Phyre2

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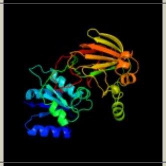
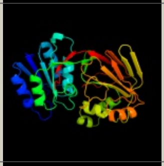
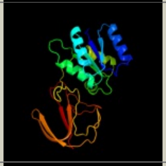
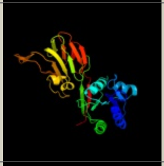
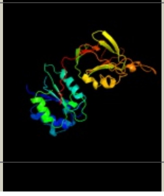
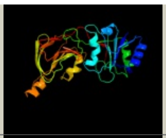
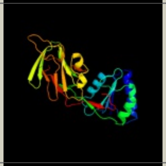
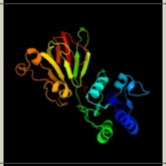
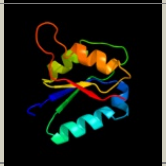
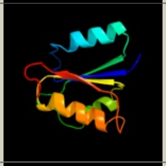
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bona1	Alignment		100.0	100	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
2	d2p1ra1	Alignment		100.0	82	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
3	c2bonB_	Alignment		100.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipid kinase; **PDBTitle:** structure of an escherichia coli lipid kinase (yegs)
4	c3s40C_	Alignment		100.0	28	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
5	c2qv7A_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase dgkb; **PDBTitle:** crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
6	d2qv7a1	Alignment		100.0	28	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
7	d2jgra1	Alignment		100.0	96	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
8	d1u0ta_	Alignment		99.6	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
9	c1yt5A_	Alignment		99.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of nad kinase from thermotoga maritima
10	c2an1D_	Alignment		99.2	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
11	c3pfnB_	Alignment		98.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase

12	c1z0zC_	Alignment		98.7	13	**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
13	d1z0sa1	Alignment		98.6	13	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
14	c2i2aA_	Alignment		98.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
15	c3afoB_	Alignment		98.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
16	c3bfjK_	Alignment		97.4	16	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
17	c3ox4D_	Alignment		97.2	15	**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
18	d1vlja_	Alignment		97.0	19	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
19	c3okfA_	Alignment		97.0	20	**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
20	d1rrma_	Alignment		96.9	13	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
21	d1jq5a_	Alignment	not modelled	96.8	20	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
22	c3ce9A_	Alignment	not modelled	96.6	16	**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
23	d1o2da_	Alignment	not modelled	96.6	19	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
24	c3lp6D_	Alignment	not modelled	96.5	27	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
25	c1ta9A_	Alignment	not modelled	96.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
26	d1o4va_	Alignment	not modelled	96.3	25	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
27	d1u11a_	Alignment	not modelled	96.2	23	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
						PDB header:lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole

28	c2fw9A_	Alignment	not modelled	96.2	23	ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
29	c2gruB_	Alignment	not modelled	96.2	20	**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+
30	d1oj7a_	Alignment	not modelled	96.1	22	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
31	c3trhI_	Alignment	not modelled	95.9	20	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
32	c3orsD_	Alignment	not modelled	95.5	20	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
33	c3iv7B_	Alignment	not modelled	95.5	12	**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
34	c3rf7A_	Alignment	not modelled	95.4	14	**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
35	c3clhA_	Alignment	not modelled	95.3	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of 3-dehydroquinate synthase (dhqs)from2 helicobacter pylori
36	d1kq3a_	Alignment	not modelled	95.3	9	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
37	d1xmpa_	Alignment	not modelled	95.2	22	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
38	c3hl0B_	Alignment	not modelled	94.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
39	d1qcza_	Alignment	not modelled	94.8	20	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
40	c3rggD_	Alignment	not modelled	94.4	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
41	c3jzdA_	Alignment	not modelled	94.3	17	**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
42	d1sg6a_	Alignment	not modelled	94.1	17	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
43	c1i3oC_	Alignment	not modelled	93.9	13	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**caspase 3; **PDBTitle:** crystal structure of the complex of xiap-bir2 and caspase 3
44	c3sipC_	Alignment	not modelled	93.7	19	**PDB header:**hydrolase/ligase/hydrolase **Chain:** C: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice and diap1-bir1 complex
45	c2wdpA_	Alignment	not modelled	93.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**caspase-6; **PDBTitle:** crystal structure of ligand free human caspase-6
46	c3uhjE_	Alignment	not modelled	93.4	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
47	c1i51A_	Alignment	not modelled	93.4	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7 subunit p20; **PDBTitle:** crystal structure of caspase-7 complexed with xiap
48	c1qduI_	Alignment	not modelled	93.4	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**caspase-8 alpha-chain; **PDBTitle:** crystal structure of the complex of caspase-8 with the tripeptide2 ketone inhibitor zevd-dcbmk
49	c3p45I_	Alignment	not modelled	93.3	12	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**caspase-6; **PDBTitle:** crystal structure of apo-caspase-6 at physiological ph
50	c1xahA_	Alignment	not modelled	93.3	16	**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+
51	c1pyoA_	Alignment	not modelled	93.3	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-2; **PDBTitle:** crystal structure of human caspase-2 in complex with acetyl-leu-asp-2 glu-ser-asp-cho
						PDB header:apoptosis

52	c3h11A_	Alignment	not modelled	92.9	8	**Chain:** A: **PDB Molecule:**casp8 and fadd-like apoptosis regulator; **PDBTitle:** zymogen caspase-8:c-flipl protease domain complex
53	d1f1ja_	Alignment	not modelled	92.7	16	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
54	c3edqC_	Alignment	not modelled	92.7	11	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**caspase-3; **PDBTitle:** crystal structure of caspase-3 with inhibitor ac-ldesd-cho
55	c2ql5A_	Alignment	not modelled	92.6	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of caspase-7 with inhibitor ac-dmqd-cho
56	c2nn3D_	Alignment	not modelled	92.6	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase-1; **PDBTitle:** structure of pro-sf-caspase-1
57	d1uz5a3	Alignment	not modelled	92.4	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
58	c2ywxA_	Alignment	not modelled	92.3	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
59	d1a9xb2	Alignment	not modelled	92.2	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
60	c2vpiA_	Alignment	not modelled	92.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
61	c3sirD_	Alignment	not modelled	91.8	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice
62	d1u9ca_	Alignment	not modelled	91.5	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
63	d1nw9b_	Alignment	not modelled	91.4	16	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
64	c2fqxA_	Alignment	not modelled	91.3	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc; **PDBTitle:** pnra from treponema pallidum complexed with guanosine
65	c2funB_	Alignment	not modelled	91.2	15	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-8; **PDBTitle:** alternative p35-caspase-8 complex
66	d2f48a1	Alignment	not modelled	91.0	16	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
67	c3zquA_	Alignment	not modelled	90.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
68	c1keeH_	Alignment	not modelled	90.8	24	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
69	c1kmcB_	Alignment	not modelled	90.6	16	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of the caspase-7 / xiap-bir2 complex
70	c3opyE_	Alignment	not modelled	90.6	12	**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	c3d54D_	Alignment	not modelled	90.6	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
72	d2ftsa3	Alignment	not modelled	90.5	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
73	c3opyG_	Alignment	not modelled	90.4	11	**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
74	c1zxxA_	Alignment	not modelled	90.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
75	c3k2qA_	Alignment	not modelled	89.3	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
76	d1qdlb_	Alignment	not modelled	89.2	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
77	d1pfka_	Alignment	not modelled	89.1	25	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
						PDB header:lyase

78	c2ejbA_	Alignment	not modelled	89.0	12	**Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
79	d1m72a_	Alignment	not modelled	89.0	15	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
80	c2hbzA_	Alignment	not modelled	88.9	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-1; **PDBTitle:** crystal structure of human caspase-1 (arg286->ala, glu390->ala) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)
81	c1nmqB_	Alignment	not modelled	88.9	13	**PDB header:**apoptosis, hydrolase **Chain:** B: **PDB Molecule:**caspase-3; **PDBTitle:** extendend tethering: in situ assembly of inhibitors
82	d1ptma_	Alignment	not modelled	88.3	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
83	d7reqa2	Alignment	not modelled	88.0	17	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
84	c2higA_	Alignment	not modelled	87.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
85	d4pfka_	Alignment	not modelled	87.9	21	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
86	c1cp3B_	Alignment	not modelled	87.8	10	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**apopain; **PDBTitle:** crystal structure of the complex of apopain with the tetrapeptide2 inhibitor ace-dvad-fmc
87	c3o8oC_	Alignment	not modelled	87.2	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
88	d1pjqa1	Alignment	not modelled	86.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
89	d2a5la1	Alignment	not modelled	86.6	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
90	c2q5cA_	Alignment	not modelled	86.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
91	c3opyB_	Alignment	not modelled	86.3	15	**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
92	c3opyH_	Alignment	not modelled	86.3	15	**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
93	c3gjzB_	Alignment	not modelled	86.0	19	**PDB header:**immune system **Chain:** B: **PDB Molecule:**microcin immunity protein mccf; **PDBTitle:** crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
94	d1i1qb_	Alignment	not modelled	85.8	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
95	c3o8nA_	Alignment	not modelled	85.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
96	c2yboA_	Alignment	not modelled	85.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
97	c2h31A_	Alignment	not modelled	85.5	13	**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
98	c2fp3A_	Alignment	not modelled	85.3	19	**PDB header:**hydrolysis/apoptosis **Chain:** A: **PDB Molecule:**caspase nc; **PDBTitle:** crystal structure of the drosophila initiator caspase dronc
99	d1mkza_	Alignment	not modelled	85.1	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
100	d1nbwb_	Alignment	not modelled	84.8	21	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Dehydratase-reactivating factor beta subunit
101	c3rfqC_	Alignment	not modelled	84.7	22	**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
102	d1di6a_	Alignment	not modelled	84.2	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
103	c2hqbA_	Alignment	not modelled	84.2	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
104	d1ujna_	Alignment	not modelled	83.8	14	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
105	d1o1ya_	Alignment	not modelled	83.7	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
106	c3f2vA_	Alignment	not modelled	83.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
107	d1xi8a3	Alignment	not modelled	83.1	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
108	d1r8ka_	Alignment	not modelled	82.9	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
109	d1t3ta2	Alignment	not modelled	82.9	8	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
110	c1rcuB_	Alignment	not modelled	82.9	31	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein vt76; **PDBTitle:** x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
111	d1rcua_	Alignment	not modelled	82.9	31	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
112	c3o8oB_	Alignment	not modelled	82.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase subunit beta; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
113	d2pjua1	Alignment	not modelled	82.6	15	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
114	d1vhqa_	Alignment	not modelled	82.5	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
115	c1zrsB_	Alignment	not modelled	82.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
116	d1g5qa_	Alignment	not modelled	81.9	10	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
117	c1sy7B_	Alignment	not modelled	81.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1; **PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
118	c3qjgD_	Alignment	not modelled	81.6	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**epidermin biosynthesis protein epid; **PDBTitle:** epidermin biosynthesis protein epid from staphylococcus aureus
119	d1qvwa_	Alignment	not modelled	81.5	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
120	d2g2ca1	Alignment	not modelled	81.5	20	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like