Phyre2

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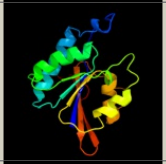
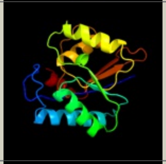
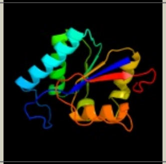
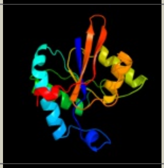
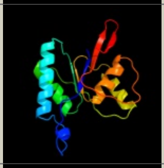
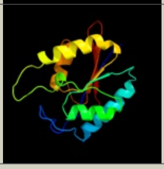
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ujcA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohistidine phosphatase sixa; **PDBTitle:** structure of the protein histidine phosphatase sixa2 complexed with tungstate
2	c3f2iD_	Alignment		100.0	24	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**alr0221 protein; **PDBTitle:** crystal structure of the alr0221 protein from nostoc, northeast2 structural genomics consortium target nsr422.
3	c2rflB_	Alignment		100.0	21	**PDB header:**hydrolase, isomerase **Chain:** B: **PDB Molecule:**putative phosphohistidine phosphatase sixa; **PDBTitle:** crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
4	c3mxoB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase pgam5, mitochondrial; **PDBTitle:** crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
5	d1e58a_	Alignment		100.0	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
6	c1yjxD_	Alignment		100.0	23	**PDB header:**isomerase, hydrolase **Chain:** D: **PDB Molecule:**phosphoglycerate mutase 1; **PDBTitle:** crystal structure of human b type phosphoglycerate mutase
7	d1riia_	Alignment		100.0	20	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
8	d1qhfa_	Alignment		100.0	21	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
9	c2a6pA_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible phosphoglycerate mutase gpm2; **PDBTitle:** structure solution to 2.2 angstrom and functional characterisation of2 the open reading frame rv3214 from mycobacterium tuberculosis
10	c3eznB_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
11	d2hhja1	Alignment		100.0	21	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase

12	c3d8hB_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glycolytic phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
13	c3r7aA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate mutase, putative; **PDBTitle:** crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
14	d1xq9a_	Alignment		100.0	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
15	d3pgma_	Alignment		100.0	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
16	c3d4iD_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sts-2 protein; **PDBTitle:** crystal structure of the 2h-phosphatase domain of sts-2
17	d1fzta_	Alignment		100.0	21	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
18	c3c7tB_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ecdysteroid-phosphate phosphatase; **PDBTitle:** crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
19	c2ikqA_	Alignment		100.0	25	**PDB header:**signaling protein, immune system **Chain:** A: **PDB Molecule:**suppressor of t-cell receptor signaling 1; **PDBTitle:** crystal structure of mouse sts-1 pgm domain in complex with phosphate
20	d1tipa_	Alignment		100.0	20	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
21	c3hjgB_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-ribazole-5'-phosphate phosphatase **PDBTitle:** crystal structure of putative alpha-ribazole-5'-phosphate2 phosphatase cobc from vibrio parahaemolyticus
22	c3dcyA_	Alignment	not modelled	100.0	21	**PDB header:**apoptosis regulator **Chain:** A: **PDB Molecule:**regulator protein; **PDBTitle:** crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
23	c3ll4B_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ykr043c; **PDBTitle:** structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
24	c3fjyB_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
25	d1v37a_	Alignment	not modelled	99.9	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
26	c3f3kA_	Alignment	not modelled	99.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ykr043c; **PDBTitle:** the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
27	c3e9eB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zgc:56074; **PDBTitle:** structure of full-length h11a mutant form of tigar from danio rerio
28	c2qniA_	Alignment	not modelled	99.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299

29	d1h2ea_	Alignment	not modelled	99.9	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
30	d1bifa2	Alignment	not modelled	99.9	20	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
31	c2i1vB_	Alignment	not modelled	99.9	20	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
32	d1k6ma2	Alignment	not modelled	99.9	20	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
33	c1k6mA_	Alignment	not modelled	99.9	22	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
34	c1bifA_	Alignment	not modelled	99.9	23	**PDB header:**bifunctional enzyme **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; **PDBTitle:** 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
35	c3eozB_	Alignment	not modelled	99.9	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
36	c2glcA_	Alignment	not modelled	98.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine acid phosphatase; **PDBTitle:** structure of francisella tularensis histidine acid2 phosphatase bound to orthovanadate
37	d1nd6a_	Alignment	not modelled	97.9	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
38	d1rpaa_	Alignment	not modelled	97.9	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
39	d1ihpa_	Alignment	not modelled	97.8	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
40	c2wniC_	Alignment	not modelled	97.7	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-phytase; **PDBTitle:** crystal structure analysis of klebsiella sp asr1 phytase
41	d1nt4a_	Alignment	not modelled	97.7	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
42	d1dkla_	Alignment	not modelled	97.6	25	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
43	d1qwoa_	Alignment	not modelled	97.4	15	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
44	d1qfxa_	Alignment	not modelled	97.3	20	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
45	c2gfiB_	Alignment	not modelled	96.8	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phytase; **PDBTitle:** crystal structure of the phytase from d. castellii at 2.3 a
46	c3nzeB_	Alignment	not modelled	69.1	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator, sugar-binding family; **PDBTitle:** the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
47	c3bk7A_	Alignment	not modelled	37.2	26	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
48	d1b5ta_	Alignment	not modelled	31.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
49	c2w48D_	Alignment	not modelled	30.0	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
50	d1lbqa_	Alignment	not modelled	27.2	15	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
51	d1l2ta_	Alignment	not modelled	25.2	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
52	c3efhB_	Alignment	not modelled	20.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
53	d2c4ka2	Alignment	not modelled	18.4	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
54	c3ss6B_	Alignment	not modelled	16.8	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
						Fold:P-loop containing nucleoside triphosphate hydrolases

55	d1cr2a_	Alignment	not modelled	16.3	12	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
56	c3ozxA_	Alignment	not modelled	14.9	23	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
57	d1dkua2	Alignment	not modelled	14.8	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
58	c3rfuC_	Alignment	not modelled	14.5	16	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
59	c1yqtA_	Alignment	not modelled	14.3	24	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
60	c1f2uD_	Alignment	not modelled	13.9	21	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
61	c3dhwC_	Alignment	not modelled	13.3	17	**PDB header:**membrane protein/hydrolase **Chain:** C: **PDB Molecule:**methionine import atp-binding protein metn; **PDBTitle:** crystal structure of methionine importer metni
62	d1j98a_	Alignment	not modelled	12.7	16	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
63	d3b48a1	Alignment	not modelled	12.7	22	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
64	c3ox4D_	Alignment	not modelled	12.7	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
65	d1vbka2	Alignment	not modelled	12.7	50	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
66	c2d62A_	Alignment	not modelled	12.2	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**multiple sugar-binding transport atp-binding **PDBTitle:** crystal structure of multiple sugar binding transport atp-2 binding protein
67	c1yveK_	Alignment	not modelled	12.2	13	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**acetohydroxy acid isomeroreductase; **PDBTitle:** acetohydroxy acid isomeroreductase complexed with nadph,2 magnesium and inhibitor ipoha (n-hydroxy-n-3 isopropyloxamate)
68	d3dhwc1	Alignment	not modelled	12.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
69	c2c4kD_	Alignment	not modelled	11.9	17	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
70	c2fmoA_	Alignment	not modelled	11.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate reductase; **PDBTitle:** ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
71	d1v93a_	Alignment	not modelled	11.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
72	c3gd7C_	Alignment	not modelled	11.1	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fusion complex of cystic fibrosis transmembrane **PDBTitle:** crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)
73	d1vlja_	Alignment	not modelled	10.6	15	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
74	d1oxxk2	Alignment	not modelled	10.5	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
75	d1rrma_	Alignment	not modelled	9.9	13	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
76	c3lopA_	Alignment	not modelled	9.1	12	**PDB header:**substrate binding protein **Chain:** A: **PDB Molecule:**substrate binding periplasmic protein; **PDBTitle:** crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
77	c1vciA_	Alignment	not modelled	9.0	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
78	c1q1bD_	Alignment	not modelled	9.0	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**maltose/maltodextrin transport atp-binding protein malk; **PDBTitle:** crystal structure of e. coli malk in the nucleotide-free form
79	c2ygrD_	Alignment	not modelled	8.9	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a;

						PDBTitle: mycobacterium tuberculosis uvra
80	d1su7a_	Alignment	not modelled	8.5	15	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
81	c1dkrB_	Alignment	not modelled	8.4	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
82	d2obba1	Alignment	not modelled	8.4	8	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
83	c2nq2C_	Alignment	not modelled	8.3	21	**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.
84	d1vjea_	Alignment	not modelled	8.1	30	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
85	c3bfjK_	Alignment	not modelled	8.0	9	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
86	c2ibyD_	Alignment	not modelled	7.9	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystallographic and kinetic studies of human mitochondrial2 acetoacetyl-coa thiolase (t2): the importance of potassium and3 chloride for its structure and function
87	c3fvqB_	Alignment	not modelled	7.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fe(3+) ions import atp-binding protein fbpc; **PDBTitle:** crystal structure of the nucleotide binding domain fbpc2 complexed with atp
88	d1g2912	Alignment	not modelled	7.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
89	d3d31a2	Alignment	not modelled	7.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
90	c3hruA_	Alignment	not modelled	7.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
91	c1u9yD_	Alignment	not modelled	7.1	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
92	c3sg0A_	Alignment	not modelled	7.1	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
93	c3lfhF_	Alignment	not modelled	7.1	29	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
94	c2it1B_	Alignment	not modelled	7.0	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin **PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii
95	d1jb7a3	Alignment	not modelled	7.0	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
96	d3beda1	Alignment	not modelled	7.0	18	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
97	d1oaoa_	Alignment	not modelled	6.5	13	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
98	c3gfoA_	Alignment	not modelled	6.5	19	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**cobalt import atp-binding protein cbio 1; **PDBTitle:** structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.
99	d2awna2	Alignment	not modelled	6.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like