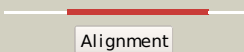
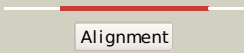
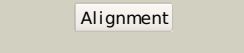
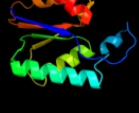
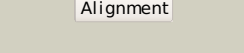
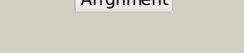
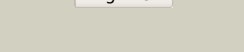
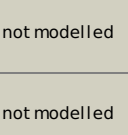


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ujcA_	 Alignment		99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
2	c2a6pA_	 Alignment		99.9	17	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
3	c3c7tB_	 Alignment		99.9	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
4	c3d4iD_	 Alignment		99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: sts-2 protein; PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2
5	c2ikqA_	 Alignment		99.9	27	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
6	c2rf1B_	 Alignment		99.9	13	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
7	c1vjxD_	 Alignment		99.9	21	PDB header: isomerase, hydrolase Chain: D: PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
8	d1fzta_	 Alignment		99.9	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
9	d1e58a_	 Alignment		99.9	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
10	c3f2iD_	 Alignment		99.9	15	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.
11	d1riia_	 Alignment		99.9	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase

12	d1qhfa_	Alignment		99.9	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
13	d1xq9a_	Alignment		99.9	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
14	c3eznB_	Alignment		99.9	22	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
15	d3pgma_	Alignment		99.9	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
16	c3fjyB_	Alignment		99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
17	d1bifa2	Alignment		99.8	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
18	d1k6ma2	Alignment		99.8	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
19	c3mxoB_	Alignment		99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgam5, mitochondrial; PDBTitle: crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
20	d1h2ea_	Alignment		99.8	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
21	c3d8hB_	Alignment	not modelled	99.8	16	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
22	c3r7aA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. Sterne
23	c3l14B_	Alignment	not modelled	99.8	25	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	c2i1vB_	Alignment	not modelled	99.8	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
25	c3f3kA_	Alignment	not modelled	99.8	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
26	d1v37a_	Alignment	not modelled	99.8	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
27	d1tipa_	Alignment	not modelled	99.8	17	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
28	c1k6mA_	Alignment	not modelled	99.8	21	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 PDB header: bifunctional enzyme

29	c1bifA_	Alignment	not modelled	99.8	19	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
30	c3dcyA_	Alignment	not modelled	99.8	18	PDB header: apoptosis regulator Chain: A: PDB Molecule: regulator protein; PDBTitle: crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
31	c2qniA_	Alignment	not modelled	99.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu0299; PDBTitle: crystal structure of uncharacterized protein atu0299
32	c3e9eB_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074; PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio
33	d2hhja1	Alignment	not modelled	99.8	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
34	c3hjgB_	Alignment	not modelled	99.8	20	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
35	c3eozB_	Alignment	not modelled	99.7	22	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
36	d1nd6a_	Alignment	not modelled	98.5	30	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
37	c2glcA_	Alignment	not modelled	98.4	25	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	98.3	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
39	c2wniC_	Alignment	not modelled	98.3	22	PDB header: hydrolase Chain: C: PDB Molecule: 3-phytase; PDBTitle: crystal structure analysis of klebsiella sp asr1 phytase
40	d1dkla_	Alignment	not modelled	98.3	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
41	d1ihpa_	Alignment	not modelled	98.3	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
42	d1nt4a_	Alignment	not modelled	98.3	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
43	d1qfxa_	Alignment	not modelled	98.0	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
44	c2gfiB_	Alignment	not modelled	97.9	31	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castellii at 2.3 a
45	d1qwoa_	Alignment	not modelled	97.9	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
46	c2c4kD_	Alignment	not modelled	46.2	16	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase- PDBTitle: crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
47	d1j5pa4	Alignment	not modelled	42.7	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	c2yl4A_	Alignment	not modelled	40.9	13	PDB header: membrane protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter, abcb10
49	d1ekja_	Alignment	not modelled	37.3	20	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
50	d1tiaa_	Alignment	not modelled	36.6	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
51	c1u9yD_	Alignment	not modelled	34.3	19	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
52	c1f0cB_	Alignment	not modelled	33.7	36	PDB header: viral protein Chain: B: PDB Molecule: ice inhibitor; PDBTitle: structure of the viral serpin crma
53	c3b5wE_	Alignment	not modelled	33.3	16	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
54	c3o0dF_	Alignment	not modelled	32.1	24	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica

					at 1.7 a2 resolution
55	d1tiba_	Alignment	not modelled	30.4	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
56	c1dkrB_	Alignment	not modelled	29.6	19 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.
57	c3efhB_	Alignment	not modelled	29.0	15 PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
58	c3dahB_	Alignment	not modelled	27.0	15 PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
59	d3tgla_	Alignment	not modelled	24.2	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
60	c3ucoB_	Alignment	not modelled	23.6	16 PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: coccomyxa beta-carbonic anhydrase in complex with iodide
61	d1lgya_	Alignment	not modelled	22.9	12 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
62	d1g5ca_	Alignment	not modelled	21.5	18 Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
63	d1t57a_	Alignment	not modelled	20.9	18 Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
64	c1ii8B_	Alignment	not modelled	20.0	10 PDB header: replication Chain: B: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
65	c3ngmB_	Alignment	not modelled	19.9	16 PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
66	c2w3nA_	Alignment	not modelled	19.4	8 PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase 2; PDBTitle: structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
67	d1l1sa_	Alignment	not modelled	19.2	12 Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
68	c3g7nA_	Alignment	not modelled	18.4	28 PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3
69	c1xexB_	Alignment	not modelled	18.2	10 PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
70	d2co5a1	Alignment	not modelled	18.1	27 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F93-like
71	d1su7a_	Alignment	not modelled	18.1	30 Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Carbon monoxide dehydrogenase
72	d1oaoa_	Alignment	not modelled	17.3	26 Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Carbon monoxide dehydrogenase
73	c2hydB_	Alignment	not modelled	17.0	21 PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
74	c1ylkA_	Alignment	not modelled	16.6	14 PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein rv1284/mt1322; PDBTitle: crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
75	d1uwca_	Alignment	not modelled	16.6	24 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
76	d1i6pa_	Alignment	not modelled	16.5	16 Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
77	c3b5xB_	Alignment	not modelled	16.4	15 PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
78	c2pd2A_	Alignment	not modelled	14.7	18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st0148; PDBTitle: crystal structure of (st0148) conserved hypothetical from sulfobolus2 tokodaii strain7
79	c1jqkE_	Alignment	not modelled	14.6	35 PDB header: oxidoreductase Chain: E: PDB Molecule: carbon monoxide dehydrogenase; PDBTitle: crystal structure of carbon monoxide dehydrogenase from2 rhodospirillum rubrum
80	d1jqka_	Alignment	not modelled	14.6	35 Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Carbon monoxide dehydrogenase

81	c2zyiB	Alignment	not modelled	14.5	10	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
82	c1f2uD	Alignment	not modelled	13.8	12	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
83	c3lp5A	Alignment	not modelled	13.7	13	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
84	c3eyxB	Alignment	not modelled	13.6	11	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
85	c2oryA	Alignment	not modelled	13.5	11	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
86	d1dkua2	Alignment	not modelled	12.7	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
87	d1vp8a	Alignment	not modelled	12.3	17	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
88	c2pjzA	Alignment	not modelled	12.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st1066; PDBTitle: the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066
89	d3b48a1	Alignment	not modelled	12.0	22	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
90	c3nhaA	Alignment	not modelled	11.9	15	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 6, mitochondrial; PDBTitle: nucleotide binding domain of human abcb6 (adp mg bound structure)
91	c2a8cE	Alignment	not modelled	11.0	16	PDB header: lyase Chain: E: PDB Molecule: carbonic anhydrase 2; PDBTitle: haemophilus influenzae beta-carbonic anhydrase
92	c3ds8A	Alignment	not modelled	10.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crystal structure of the gene lin2722 products from listeria2 innocua
93	d2c4ka2	Alignment	not modelled	10.9	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
94	c2l9dA	Alignment	not modelled	10.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112
95	c2p51A	Alignment	not modelled	10.6	13	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: spcc18.06c protein; PDBTitle: crystal structure of the s. pombe pop2p deadenylation2 subunit
96	c2a5vB	Alignment	not modelled	10.4	18	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase (carbonate dehydratase) (carbonic PDBTitle: crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
97	d1pf4a1	Alignment	not modelled	10.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
98	c2olkD	Alignment	not modelled	10.2	16	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
99	d2h1qa1	Alignment	not modelled	9.9	12	Fold: PLP-dependent transferase-like Superfamily: Dhaf3308-like Family: Dhaf3308-like