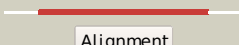

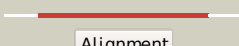

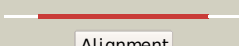

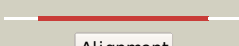











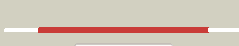











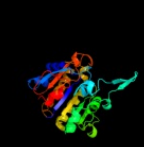

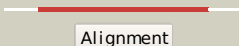

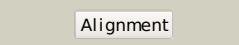

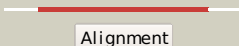
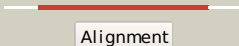
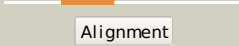

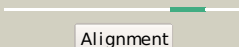

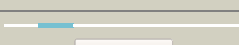
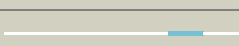


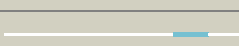

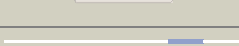

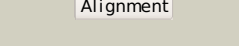

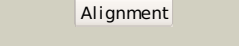
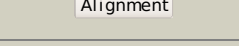
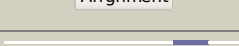



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3m8yC_	 Alignment		100.0	26	PDB header: isomerase Chain: C; PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
2	c2i09A_	 Alignment		100.0	28	PDB header: isomerase Chain: A; PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
3	d1p49a_	 Alignment		100.0	11	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
4	c3b5qB_	 Alignment		100.0	12	PDB header: hydrolase Chain: B; PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
5	d1lauka_	 Alignment		100.0	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
6	c2zktB_	 Alignment		100.0	13	PDB header: isomerase Chain: B; PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
7	c3ed4A_	 Alignment		100.0	12	PDB header: transferase Chain: A; PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
8	d1hdha_	 Alignment		100.0	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
9	c2vqrA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: putative sulfatase; PDBTitle: crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily
10	c2qzuA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
11	d1fsua_	 Alignment		100.0	14	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase

12	d2i09a1	Alignment		100.0	28	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
13	c3lxqB	Alignment		100.0	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp1736; PDBTitle: the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
14	c2w8dB	Alignment		100.0	11	PDB header: transferase Chain: B: PDB Molecule: processed glycerol phosphate lipoteichoic acid synthase 2; PDBTitle: distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
15	c2w5tA	Alignment		100.0	11	PDB header: transferase Chain: A: PDB Molecule: processed glycerol phosphate lipoteichoic acid PDBTitle: structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
16	d1o98a2	Alignment		100.0	21	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
17	c3q3qA	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
18	c2qsoB	Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase-nucleotide pyrophosphatase; PDBTitle: structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
19	c3szzA	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphonoacetate hydrolase; PDBTitle: crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
20	d1ei6a	Alignment		100.0	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase
21	c2xrgA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
22	c2xr9A	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
23	d1y6va1	Alignment	not modelled	100.0	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
24	c1ew2A	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase; PDBTitle: crystal structure of a human phosphatase
25	d1zeda1	Alignment	not modelled	100.0	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
26	d1k7ha	Alignment	not modelled	100.0	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
27	c2iucB	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic2 bacterium tab5
28	c3e2dB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase

29	c1o98A	 Alignment	not modelled	100.0	24	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
30	c3a52A	 Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkaline phosphatase from2 psychrophile shewanella sp.
31	c2w0yB	 Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
32	c2x98A	 Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
33	c3igzB	 Alignment	not modelled	99.9	24	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
34	c3iddA	 Alignment	not modelled	99.9	15	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
35	c2d1gB	 Alignment	not modelled	99.4	11	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
36	d2i09a2	 Alignment	not modelled	87.2	7	Fold: DeoB insert domain-like Superfamily: DeoB insert domain-like Family: DeoB insert domain-like
37	d1b4ub	 Alignment	not modelled	68.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
38	d1j33a	 Alignment	not modelled	46.4	32	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
39	c3oaaO	 Alignment	not modelled	40.4	20	PDB header: hydrolase/transport protein Chain: O: PDB Molecule: atp synthase gamma chain; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
40	c3f5dA	 Alignment	not modelled	39.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from2 bacillus subtilis
41	c3cagF	 Alignment	not modelled	34.9	33	PDB header: dna binding protein Chain: F: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
42	d2p5ma1	 Alignment	not modelled	33.0	14	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
43	d1b4ba	 Alignment	not modelled	31.6	19	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
44	c2xokG	 Alignment	not modelled	31.4	17	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: refined structure of yeast f1c10 atpase complex to 3 a2 resolution
45	c3ereD	 Alignment	not modelled	29.7	33	PDB header: dna binding protein/dna Chain: D: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
46	c1b4aA	 Alignment	not modelled	23.3	19	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
47	d1l5oa	 Alignment	not modelled	20.9	35	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
48	d1xxaa	 Alignment	not modelled	20.4	24	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
49	d1a05a	 Alignment	not modelled	19.4	23	Fold: Isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
50	d2nlyal	 Alignment	not modelled	19.3	40	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase
51	d1w0da	 Alignment	not modelled	16.2	23	Fold: Isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
52	d1fs0g	 Alignment	not modelled	15.7	16	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
53	c3v4gA	 Alignment	not modelled	15.1	14	PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: 1.60 angstrom resolution crystal structure of an arginine

						repressor2 from vibrio vulnificus cmcp6
54	c3e20C_	Alignment	not modelled	14.4	8	PDB header: translation Chain: C: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
55	c3pnuA_	Alignment	not modelled	13.6	17	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
56	d1dc1a_	Alignment	not modelled	11.9	10	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease BsobI
57	d1dt9a3	Alignment	not modelled	11.2	13	Fold: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Superfamily: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Family: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
58	c1zzgB_	Alignment	not modelled	11.2	12	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
59	d1t61a1	Alignment	not modelled	11.1	10	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
60	c2w6jG_	Alignment	not modelled	10.8	33	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
61	c3p19A_	Alignment	not modelled	10.4	40	PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
62	d1xo1a2	Alignment	not modelled	9.9	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
63	c3ff1B_	Alignment	not modelled	9.7	20	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of glucose 6-phosphate isomerase from staphylococcus aureus
64	c1yx3A_	Alignment	not modelled	9.5	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dsrC; PDBTitle: nmr structure of allochromatium vinosum dsrC: northeast2 structural genomics consortium target op4
65	d1nfga2	Alignment	not modelled	9.5	23	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
66	c2qe7G_	Alignment	not modelled	9.2	33	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
67	d1tfr2	Alignment	not modelled	9.1	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
68	d2jdig1	Alignment	not modelled	9.0	33	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
69	d1szpb1	Alignment	not modelled	9.0	14	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
70	c3ajfA_	Alignment	not modelled	8.9	16	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: structural insights into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
71	d1gkra2	Alignment	not modelled	8.8	23	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
72	d1uqra_	Alignment	not modelled	8.8	56	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
73	d1k1da2	Alignment	not modelled	8.4	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
74	c2q8nB_	Alignment	not modelled	8.3	8	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
75	d1fe0a_	Alignment	not modelled	8.3	25	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
76	d1p94a_	Alignment	not modelled	8.3	17	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
77	d1yzfa1	Alignment	not modelled	8.3	50	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: TAP-like
78	d1ji8a_	Alignment	not modelled	8.2	24	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
79	d1c7qa_	Alignment	not modelled	8.2	16	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI

80	d1dzfa1	Alignment	not modelled	8.1	15	Fold: Restriction endonuclease-like Superfamily: Eukaryotic RPB5 N-terminal domain Family: Eukaryotic RPB5 N-terminal domain
81	d2i5ia1	Alignment	not modelled	7.9	14	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: YdjC-like
82	c2o2cB_	Alignment	not modelled	7.8	8	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase, glycosomal; PDBTitle: crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
83	c1ly1A_	Alignment	not modelled	7.6	11	PDB header: transferase Chain: A: PDB Molecule: polynucleotide kinase; PDBTitle: structure and mechanism of t4 polynucleotide kinase
84	d1ly1a_	Alignment	not modelled	7.6	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
85	d1qrda_	Alignment	not modelled	7.4	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
86	c2e67D_	Alignment	not modelled	7.2	27	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein tthb029; PDBTitle: crystal structure of the hypothetical protein tthb029 from thermus2 thermophilus hb8
87	d2v4jc1	Alignment	not modelled	7.2	18	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
88	d2eg6a1	Alignment	not modelled	7.1	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
89	c3jzeC_	Alignment	not modelled	7.0	14	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. It2
90	d1ypra_	Alignment	not modelled	7.0	10	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
91	d1ynya2	Alignment	not modelled	6.9	27	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
92	d1hm5a_	Alignment	not modelled	6.8	4	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
93	c3nbuC_	Alignment	not modelled	6.8	8	PDB header: isomerase Chain: C: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of pgi glucosephosphate isomerase
94	c3c9pA_	Alignment	not modelled	6.7	3	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sp1917; PDBTitle: crystal structure of uncharacterized protein sp1917
95	c3hjbA_	Alignment	not modelled	6.5	8	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
96	d1u0fa_	Alignment	not modelled	6.5	4	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
97	d1f2ka_	Alignment	not modelled	6.5	13	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
98	c1yypA_	Alignment	not modelled	6.3	11	PDB header: replication/transferase Chain: A: PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of cytomegalovirus ul44 bound to c-terminal peptide2 from cmv ul54
99	d1iata_	Alignment	not modelled	6.1	4	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI