Phyre^2

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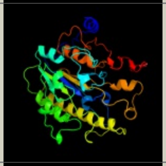
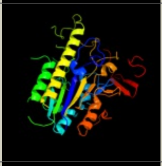
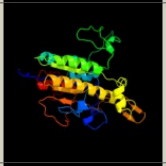
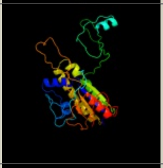
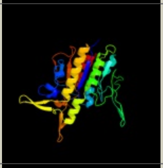
Description	P75785
Date	Thu Jan 5 12:14:07 GMT 2012
Unique Job ID	243b30e9e423b203

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w8dB_	Alignment		100.0	13	**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
2	c2w5tA_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
3	c3lxqB_	Alignment		100.0	14	**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
4	c3ed4A_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
5	c2qzuA_	Alignment		100.0	17	**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
6	d1fsua_	Alignment		100.0	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
7	d1auka_	Alignment		100.0	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
8	c3b5qB_	Alignment		100.0	14	**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
9	d1hdha_	Alignment		100.0	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
10	c2vqrA_	Alignment		100.0	17	**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
11	d1p49a_	Alignment		100.0	15	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase

12	d1o98a2	Alignment		100.0	9	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
13	d2i09a1	Alignment		100.0	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
14	c3m8yC_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
15	c2zktB_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
16	c3q3qA_	Alignment		100.0	16	**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	c2gsoB_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
18	c2i09A_	Alignment		99.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
19	c3szzA_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
20	c2xr9A_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
21	c2xrgA_	Alignment	not modelled	99.9	15	**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	d1ei6a_	Alignment	not modelled	99.8	11	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
23	c1o98A_	Alignment	not modelled	99.7	12	**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	c2d1gB_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
25	c3igzB_	Alignment	not modelled	99.5	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
26	c2iucB_	Alignment	not modelled	99.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
27	c2w0yB_	Alignment	not modelled	99.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
28	d1y6va1	Alignment	not modelled	99.0	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase

29	c2x98A_	Alignment	not modelled	98.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
30	d1zeda1	Alignment	not modelled	98.8	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
31	c1ew2A_	Alignment	not modelled	98.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase
32	c3a52A_	Alignment	not modelled	98.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
33	d1k7ha_	Alignment	not modelled	98.6	11	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
34	c3e2dB_	Alignment	not modelled	98.5	14	**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
35	c3iddA_	Alignment	not modelled	91.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
36	c3bijC_	Alignment	not modelled	45.1	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein gsu0716; **PDBTitle:** crystal structure of protein gsu0716 from geobacter2 sulfurreducens. northeast structural genomics target gsr13
37	d1uzdc1	Alignment	not modelled	43.1	24	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
38	d1b4ub_	Alignment	not modelled	36.8	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
39	d1ej7s_	Alignment	not modelled	35.1	20	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
40	d8ruci_	Alignment	not modelled	29.9	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
41	d2z1aa2	Alignment	not modelled	27.0	11	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
42	c2jcmA_	Alignment	not modelled	24.3	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic purine 5'-nucleotidase; **PDBTitle:** crystal structure of human cytosolic 5'-nucleotidase ii in2 complex with beryllium trifluoride
43	c2xokG_	Alignment	not modelled	21.9	21	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** refined structure of yeast f1c10 atpase complex to 3 a2 resolution
44	c3e4cB_	Alignment	not modelled	19.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** procaspase-1 zymogen domain crystal strucutre
45	d1l5oa_	Alignment	not modelled	18.3	42	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
46	d1j33a_	Alignment	not modelled	17.2	33	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
47	c3uoaB_	Alignment	not modelled	16.9	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** crystal structure of the malt1 paracaspase (p21 form)
48	d2dlxa1	Alignment	not modelled	16.7	4	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain
49	d1xo1a2	Alignment	not modelled	15.2	12	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
50	d1s1qa_	Alignment	not modelled	14.8	8	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
51	d2bdea1	Alignment	not modelled	13.0	29	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**5' nucleotidase-like
52	d2fiqa1	Alignment	not modelled	12.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
53	d1a8la1	Alignment	not modelled	11.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
54	c2xmoB_	Alignment	not modelled	11.5	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein;

						PDBTitle: the crystal structure of lmo2642
55	d2iuba2	Alignment	not modelled	10.0	25	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
56	d1usha2	Alignment	not modelled	8.5	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
57	c2hy1A_	Alignment	not modelled	8.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
58	d2hy1a1	Alignment	not modelled	8.3	33	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
59	c3bd0D_	Alignment	not modelled	8.3	15	**PDB header:**peptide binding protein **Chain:** D: **PDB Molecule:**protein memo1; **PDBTitle:** crystal structure of memo, form ii
60	c2hbzA_	Alignment	not modelled	8.3	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-1; **PDBTitle:** crystal structure of human caspase-1 (arg286->ala, glu390->ala) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)
61	d1yj5a1	Alignment	not modelled	7.8	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
62	d2hrca1	Alignment	not modelled	7.7	25	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
63	d1a3xa3	Alignment	not modelled	7.1	3	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
64	c3ib7A_	Alignment	not modelled	7.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
65	d1szpb1	Alignment	not modelled	7.0	17	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
66	c3gnjD_	Alignment	not modelled	7.0	10	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**thioredoxin domain protein; **PDBTitle:** the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
67	d1tfra2	Alignment	not modelled	7.0	28	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
68	d1xfla_	Alignment	not modelled	6.8	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
69	c2w6jG_	Alignment	not modelled	6.6	24	**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.
70	c2dfjA_	Alignment	not modelled	6.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
71	c1o7dA_	Alignment	not modelled	6.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
72	d1wdds_	Alignment	not modelled	6.0	25	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
73	d2nxfa1	Alignment	not modelled	6.0	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
74	d1dt9a3	Alignment	not modelled	5.8	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
75	c3mk7F_	Alignment	not modelled	5.7	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
76	d2fwha1	Alignment	not modelled	5.6	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
77	d2g50a3	Alignment	not modelled	5.6	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
78	c2z1aA_	Alignment	not modelled	5.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
79	d2jdig1	Alignment	not modelled	5.5	22	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
						Fold:7-stranded beta/alpha barrel

80	d3bvua3	Alignment	not modelled	5.4	7	**Superfamily:**Glycoside hydrolase/deacetylase **Family:**alpha-mannosidase
81	c2fp3A_	Alignment	not modelled	5.4	14	**PDB header:**hydrolysis/apoptosis **Chain:** A: **PDB Molecule:**caspase nc; **PDBTitle:** crystal structure of the drosophila initiator caspase dronc
82	c1cp3B_	Alignment	not modelled	5.1	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**apopain; **PDBTitle:** crystal structure of the complex of apopain with the tetrapeptide2 inhibitor ace-dvad-fmc
83	d3c9fa2	Alignment	not modelled	5.1	7	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain