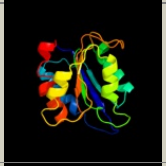
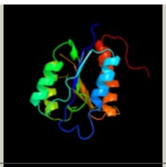
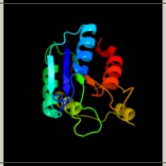
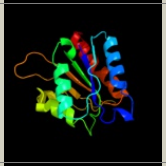
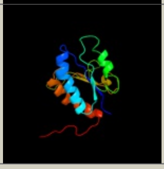
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AEZ9
Date	Thu Jan 5 11:24:43 GMT 2012
Unique Job ID	366d9a69d91f1ad5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mkza_	Alignment		100.0	98	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
2	d1y5ea1	Alignment		100.0	42	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
3	c3rfqC_	Alignment		100.0	28	**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
4	c2pjkA_	Alignment		100.0	29	**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
5	c2is8A_	Alignment		100.0	33	**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
6	d1uuya_	Alignment		100.0	31	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
7	d2f7wa1	Alignment		100.0	26	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
8	d1jlja_	Alignment		100.0	31	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
9	c2g4rB_	Alignment		100.0	29	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
10	d2g2ca1	Alignment		100.0	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
11	d1di6a_	Alignment		100.0	26	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like

12	c2nqqA_	Alignment		100.0	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
13	c3kbqA_	Alignment		100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
14	c2fu3A_	Alignment		100.0	21	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
15	d2nqra3	Alignment		100.0	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
16	d2ftsa3	Alignment		100.0	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
17	c1uz5A_	Alignment		100.0	20	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
18	d1uz5a3	Alignment		99.9	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
19	d1wu2a3	Alignment		99.9	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
20	c1wu2B_	Alignment		99.9	16	**PDB header:**structural genomics,biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis moea protein; **PDBTitle:** crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
21	d1xi8a3	Alignment	not modelled	99.9	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
22	d1wl8a1	Alignment	not modelled	93.0	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
23	d1nn4a_	Alignment	not modelled	92.5	20	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
24	c3qd5B_	Alignment	not modelled	92.3	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
25	c3he8A_	Alignment	not modelled	92.3	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
26	c2xecD_	Alignment	not modelled	91.7	11	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
27	d1o1xa_	Alignment	not modelled	91.6	23	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
28	d1i7qb_	Alignment	not modelled	91.6	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
						PDB header:isomerase

29	c3k7pA_	Alignment	not modelled	90.9	14	**Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
30	c3onoA_	Alignment	not modelled	90.7	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
31	c3rgwS_	Alignment	not modelled	90.6	13	**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
32	c2yxbA_	Alignment	not modelled	90.5	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
33	d1a9xb2	Alignment	not modelled	90.3	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
34	c2ppwA_	Alignment	not modelled	89.8	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
35	d1i1qb_	Alignment	not modelled	89.5	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
36	c3m1pA_	Alignment	not modelled	89.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
37	c3s5pA_	Alignment	not modelled	89.2	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
38	d2a9va1	Alignment	not modelled	89.0	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
39	c3a9rA_	Alignment	not modelled	88.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-arabinose isomerase; **PDBTitle:** x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
40	c3p2yA_	Alignment	not modelled	88.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
41	d1gpma2	Alignment	not modelled	88.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
42	d2nu7b1	Alignment	not modelled	87.5	13	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
43	d1vcoa1	Alignment	not modelled	87.3	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
44	d2vvpa1	Alignment	not modelled	86.9	15	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
45	d1pjca1	Alignment	not modelled	86.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
46	d1frfs_	Alignment	not modelled	85.3	12	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
47	c2vpiA_	Alignment	not modelled	85.2	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
48	c1z0zC_	Alignment	not modelled	84.9	15	**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
49	d1z0sa1	Alignment	not modelled	84.8	15	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
50	c3l4eA_	Alignment	not modelled	83.9	15	**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
51	d1yq9a1	Alignment	not modelled	83.9	13	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
52	c1zrsB_	Alignment	not modelled	83.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
53	c3c5yD_	Alignment	not modelled	83.4	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
54	c3hr4C_	Alignment	not modelled	82.7	8	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex

55	c2wpnA_	Alignment	not modelled	82.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [nifese] hydrogenase, small subunit; **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
56	d1iowa1	Alignment	not modelled	82.4	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
57	c3n0vD_	Alignment	not modelled	82.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
58	d1e3da_	Alignment	not modelled	81.6	11	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
59	c3myrE_	Alignment	not modelled	81.5	11	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
60	d1v93a_	Alignment	not modelled	81.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
61	d1tlla2	Alignment	not modelled	81.3	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
62	c3cq9C_	Alignment	not modelled	81.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uncharacterized protein lp_1622; **PDBTitle:** crystal structure of the lp_1622 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr114
63	c3melC_	Alignment	not modelled	80.9	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase family protein; **PDBTitle:** crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150
64	d1jq5a_	Alignment	not modelled	80.6	10	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
65	c3d54D_	Alignment	not modelled	80.3	10	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
66	c3ihkC_	Alignment	not modelled	80.3	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83
67	d1ka9h_	Alignment	not modelled	80.0	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
68	c3l6dB_	Alignment	not modelled	80.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
69	d1wuis1	Alignment	not modelled	79.9	10	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
70	d1ja1a2	Alignment	not modelled	79.9	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
71	c2vk2A_	Alignment	not modelled	79.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
72	c1j9zB_	Alignment	not modelled	79.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
73	c3ce9A_	Alignment	not modelled	79.5	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
74	c2qvcC_	Alignment	not modelled	78.2	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**sugar abc transporter, periplasmic sugar-binding **PDBTitle:** crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
75	d1o7ja_	Alignment	not modelled	78.2	23	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
76	d1ydga_	Alignment	not modelled	78.2	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
77	c3en0A_	Alignment	not modelled	78.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
78	c3louB_	Alignment	not modelled	76.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1) from burkholderia mallei atcc 23344 at 1.90 a resolution
79	c1h2aS_	Alignment	not modelled	76.8	10	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio

						vulgaris
80	c1tllA_	Alignment	not modelled	76.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
81	c3o1lB_	Alignment	not modelled	76.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
82	c3lm8D_	Alignment	not modelled	75.7	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine pyrophosphokinase; **PDBTitle:** crystal structure of thiamine pyrophosphokinase from2 bacillus subtilis, northeast structural genomics consortium3 target sr677
83	d1bvyf_	Alignment	not modelled	75.5	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
84	c1bvyF_	Alignment	not modelled	75.5	7	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
85	d1u2ma_	Alignment	not modelled	75.4	18	**Fold:**OmpH-like **Superfamily:**OmpH-like **Family:**OmpH-like
86	d2qv7a1	Alignment	not modelled	74.9	15	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
87	d1tjya_	Alignment	not modelled	74.8	10	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
88	c3kklA_	Alignment	not modelled	74.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
89	c3h5lB_	Alignment	not modelled	74.6	24	**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
90	c1fuiB_	Alignment	not modelled	73.3	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
91	c3r74B_	Alignment	not modelled	73.3	16	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
92	d1s1ma1	Alignment	not modelled	72.8	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
93	c2an1D_	Alignment	not modelled	72.3	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
94	d2naca2	Alignment	not modelled	71.7	19	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
95	d1a9xa3	Alignment	not modelled	71.6	33	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
96	c1np3B_	Alignment	not modelled	71.5	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
97	d2auna2	Alignment	not modelled	71.5	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
98	c3s40C_	Alignment	not modelled	71.4	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
99	d1fmfa_	Alignment	not modelled	71.1	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
100	d2b4aa1	Alignment	not modelled	69.3	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
101	d7reqa2	Alignment	not modelled	69.1	18	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
102	d1zl0a2	Alignment	not modelled	68.1	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
103	d1t0ba_	Alignment	not modelled	67.5	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**ThuA-like
104	d1n57a_	Alignment	not modelled	67.2	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
105	d2nv0a1	Alignment	not modelled	66.7	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like

						Family: Class I glutamine amidotransferases (GAT)
106	c1l9xA_	Alignment	not modelled	65.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
107	d1l9xa_	Alignment	not modelled	65.9	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
108	d1nyra1	Alignment	not modelled	65.8	13	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
109	c2g04B_	Alignment	not modelled	65.7	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable fatty-acid-coa racemase far; **PDBTitle:** crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
110	c2i2aA_	Alignment	not modelled	65.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
111	d1cc1s_	Alignment	not modelled	65.0	12	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
112	d1i36a2	Alignment	not modelled	64.2	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
113	d1qf6a1	Alignment	not modelled	63.9	19	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
114	d1dxya2	Alignment	not modelled	63.8	12	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
115	d1vpda2	Alignment	not modelled	63.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
116	d1o2da_	Alignment	not modelled	63.7	19	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
117	c3lftA_	Alignment	not modelled	63.4	14	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
118	c2ywcC_	Alignment	not modelled	63.3	14	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
119	d2bona1	Alignment	not modelled	63.2	15	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
120	c2eezG_	Alignment	not modelled	63.1	14	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase from themus thermophilus