








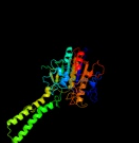











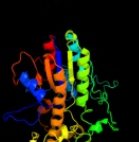


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3m8yC_	 Alignment		100.0	46	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
2	c2i09A_	 Alignment		100.0	38	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
3	c2zktB_	 Alignment		100.0	16	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
4	d1hdha_	 Alignment		100.0	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
5	d1p49a_	 Alignment		100.0	14	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
6	c2qzuA_	 Alignment		100.0	14	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
7	d1lauka_	 Alignment		100.0	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
8	c3ed4A_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
9	d1fsua_	 Alignment		100.0	14	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
10	c3b5qB_	 Alignment		100.0	10	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
11	c2vqrA_	 Alignment		100.0	15	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

12	c3lxqB_	Alignment		100.0	17	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
13	c2w8dB_	Alignment		100.0	14	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
14	c2w5tA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: processed glycerol phosphate lipoteichoic acid PDBTitle: structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
15	d2i09a1	Alignment		100.0	37	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
16	c3q3qA_	Alignment		100.0	15	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
17	d1o98a2	Alignment		100.0	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
18	c2qsoB_	Alignment		100.0	12	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	13	PDB header: hydrolase Chain: A: PDB Molecule: phosphonoacetate hydrolase; PDBTitle: crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
20	c2xrgA_	Alignment		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
21	d1ei6a_	Alignment	not modelled	100.0	12	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase
22	c2xr9A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
23	c1o98A_	Alignment	not modelled	99.9	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
24	c3iddA_	Alignment	not modelled	99.9	19	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
25	c3igzB_	Alignment	not modelled	99.9	26	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
26	d1zeda1	Alignment	not modelled	99.5	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
27	d1y6va1	Alignment	not modelled	99.5	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
28	c1ew2A_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase; PDBTitle: crystal structure of a human phosphatase

29	c2d1gB_	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
30	c2iucB_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic2 bacterium tab5
31	d1k7ha_	Alignment	not modelled	99.4	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
32	c3a52A_	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkaine phosphatase from2 psychrophile shewanella sp.
33	c3e2dB_	Alignment	not modelled	99.2	17	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
34	c2w0yB_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
35	c2x98A_	Alignment	not modelled	99.1	18	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
36	d2i09a2	Alignment	not modelled	98.6	44	Fold: DeoB insert domain-like Superfamily: DeoB insert domain-like Family: DeoB insert domain-like
37	d1b4ub_	Alignment	not modelled	62.6	10	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
38	c3oaaO_	Alignment	not modelled	60.2	18	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
39	d1fs0g_	Alignment	not modelled	33.7	16	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
40	c2xokG_	Alignment	not modelled	30.3	31	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: refined structure of yeast f1c10 atpase complex to 3 a2 resolution
41	c3e20C_	Alignment	not modelled	27.3	12	PDB header: translation Chain: C: PDB Molecule: eukaryotic peptid chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
42	d1t6la1	Alignment	not modelled	27.1	11	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
43	c3f5dA_	Alignment	not modelled	23.4	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from2 bacillus subtilis
44	d1nfga2	Alignment	not modelled	22.9	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
45	c2vbgB_	Alignment	not modelled	22.5	8	PDB header: lyase Chain: B: PDB Molecule: branched-chain alpha-ketoacid decarboxylase; PDBTitle: the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
46	c3jzeC_	Alignment	not modelled	22.5	16	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. lt2
47	d1j33a_	Alignment	not modelled	22.3	30	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	c1ovmC_	Alignment	not modelled	22.1	12	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
49	d1ovma3	Alignment	not modelled	21.6	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
50	c1zzgB_	Alignment	not modelled	21.4	13	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
51	c3pnuA_	Alignment	not modelled	20.6	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
52	d1dt9a3	Alignment	not modelled	20.4	4	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
						Fold: Thiamin diphosphate-binding fold (THDP-binding)

53	d2ji7a3	Alignment	not modelled	20.4	12	Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
54	c3cagF_	Alignment	not modelled	20.2	24	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.
55	d2jdig1	Alignment	not modelled	20.1	22	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
56	d2p5ma1	Alignment	not modelled	19.9	38	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
57	d1b4ba_	Alignment	not modelled	19.1	29	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
58	c3ff1B_	Alignment	not modelled	19.1	21	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of glucose 6-phosphate isomerase from staphylococcus aureus
59	c2w6jG_	Alignment	not modelled	18.5	21	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.
60	c3eyaE_	Alignment	not modelled	18.3	11	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
61	c2q8nB_	Alignment	not modelled	17.4	4	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
62	d1c7qa_	Alignment	not modelled	17.4	17	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
63	d2pg4a1	Alignment	not modelled	17.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F93-like
64	c3ereD_	Alignment	not modelled	16.0	24	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
65	c3p19A_	Alignment	not modelled	16.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
66	c2o2cB_	Alignment	not modelled	15.6	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
67	d1l5oa_	Alignment	not modelled	15.5	50	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
68	d1dc1a_	Alignment	not modelled	15.1	26	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease BsoBI
69	d2eg6a1	Alignment	not modelled	14.7	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
70	c2f00A_	Alignment	not modelled	13.8	10	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murC
71	c1yypA_	Alignment	not modelled	13.8	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
72	c3nbuC_	Alignment	not modelled	13.8	4	PDB header: isomerase Chain: C: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of pgi glucosephosphate isomerase
73	c2nxwB_	Alignment	not modelled	13.5	12	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasiliense
74	c3hjbA_	Alignment	not modelled	12.9	4	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.
75	d1u0fa_	Alignment	not modelled	12.9	8	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
76	d2ez9a3	Alignment	not modelled	12.8	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
77	d1gkra2	Alignment	not modelled	12.7	28	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
78	d1hm5a_	Alignment	not modelled	12.5	8	Fold: SIS domain Superfamily: SIS domain

					Family: Phosphoglucose isomerase, PGI
79	d1ynya2	Alignment	not modelled	12.5	20 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
80	d1q50a_	Alignment	not modelled	12.4	13 Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
81	c2qe7G_	Alignment	not modelled	12.3	27 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
82	c1t10A_	Alignment	not modelled	12.3	13 PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
83	c2w93A_	Alignment	not modelled	12.3	8 PDB header: lyase Chain: A: PDB Molecule: pyruvate decarboxylase isozyme 1; PDBTitle: crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
84	c2ejbA_	Alignment	not modelled	12.2	16 PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
85	c3ljka_	Alignment	not modelled	12.2	13 PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: glucose-6-phosphate isomerase from francisella tularensis.
86	d1jsca3	Alignment	not modelled	12.0	9 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
87	c1b4aA_	Alignment	not modelled	11.7	29 PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
88	d1iata_	Alignment	not modelled	11.7	8 Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
89	c3kpgA_	Alignment	not modelled	11.5	23 PDB header: oxidoreductase Chain: A: PDB Molecule: sulfide-quinone reductase, putative; PDBTitle: crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
90	c2o15B_	Alignment	not modelled	11.3	12 PDB header: transcription regulator Chain: B: PDB Molecule: pai 2 protein; PDBTitle: crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus
91	d1xxaa_	Alignment	not modelled	11.3	29 Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
92	d1t9ba3	Alignment	not modelled	11.3	10 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
93	c3zquA_	Alignment	not modelled	11.2	21 PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
94	d2hxma1	Alignment	not modelled	11.1	4 Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
95	d1laue_	Alignment	not modelled	10.7	8 Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
96	d1k1da2	Alignment	not modelled	10.5	22 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
97	d1gzda_	Alignment	not modelled	10.4	8 Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
98	c2pgnA_	Alignment	not modelled	10.2	10 PDB header: hydrolase Chain: A: PDB Molecule: cyclohexane-1,2-dione hydrolase (cdh); PDBTitle: the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
99	d1q6za3	Alignment	not modelled	10.1	13 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module