Phyre2

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Description	P04079
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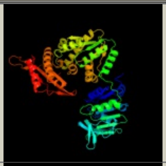
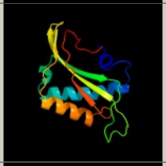
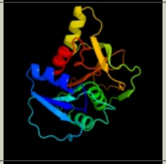
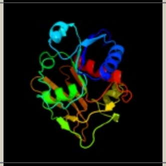
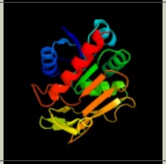
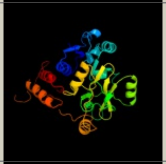
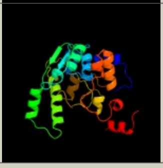
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gpmD_	Alignment		100.0	100	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
2	c2vxoB_	Alignment		100.0	41	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
3	c3uowB_	Alignment		100.0	44	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
4	c2ywcC_	Alignment		100.0	51	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
5	c3tqiB_	Alignment		100.0	64	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
6	c2dplA_	Alignment		100.0	52	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3
7	d1gpma3	Alignment		100.0	100	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**GMP synthetase C-terminal dimerisation domain **Family:**GMP synthetase C-terminal dimerisation domain
8	d1gpma2	Alignment		100.0	100	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
9	c2vpiA_	Alignment		100.0	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
10	d1wl8a1	Alignment		100.0	36	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
11	c1keeH_	Alignment		100.0	21	**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

12	d2a9va1	Alignment		100.0	31	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
13	d1i7qb_	Alignment		100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
14	c3r74B_	Alignment		100.0	17	**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
15	d1qdlb_	Alignment		100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
16	d1a9xb2	Alignment		100.0	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
17	d1gpma1	Alignment		100.0	100	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
18	d1i1qb_	Alignment		100.0	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
19	c1jvnB_	Alignment		100.0	16	**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
20	c3q4gA_	Alignment		100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
21	c3dpiA_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
22	d1kqpa_	Alignment	not modelled	100.0	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
23	d1wxia1	Alignment	not modelled	100.0	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
24	c2derA_	Alignment	not modelled	100.0	27	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma; **PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
25	d1jvna2	Alignment	not modelled	100.0	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
26	d1o1ya_	Alignment	not modelled	100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
27	c3d54D_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
28	c2hmaA_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae

29	c3l83A_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
30	d1ka9h_	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
31	c3l7nA_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
32	c3fiuD_	Alignment	not modelled	99.9	18	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
33	d1k9vf_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
34	d1s1ma1	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
35	c3fijD_	Alignment	not modelled	99.9	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
36	d1q7ra_	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
37	c3p52B_	Alignment	not modelled	99.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
38	d1vcoa1	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
39	c2ywjA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
40	c1l9xA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
41	d1l9xa_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
42	d2nv0a1	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
43	c2ywdA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of glutamine amidotransferase
44	c2issF_	Alignment	not modelled	99.9	20	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
45	c2e18B_	Alignment	not modelled	99.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3
46	c2w7tA_	Alignment	not modelled	99.9	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
47	c3nvaB_	Alignment	not modelled	99.9	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
48	c1vcnA_	Alignment	not modelled	99.9	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
49	c2ad5B_	Alignment	not modelled	99.9	20	**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.
50	c2v4uA_	Alignment	not modelled	99.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthase 2; **PDBTitle:** human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
51	d1t3ta2	Alignment	not modelled	99.9	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
52	c2c5sA_	Alignment	not modelled	99.9	21	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
53	d2c5sa1	Alignment	not modelled	99.9	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
54	d1xnga1	Alignment	not modelled	99.9	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases

55	d2abwa1	Alignment	not modelled	99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
56	d2ghra1	Alignment	not modelled	99.9	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
57	c3n05B_	Alignment	not modelled	99.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
58	c2h2wA_	Alignment	not modelled	99.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
59	c3bl5E_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
60	d1wy5a1	Alignment	not modelled	99.8	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
61	d1ni5a1	Alignment	not modelled	99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
62	c2e21A_	Alignment	not modelled	99.8	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
63	c3a2kB_	Alignment	not modelled	99.8	19	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
64	d2pg3a1	Alignment	not modelled	99.8	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
65	d1j20a1	Alignment	not modelled	99.8	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
66	c3k32D_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized protein mj0690; **PDBTitle:** the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
67	d1vl2a1	Alignment	not modelled	99.7	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
68	c1ni5A_	Alignment	not modelled	99.7	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
69	c2nz2A_	Alignment	not modelled	99.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
70	c3ilvA_	Alignment	not modelled	99.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
71	d1k92a1	Alignment	not modelled	99.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
72	c1vl2C_	Alignment	not modelled	99.7	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
73	d1vbka1	Alignment	not modelled	99.7	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
74	c1kh2D_	Alignment	not modelled	99.7	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
75	c3dlaD_	Alignment	not modelled	99.6	11	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
76	d1sura_	Alignment	not modelled	99.6	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
77	c1k97A_	Alignment	not modelled	99.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
78	c2o8vA_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
79	c2goyC_	Alignment	not modelled	99.4	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
80	d1zuna1	Alignment	not modelled	99.3	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like

81	c1vbkA_	Alignment	not modelled	99.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
82	c1zunA_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
83	c2oq2B_	Alignment	not modelled	98.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
84	d1ru8a_	Alignment	not modelled	98.9	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
85	d1ct9a1	Alignment	not modelled	98.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
86	c3g59A_	Alignment	not modelled	98.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fmn adenylyltransferase; **PDBTitle:** crystal structure of candida glabrata fmn2 adenylyltransferase in complex with atp
87	c1ct9D_	Alignment	not modelled	98.8	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli
88	d1q15a1	Alignment	not modelled	98.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
89	d1jgta1	Alignment	not modelled	98.7	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
90	c1q15A_	Alignment	not modelled	98.7	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
91	c2wsiA_	Alignment	not modelled	98.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fad synthetase; **PDBTitle:** crystal structure of yeast fad synthetase (fad1) in complex2 with fad
92	c1m1zB_	Alignment	not modelled	98.5	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
93	c1t3tA_	Alignment	not modelled	98.5	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
94	d2d13a1	Alignment	not modelled	98.1	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
95	c3uk7B_	Alignment	not modelled	97.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
96	c1sy7B_	Alignment	not modelled	97.5	13	**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.
97	c3l3bA_	Alignment	not modelled	97.2	25	**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
98	d1vhqa_	Alignment	not modelled	97.1	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
99	d1sy7a1	Alignment	not modelled	97.0	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
100	d1p80a1	Alignment	not modelled	96.9	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
101	c3cneD_	Alignment	not modelled	96.8	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative protease i; **PDBTitle:** crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
102	c3fseB_	Alignment	not modelled	96.8	23	**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
103	c3n7tA_	Alignment	not modelled	96.6	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**macrophage binding protein; **PDBTitle:** crystal structure of a macrophage binding protein from coccidioides2 immitis
104	d1qvwa_	Alignment	not modelled	96.5	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
105	d1n57a_	Alignment	not modelled	96.2	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
106	d1p5fa_	Alignment	not modelled	96.1	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like

						Family:DJ-1/PfpI
107	d1oi4a1	Alignment	not modelled	96.0	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
108	d1u9ca_	Alignment	not modelled	95.9	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
109	c3kklA_	Alignment	not modelled	95.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
110	c3l4eA_	Alignment	not modelled	95.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
111	c1p81A_	Alignment	not modelled	95.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli
112	d1g2ia_	Alignment	not modelled	95.3	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
113	d1fyea_	Alignment	not modelled	94.8	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
114	c3ot1B_	Alignment	not modelled	94.5	18	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**4-methyl-5(b-hydroxyethyl)-thiazole monophosphate **PDBTitle:** crystal structure of vc2308 protein
115	c3f5dA_	Alignment	not modelled	93.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis
116	d1xi8a3	Alignment	not modelled	93.2	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
117	c2vrnA_	Alignment	not modelled	93.0	14	**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
118	d2fexa1	Alignment	not modelled	92.7	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
119	d2ab0a1	Alignment	not modelled	92.7	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
120	d2jfga1	Alignment	not modelled	91.4	16	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain