Phyre2

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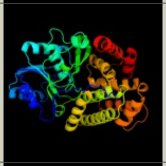
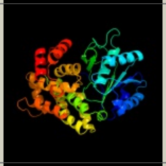
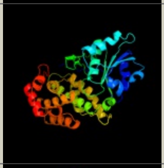
Description	P76553
Date	Thu Jan 5 12:24:31 GMT 2012
Unique Job ID	c7d2bf2502a6ed3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bfjK_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
2	c3ox4D_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
3	d1vlja_	Alignment		100.0	21	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
4	d1rrma_	Alignment		100.0	38	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
5	d1oj7a_	Alignment		100.0	23	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
6	d1o2da_	Alignment		100.0	30	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
7	c3hl0B_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
8	c3iv7B_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alcohol dehydrogenase iv; **PDBTitle:** crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
9	c3rf7A_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
10	c3jzdA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
11	d1jq5a_	Alignment		100.0	23	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase

12	c1ta9A_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
13	c3uhjE_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
14	d1kq3a_	Alignment		100.0	24	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
15	c3ce9A_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
16	c3okfA_	Alignment		100.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
17	d1sg6a_	Alignment		100.0	15	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
18	c1xahA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of staphlyococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+
19	c3clhA_	Alignment		100.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of 3-dehydroquinate synthase (dhqs)from2 helicobacter pylori
20	c2gruB_	Alignment		100.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-deoxy-scyllo-inosose synthase; **PDBTitle:** crystal structure of 2-deoxy-scyllo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
21	d1ujna_	Alignment	not modelled	100.0	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
22	c3orsD_	Alignment	not modelled	97.1	22	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
23	d1qcza_	Alignment	not modelled	97.0	14	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
24	d1o4va_	Alignment	not modelled	97.0	16	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
25	c3rggD_	Alignment	not modelled	97.0	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
26	c2fw9A_	Alignment	not modelled	96.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
						Fold: Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole

27	d1u11a_	Alignment	not modelled	96.9	15	carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
28	c3lp6D_	Alignment	not modelled	96.9	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
29	d2p1ra1	Alignment	not modelled	96.7	21	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
30	d1xmpa_	Alignment	not modelled	96.6	18	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
31	c3trhI_	Alignment	not modelled	96.6	19	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
32	d2jgra1	Alignment	not modelled	96.5	16	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
33	d2bona1	Alignment	not modelled	96.4	16	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
34	c2h31A_	Alignment	not modelled	96.2	15	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
35	d1u0ta_	Alignment	not modelled	95.7	24	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
36	c2ywxA_	Alignment	not modelled	95.3	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
37	d1qo0a_	Alignment	not modelled	95.1	10	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
38	c2qv7A_	Alignment	not modelled	94.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase dgkb; **PDBTitle:** crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
39	d1pfka_	Alignment	not modelled	94.1	28	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
40	d4pfka_	Alignment	not modelled	94.0	26	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
41	c1zxxA_	Alignment	not modelled	93.9	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
42	c3s40C_	Alignment	not modelled	93.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
43	c2j37W_	Alignment	not modelled	92.9	18	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
44	c2an1D_	Alignment	not modelled	92.6	27	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
45	c2iy3A_	Alignment	not modelled	92.3	15	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
46	c3pfnB_	Alignment	not modelled	92.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
47	c2bonB_	Alignment	not modelled	92.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipid kinase; **PDBTitle:** structure of an escherichia coli lipid kinase (yegs)
48	c3opyB_	Alignment	not modelled	92.1	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
49	c3opyH_	Alignment	not modelled	92.1	22	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
50	d2f48a1	Alignment	not modelled	91.7	15	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
51	c3rfqC_	Alignment	not modelled	91.5	21	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
						PDB header:transport protein

52	c3snrA_	Alignment	not modelled	91.4	12	**Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
53	c3sg0A_	Alignment	not modelled	91.1	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
54	c3dm5A_	Alignment	not modelled	90.9	24	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
55	c3opyG_	Alignment	not modelled	90.6	18	**PDB header:**transferase **Chain:** G: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
56	c3opyE_	Alignment	not modelled	90.3	21	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
57	c1z0zC_	Alignment	not modelled	90.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
58	d1z0sa1	Alignment	not modelled	90.0	22	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
59	c3o8oB_	Alignment	not modelled	89.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase subunit beta; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
60	c3hi0B_	Alignment	not modelled	89.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
61	c3i45A_	Alignment	not modelled	89.4	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of putative twin-arginine translocation pathway2 signal protein from rhodospirillum rubrum atcc 11170
62	c3k2qA_	Alignment	not modelled	89.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
63	c2j289_	Alignment	not modelled	89.3	22	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
64	d1ewka_	Alignment	not modelled	89.2	4	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
65	c3i09A_	Alignment	not modelled	89.1	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic branched-chain amino acid-binding protein; **PDBTitle:** crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
66	c3eafA_	Alignment	not modelled	89.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
67	d2qv7a1	Alignment	not modelled	89.0	16	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
68	c2higA_	Alignment	not modelled	88.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
69	c3o8nA_	Alignment	not modelled	88.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
70	c1qzwC_	Alignment	not modelled	88.7	18	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
71	c3o8oC_	Alignment	not modelled	88.5	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
72	c1t6dB_	Alignment	not modelled	88.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
73	c3mdqA_	Alignment	not modelled	88.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
74	c3n0wA_	Alignment	not modelled	87.8	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc branched chain amino acid family transporter, **PDBTitle:** crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bxe_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
75	d1xi8a3	Alignment	not modelled	87.4	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like

76	d2g2ca1	Alignment	not modelled	87.1	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
77	d1v4va_	Alignment	not modelled	87.1	24	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
78	c3cf4G_	Alignment	not modelled	86.7	12	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
79	c2i2aA_	Alignment	not modelled	86.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
80	d1vh3a_	Alignment	not modelled	86.7	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
81	c2q5cA_	Alignment	not modelled	86.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
82	c3lopA_	Alignment	not modelled	86.0	16	**PDB header:**substrate binding protein **Chain:** A: **PDB Molecule:**substrate binding periplasmic protein; **PDBTitle:** crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
83	c2floA_	Alignment	not modelled	85.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
84	c3tqrA_	Alignment	not modelled	85.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
85	c3nhzA_	Alignment	not modelled	85.1	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
86	c2g4rB_	Alignment	not modelled	85.0	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
87	d2ji7a1	Alignment	not modelled	84.9	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
88	d1y5ea1	Alignment	not modelled	84.7	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
89	c3cerD_	Alignment	not modelled	84.1	17	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**possible exopolyphosphatase-like protein; **PDBTitle:** crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
90	c3khtA_	Alignment	not modelled	83.6	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
91	c2is8A_	Alignment	not modelled	83.6	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
92	d2f7wa1	Alignment	not modelled	82.7	10	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
93	c3dcjA_	Alignment	not modelled	82.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
94	c2zwmA_	Alignment	not modelled	81.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
95	c2yhsA_	Alignment	not modelled	81.8	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
96	d1zpda1	Alignment	not modelled	81.8	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
97	c2xecD_	Alignment	not modelled	81.7	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
98	d2pjua1	Alignment	not modelled	81.7	15	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
99	c3l4eA_	Alignment	not modelled	81.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
100	d2ihta1	Alignment	not modelled	81.6	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain

101	c2hqbA_	Alignment	not modelled	81.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional activator of comk gene; **PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
102	c3h5lB_	Alignment	not modelled	81.4	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative branched-chain amino acid abc **PDBTitle:** crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
103	d1mkza_	Alignment	not modelled	80.8	12	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
104	c1vmaA_	Alignment	not modelled	80.5	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
105	d1zesa1	Alignment	not modelled	80.5	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
106	c3q41B_	Alignment	not modelled	80.2	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1; **PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd)
107	d2bw0a2	Alignment	not modelled	80.2	11	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
108	c3grcD_	Alignment	not modelled	80.1	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
109	c3dmdA_	Alignment	not modelled	79.4	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
110	c3a0rB_	Alignment	not modelled	79.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
111	d1a9xa4	Alignment	not modelled	79.2	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
112	c3b9qA_	Alignment	not modelled	78.1	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
113	d2a9pa1	Alignment	not modelled	78.1	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
114	c2o6lA_	Alignment	not modelled	78.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucuronosyltransferase 2b7; **PDBTitle:** crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
115	c2pgnA_	Alignment	not modelled	77.9	20	**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
116	c2e4wA_	Alignment	not modelled	77.8	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**metabotropic glutamate receptor 3; **PDBTitle:** crystal structure of the extracellular region of the group ii2 metabotropic glutamate receptor complexed with 1s,3s-acpd
117	c1ny5A_	Alignment	not modelled	77.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
118	d1di6a_	Alignment	not modelled	77.3	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
119	d1xhfa1	Alignment	not modelled	77.1	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
120	d1t9ba1	Alignment	not modelled	77.0	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain