Phyre²

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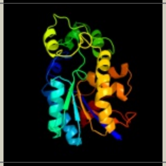
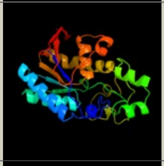
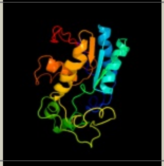
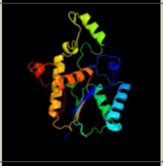
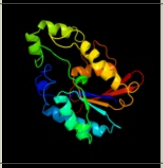
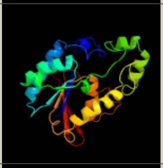
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e58a_	Alignment		100.0	99	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
2	d1xq9a_	Alignment		100.0	60	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
3	c1yjxD_	Alignment		100.0	58	**PDB header:**isomerase, hydrolase **Chain:** D: **PDB Molecule:**phosphoglycerate mutase 1; **PDBTitle:** crystal structure of human b type phosphoglycerate mutase
4	d1qhfa_	Alignment		100.0	54	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
5	d2hhja1	Alignment		100.0	46	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
6	c3eznB_	Alignment		100.0	65	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
7	d1riia_	Alignment		100.0	50	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
8	c3d8hB_	Alignment		100.0	58	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glycolytic phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
9	d3pgma_	Alignment		100.0	51	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
10	d1fzta_	Alignment		100.0	51	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
11	c3r7aA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate mutase, putative; **PDBTitle:** crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne

12	c1k6mA_	Alignment		100.0	31	**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
13	c3ll4B_	Alignment		100.0	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
14	c2i1vB_	Alignment		100.0	31	**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
15	c1bifA_	Alignment		100.0	27	**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
16	c3f3kA_	Alignment		100.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ykr043c; **PDBTitle:** the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
17	d1bifa2	Alignment		100.0	27	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
18	c3dcyA_	Alignment		100.0	28	**PDB header:**apoptosis regulator **Chain:** A: **PDB Molecule:**regulator protein; **PDBTitle:** crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
19	c2a6pA_	Alignment		100.0	27	**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
20	d1h2ea_	Alignment		100.0	28	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
21	d1k6ma2	Alignment	not modelled	100.0	31	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
22	c3e9eB_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zgc:56074; **PDBTitle:** structure of full-length h11a mutant form of tigar from danio rerio
23	d1tipa_	Alignment	not modelled	100.0	29	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
24	c3d4iD_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sts-2 protein; **PDBTitle:** crystal structure of the 2h-phosphatase domain of sts-2
25	c2ikqA_	Alignment	not modelled	100.0	23	**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
26	c3mxoB_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase pgam5, mitochondrial; **PDBTitle:** crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
27	c3hjgB_	Alignment	not modelled	100.0	21	**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
28	c3c7tB_	Alignment	not modelled	100.0	22	**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
29	c2qniA_	Alignment	not modelled	100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
30	d1v37a_	Alignment	not modelled	100.0	29	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
31	c3eozB_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
32	c1ujcA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohistidine phosphatase sixa; **PDBTitle:** structure of the protein histidine phosphatase sixa2 complexed with tungstate
33	c2rflB_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase, isomerase **Chain:** B: **PDB Molecule:**putative phosphohistidine phosphatase sixa; **PDBTitle:** crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
34	c3f2iD_	Alignment	not modelled	100.0	26	**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.
35	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
36	d1nd6a_	Alignment	not modelled	98.7	14	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
37	c2glcA_	Alignment	not modelled	98.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine acid phosphatase; **PDBTitle:** structure of francisella tularensis histidine acid2 phosphatase bound to orthovanadate
38	d1rpaa_	Alignment	not modelled	98.1	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
39	d1ihpa_	Alignment	not modelled	97.9	26	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
40	c2wniC_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-phytase; **PDBTitle:** crystal structure analysis of klebsiella sp asr1 phytase
41	d1dkla_	Alignment	not modelled	97.7	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
42	d1qfxa_	Alignment	not modelled	97.7	24	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
43	d1qwoa_	Alignment	not modelled	97.6	14	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
44	d1nt4a_	Alignment	not modelled	97.6	20	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
45	c2gfiB_	Alignment	not modelled	97.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phytase; **PDBTitle:** crystal structure of the phytase from d. castellii at 2.3 a
46	c2xt6B_	Alignment	not modelled	60.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
47	c2yicC_	Alignment	not modelled	45.3	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
48	d1vjea_	Alignment	not modelled	23.7	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
49	c3lfhF_	Alignment	not modelled	22.7	26	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
50	d1ohea1	Alignment	not modelled	21.9	8	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
51	c3u7vA_	Alignment	not modelled	21.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
52	c1xb4C_	Alignment	not modelled	17.1	13	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**hypothetical 23.6 kda protein in yuh1-ura8 **PDBTitle:** crystal structure of subunit vps25 of the endosomal2 trafficking complex escrt-ii
53	d1j98a_	Alignment	not modelled	16.0	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
54	d1jl3a_	Alignment	not modelled	15.9	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein

						phosphatases
55	c2jzcA_	Alignment	not modelled	13.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine transferase subunit **PDBTitle:** nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
56	d1tiaa_	Alignment	not modelled	13.5	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
57	d1xb4a2	Alignment	not modelled	13.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
58	c3g7nA_	Alignment	not modelled	12.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3
59	d1p9oa_	Alignment	not modelled	12.4	18	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
60	d3tgla_	Alignment	not modelled	12.3	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
61	c3mtqA_	Alignment	not modelled	11.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphoenolpyruvate-dependent sugar **PDBTitle:** crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
62	d1dg9a_	Alignment	not modelled	11.4	20	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
63	d3c70a1	Alignment	not modelled	11.3	40	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
64	d2hk6a1	Alignment	not modelled	10.8	12	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
65	d1tiba_	Alignment	not modelled	10.7	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
66	c2wmyH_	Alignment	not modelled	10.4	15	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**putative acid phosphatase wzb; **PDBTitle:** crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
67	c3o0dF_	Alignment	not modelled	9.5	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
68	d2vcha1	Alignment	not modelled	9.4	10	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
69	c3ngmB_	Alignment	not modelled	9.4	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**extracellular lipase; **PDBTitle:** crystal structure of lipase from gibberella zeae
70	d2acva1	Alignment	not modelled	9.3	10	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
71	d1npya1	Alignment	not modelled	9.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
72	c2olkD_	Alignment	not modelled	9.2	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acid abc transporter; **PDBTitle:** abc protein artp in complex with adp-beta-s
73	c2gwoC_	Alignment	not modelled	8.6	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dual specificity protein phosphatase 13; **PDBTitle:** crystal structure of tmdp
74	d3beda1	Alignment	not modelled	8.5	18	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
75	c2jh3C_	Alignment	not modelled	8.4	23	**PDB header:**ribosomal protein **Chain:** C: **PDB Molecule:**ribosomal protein s2-related protein; **PDBTitle:** the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
76	d1pdoa_	Alignment	not modelled	8.3	28	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
77	c3efhB_	Alignment	not modelled	8.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
78	c3cmmA_	Alignment	not modelled	8.2	18	**PDB header:**ligase/protein binding **Chain:** A: **PDB Molecule:**ubiquitin-activating enzyme e1 1; **PDBTitle:** crystal structure of the uba1-ubiquitin complex
79	c2ri0B_	Alignment	not modelled	8.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans

80	c2zqeA_	Alignment	not modelled	8.2	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
81	c1f0cB_	Alignment	not modelled	8.0	33	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**ice inhibitor; **PDBTitle:** structure of the viral serpin crma
82	c2o6lA_	Alignment	not modelled	8.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucuronosyltransferase 2b7; **PDBTitle:** crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
83	c3hbjA_	Alignment	not modelled	7.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**flavonoid 3-o-glucosyltransferase; **PDBTitle:** structure of ugt78g1 complexed with udp
84	c2gi4A_	Alignment	not modelled	7.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
85	c1yqtA_	Alignment	not modelled	7.2	17	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
86	c3quaA_	Alignment	not modelled	7.1	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis
87	c2e0tA_	Alignment	not modelled	7.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 26; **PDBTitle:** crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
88	d3b48a1	Alignment	not modelled	6.8	10	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
89	c2ijoA_	Alignment	not modelled	6.5	28	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** crystal structure of the west nile virus ns2b-ns3 protease2 complexed with bovine pancreatic trypsin inhibitor
90	c3e90C_	Alignment	not modelled	6.5	28	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ns2b cofactor; **PDBTitle:** west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
91	c3iabB_	Alignment	not modelled	6.4	8	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**ribonucleases p/mrp protein subunit pop7; **PDBTitle:** crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
92	c3lkwA_	Alignment	not modelled	6.3	25	**PDB header:**viral protein,hydrolase **Chain:** A: **PDB Molecule:**fusion protein of nonstructural protein 2b and **PDBTitle:** crystal structure of dengue virus 1 ns2b/ns3 protease active2 site mutant
93	c2fekA_	Alignment	not modelled	6.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
94	c1u2pA_	Alignment	not modelled	6.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
95	d1d1qa_	Alignment	not modelled	6.0	26	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
96	c1f2uD_	Alignment	not modelled	6.0	17	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
97	c2d2fA_	Alignment	not modelled	5.8	6	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
98	c2imgA_	Alignment	not modelled	5.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 23; **PDBTitle:** crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
99	c2wgpA_	Alignment	not modelled	5.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 14; **PDBTitle:** crystal structure of human dual specificity phosphatase 14