Phyre^2

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Description	P39349
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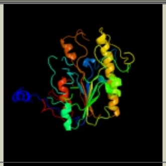
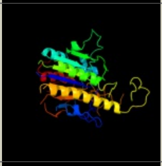
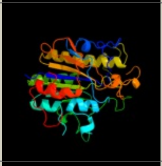
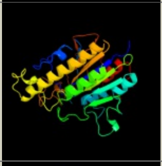
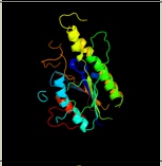
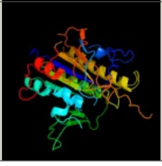
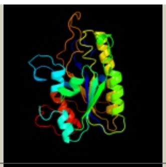
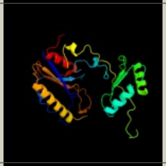
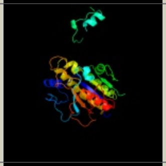
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w8dB_	Alignment		100.0	12	**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	12	**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	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
4	c3ed4A_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
5	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
6	d1auka_	Alignment		100.0	15	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
7	d1fsua_	Alignment		100.0	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
8	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
9	d1hdha_	Alignment		100.0	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
10	c2vqrA_	Alignment		100.0	16	**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	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
14	c3m8yC_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
15	d2i09a1	Alignment		100.0	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
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		100.0	14	**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	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
19	c2xrgA_	Alignment		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
20	c2xr9A_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
21	c3szzA_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
22	d1ei6a_	Alignment	not modelled	99.9	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
23	c1o98A_	Alignment	not modelled	99.7	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	12	**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	99.6	17	**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	99.4	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	99.3	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
28	c1ew2A_	Alignment	not modelled	99.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase

29	d1zeda1	Alignment	not modelled	99.2	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
30	c2w0yB_	Alignment	not modelled	99.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
31	d1k7ha_	Alignment	not modelled	99.1	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
32	c2x98A_	Alignment	not modelled	99.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
33	c3a52A_	Alignment	not modelled	99.0	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	98.7	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
35	c3iddA_	Alignment	not modelled	96.7	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
36	d1b4ub_	Alignment	not modelled	42.4	5	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
37	c3bijC_	Alignment	not modelled	38.2	18	**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
38	d1j33a_	Alignment	not modelled	28.7	13	**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	d1l5oa_	Alignment	not modelled	24.9	7	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
40	c3ib7A_	Alignment	not modelled	22.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
41	d1xo1a2	Alignment	not modelled	22.6	12	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
42	d3c9fa2	Alignment	not modelled	22.0	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
43	c2xokG_	Alignment	not modelled	21.3	11	**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	c2hy1A_	Alignment	not modelled	20.6	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
45	d2hy1a1	Alignment	not modelled	20.6	31	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
46	c3e4cB_	Alignment	not modelled	19.1	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** procaspase-1 zymogen domain crystal strucutre
47	d1s1qa_	Alignment	not modelled	19.0	12	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
48	d1usha2	Alignment	not modelled	16.9	11	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
49	d1uzdc1	Alignment	not modelled	14.7	9	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
50	d1yj5a1	Alignment	not modelled	13.1	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
51	d2p0va1	Alignment	not modelled	12.2	11	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
52	c2p0vA_	Alignment	not modelled	12.2	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
53	d1ej7s_	Alignment	not modelled	12.0	11	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
54	d2z1aa2	Alignment	not modelled	11.9	8	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal

						domain
55	d1tfra2	Alignment	not modelled	11.8	15	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
56	d2hrca1	Alignment	not modelled	11.0	7	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
57	c3uoaB_	Alignment	not modelled	10.6	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)
58	c2jcmA_	Alignment	not modelled	9.1	14	**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
59	d8ruci_	Alignment	not modelled	8.9	11	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
60	c1oidA_	Alignment	not modelled	8.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein usha; **PDBTitle:** 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
61	c2dfjA_	Alignment	not modelled	8.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
62	d2jdig1	Alignment	not modelled	7.7	17	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
63	d1jb0i_	Alignment	not modelled	7.2	23	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
64	d2hk6a1	Alignment	not modelled	7.2	11	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
65	c3a0hk_	Alignment	not modelled	7.2	38	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
66	d1yp2a2	Alignment	not modelled	7.1	3	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
67	d1cmwa2	Alignment	not modelled	6.4	13	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
68	d2nxfa1	Alignment	not modelled	6.1	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
69	c3c9fB_	Alignment	not modelled	6.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314
70	d1fs0g_	Alignment	not modelled	5.8	20	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
71	c3a0bK_	Alignment	not modelled	5.7	38	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
72	c3a0bk_	Alignment	not modelled	5.7	38	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
73	c2w6jG_	Alignment	not modelled	5.7	17	**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.
74	c1oy8A_	Alignment	not modelled	5.7	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
75	c2hbzA_	Alignment	not modelled	5.6	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)
76	c3e20C_	Alignment	not modelled	5.6	12	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
77	d1a9xa3	Alignment	not modelled	5.5	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
78	c3oaaO_	Alignment	not modelled	5.2	12	**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
79	d1szpb1	Alignment	not modelled	5.2	17	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
80	c3zvmA_	Alignment	not modelled	5.1	26	**PDB header:**hydrolase/transferase/dna **Chain:** A: **PDB Molecule:**bifunctional polynucleotide phosphatase/kinase; **PDBTitle:** the structural basis for substrate recognition by

						mammalian2 polynucleotide kinase 3' phosphatase
81	d1dt9a3	Alignment	not modelled	5.1	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