Phyre^2

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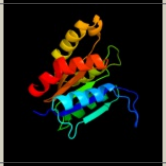
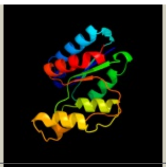
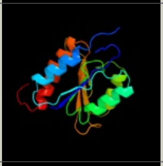
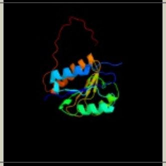
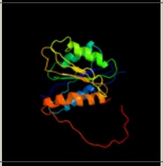
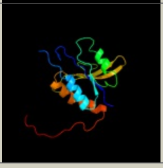
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1di6a_	Alignment		100.0	99	**Fold:** Molybdenum cofactor biosynthesis proteins **Superfamily:** Molybdenum cofactor biosynthesis proteins **Family:** MogA-like
2	d2f7wa1	Alignment		100.0	57	**Fold:** Molybdenum cofactor biosynthesis proteins **Superfamily:** Molybdenum cofactor biosynthesis proteins **Family:** MogA-like
3	d1uuya_	Alignment		100.0	34	**Fold:** Molybdenum cofactor biosynthesis proteins **Superfamily:** Molybdenum cofactor biosynthesis proteins **Family:** MogA-like
4	c2is8A_	Alignment		100.0	42	**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
5	d1jlja_	Alignment		100.0	36	**Fold:** Molybdenum cofactor biosynthesis proteins **Superfamily:** Molybdenum cofactor biosynthesis proteins **Family:** MogA-like
6	d1mkza_	Alignment		100.0	27	**Fold:** Molybdenum cofactor biosynthesis proteins **Superfamily:** Molybdenum cofactor biosynthesis proteins **Family:** MogA-like
7	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
8	c2pjkA_	Alignment		100.0	23	**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
9	c2g4rB_	Alignment		100.0	31	**PDB header:** biosynthetic protein **Chain:** B: **PDB Molecule:** molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
10	d1y5ea1	Alignment		100.0	30	**Fold:** Molybdenum cofactor biosynthesis proteins **Superfamily:** Molybdenum cofactor biosynthesis proteins **Family:** MogA-like
11	d2g2ca1	Alignment		100.0	20	**Fold:** Molybdenum cofactor biosynthesis proteins **Superfamily:** Molybdenum cofactor biosynthesis proteins **Family:** MogA-like

12	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
13	d2nqra3	Alignment		100.0	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
14	d2ftsa3	Alignment		100.0	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
15	c2nqqA_	Alignment		99.9	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
16	c2fu3A_	Alignment		99.9	12	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
17	c1uz5A_	Alignment		99.9	14	**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	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
19	d1wu2a3	Alignment		99.9	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
20	c1wu2B_	Alignment		99.8	18	**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	99.7	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
22	d1gpma2	Alignment	not modelled	93.1	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
23	d1wl8a1	Alignment	not modelled	92.5	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
24	c3qd5B_	Alignment	not modelled	92.0	17	**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	d1s1ma1	Alignment	not modelled	90.7	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
26	d2a9va1	Alignment	not modelled	88.9	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
27	c3onoA_	Alignment	not modelled	84.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
28	d1i7qb_	Alignment	not modelled	83.6	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
						PDB header:isomerase

29	c2xecD_	Alignment	not modelled	83.5	17	**Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
30	d1di0a_	Alignment	not modelled	82.6	12	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
31	d1u2ma_	Alignment	not modelled	82.4	17	**Fold:**OmpH-like **Superfamily:**OmpH-like **Family:**OmpH-like
32	d1rvv1_	Alignment	not modelled	82.2	15	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
33	d1nqua_	Alignment	not modelled	81.9	15	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
34	c3s99A_	Alignment	not modelled	81.2	13	**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
35	c3c5yD_	Alignment	not modelled	81.1	20	**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
36	c2ppwA_	Alignment	not modelled	80.4	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
37	d1jrla_	Alignment	not modelled	80.3	18	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**TAP-like
38	d1iofa_	Alignment	not modelled	78.8	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
39	d1a9xb2	Alignment	not modelled	78.6	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
40	d1qf6a1	Alignment	not modelled	78.5	18	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
41	c3he8A_	Alignment	not modelled	78.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
42	d1k9vf_	Alignment	not modelled	78.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
43	d1q7ra_	Alignment	not modelled	76.3	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
44	c2obxH_	Alignment	not modelled	75.9	19	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh2 from mesorhizobium loti (gene mll7281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
45	c2fqxA_	Alignment	not modelled	75.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc; **PDBTitle:** pnra from treponema pallidum complexed with guanosine
46	c3hp4A_	Alignment	not modelled	74.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gdsl-esterase; **PDBTitle:** crystal structure of psychrotrophic esterase esta from2 pseudoalteromonas sp. 643a inhibited by monoethylphosphonate
47	d2bona1	Alignment	not modelled	74.3	15	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
48	d1vcoa1	Alignment	not modelled	72.7	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
49	d1i1qb_	Alignment	not modelled	69.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
50	c3a9rA_	Alignment	not modelled	69.7	14	**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
51	d1nn4a_	Alignment	not modelled	68.8	12	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
52	d1dhsa_	Alignment	not modelled	68.0	32	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Deoxyhypusine synthase, DHS
53	d2naca2	Alignment	not modelled	68.0	14	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
54	d1o1xa_	Alignment	not modelled	67.2	8	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB

55	c1z0zC_	Alignment	not modelled	66.3	25	**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
56	d1z0sa1	Alignment	not modelled	66.3	25	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
57	c3pu6A_	Alignment	not modelled	65.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of an uncharacterized protein from wolinella2 succinogenes
58	d1nyra1	Alignment	not modelled	65.6	13	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
59	c2bonB_	Alignment	not modelled	64.4	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipid kinase; **PDBTitle:** structure of an escherichia coli lipid kinase (yegs)
60	d1ka9h_	Alignment	not modelled	64.1	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
61	c2v4uA_	Alignment	not modelled	62.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthase 2; **PDBTitle:** human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
62	c3giuA_	Alignment	not modelled	62.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrrolidone-carboxylate peptidase; **PDBTitle:** 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
63	c3cq9C_	Alignment	not modelled	62.4	17	**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
64	d2g4ca1	Alignment	not modelled	62.3	15	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
65	d2qv7a1	Alignment	not modelled	61.9	13	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
66	d2vvpa1	Alignment	not modelled	61.8	13	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
67	d1fuia2	Alignment	not modelled	61.7	14	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
68	d2jgra1	Alignment	not modelled	61.4	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
69	c2pjuD_	Alignment	not modelled	61.0	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
70	d1a2za_	Alignment	not modelled	61.0	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
71	c3lacA_	Alignment	not modelled	60.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrrolidone-carboxylate peptidase; **PDBTitle:** crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp
72	d2nv0a1	Alignment	not modelled	60.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
73	d1jq5a_	Alignment	not modelled	59.8	13	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
74	d1auga_	Alignment	not modelled	59.3	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
75	c3s5pA_	Alignment	not modelled	59.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
76	c3l4eA_	Alignment	not modelled	58.8	17	**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
77	d1xrsa_	Alignment	not modelled	58.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**D-lysine 5,6-aminomutase alpha subunit, KamD
78	d1cfza_	Alignment	not modelled	58.5	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Hydrogenase maturating endopeptidase HybD
79	d1c2ya_	Alignment	not modelled	58.3	10	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
80	d2ajta2	Alignment	not modelled	58.3	10	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains

						Family: AraA N-terminal and middle domain-like
81	d1o2da_	Alignment	not modelled	58.2	17	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
82	d1saza2	Alignment	not modelled	57.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
83	c2vk2A_	Alignment	not modelled	57.8	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
84	c3en0A_	Alignment	not modelled	56.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
85	c3hr4C_	Alignment	not modelled	56.8	12	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
86	c3ihkC_	Alignment	not modelled	53.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83
87	d1vlja_	Alignment	not modelled	53.3	13	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
88	d2p1ra1	Alignment	not modelled	52.5	16	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
89	c3orsD_	Alignment	not modelled	52.1	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
90	c2i2aA_	Alignment	not modelled	51.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
91	d3clsc1	Alignment	not modelled	51.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
92	d2pjua1	Alignment	not modelled	50.6	6	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
93	c3lftA_	Alignment	not modelled	50.0	15	**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
94	c2ywcC_	Alignment	not modelled	49.8	10	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
95	c2j37W_	Alignment	not modelled	49.0	13	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
96	d1ja1a2	Alignment	not modelled	48.9	5	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
97	c2vptA_	Alignment	not modelled	48.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipolytic enzyme; **PDBTitle:** clostridium thermocellum family 3 carbohydrate esterase
98	d1jr2a_	Alignment	not modelled	48.6	9	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
99	c1jr2A_	Alignment	not modelled	48.6	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
100	c1keeH_	Alignment	not modelled	48.5	23	**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
101	c3m1pA_	Alignment	not modelled	48.2	12	**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
102	c3k7pA_	Alignment	not modelled	48.2	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
103	c3lm8D_	Alignment	not modelled	47.5	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine pyrophosphokinase; **PDBTitle:** crystal structure of thiamine pyrophosphokinase from2 bacillus subtilis, northeast structural genomics consortium3 target sr677
104	c3ce9A_	Alignment	not modelled	47.4	10	**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
105	c1bvyF_	Alignment	not modelled	47.2	17	**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)
						Fold: Flavodoxin-like

106	d1bvyf_	Alignment	not modelled	47.2	17	**Superfamily:**Flavoproteins **Family:**Flavodoxin-related
107	c3r74B_	Alignment	not modelled	47.0	18	**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
108	c2an1D_	Alignment	not modelled	46.3	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
109	c2iy3A_	Alignment	not modelled	46.2	18	**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
110	d1vjga_	Alignment	not modelled	46.2	13	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Hypothetical protein alr1529
111	d1twda_	Alignment	not modelled	45.4	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
112	c2issF_	Alignment	not modelled	44.8	26	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
113	c3mk3L_	Alignment	not modelled	44.7	12	**PDB header:**transferase **Chain:** L: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase; **PDBTitle:** crystal structure of lumazine synthase from salmonella typhimurium lt2
114	d1wsaa_	Alignment	not modelled	44.2	11	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
115	d1iu8a_	Alignment	not modelled	43.6	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
116	c3melC_	Alignment	not modelled	43.1	15	**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
117	c3iwpK_	Alignment	not modelled	43.0	16	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
118	d1o94c_	Alignment	not modelled	43.0	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
119	c2r47C_	Alignment	not modelled	42.2	7	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein mth_862; **PDBTitle:** crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
120	c3s40C_	Alignment	not modelled	42.2	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne