crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
85	c1f0cB_	Alignment	not modelled	7.4	41	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**ice inhibitor; **PDBTitle:** structure of the viral serpin crma
86	c3lvtA_	Alignment	not modelled	7.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase, family 38; **PDBTitle:** the crystal structure of a protein in the glycosyl hydrolase2 family 38 from enterococcus faecalis to 2.55a
87	c2wk1A_	Alignment	not modelled	7.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**novp; **PDBTitle:** structure of the o-methyltransferase novp
88	c3osuA_	Alignment	not modelled	7.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of the 3-oxoacyl-acyl carrier protein reductase,2 fabg, from staphylococcus aureus
89	c2dgdD_	Alignment	not modelled	7.0	19	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
90	c2zfhA_	Alignment	not modelled	7.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cuta; **PDBTitle:** crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
91	d1rypl_	Alignment	not modelled	6.8	10	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
92	d1p1la_	Alignment	not modelled	6.7	47	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
93	d1nzaa_	Alignment	not modelled	6.7	29	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
94	d1ukua_	Alignment	not modelled	6.6	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
95	c2e7vA_	Alignment	not modelled	6.5	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transmembrane protease; **PDBTitle:** crystal structure of sea domain of transmembrane protease2 from mus musculus
96	d2nxca1	Alignment	not modelled	6.5	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
97	c1ep3B_	Alignment	not modelled	6.5	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydroorotate dehydrogenase b (pyrk subunit); **PDBTitle:** crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
98	c1xk8A_	Alignment	not modelled	6.5	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**divalent cation tolerant protein cuta; **PDBTitle:** divalent cation tolerant protein cuta from homo sapiens2 o60888
99	d2zfha1	Alignment	not modelled	6.5	29	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)