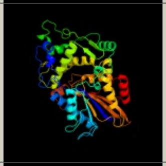
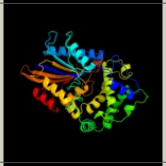
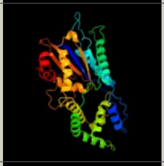
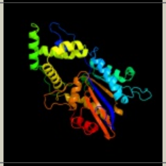
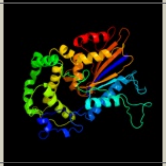
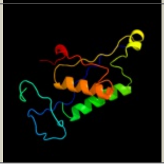
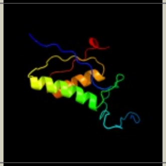
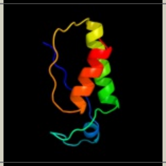
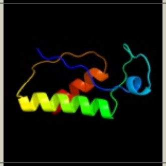
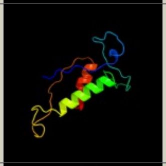
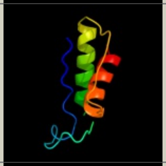
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P19926
Date	Thu Jan 5 11:37:37 GMT 2012
Unique Job ID	5e6648266397b89e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nt4a_	Alignment		100.0	100	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
2	d1dkla_	Alignment		100.0	32	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
3	c2wniC_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-phytase; **PDBTitle:** crystal structure analysis of klebsiella sp asr1 phytase
4	d1ihpa_	Alignment		100.0	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
5	d1qfxa_	Alignment		100.0	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
6	c2gfiB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phytase; **PDBTitle:** crystal structure of the phytase from d. castellii at 2.3 a
7	c2glcA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine acid phosphatase; **PDBTitle:** structure of francisella tularensis histidine acid2 phosphatase bound to orthovanadate
8	d1rpaa_	Alignment		100.0	21	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
9	d1nd6a_	Alignment		100.0	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
10	d1qwoa_	Alignment		100.0	14	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
11	c2ikqA_	Alignment		98.5	16	**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	14	**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	21	**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		97.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohistidine phosphatase sixa; **PDBTitle:** structure of the protein histidine phosphatase sixa2 complexed with tungstate
15	c1yjxD_	Alignment		97.9	19	**PDB header:**isomerase, hydrolase **Chain:** D: **PDB Molecule:**phosphoglycerate mutase 1; **PDBTitle:** crystal structure of human b type phosphoglycerate mutase
16	c3eznB_	Alignment		97.9	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
17	d1xq9a_	Alignment		97.8	29	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
18	d3pgma_	Alignment		97.8	23	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
19	d1e58a_	Alignment		97.7	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
20	d1qhfa_	Alignment		97.7	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
21	d1riia_	Alignment	not modelled	97.7	29	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
22	c2rflB_	Alignment	not modelled	97.7	16	**PDB header:**hydrolase, isomerase **Chain:** B: **PDB Molecule:**putative phosphohistidine phosphatase sixa; **PDBTitle:** crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
23	c3f2iD_	Alignment	not modelled	97.7	20	**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.
24	c3d8hB_	Alignment	not modelled	97.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glycolytic phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
25	c3dcyA_	Alignment	not modelled	97.7	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.
26	d1fzta_	Alignment	not modelled	97.6	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
27	c3ll4B_	Alignment	not modelled	97.6	14	**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
28	c3r7aA_	Alignment	not modelled	97.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate mutase, putative; **PDBTitle:** crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne

29	d1k6ma2	Alignment	not modelled	97.5	16	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
30	c2a6pA_	Alignment	not modelled	97.5	22	**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
31	c3mxoB_	Alignment	not modelled	97.5	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)
32	c3e9eB_	Alignment	not modelled	97.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zgc:56074; **PDBTitle:** structure of full-length h11a mutant form of tigar from danio rerio
33	c3fjyB_	Alignment	not modelled	97.4	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
34	c3eozB_	Alignment	not modelled	97.4	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
35	c2i1vB_	Alignment	not modelled	97.4	19	**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
36	d2hhja1	Alignment	not modelled	97.4	15	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
37	d1bifa2	Alignment	not modelled	97.3	16	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
38	c3f3kA_	Alignment	not modelled	97.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ykr043c; **PDBTitle:** the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
39	c1k6mA_	Alignment	not modelled	97.2	16	**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
40	d1tipa_	Alignment	not modelled	97.2	15	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
41	c2qniA_	Alignment	not modelled	97.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
42	c1bifA_	Alignment	not modelled	97.0	16	**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
43	d1h2ea_	Alignment	not modelled	96.8	25	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
44	c3hjgB_	Alignment	not modelled	96.4	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	d1v37a_	Alignment	not modelled	96.3	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
46	c2l3hA_	Alignment	not modelled	61.4	22	**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	d1mg7a1	Alignment	not modelled	12.9	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Early switch protein XOL-1, N-terminal domain
48	d1avsa_	Alignment	not modelled	10.5	17	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
49	d3bida1	Alignment	not modelled	10.1	19	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
50	d1h6pa_	Alignment	not modelled	9.3	5	**Fold:**Telomeric repeat binding factor (TRF) dimerisation domain **Superfamily:**Telomeric repeat binding factor (TRF) dimerisation domain **Family:**Telomeric repeat binding factor (TRF) dimerisation domain
51	d2ca1a1	Alignment	not modelled	9.3	13	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
52	d1rhoa_	Alignment	not modelled	9.0	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
53	d1fsoa_	Alignment	not modelled	9.0	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
						PDB header:gene regulation

54	c1mg7B_	Alignment	not modelled	9.0	20	**Chain:** B: **PDB Molecule:**early switch protein xol-1 2.2k splice form; **PDBTitle:** crystal structure of xol-1
55	d1p2za2	Alignment	not modelled	8.7	38	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Adenovirus hexon
56	d2k7ia1	Alignment	not modelled	8.7	20	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
57	c2k7iB_	Alignment	not modelled	8.7	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0339 protein atu0232; **PDBTitle:** solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
58	d1ajwa_	Alignment	not modelled	8.5	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
59	d1ehia1	Alignment	not modelled	8.4	24	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
60	d2k8ea1	Alignment	not modelled	8.1	19	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
61	d2k49a2	Alignment	not modelled	7.8	6	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
62	d1doab_	Alignment	not modelled	7.6	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
63	d1kmta_	Alignment	not modelled	7.4	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
64	c2z4tA_	Alignment	not modelled	6.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-galactoside alpha-2,6-sialyltransferase; **PDBTitle:** crystal structure of vibrionaceae photobacterium sp. jt-ish-224 2,6-2 sialyltransferase in a ternary complex with donor product cmp and3 accepter substrate lactose
65	d1hh4e_	Alignment	not modelled	6.1	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
66	d1vk9a_	Alignment	not modelled	6.0	33	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Hypothetical protein TM1506
67	d1ds6b_	Alignment	not modelled	5.8	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
68	d1v7za_	Alignment	not modelled	5.6	18	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
69	d2odka1	Alignment	not modelled	5.6	29	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
70	d1wrka1	Alignment	not modelled	5.3	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like