Phyre2

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Description	P25549
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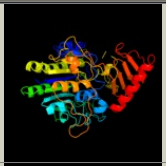
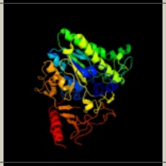
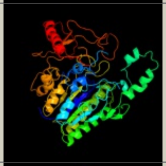
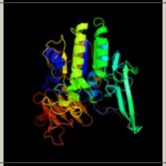
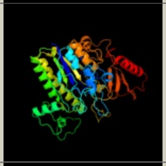
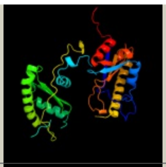
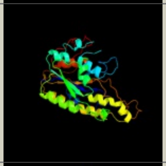
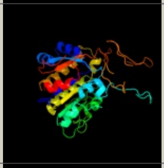
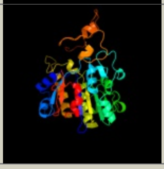
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hdha_	Alignment		100.0	26	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
2	d1auka_	Alignment		100.0	27	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
3	d1p49a_	Alignment		100.0	26	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
4	c3ed4A_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
5	d1fsua_	Alignment		100.0	26	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
6	c2qzuA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
7	c2vqrA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase; **PDBTitle:** crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily
8	c3b5qB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
9	c3lxqB_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp1736; **PDBTitle:** the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
10	c2w8dB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid synthase 2; **PDBTitle:** distinct and essential morphogenic functions for wall- and2 lipo-teichoic acids in bacillus subtilis
11	c2w5tA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.

12	c2zktB_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
13	c3m8yC_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
14	c3q3qA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
15	d1o98a2	Alignment		100.0	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
16	c2gsoB_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
17	c2i09A_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
18	c3szzA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
19	d2i09a1	Alignment		100.0	20	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
20	d1ei6a_	Alignment		100.0	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
21	c2xrgA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
22	c2xr9A_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
23	c1o98A_	Alignment	not modelled	99.7	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
24	c2d1gB_	Alignment	not modelled	99.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
25	c3igzB_	Alignment	not modelled	99.6	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
26	c2iucB_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
27	d1y6va1	Alignment	not modelled	99.4	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
28	c1ew2A_	Alignment	not modelled	99.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase;

						PDBTitle: crystal structure of a human phosphatase
29	d1zeda1	Alignment	not modelled	99.3	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
30	d1k7ha_	Alignment	not modelled	99.2	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
31	c3a52A_	Alignment	not modelled	99.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
32	c2w0yB_	Alignment	not modelled	99.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
33	c2x98A_	Alignment	not modelled	99.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
34	c3e2dB_	Alignment	not modelled	98.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
35	c3iddA_	Alignment	not modelled	94.5	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
36	d1b4ub_	Alignment	not modelled	41.6	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
37	d1xo1a2	Alignment	not modelled	34.1	19	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
38	c3oaaO_	Alignment	not modelled	32.1	21	**PDB header:**hydrolase/transport protein **Chain:** O: **PDB Molecule:**atp synthase gamma chain; **PDBTitle:** structure of the e.coli f1-atp synthase inhibited by subunit epsilon
39	d1okga1	Alignment	not modelled	26.5	13	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
40	d1skyb3	Alignment	not modelled	23.1	36	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
41	d1fx0a3	Alignment	not modelled	23.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
42	d1tfra2	Alignment	not modelled	22.0	31	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
43	c2d0jD_	Alignment	not modelled	21.4	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
44	d1l5oa_	Alignment	not modelled	20.7	30	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
45	c2ihnA_	Alignment	not modelled	19.1	35	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
46	d1fs0g_	Alignment	not modelled	18.6	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
47	c3dqzB_	Alignment	not modelled	18.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein; **PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis2 thaliana
48	c3a5dM_	Alignment	not modelled	17.8	15	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**v-type atp synthase beta chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
49	d2b8ea1	Alignment	not modelled	17.4	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
50	d1j33a_	Alignment	not modelled	17.3	17	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
51	d1skye3	Alignment	not modelled	17.2	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
52	d1dc1a_	Alignment	not modelled	17.0	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BsobI
53	d1mm0a_	Alignment	not modelled	16.7	13	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Insect defensins
						Fold: Nucleotide-diphospho-sugar transferases

54	d3cu0a1	Alignment	not modelled	16.5	27	**Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
55	c3anyB_	Alignment	not modelled	16.2	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
56	c1okgA_	Alignment	not modelled	16.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
57	d1cmwa2	Alignment	not modelled	16.1	42	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
58	d2qalk1	Alignment	not modelled	15.2	31	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
59	c3oaaC_	Alignment	not modelled	15.0	30	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** structure of the e.coli f1-atp synthase inhibited by subunit epsilon
60	d2cz4a1	Alignment	not modelled	14.7	11	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
61	c2k23A_	Alignment	not modelled	14.6	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 2; **PDBTitle:** solution structure analysis of the rlcn2
62	d1v82a_	Alignment	not modelled	14.1	24	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
63	c3absD_	Alignment	not modelled	14.1	19	**PDB header:**lyase **Chain:** D: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
64	c3cagF_	Alignment	not modelled	13.6	15	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
65	d1szpb1	Alignment	not modelled	13.3	21	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
66	d1srva_	Alignment	not modelled	13.1	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
67	d2b6fa1	Alignment	not modelled	13.0	12	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Sulfiredoxin-like
68	c1w0jB_	Alignment	not modelled	12.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase alpha chain heart isoform, **PDBTitle:** beryllium fluoride inhibited bovine f1-atpase
69	c3ereD_	Alignment	not modelled	12.5	15	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
70	c3olhA_	Alignment	not modelled	12.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
71	d1b4ba_	Alignment	not modelled	12.4	15	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
72	c2w6jG_	Alignment	not modelled	12.4	27	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
73	d2p5ma1	Alignment	not modelled	12.3	15	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
74	c3ippA_	Alignment	not modelled	12.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
75	c3icgD_	Alignment	not modelled	12.1	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase d; **PDBTitle:** crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
76	c2qe7C_	Alignment	not modelled	12.0	32	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
77	c2r9vA_	Alignment	not modelled	12.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
78	c3k1tA_	Alignment	not modelled	11.9	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution

79	c3jviA_	Alignment	not modelled	11.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
80	c1kmhA_	Alignment	not modelled	11.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atpase alpha subunit; **PDBTitle:** crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
81	d1exsa_	Alignment	not modelled	11.5	4	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
82	c2pn1A_	Alignment	not modelled	11.3	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoylphosphate synthase large subunit; **PDBTitle:** crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
83	d1we3a2	Alignment	not modelled	11.3	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
84	d1gt1a_	Alignment	not modelled	11.2	18	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
85	d1oela2	Alignment	not modelled	11.2	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
86	d2uubk1	Alignment	not modelled	11.1	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
87	d1dzka_	Alignment	not modelled	11.0	11	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
88	c2dajA_	Alignment	not modelled	11.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa0977 protein; **PDBTitle:** solution structure of the novel identified ubiquitin-like2 domain in the human cobl-like 1 protein
89	c2w6fA_	Alignment	not modelled	10.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha heart isoform, **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 2.
90	c3bijC_	Alignment	not modelled	10.7	11	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein gsu0716; **PDBTitle:** crystal structure of protein gsu0716 from geobacter2 sulfurreducens. northeast structural genomics target gsr13
91	c2c61A_	Alignment	not modelled	10.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a-type atp synthase non-catalytic subunit b; **PDBTitle:** crystal structure of the non-catalytic b subunit of a-type2 atpase from m. mazei go1
92	d2jdia3	Alignment	not modelled	10.5	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
93	c2qe7G_	Alignment	not modelled	10.2	56	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
94	c3d4rE_	Alignment	not modelled	10.1	23	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**domain of unknown function from the pfam-b_34464 family; **PDBTitle:** crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
95	c2fa5B_	Alignment	not modelled	10.1	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator marr/emrr family; **PDBTitle:** the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
96	d1kida_	Alignment	not modelled	10.0	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
97	c3e20C_	Alignment	not modelled	9.9	16	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
98	c3bbnK_	Alignment	not modelled	9.9	29	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**ribosomal protein s11; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
99	d1g8fa3	Alignment	not modelled	9.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain