Phyre^2

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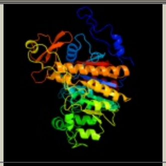
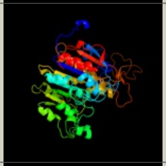
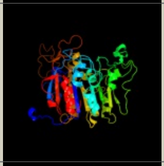
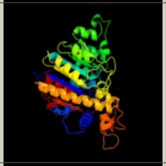
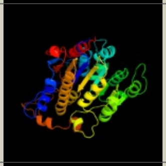
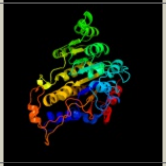
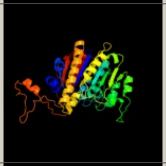
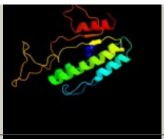
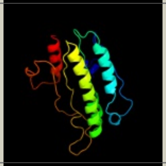
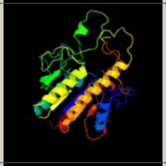
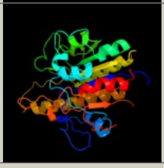
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y6va1	Alignment		100.0	100	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
2	d1k7ha_	Alignment		100.0	34	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
3	d1zeda1	Alignment		100.0	34	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
4	c1ew2A_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase
5	c2x98A_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
6	c2w0yB_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
7	c3e2dB_	Alignment		100.0	34	**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
8	c3a52A_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
9	c2iucB_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
10	c3m8yC_	Alignment		99.9	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
11	c2i09A_	Alignment		99.9	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans

12	c3igzB_	Alignment		99.7	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
13	d1o98a2	Alignment		99.6	22	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
14	c1o98A_	Alignment		99.6	19	**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
15	d1hdha_	Alignment		99.5	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
16	c3ed4A_	Alignment		99.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
17	d1auka_	Alignment		99.4	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
18	c3q3qA_	Alignment		99.4	21	**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
19	c2zktB_	Alignment		99.4	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
20	c3lxqB_	Alignment		99.4	22	**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
21	d2i09a1	Alignment	not modelled	99.3	18	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
22	d1p49a_	Alignment	not modelled	99.3	15	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
23	d1fsua_	Alignment	not modelled	99.3	21	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
24	c2vqrA_	Alignment	not modelled	99.2	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
25	c2w8dB_	Alignment	not modelled	99.2	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
26	c2qzuA_	Alignment	not modelled	99.2	15	**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
27	c2w5tA_	Alignment	not modelled	99.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide

28	c2xrgA_	Alignment	not modelled	99.1	25	pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
29	c2xr9A_	Alignment	not modelled	99.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
30	c3b5qB_	Alignment	not modelled	99.0	21	**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
31	c3szzA_	Alignment	not modelled	98.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
32	d1ei6a_	Alignment	not modelled	98.4	24	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
33	c2gsoB_	Alignment	not modelled	98.2	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
34	c2d1gB_	Alignment	not modelled	96.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
35	c3iddA_	Alignment	not modelled	79.0	27	**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	76.8	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
37	c1q14A_	Alignment	not modelled	47.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
38	c1h2aS_	Alignment	not modelled	40.0	39	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
39	d1wuis1	Alignment	not modelled	40.0	39	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
40	d1j8fa_	Alignment	not modelled	39.5	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
41	d2ihta3	Alignment	not modelled	35.0	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
42	d1frfs_	Alignment	not modelled	31.8	25	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
43	d1j83a_	Alignment	not modelled	30.9	20	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 17 carbohydrate binding module, CBM17
44	c3glsC_	Alignment	not modelled	28.9	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
45	d1q1aa_	Alignment	not modelled	26.3	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
46	c2q1wC_	Alignment	not modelled	24.6	13	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
47	c3euaD_	Alignment	not modelled	23.8	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
48	c2pjuD_	Alignment	not modelled	21.7	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
49	d1e3da_	Alignment	not modelled	21.2	29	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
50	d2a84a1	Alignment	not modelled	19.7	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
51	c3bq9A_	Alignment	not modelled	19.5	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
52	c3t9qB_	Alignment	not modelled	17.7	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**stage ii sporulation protein e; **PDBTitle:** structure of the phosphatase domain of the cell fate determinant2 spoiie from bacillus subtilis (mn presoaked)
						Fold: Chelatase-like

53	d2pjua1	Alignment	not modelled	17.0	18	**Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
54	c3cdiA_	Alignment	not modelled	15.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide phosphorylase; **PDBTitle:** crystal structure of e. coli pnpase
55	c3absD_	Alignment	not modelled	15.0	30	**PDB header:**lyase **Chain:** D: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
56	c3anyB_	Alignment	not modelled	15.0	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
57	c3pu9A_	Alignment	not modelled	14.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein serine/threonine phosphatase; **PDBTitle:** crystal structure of serine/threonine phosphatase sphaerobacter2 thermophilus dsm 20745
58	d1w0da_	Alignment	not modelled	14.8	25	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
59	c3fkjA_	Alignment	not modelled	14.8	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
60	c3b3jA_	Alignment	not modelled	13.9	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
61	c3u1hA_	Alignment	not modelled	13.9	45	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
62	d2d0oa2	Alignment	not modelled	13.7	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
63	c2pr7A_	Alignment	not modelled	13.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family; **PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
64	c1okjB_	Alignment	not modelled	13.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protease yeaz; **PDBTitle:** crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
65	c2q5cA_	Alignment	not modelled	12.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
66	d1qh8a_	Alignment	not modelled	12.4	6	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
67	d1u7pa_	Alignment	not modelled	12.1	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
68	d1uhma_	Alignment	not modelled	12.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
69	d1ybha3	Alignment	not modelled	12.0	26	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
70	c2x48B_	Alignment	not modelled	11.9	15	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
71	c2i56A_	Alignment	not modelled	11.8	15	**PDB header:**isomerase, metal-binding protein **Chain:** A: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
72	d1pvda3	Alignment	not modelled	11.3	43	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
73	c3rgwS_	Alignment	not modelled	11.0	29	**PDB header:**oxidoreductase/oxidoreductase **Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk; **PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
74	d2fhza1	Alignment	not modelled	10.9	23	**Fold:**ImmE5-like **Superfamily:**ImmE5-like **Family:**ImmE5-like
75	c3bz6A_	Alignment	not modelled	10.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0502 protein pspto_2686; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 pseudomonas syringae pv. tomato str. dc3000
76	d1ek6a_	Alignment	not modelled	10.8	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
77	c3blxL_	Alignment	not modelled	10.7	18	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 2;

						PDBTitle: yeast isocitrate dehydrogenase (apo form)
78	d1cc1s_	Alignment	not modelled	10.6	38	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
79	c2kjwA_	Alignment	not modelled	10.5	38	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55
80	c3cdjA_	Alignment	not modelled	10.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide phosphorylase; **PDBTitle:** crystal structure of the e. coli kh/s1 domain truncated2 pnpase
81	d1g6q1_	Alignment	not modelled	10.2	29	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
82	d1e3ha5	Alignment	not modelled	10.2	10	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
83	c3enkB_	Alignment	not modelled	10.2	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
84	d1xlma_	Alignment	not modelled	10.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
85	c3gxxB_	Alignment	not modelled	10.0	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
86	c2dfxl_	Alignment	not modelled	9.9	23	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**colicin-e5 immunity protein; **PDBTitle:** crystal structure of the carboxy terminal domain of colicin2 e5 complexed with its inhibitor
87	c1t9dB_	Alignment	not modelled	9.9	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetolactate synthase, mitochondrial; **PDBTitle:** crystal structure of yeast acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
88	c3es2A_	Alignment	not modelled	9.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of the c-terminal phosphatase domain of p.2 aeruginonsa rssb
89	d1ghca_	Alignment	not modelled	9.2	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
90	d1tfra2	Alignment	not modelled	9.1	18	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
91	d1p4da_	Alignment	not modelled	9.0	23	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
92	d1a05a_	Alignment	not modelled	8.9	45	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
93	d1lxna_	Alignment	not modelled	8.9	24	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
94	d1t9ba3	Alignment	not modelled	8.9	38	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
95	d2blna1	Alignment	not modelled	8.9	5	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
96	c1zorB_	Alignment	not modelled	8.7	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
97	d1qyia_	Alignment	not modelled	8.6	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
98	c3ir9A_	Alignment	not modelled	8.6	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
99	c3r6mD_	Alignment	not modelled	8.5	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**yeaz, resuscitation promoting factor; **PDBTitle:** crystal structure of vibrio parahaemolyticus yeaz