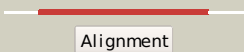

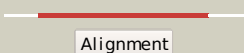

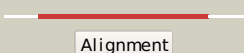

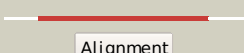



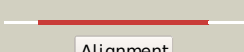

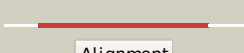

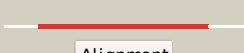













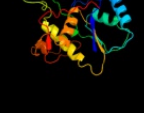

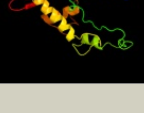


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h2ea_	 Alignment		100.0	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
2	d1e58a_	 Alignment		100.0	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
3	c1yjd_	 Alignment		100.0	23	PDB header: isomerase, hydrolase Chain: D: PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
4	c2a6pA_	 Alignment		100.0	24	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
5	d1xq9a_	 Alignment		100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
6	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
7	c3r7aA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
8	d1riia_	 Alignment		100.0	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
9	c2ilvB_	 Alignment		100.0	27	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
10	d1qhfa_	 Alignment		100.0	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
11	d2hhja1	 Alignment		100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase

12	c1k6mA	Alignment		100.0	25	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	d1bifa2	Alignment		100.0	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
14	d1fzta	Alignment		100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
15	c3d8hB	Alignment		100.0	23	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
16	d1tipa	Alignment		100.0	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
17	c1bifa	Alignment		100.0	24	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
18	c3ll4B	Alignment		100.0	22	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
19	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.
20	c3hjgB	Alignment		100.0	22	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
21	d1k6ma2	Alignment	not modelled	100.0	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
22	c3dcyA	Alignment	not modelled	100.0	23	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	d3pgma	Alignment	not modelled	100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
24	c3e9eB	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074; PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio
25	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
26	c2ikqA	Alignment	not modelled	100.0	21	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
27	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
28	d1v37a	Alignment	not modelled	100.0	32	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
						PDB header: hydrolase

29	c3mxB	Alignment	not modelled	100.0	21	Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgm5, mitochondrial; PDBTitle: crystal structure oh human phosphoglycerate mutase family member 52 (pgm5)
30	c3c7tB	Alignment	not modelled	100.0	20	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
31	c3eozB	Alignment	not modelled	100.0	20	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	21	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	99.9	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	99.9	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.
35	c3fjyB	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
36	c2glcA	Alignment	not modelled	97.7	27	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	97.6	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
38	d1rpaa	Alignment	not modelled	97.5	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
39	d1ihpa	Alignment	not modelled	97.4	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
40	d1dkla	Alignment	not modelled	97.1	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
41	c2wniC	Alignment	not modelled	97.0	21	PDB header: hydrolase Chain: C: PDB Molecule: 3-phytase; PDBTitle: crystal structure analysis of klebsiella sp asr1 phytase
42	d1nt4a	Alignment	not modelled	97.0	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
43	d1qwoa	Alignment	not modelled	97.0	16	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
44	d1qfxa	Alignment	not modelled	96.7	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
45	c2gfiB	Alignment	not modelled	96.4	20	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castellii at 2.3 a
46	d1ttaa	Alignment	not modelled	61.1	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
47	c3o0dF	Alignment	not modelled	53.4	17	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
48	d1tiba	Alignment	not modelled	52.9	7	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
49	c3ngmB	Alignment	not modelled	52.1	14	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
50	d3tgla	Alignment	not modelled	44.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
51	d1uwca	Alignment	not modelled	35.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
52	c3g7nA	Alignment	not modelled	33.0	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3
53	c2jkbB	Alignment	not modelled	33.0	11	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 - monophosphate) (orthorhombic crystal form)
54	c2p10D	Alignment	not modelled	29.2	18	PDB header: hydrolase Chain: D: PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15

						a resolution
55	c3hbjA_	Alignment	not modelled	27.7	30	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
56	d2vcha1	Alignment	not modelled	27.3	30	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
57	d1lgya_	Alignment	not modelled	25.8	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
58	c2o6lA_	Alignment	not modelled	25.4	25	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
59	c2jzcA_	Alignment	not modelled	24.1	38	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
60	c3nmeA_	Alignment	not modelled	22.8	10	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
61	d2acva1	Alignment	not modelled	22.7	40	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
62	d2pq6a1	Alignment	not modelled	21.8	25	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
63	c3lp5A_	Alignment	not modelled	21.3	9	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
64	d2ejna1	Alignment	not modelled	20.1	36	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
65	c2oudA_	Alignment	not modelled	19.9	23	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
66	dlyfza1	Alignment	not modelled	19.4	9	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
67	clyfzA_	Alignment	not modelled	19.4	9	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
68	d2c1xa1	Alignment	not modelled	19.0	35	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
69	d1l1sa_	Alignment	not modelled	17.3	14	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
70	c3mtqA_	Alignment	not modelled	17.1	14	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
71	c3o7mD_	Alignment	not modelled	16.8	11	PDB header: transferase Chain: D: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
72	d1jl3a_	Alignment	not modelled	16.7	10	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
73	c3ds8A_	Alignment	not modelled	16.6	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crystal structure of the gene lin2722 products from listeria2 innocua
74	c1yn9B_	Alignment	not modelled	16.3	12	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
75	c3e90C_	Alignment	not modelled	16.2	21	PDB header: hydrolase Chain: C: PDB Molecule: ns2b cofactor; PDBTitle: west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kr-h
76	c2ijoA_	Alignment	not modelled	16.0	21	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
77	c3iabB_	Alignment	not modelled	15.4	11	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
78	c2wmyh1	Alignment	not modelled	14.5	20	PDB header: hydrolase Chain: H: PDB Molecule: putative acid phosphatase wzb;

78	c2wmyt_	Alignment	not modelled	14.3	20	PDBTitle: crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate. Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
79	d1dg9a_	Alignment	not modelled	14.3	20	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrenchelatase
80	d2hk6a1	Alignment	not modelled	13.7	13	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
81	c2oryA_	Alignment	not modelled	12.5	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
82	d1fsga_	Alignment	not modelled	12.1	10	Fold: Chelatase-like Superfamily: Chelatase Family: Cobalt chelatase CbiK
83	d1qgoa_	Alignment	not modelled	12.1	10	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase; PDBTitle: structure-assisted discovery of variola major h12 phosphatase inhibitors
84	c2p4dA_	Alignment	not modelled	12.0	17	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folypolyglutamate synthetase, C-terminal domain
85	d2gc6a1	Alignment	not modelled	11.7	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
86	d1nula_	Alignment	not modelled	11.6	22	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
87	d2i09a1	Alignment	not modelled	11.6	7	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
88	d1j3wa_	Alignment	not modelled	11.5	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
89	d1nvtal	Alignment	not modelled	11.3	11	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
90	d1rxda_	Alignment	not modelled	11.0	12	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
91	c1u2pA_	Alignment	not modelled	10.8	11	PDB header: transferase Chain: F: PDB Molecule: phosphotransferase system, mannose/fructose-specific PDBTitle: crystal structure of manxa from thermoanaerobacter tengcongensis
92	c3lfhF_	Alignment	not modelled	10.7	23	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
93	c2imgA_	Alignment	not modelled	10.6	15	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
94	c2fekA_	Alignment	not modelled	10.6	30	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 14; PDBTitle: crystal structure of human dual specificity phosphatase 14
95	c2wgpA_	Alignment	not modelled	10.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st0148; PDBTitle: crystal structure of (st0148) conserved hypothetical from sulfolobus2 tokodaii strain7
96	c2pd2A_	Alignment	not modelled	10.3	25	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
97	d1d1qa_	Alignment	not modelled	10.2	11	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
98	c2g6zB_	Alignment	not modelled	10.1	14	PDB header: hydrolase Chain: B: PDB Molecule: htlv-i capsid protein; PDBTitle: solution structure of htlv-i capsid protein
99	c1qrjB_	Alignment	not modelled	9.9	14	