Phyre^2

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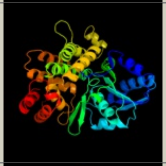
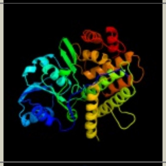
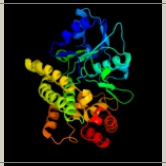
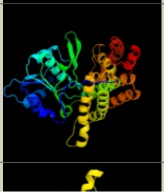
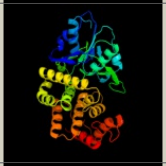
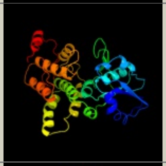
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ta9A_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
2	d1jq5a_	Alignment		100.0	30	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
3	c3uhjE_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
4	d1kq3a_	Alignment		100.0	32	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
5	c3ox4D_	Alignment		100.0	16	**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
6	c3bfjK_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
7	d1vlja_	Alignment		100.0	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
8	d1rrma_	Alignment		100.0	17	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
9	d1oj7a_	Alignment		100.0	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
10	c3iv7B_	Alignment		100.0	18	**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
11	c3hl0B_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
						

12	c3jzdA_	Alignment		100.0	19	**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
13	d1o2da_	Alignment		100.0	20	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
14	c3ce9A_	Alignment		100.0	14	**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
15	c3rf7A_	Alignment		100.0	17	**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
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	15	**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	11	**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	17	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
22	c3orsD_	Alignment	not modelled	97.2	15	**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	d2jgra1	Alignment	not modelled	97.2	14	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
24	c3rggD_	Alignment	not modelled	97.2	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
25	d1qcza_	Alignment	not modelled	97.2	18	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
26	d1o4va_	Alignment	not modelled	97.1	18	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
27	c2fw9A_	Alignment	not modelled	97.1	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

28	d1u11a_	Alignment	not modelled	97.0	13	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
29	c2qv7A_	Alignment	not modelled	97.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase dgkb; **PDBTitle:** crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
30	c3lp6D_	Alignment	not modelled	97.0	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
31	d2qv7a1	Alignment	not modelled	97.0	16	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
32	d2p1ra1	Alignment	not modelled	96.8	14	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
33	d1xmpa_	Alignment	not modelled	96.8	14	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
34	c2bonB_	Alignment	not modelled	96.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipid kinase; **PDBTitle:** structure of an escherichia coli lipid kinase (yegs)
35	c3s40C_	Alignment	not modelled	96.6	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
36	d2bona1	Alignment	not modelled	96.6	13	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
37	c3trhI_	Alignment	not modelled	96.6	12	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
38	d1u0ta_	Alignment	not modelled	96.3	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
39	c2ywxA_	Alignment	not modelled	96.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
40	c2h31A_	Alignment	not modelled	96.1	17	**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
41	c2an1D_	Alignment	not modelled	92.7	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
42	c1z0zC_	Alignment	not modelled	90.9	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
43	c3pfnB_	Alignment	not modelled	90.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
44	c2i2aA_	Alignment	not modelled	90.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
45	d1z0sa1	Alignment	not modelled	90.8	22	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
46	c2xecD_	Alignment	not modelled	90.7	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
47	d2ji7a1	Alignment	not modelled	89.9	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
48	c1yt5A_	Alignment	not modelled	87.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of nad kinase from thermotoga maritima
49	c2q5cA_	Alignment	not modelled	86.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
50	d1v4va_	Alignment	not modelled	86.4	27	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
51	c3afoB_	Alignment	not modelled	85.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
52	c2hqbA_	Alignment	not modelled	85.8	10	**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
53	d1pvda1	Alignment	not modelled	85.4	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
54	d1ovma1	Alignment	not modelled	85.2	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
55	d2pjua1	Alignment	not modelled	83.8	10	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
56	d1q6za1	Alignment	not modelled	83.5	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
57	d1pfka_	Alignment	not modelled	82.7	15	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
58	d2ez9a1	Alignment	not modelled	82.6	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
59	d1ybha1	Alignment	not modelled	81.3	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
60	c3hi0B_	Alignment	not modelled	81.0	14	**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	c2fqxA_	Alignment	not modelled	80.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc; **PDBTitle:** pnra from treponema pallidum complexed with guanosine
62	c1zxxA_	Alignment	not modelled	80.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
63	d4pfka_	Alignment	not modelled	80.2	20	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
64	d2ihta1	Alignment	not modelled	80.1	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
65	d1zpda1	Alignment	not modelled	79.9	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
66	c3opyB_	Alignment	not modelled	79.6	25	**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
67	c3opyH_	Alignment	not modelled	79.6	25	**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
68	c3rfqC_	Alignment	not modelled	78.9	13	**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
69	c2floA_	Alignment	not modelled	78.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
70	c3opyE_	Alignment	not modelled	78.5	16	**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
71	c3o8oB_	Alignment	not modelled	77.8	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase subunit beta; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
72	d1t9ba1	Alignment	not modelled	76.6	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
73	d1xi8a3	Alignment	not modelled	76.6	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
74	c1t6dB_	Alignment	not modelled	76.0	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
75	c3opyG_	Alignment	not modelled	75.7	16	**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
76	c3mdqA_	Alignment	not modelled	75.6	9	**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
77	d2djia1	Alignment	not modelled	74.1	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
78	d2g2ca1	Alignment	not modelled	72.6	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like

79	c2higA_	Alignment	not modelled	72.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
80	c3k2qA_	Alignment	not modelled	72.1	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
81	c2g4rB_	Alignment	not modelled	71.7	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
82	c3cerD_	Alignment	not modelled	71.4	10	**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
83	d3ckma1	Alignment	not modelled	67.9	8	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
84	d2f48a1	Alignment	not modelled	66.5	17	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
85	c3cf4G_	Alignment	not modelled	66.5	8	**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
86	c2x7jA_	Alignment	not modelled	65.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
87	c3o8oC_	Alignment	not modelled	65.8	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
88	d1o8bb1	Alignment	not modelled	64.2	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
89	c1powA_	Alignment	not modelled	64.2	16	**PDB header:**oxidoreductase(oxygen as acceptor) **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
90	d1ozha1	Alignment	not modelled	63.8	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
91	c2dgdD_	Alignment	not modelled	63.7	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
92	c2j289_	Alignment	not modelled	63.5	15	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
93	c3o8nA_	Alignment	not modelled	63.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
94	c3l4eA_	Alignment	not modelled	60.9	16	**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
95	c2pjuD_	Alignment	not modelled	60.8	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
96	c2j37W_	Alignment	not modelled	58.8	9	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
97	c3sg0A_	Alignment	not modelled	58.4	12	**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
98	c3nhzA_	Alignment	not modelled	58.3	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
99	c3rfoA_	Alignment	not modelled	58.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
100	c3dm5A_	Alignment	not modelled	57.8	11	**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.
101	c2og2A_	Alignment	not modelled	56.1	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
102	d1y5ea1	Alignment	not modelled	55.9	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like

103	d1vmea1	Alignment	not modelled	55.6	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
104	c2cnwF_	Alignment	not modelled	55.6	16	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
105	c2iy3A_	Alignment	not modelled	54.7	11	**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
106	d1mkza_	Alignment	not modelled	54.5	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
107	c2w93A_	Alignment	not modelled	53.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pyruvate decarboxylase isozyme 1; **PDBTitle:** crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
108	c3s99A_	Alignment	not modelled	53.3	6	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**basic membrane lipoprotein; **PDBTitle:** crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
109	c2pjkA_	Alignment	not modelled	53.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
110	d1fmta2	Alignment	not modelled	52.3	14	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
111	c2zwmA_	Alignment	not modelled	52.3	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
112	c3hbmA_	Alignment	not modelled	52.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
113	d1di6a_	Alignment	not modelled	52.0	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
114	c3u7jA_	Alignment	not modelled	51.7	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
115	c3b9qA_	Alignment	not modelled	51.6	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
116	c2is8A_	Alignment	not modelled	50.6	8	**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
117	d2a9pa1	Alignment	not modelled	49.9	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
118	c1qzwC_	Alignment	not modelled	48.8	14	**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
119	d1u3da2	Alignment	not modelled	48.6	11	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
120	c3i09A_	Alignment	not modelled	46.9	8	**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