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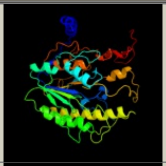
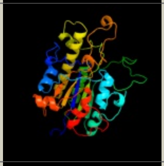
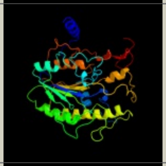
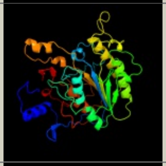
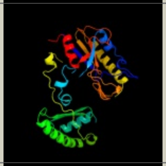
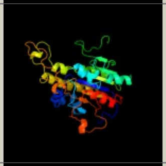
Description	P42640
Date	Thu Jan 5 12:02:01 GMT 2012
Unique Job ID	a2a42925ec7eef37

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	c3ed4A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
3	d1fsua_	Alignment		100.0	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
4	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
5	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.
6	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
7	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
8	d1auka_	Alignment		100.0	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
9	d1hdha_	Alignment		100.0	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
10	d1p49a_	Alignment		100.0	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
11	c2vqrA_	Alignment		100.0	18	**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	d1o98a2	Alignment		100.0	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
13	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
14	c3m8yC_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
15	d2i09a1	Alignment		100.0	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
16	c2gsoB_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
17	c3q3qA_	Alignment		99.9	22	**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	c2i09A_	Alignment		99.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
19	c3szzA_	Alignment		99.9	14	**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		99.9	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
21	c2xrgA_	Alignment	not modelled	99.9	16	**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	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
23	c1o98A_	Alignment	not modelled	99.6	13	**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	c3igzB_	Alignment	not modelled	99.6	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
25	c2d1gB_	Alignment	not modelled	99.4	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
26	c2iucB_	Alignment	not modelled	98.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
27	d1y6va1	Alignment	not modelled	98.5	18	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
28	c1ew2A_	Alignment	not modelled	98.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase;

						PDBTitle: crystal structure of a human phosphatase
29	c2w0yB_	Alignment	not modelled	98.4	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
30	d1zeda1	Alignment	not modelled	98.4	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
31	d1k7ha_	Alignment	not modelled	98.4	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
32	c2x98A_	Alignment	not modelled	98.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
33	c3a52A_	Alignment	not modelled	98.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
34	c3e2dB_	Alignment	not modelled	98.0	19	**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	87.8	20	**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	63.4	15	**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	c3uoaB_	Alignment	not modelled	58.2	21	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** crystal structure of the malt1 paracaspase (p21 form)
38	d1b4ub_	Alignment	not modelled	56.5	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
39	d2nxfa1	Alignment	not modelled	43.8	12	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
40	d1s1qa_	Alignment	not modelled	32.7	14	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
41	d1qnra_	Alignment	not modelled	31.1	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
42	d1j33a_	Alignment	not modelled	29.1	54	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
43	d1l5oa_	Alignment	not modelled	28.3	38	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
44	d1cmwa2	Alignment	not modelled	20.0	8	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
45	c2jcmA_	Alignment	not modelled	15.5	24	**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
46	d1ma3a_	Alignment	not modelled	12.6	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
47	d2bdea1	Alignment	not modelled	11.3	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**5' nucleotidase-like
48	d1txla_	Alignment	not modelled	10.2	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Hypothetical protein YodA
49	c1txlA_	Alignment	not modelled	10.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**metal-binding protein yoda; **PDBTitle:** crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149
50	d2hy1a1	Alignment	not modelled	10.1	27	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
51	c2hy1A_	Alignment	not modelled	10.1	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
52	d1yj5a1	Alignment	not modelled	10.0	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
53	c3t1iC_	Alignment	not modelled	10.0	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
						Fold: PreATP-grasp domain

54	d2r7ka1	Alignment	not modelled	10.0	18	**Superfamily:**PreATP-grasp domain **Family:**PurP N-terminal domain-like
55	c3ib7A_	Alignment	not modelled	9.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
56	c2xokG_	Alignment	not modelled	9.4	19	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** refined structure of yeast f1c10 atpase complex to 3 a2 resolution
57	c2funB_	Alignment	not modelled	9.4	12	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-8; **PDBTitle:** alternative p35-caspase-8 complex
58	c3oaaO_	Alignment	not modelled	9.3	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
59	d1fs0g_	Alignment	not modelled	9.2	21	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
60	c3e4cB_	Alignment	not modelled	9.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** procaspase-1 zymogen domain crystal strucutre
61	d1j08a1	Alignment	not modelled	8.9	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
62	c3g7kD_	Alignment	not modelled	8.9	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**3-methylitaconate isomerase; **PDBTitle:** crystal structure of methylitaconate-delta-isomerase
63	d1umdb1	Alignment	not modelled	8.8	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
64	d1v8za1	Alignment	not modelled	8.5	4	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
65	d2jdig1	Alignment	not modelled	8.5	30	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
66	c2w6jG_	Alignment	not modelled	8.4	20	**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.
67	c2qe7G_	Alignment	not modelled	8.3	30	**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
68	c3k35D_	Alignment	not modelled	8.1	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
69	d1szpb1	Alignment	not modelled	8.1	14	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
70	d1nw9b_	Alignment	not modelled	7.9	12	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
71	d1xo1a2	Alignment	not modelled	7.7	13	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
72	c3eypB_	Alignment	not modelled	7.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
73	d1uzxa_	Alignment	not modelled	7.2	9	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
74	c3qfnA_	Alignment	not modelled	7.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
75	d1yc5a1	Alignment	not modelled	7.2	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
76	d2z1aa2	Alignment	not modelled	7.1	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
77	c1cp3B_	Alignment	not modelled	7.0	21	**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
78	d1n57a_	Alignment	not modelled	6.9	8	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
79	d1tfra2	Alignment	not modelled	6.8	8	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain

80	d1uf3a_	Alignment	not modelled	6.7	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
81	d2pw6a1	Alignment	not modelled	6.7	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
82	d1a8la1	Alignment	not modelled	6.6	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
83	c2o2jA_	Alignment	not modelled	6.6	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
84	c3auzA_	Alignment	not modelled	6.5	9	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
85	c2xmoB_	Alignment	not modelled	6.4	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
86	c3pkiF_	Alignment	not modelled	6.4	8	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
87	d1usha2	Alignment	not modelled	6.3	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
88	c2x7lP_	Alignment	not modelled	6.3	45	**PDB header:**immune system **Chain:** P: **PDB Molecule:**hiv rev; **PDBTitle:** implications of the hiv-1 rev dimer structure at 3.2a2 resolution for multimeric binding to the rev response3 element
89	d1ex9a_	Alignment	not modelled	6.2	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
90	c1kmcB_	Alignment	not modelled	6.2	19	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of the caspase-7 / xiap-bir2 complex
91	d1m7ta_	Alignment	not modelled	6.2	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
92	d2ozlb1	Alignment	not modelled	6.1	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
93	c3siqF_	Alignment	not modelled	6.1	14	**PDB header:**ligase **Chain:** F: **PDB Molecule:**apoptosis 1 inhibitor; **PDBTitle:** crystal structure of autoinhibited diap1-bir1 domain
94	d1hlga_	Alignment	not modelled	6.0	9	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
95	c2kncA_	Alignment	not modelled	6.0	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
96	d1w85b1	Alignment	not modelled	6.0	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
97	d1uzdc1	Alignment	not modelled	6.0	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
98	c1w8xP_	Alignment	not modelled	5.9	10	**PDB header:**virus **Chain:** P: **PDB Molecule:**protein p16; **PDBTitle:** structural analysis of prd1
99	d1ej7s_	Alignment	not modelled	5.9	15	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit