Phyre^2

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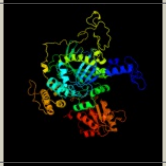
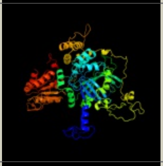
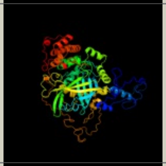
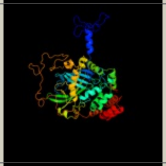
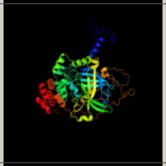
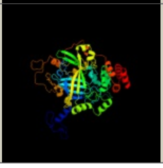
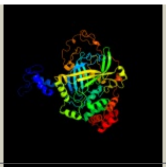
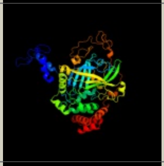
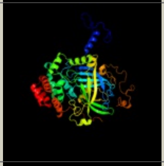
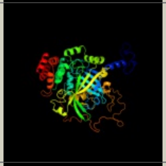
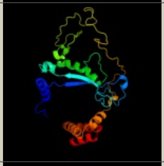
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1p81A_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli
2	c3ej6D_	Alignment		100.0	44	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
3	c2iufA_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase; **PDBTitle:** the structures of penicillium vitale catalase: resting2 state, oxidised state (compound i) and complex with3 aminotriazole
4	c1sy7B_	Alignment		100.0	50	**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.
5	d1p80a2	Alignment		100.0	100	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
6	c2j2mD_	Alignment		100.0	43	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase; **PDBTitle:** crystal structure analysis of catalase from exiguobacterium2 oxidotolerans
7	d1qwla_	Alignment		100.0	44	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
8	d1e93a_	Alignment		100.0	42	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
9	d1gwea_	Alignment		100.0	38	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
10	d1m7sa_	Alignment		100.0	39	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
11	d1si8a_	Alignment		100.0	44	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases

12	d4blca_	Alignment		100.0	40	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
13	d1dgfa_	Alignment		100.0	39	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
14	c2xq1M_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**peroxisomal catalase; **PDBTitle:** crystal structure of peroxisomal catalase from the yeast hansenula2 polymorpha
15	d1a4ea_	Alignment		100.0	39	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
16	c1f4jC_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**catalase; **PDBTitle:** structure of tetragonal crystals of human erythrocyte2 catalase
17	c1ye9E_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of proteolytically truncated catalase2 hpii from e. coli
18	c1ye9A_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of proteolytically truncated catalase2 hpii from e. coli
19	d1u5ua_	Alignment		100.0	18	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Allene oxide synthase
20	c3e4wB_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a 33kda catalase-related protein from2 mycobacterium avium subsp. paratuberculosis. p2(1)2(1)2(1) crystal3 form.
21	c3dy5A_	Alignment	not modelled	100.0	19	**PDB header:**lyase, oxidoreductase **Chain:** A: **PDB Molecule:**allene oxide synthase-lipoxygenase protein; **PDBTitle:** allene oxide synthase 8r-lipoxygenase from plexaura homomalla
22	d1p80a1	Alignment	not modelled	100.0	100	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
23	d1sy7a1	Alignment	not modelled	100.0	30	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
24	c3fseB_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and **PDBTitle:** crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
25	d1g2ia_	Alignment	not modelled	99.6	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
26	d1oi4a1	Alignment	not modelled	99.6	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
27	c3uk7B_	Alignment	not modelled	99.5	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
28	c2vrnA_	Alignment	not modelled	99.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease i; **PDBTitle:** the structure of the stress response protein dr1199 from2

						deinococcus radiodurans: a member of the dj-1 superfamily
29	c3cneD_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative protease i; **PDBTitle:** crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
30	c3ot1B_	Alignment	not modelled	99.4	15	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**4-methyl-5(b-hydroxyethyl)-thiazole monophosphate **PDBTitle:** crystal structure of vc2308 protein
31	d1p5fa_	Alignment	not modelled	99.4	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
32	d1vhqa_	Alignment	not modelled	99.4	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
33	c3kklA_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
34	d2fexa1	Alignment	not modelled	99.3	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
35	c3ewnA_	Alignment	not modelled	99.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of a thij/pfpi family protein from pseudomonas2 syringae
36	c3mgkA_	Alignment	not modelled	99.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**intracellular protease/amidase related enzyme **PDBTitle:** crystal structure of probable protease/amidase from2 clostridium acetobutylicum atcc 824
37	c3efeC_	Alignment	not modelled	99.2	13	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
38	c3l3bA_	Alignment	not modelled	99.2	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
39	c3nooB_	Alignment	not modelled	99.2	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
40	d1u9ca_	Alignment	not modelled	99.2	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
41	c3f5dA_	Alignment	not modelled	99.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis
42	d2ab0a1	Alignment	not modelled	99.1	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
43	d1qvwa_	Alignment	not modelled	99.1	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
44	c3graA_	Alignment	not modelled	99.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, arac family; **PDBTitle:** crystal structure of arac family transcriptional regulator from2 pseudomonas putida
45	c3n7tA_	Alignment	not modelled	99.0	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**macrophage binding protein; **PDBTitle:** crystal structure of a macrophage binding protein from coccidioides2 immitis
46	c3bhnA_	Alignment	not modelled	98.9	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thij/pfpi domain protein; **PDBTitle:** crystal structure of a dj-1/pfpi-like protein (shew_2856) from2 shewanella loihica pv-4 at 1.76 a resolution
47	c3er6D_	Alignment	not modelled	98.8	10	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative transcriptional regulator protein; **PDBTitle:** crystal structure of a putative transcriptional regulator2 protein from vibrio parahaemolyticus
48	d1n57a_	Alignment	not modelled	98.8	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
49	d1t3ta2	Alignment	not modelled	97.8	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
50	d1q7ra_	Alignment	not modelled	97.4	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
51	c3d54D_	Alignment	not modelled	97.2	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
52	d1o1ya_	Alignment	not modelled	97.1	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
53	d2nv0a1	Alignment	not modelled	97.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
54	d1ka9h_	Alignment	not modelled	97.0	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like

						Family: Class I glutamine amidotransferases (GAT)
55	c2issF_	Alignment	not modelled	96.9	21	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
56	c2ywjA_	Alignment	not modelled	96.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
57	c3l7nA_	Alignment	not modelled	96.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
58	d1a9xb2	Alignment	not modelled	96.4	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
59	c2ywdA_	Alignment	not modelled	96.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of glutamine amidotransferase
60	d2abwa1	Alignment	not modelled	96.0	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
61	d1jvna2	Alignment	not modelled	96.0	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
62	d1wl8a1	Alignment	not modelled	95.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
63	d1k9vf_	Alignment	not modelled	95.7	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
64	c3l83A_	Alignment	not modelled	95.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
65	c1keeH_	Alignment	not modelled	95.4	19	**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
66	d1i1qb_	Alignment	not modelled	95.3	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
67	d1gpma2	Alignment	not modelled	95.2	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
68	d1vcoa1	Alignment	not modelled	95.2	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
69	d2a9va1	Alignment	not modelled	95.0	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
70	c3r74B_	Alignment	not modelled	94.9	15	**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
71	c3fijD_	Alignment	not modelled	94.6	16	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
72	c1jvnB_	Alignment	not modelled	94.5	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
73	d2ghra1	Alignment	not modelled	94.5	8	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
74	d1qdlb_	Alignment	not modelled	93.9	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
75	c1vcnA_	Alignment	not modelled	93.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
76	c2w7tA_	Alignment	not modelled	93.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
77	c2ad5B_	Alignment	not modelled	92.5	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
78	c1t3tA_	Alignment	not modelled	92.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
79	c1l9xA_	Alignment	not modelled	92.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
						Fold: Flavodoxin-like

80	d1l9xa_	Alignment	not modelled	92.0	14	**Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
81	d1i7qb_	Alignment	not modelled	92.0	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
82	c3nvaB_	Alignment	not modelled	90.8	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
83	d1s1ma1	Alignment	not modelled	89.5	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
84	c3tqiB_	Alignment	not modelled	87.9	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
85	c3l4eA_	Alignment	not modelled	85.7	18	**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
86	c2vpiA_	Alignment	not modelled	85.5	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
87	c2v4uA_	Alignment	not modelled	85.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthase 2; **PDBTitle:** human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
88	c3lqkA_	Alignment	not modelled	84.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
89	c1gpmD_	Alignment	not modelled	83.9	14	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
90	c3mcuF_	Alignment	not modelled	83.8	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dipicolinate synthase, b chain; **PDBTitle:** crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
91	c2ywcC_	Alignment	not modelled	82.1	19	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
92	d1u9ya1	Alignment	not modelled	79.4	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
93	d1tc1a_	Alignment	not modelled	77.4	8	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
94	c3m4xA_	Alignment	not modelled	74.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
95	d2qv7a1	Alignment	not modelled	74.1	16	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
96	c3uowB_	Alignment	not modelled	70.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
97	c3ragA_	Alignment	not modelled	70.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
98	d2c4ka1	Alignment	not modelled	70.5	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
99	c2qv7A_	Alignment	not modelled	69.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase dgkb; **PDBTitle:** crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
100	d1vcha1	Alignment	not modelled	69.4	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
101	c2f59B_	Alignment	not modelled	66.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
102	d1dkua1	Alignment	not modelled	66.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
103	c3m6wA_	Alignment	not modelled	66.1	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
104	d1l5xa_	Alignment	not modelled	65.4	13	**Fold:**SurE-like **Superfamily:**SurE-like **Family:**SurE-like
105	c3lpnB_	Alignment	not modelled	63.5	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of the phosphoribosylpyrophosphate

						(prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
106	c3k9cA_	Alignment	not modelled	61.5	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
107	d1dxha2	Alignment	not modelled	61.5	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
108	d2gmqa1	Alignment	not modelled	60.5	29	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PrgU-like
109	c3okfA_	Alignment	not modelled	59.8	23	**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
110	c2phjA_	Alignment	not modelled	57.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of sure protein from aquifex aeolicus
111	d1gph11	Alignment	not modelled	57.4	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
112	c3dahB_	Alignment	not modelled	57.2	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
113	c2vxoB_	Alignment	not modelled	57.0	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
114	c2v4oB_	Alignment	not modelled	56.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**multifunctional protein sur e; **PDBTitle:** crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
115	c2xggB_	Alignment	not modelled	55.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**microneme protein 2; **PDBTitle:** structure of toxoplasma gondii micronemal protein 2 a_i2 domain
116	c2frxD_	Alignment	not modelled	54.4	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
117	c2e6gI_	Alignment	not modelled	53.5	18	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of the stationary phase survival protein sure from2 thermus thermophilus hb8 in complex with phosphate
118	c2c4kD_	Alignment	not modelled	52.3	19	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
119	d2g0ta1	Alignment	not modelled	51.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
120	c2obxH_	Alignment	not modelled	50.6	12	**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