Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AFR2
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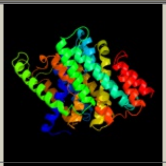
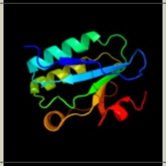
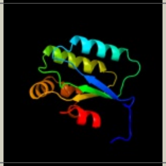
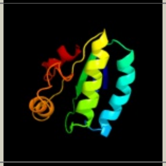
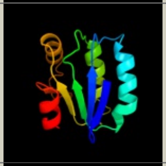
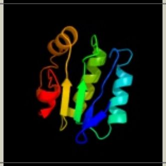
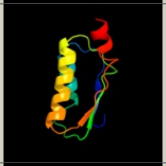
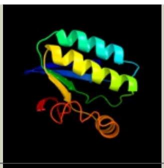
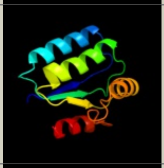
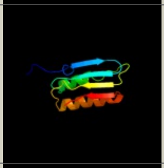
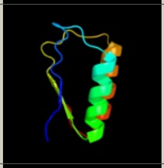
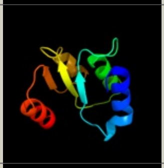
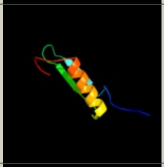
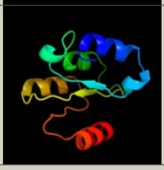
Unique Job ID	db9cf24852b95d1c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qe7A_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uracil permease; **PDBTitle:** crystal structure of uracil transporter--uraa
2	c3ny7A_	Alignment		99.9	98	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sulfate transporter; **PDBTitle:** stas domain of ychm bound to acp
3	c3lloA_	Alignment		99.9	17	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**prestin; **PDBTitle:** crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
4	c3mglA_	Alignment		99.9	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate permease family protein; **PDBTitle:** crystal structure of permease family protein from vibrio2 cholerae
5	c3oirA_	Alignment		99.9	28	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter sulfate transporter family protein; **PDBTitle:** crystal structure of sulfate transporter family protein from wolinella2 succinogenes
6	c2klnA_	Alignment		99.8	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable sulphate-transport transmembrane protein, cog0659; **PDBTitle:** solution structure of stas domain of rv1739c from m. tuberculosis
7	d1auza_	Alignment		99.7	26	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
8	d1th8b_	Alignment		99.7	25	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
9	c3f43A_	Alignment		99.6	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative anti-sigma factor antagonist tm1081; **PDBTitle:** crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
10	c3lklB_	Alignment		99.6	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**antisigma-factor antagonist stas; **PDBTitle:** crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
11	c2vy9A_	Alignment		99.6	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**anti-sigma-factor antagonist; **PDBTitle:** molecular architecture of the stressosome, a signal2 integration and transduction hub

12	d1vc1a_	Alignment		99.5	18	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
13	c3t6oA_	Alignment		99.4	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter/antisigma-factor antagonist stas; **PDBTitle:** the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
14	d1h4xa_	Alignment		99.3	14	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
15	c3ih9A_	Alignment		95.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure analysis of mglu in its tris form
16	c3bezC_	Alignment		74.2	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease 4; **PDBTitle:** crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
17	d2nu7b1	Alignment		72.1	12	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
18	d1mvoa_	Alignment		70.8	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
19	c2dfwA_	Alignment		69.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
20	c3b2nA_	Alignment		68.6	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
21	c3bl4B_	Alignment	not modelled	66.7	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
22	d1l7vc_	Alignment	not modelled	60.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
23	c1yqtA_	Alignment	not modelled	57.4	18	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
24	d2hyda1	Alignment	not modelled	55.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
25	c3jteA_	Alignment	not modelled	55.2	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
26	d1dz3a_	Alignment	not modelled	48.3	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
27	d2q3la1	Alignment	not modelled	48.0	15	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Sfri0576-like
28	c3gfzB_	Alignment	not modelled	46.4	12	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
						PDB header:structural genomics, unknown function

29	c2qy6A_	Alignment	not modelled	45.5	19	**Chain:** A: **PDB Molecule:**upf0209 protein yfck; **PDBTitle:** crystal structure of the n-terminal domain of upf0209 protein yfck2 from escherichia coli o157:h7
30	c2pr7A_	Alignment	not modelled	45.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family; **PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
31	c2deoA_	Alignment	not modelled	43.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**441aa long hypothetical nfed protein; **PDBTitle:** 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
32	c3hv9A_	Alignment	not modelled	43.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
33	c2zwmA_	Alignment	not modelled	42.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
34	d1a04a2	Alignment	not modelled	41.0	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
35	d1tg6a1	Alignment	not modelled	40.7	13	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
36	c3hvbB_	Alignment	not modelled	38.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa
37	d1pf4a1	Alignment	not modelled	37.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
38	c3ozxA_	Alignment	not modelled	36.9	13	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
39	c2yz2B_	Alignment	not modelled	36.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative abc transporter atp-binding protein tm_0222; **PDBTitle:** crystal structure of the abc transporter in the cobalt transport2 system
40	d1ys7a2	Alignment	not modelled	36.0	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	c3i42A_	Alignment	not modelled	35.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey- **PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
42	c3eulB_	Alignment	not modelled	34.0	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**possible nitrate/nitrite response transcriptional **PDBTitle:** structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
43	c2qv0A_	Alignment	not modelled	33.8	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
44	d2awna2	Alignment	not modelled	33.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
45	d1ji0a_	Alignment	not modelled	33.2	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
46	d1u0sy_	Alignment	not modelled	32.9	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	c2q3eH_	Alignment	not modelled	32.6	14	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
48	d2csua3	Alignment	not modelled	31.9	15	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
49	c3cz5B_	Alignment	not modelled	31.7	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two-component response regulator, luxr family; **PDBTitle:** crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
50	d1b0ua_	Alignment	not modelled	30.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
51	c3nhaA_	Alignment	not modelled	30.2	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 6, mitochondrial; **PDBTitle:** nucleotide binding domain of human abcb6 (adp mg bound structure)
52	c2r6fA_	Alignment	not modelled	29.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
53	c2it1B_	Alignment	not modelled	29.0	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin

						PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
54	d1jbea_	Alignment	not modelled	28.4	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
55	c3nhzA_	Alignment	not modelled	28.2	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
56	c3dcmX_	Alignment	not modelled	27.9	2	**PDB header:**transferase **Chain:** X: **PDB Molecule:**uncharacterized protein tm_1570; **PDBTitle:** crystal structure of the thermotoga maritima spout family2 rna-methyltransferase protein tm1570 in complex with s-3 adenosyl-l-methionine
57	c2pcjB_	Alignment	not modelled	27.8	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipoprotein-releasing system atp-binding protein lold; **PDBTitle:** crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
58	d1mv5a_	Alignment	not modelled	27.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
59	d1peya_	Alignment	not modelled	25.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
60	d1krwa_	Alignment	not modelled	25.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	d1s8na_	Alignment	not modelled	25.1	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	d1g6ha_	Alignment	not modelled	23.9	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
63	c2r6oB_	Alignment	not modelled	23.6	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase (ggdef & eal **PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
64	c3hdgE_	Alignment	not modelled	23.5	13	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
65	c3kthD_	Alignment	not modelled	22.8	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** structure of clpp from bacillus subtilis in orthorombic crystal form
66	c2nq2C_	Alignment	not modelled	22.2	10	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**hypothetical abc transporter atp-binding protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
67	d2cbya1	Alignment	not modelled	22.0	9	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
68	d1xhfa1	Alignment	not modelled	22.0	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
69	c2csuB_	Alignment	not modelled	21.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
70	c3hn7A_	Alignment	not modelled	21.3	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
71	c1vciA_	Alignment	not modelled	21.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar-binding transport atp-binding protein; **PDBTitle:** crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
72	d2iw0a1	Alignment	not modelled	21.0	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
73	c3g5uB_	Alignment	not modelled	20.9	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**multidrug resistance protein 1a; **PDBTitle:** structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
74	d1jj7a_	Alignment	not modelled	20.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
75	c1eucB_	Alignment	not modelled	20.7	6	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
76	c3llmB_	Alignment	not modelled	19.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase a; **PDBTitle:** crystal structure analysis of a rna helicase
77	d2ayxa1	Alignment	not modelled	19.7	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

78	c1e1cA_	Alignment	not modelled	19.6	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase alpha chain; **PDBTitle:** methylmalonyl-coa mutase h244a mutant
79	d1zesa1	Alignment	not modelled	19.2	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
80	c1tg6G_	Alignment	not modelled	19.2	13	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**putative atp-dependent clp protease proteolytic subunit; **PDBTitle:** crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
81	c3lpzA_	Alignment	not modelled	19.1	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**get4 (yor164c homolog); **PDBTitle:** crystal structure of c. therm. get4
82	c2rjnA_	Alignment	not modelled	19.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
83	c3a0rB_	Alignment	not modelled	18.8	12	**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)
84	c3nvbA_	Alignment	not modelled	18.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
85	c2cbyG_	Alignment	not modelled	17.7	9	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp-dependent clp protease proteolytic subunit 1; **PDBTitle:** crystal structure of the atp-dependent clp protease2 proteolytic subunit 1 (clpp1) from mycobacterium3 tuberculosis
86	c2zayA_	Alignment	not modelled	17.2	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
87	c3pihA_	Alignment	not modelled	16.9	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
88	d2basa1	Alignment	not modelled	16.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
89	c1wazA_	Alignment	not modelled	16.1	28	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
90	c1oxtB_	Alignment	not modelled	16.0	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, atp binding protein; **PDBTitle:** crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
91	c3s83A_	Alignment	not modelled	16.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
92	c3u5cH_	Alignment	not modelled	15.8	4	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**40s ribosomal protein s7-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
93	d1jb0i_	Alignment	not modelled	15.7	19	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
94	c2d2fA_	Alignment	not modelled	15.5	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
95	c2nu9E_	Alignment	not modelled	15.4	12	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
96	c2hx1D_	Alignment	not modelled	15.3	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had **PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
97	c2pzfB_	Alignment	not modelled	15.3	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cystic fibrosis transmembrane conductance regulator; **PDBTitle:** minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
98	d1heya_	Alignment	not modelled	14.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
99	d1yg6a1	Alignment	not modelled	14.9	8	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit