Phyre2

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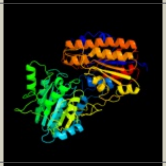
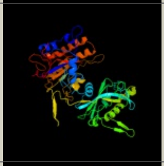
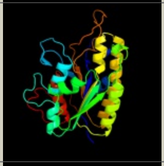
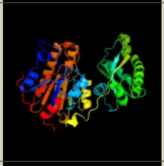
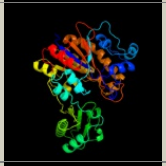
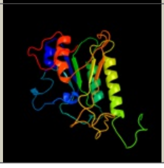
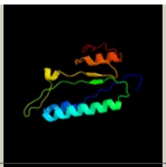
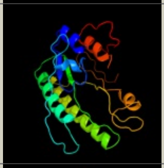
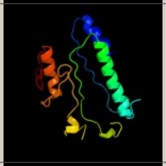
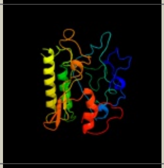
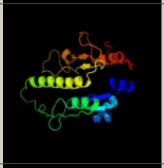
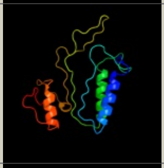
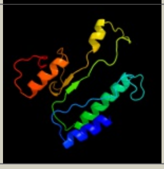
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1o98A_	Alignment		100.0	50	**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
2	c3igzB_	Alignment		100.0	34	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
3	d1o98a1	Alignment		100.0	42	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
4	c3iddA_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
5	d1o98a2	Alignment		100.0	60	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
6	c2zktB_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
7	c2i09A_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
8	c3m8yC_	Alignment		99.9	25	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
9	d2i09a1	Alignment		99.9	26	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
10	c3lxqB_	Alignment		99.8	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
11	d1fsua_	Alignment		99.8	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase

12	c3q3qA_	Alignment		99.8	29	**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
13	d1hdha_	Alignment		99.8	21	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
14	c3b5qB_	Alignment		99.7	21	**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
15	d1auka_	Alignment		99.7	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
16	c2qzuA_	Alignment		99.7	13	**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
17	c3ed4A_	Alignment		99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
18	d1p49a_	Alignment		99.7	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
19	c2vqrA_	Alignment		99.7	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
20	c2w5tA_	Alignment		99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
21	c2xrgA_	Alignment	not modelled	99.7	13	**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	c2w8dB_	Alignment	not modelled	99.7	13	**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
23	c2xr9A_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
24	d1y6va1	Alignment	not modelled	99.5	20	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
25	c2iucB_	Alignment	not modelled	99.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
26	c3a52A_	Alignment	not modelled	99.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
27	c1ew2A_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase
28	d1k7ha_	Alignment	not modelled	99.4	21	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase

29	d1zeda1	Alignment	not modelled	99.4	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
30	c2gsoB_	Alignment	not modelled	99.3	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
31	c2w0yB_	Alignment	not modelled	99.3	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
32	c2x98A_	Alignment	not modelled	99.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
33	c3e2dB_	Alignment	not modelled	99.0	19	**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
34	d1ei6a_	Alignment	not modelled	98.2	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
35	c3szzA_	Alignment	not modelled	97.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
36	c2d1gB_	Alignment	not modelled	97.4	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
37	c3m0zD_	Alignment	not modelled	91.9	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of putative aldolase from klebsiella2 pneumoniae.
38	c3m6yA_	Alignment	not modelled	79.6	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
39	c3muxB_	Alignment	not modelled	75.3	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative 4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
40	c1qzwC_	Alignment	not modelled	47.3	18	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
41	d1vyva2	Alignment	not modelled	46.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
42	c3ib7A_	Alignment	not modelled	46.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
43	c3tovB_	Alignment	not modelled	44.0	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
44	c2j37W_	Alignment	not modelled	43.9	17	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
45	c2iy3A_	Alignment	not modelled	28.9	15	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
46	d2nxfa1	Alignment	not modelled	27.8	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
47	d1vyua2	Alignment	not modelled	26.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
48	d2z3va1	Alignment	not modelled	24.3	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
49	d1iq0a1	Alignment	not modelled	24.0	33	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
50	d1whua_	Alignment	not modelled	23.8	55	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 **Family:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
51	d1o57a1	Alignment	not modelled	23.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
52	d1f7ua1	Alignment	not modelled	23.3	17	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
53	d1ydga_	Alignment	not modelled	22.7	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins

						Family: WrbA-like
54	c2ip1A_	Alignment	not modelled	22.1	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
55	c2j289_	Alignment	not modelled	21.2	15	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
56	c3dm5A_	Alignment	not modelled	20.0	17	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
57	d1pkxa1	Alignment	not modelled	19.9	17	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
58	c4a1oB_	Alignment	not modelled	18.6	12	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
59	d2a9pa1	Alignment	not modelled	17.6	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
60	c3m6mF_	Alignment	not modelled	17.5	26	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
61	d1s8na_	Alignment	not modelled	15.3	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	d1ys7a2	Alignment	not modelled	14.9	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
63	c3cwoX_	Alignment	not modelled	14.4	25	**PDB header:**de novo protein **Chain:** X: **PDB Molecule:**beta/alpha-barrel protein based on 1thf and 1tmy; **PDBTitle:** a beta/alpha-barrel built by the combination of fragments2 from different folds
64	c3oaaO_	Alignment	not modelled	14.0	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
65	d1u0sy_	Alignment	not modelled	14.0	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
66	c2nwqA_	Alignment	not modelled	14.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable short-chain dehydrogenase; **PDBTitle:** short chain dehydrogenase from pseudomonas aeruginosa
67	d1g8fa3	Alignment	not modelled	13.6	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
68	c2vy9A_	Alignment	not modelled	13.2	16	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**anti-sigma-factor antagonist; **PDBTitle:** molecular architecture of the stressosome, a signal2 integration and transduction hub
69	c3qg5D_	Alignment	not modelled	13.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
70	c3dzdA_	Alignment	not modelled	13.2	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
71	d2enda_	Alignment	not modelled	12.6	63	**Fold:**T4 endonuclease V **Superfamily:**T4 endonuclease V **Family:**T4 endonuclease V
72	d1q74a_	Alignment	not modelled	12.6	16	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
73	d2f99a1	Alignment	not modelled	12.6	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
74	c2qy9A_	Alignment	not modelled	11.8	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
75	d2b7oa1	Alignment	not modelled	11.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
76	d1c8ba_	Alignment	not modelled	11.7	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
77	c3hv0A_	Alignment	not modelled	11.6	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
78	c2q8uA_	Alignment	not modelled	11.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative; **PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
						PDB header:oxidoreductase

79	c3lcmB_	Alignment	not modelled	10.6	13	**Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
80	c1iq0A_	Alignment	not modelled	10.3	35	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** thermus thermophilus arginyl-trna synthetase
81	c2j48A_	Alignment	not modelled	10.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
82	c3t8yA_	Alignment	not modelled	10.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
83	c2gwrA_	Alignment	not modelled	9.9	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dna-binding response regulator mtra; **PDBTitle:** crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
84	c2g2qB_	Alignment	not modelled	9.7	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the crystal structure of g4, the poxviral disulfide oxidoreductase2 essential for cytoplasmic disulfide bond formation
85	c3grcD_	Alignment	not modelled	9.5	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
86	c2xmoB_	Alignment	not modelled	9.3	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
87	c2og2A_	Alignment	not modelled	9.3	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
88	c2zwmA_	Alignment	not modelled	9.1	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
89	d1fs0g_	Alignment	not modelled	8.9	15	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
90	c3a0rB_	Alignment	not modelled	8.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
91	d1lpbb2	Alignment	not modelled	8.8	44	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
92	d2qwxa1	Alignment	not modelled	8.8	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
93	d1mb3a_	Alignment	not modelled	8.7	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
94	c3cu5B_	Alignment	not modelled	8.7	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two component transcriptional regulator, arac family; **PDBTitle:** crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
95	c3bh1A_	Alignment	not modelled	8.6	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0371 protein dip2346; **PDBTitle:** crystal structure of protein dip2346 from corynebacterium diphtheriae
96	c2qv0A_	Alignment	not modelled	8.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
97	d1dz3a_	Alignment	not modelled	8.4	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
98	d1hska2	Alignment	not modelled	8.4	23	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
99	c2xokG_	Alignment	not modelled	8.4	33	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** refined structure of yeast f1c10 atpase complex to 3 a2 resolution