Phyre2

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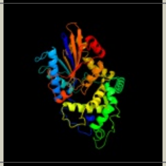
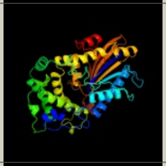
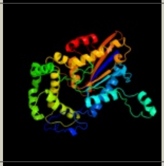
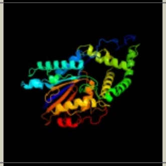
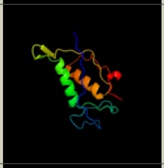
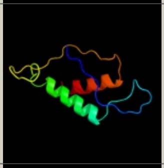
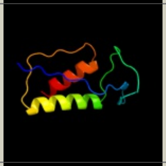
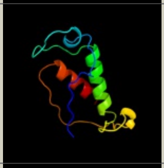
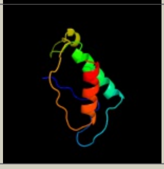
Description	P07102
Date	Thu Jan 5 11:00:08 GMT 2012
Unique Job ID	6fa11ac28930314e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dkla_	Alignment		100.0	100	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
2	d1nt4a_	Alignment		100.0	31	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
3	c2wniC_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-phytase; **PDBTitle:** crystal structure analysis of klebsiella sp asr1 phytase
4	d1rpaa_	Alignment		100.0	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
5	c2glcA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine acid phosphatase; **PDBTitle:** structure of francisella tularensis histidine acid2 phosphatase bound to orthovanadate
6	d1nd6a_	Alignment		100.0	20	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
7	d1ihpa_	Alignment		100.0	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
8	d1qfxa_	Alignment		100.0	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
9	c2gfiB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phytase; **PDBTitle:** crystal structure of the phytase from d. castellii at 2.3 a
10	d1qwoa_	Alignment		100.0	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
11	c2ikqA_	Alignment		98.6	15	**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

12	c3d4iD_	Alignment		98.4	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sts-2 protein; **PDBTitle:** crystal structure of the 2h-phosphatase domain of sts-2
13	c3c7tB_	Alignment		98.2	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
14	c1ujcA_	Alignment		98.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohistidine phosphatase sixa; **PDBTitle:** structure of the protein histidine phosphatase sixa2 complexed with tungstate
15	c3eznB_	Alignment		98.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
16	c1yjxD_	Alignment		97.9	22	**PDB header:**isomerase, hydrolase **Chain:** D: **PDB Molecule:**phosphoglycerate mutase 1; **PDBTitle:** crystal structure of human b type phosphoglycerate mutase
17	d1xq9a_	Alignment		97.8	23	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
18	d1e58a_	Alignment		97.8	16	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
19	d3pgma_	Alignment		97.8	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
20	d1qhfa_	Alignment		97.8	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
21	d1riia_	Alignment	not modelled	97.8	16	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
22	c3ll4B_	Alignment	not modelled	97.8	20	**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
23	c2i1vB_	Alignment	not modelled	97.7	17	**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
24	d1fzta_	Alignment	not modelled	97.7	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
25	c3d8hB_	Alignment	not modelled	97.7	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glycolytic phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
26	d1k6ma2	Alignment	not modelled	97.7	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
27	c2rflB_	Alignment	not modelled	97.6	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
28	c3f3kA_	Alignment	not modelled	97.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ykr043c; **PDBTitle:** the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.

29	c2a6pA_	Alignment	not modelled	97.6	23	**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
30	c3f2iD_	Alignment	not modelled	97.6	21	**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.
31	c3dcyA_	Alignment	not modelled	97.6	16	**PDB header:**apoptosis regulator **Chain:** A: **PDB Molecule:**regulator protein; **PDBTitle:** crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
32	c3r7aA_	Alignment	not modelled	97.5	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate mutase, putative; **PDBTitle:** crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
33	c1k6mA_	Alignment	not modelled	97.5	19	**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	d1bifa2	Alignment	not modelled	97.5	21	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
35	c3mxoB_	Alignment	not modelled	97.5	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase pgam5, mitochondrial; **PDBTitle:** crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
36	c3e9eB_	Alignment	not modelled	97.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zgc:56074; **PDBTitle:** structure of full-length h11a mutant form of tigar from danio rerio
37	d1tipa_	Alignment	not modelled	97.4	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
38	c3eozB_	Alignment	not modelled	97.4	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
39	d2hhja1	Alignment	not modelled	97.4	16	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
40	c1bifA_	Alignment	not modelled	97.4	21	**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
41	c3fjyB_	Alignment	not modelled	97.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
42	c2qniA_	Alignment	not modelled	97.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
43	d1v37a_	Alignment	not modelled	96.7	23	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
44	c3hjgB_	Alignment	not modelled	96.7	12	**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
45	d1h2ea_	Alignment	not modelled	96.7	27	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
46	c2l3hA_	Alignment	not modelled	68.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prostatic acid phosphatase; **PDBTitle:** nmr structure in a membrane environment reveals putative amyloidogenic2 regions of the sevi precursor peptide pap248-286
47	d1p2za2	Alignment	not modelled	21.8	31	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Adenovirus hexon
48	d1rhoa_	Alignment	not modelled	13.1	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
49	d1fsoa_	Alignment	not modelled	12.9	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
50	d1ajwa_	Alignment	not modelled	12.9	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
51	c2k87A_	Alignment	not modelled	12.8	13	**PDB header:**viral protein, rna binding protein **Chain:** A: **PDB Molecule:**non-structural protein 3 of replicase polyprotein 1a; **PDBTitle:** nmr structure of a putative rna binding protein (sars1) from sars2 coronavirus
52	d1mg7a1	Alignment	not modelled	11.2	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Early switch protein XOL-1, N-terminal domain
53	c2bviK_	Alignment	not modelled	11.2	30	**PDB header:**virus **Chain:** K: **PDB Molecule:**hexon protein; **PDBTitle:** the quasi-atomic model of human adenovirus type 52 capsid (part 2)

54	c2k6uA_	Alignment	not modelled	10.9	27	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like 3 a chain; **PDBTitle:** the solution structure of a conformationally restricted2 fully active derivative of the human relaxin-like factor3 (rlf)
55	d1doab_	Alignment	not modelled	10.7	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
56	c2h8bA_	Alignment	not modelled	10.5	27	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**insulin-like 3; **PDBTitle:** solution structure of insl3
57	d1kmta_	Alignment	not modelled	10.1	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
58	d1ds6b_	Alignment	not modelled	8.5	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
59	d1hh4e_	Alignment	not modelled	8.3	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
60	c2k6tA_	Alignment	not modelled	8.3	27	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like 3 a chain; **PDBTitle:** solution structure of the relaxin-like factor
61	c1mg7B_	Alignment	not modelled	7.4	20	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**early switch protein xol-1 2.2k splice form; **PDBTitle:** crystal structure of xol-1
62	c2qz5A_	Alignment	not modelled	6.0	10	**PDB header:**signaling protein, lipid binding protein **Chain:** A: **PDB Molecule:**axin interactor, dorsalization associated **PDBTitle:** crystal structure of the c-terminal domain of aida
63	d1v7za_	Alignment	not modelled	5.7	21	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
64	d1egaa2	Alignment	not modelled	5.6	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
65	d2zdra2	Alignment	not modelled	5.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like