Phyre2

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Description	P15254
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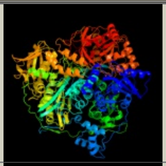
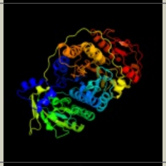
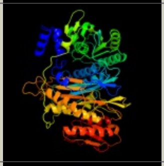
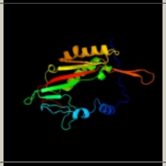
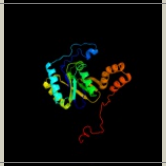
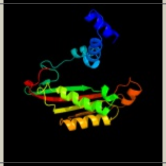
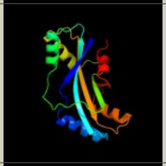
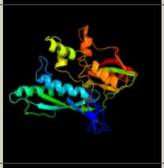
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1t3tA_	Alignment		100.0	94	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
2	c3ac6A_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 2; **PDBTitle:** crystal structure of purl from thermus thermophilus
3	c3d54I_	Alignment		100.0	25	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** stucture of purlqs from thermotoga maritima
4	c2hs0A_	Alignment		100.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** t. maritima purl complexed with atp
5	d1t3ta2	Alignment		100.0	94	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
6	d1t3ta4	Alignment		100.0	97	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
7	d1t3ta5	Alignment		100.0	95	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
8	d1t3ta7	Alignment		100.0	89	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
9	d1vk3a1	Alignment		100.0	36	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
10	d1t3ta3	Alignment		100.0	88	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**FGAM synthase PurL, PurS-like domain
11	d1t3ta6	Alignment		100.0	98	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like

12	d1vk3a2	Alignment		100.0	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
13	c3mcqA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine-monophosphate kinase; **PDBTitle:** crystal structure of thiamine-monophosphate kinase (mfla_0573) from2 methylobacillus flagellatus kt at 1.91 a resolution
14	c3d54D_	Alignment		100.0	30	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
15	d1vk3a3	Alignment		100.0	26	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
16	c2z1eA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hype from thermococcus kodakaraensis (outward2 form)
17	c2btuB_	Alignment		100.0	18	**PDB header:**synthase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole synthetase; **PDBTitle:** crystal structure of phosphoribosylformylglycinamidine2 cyclo-ligase from bacillus anthracis at 2.3a resolution.
18	c2yxzA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin-monophosphate kinase; **PDBTitle:** crystal structure of tt0281 from thermus thermophilus hb8
19	c2rb9D_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hype protein; **PDBTitle:** crystal structure of e.coli hype
20	c2z1tA_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hydrogenase maturation protein hype
21	c2zauB_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
22	c2zodB_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
23	c1cliD_	Alignment	not modelled	100.0	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**protein (phosphoribosyl-aminoimidazole synthetase); **PDBTitle:** x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
24	c2v9yA_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** human aminoimidazole ribonucleotide synthetase
25	c3m84A_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
26	c3fd5B_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase 1; **PDBTitle:** crystal structure of human selenophosphate synthetase 12 complex with ampcp
27	c2z01A_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 synthetase from geobacillus kaustophilus

28	c3c9uB_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** aathil complexed with adp and tpp
29	d1t3ta1	Alignment	not modelled	99.9	94	**Fold:**RuvA C-terminal domain-like **Superfamily:**FGAM synthase PurL, linker domain **Family:**FGAM synthase PurL, linker domain
30	c1vqvB_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** crystal structure of thiamine monophosphate kinase (thil)2 from aquifex aeolicus
31	d1clia2	Alignment	not modelled	99.8	13	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
32	d2z1ea2	Alignment	not modelled	99.8	21	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
33	d2zoda2	Alignment	not modelled	99.8	21	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
34	c3mdoB_	Alignment	not modelled	99.6	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of a putative phosphoribosylformylglycinamidine2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
35	c3fijD_	Alignment	not modelled	99.6	16	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
36	d1ka9h_	Alignment	not modelled	99.5	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
37	d3c9ua2	Alignment	not modelled	99.5	12	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
38	c1jvnB_	Alignment	not modelled	99.4	18	**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
39	d1jvna2	Alignment	not modelled	99.3	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
40	d2nv0a1	Alignment	not modelled	99.3	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
41	d2abwa1	Alignment	not modelled	99.3	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
42	d1qdlb_	Alignment	not modelled	99.2	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
43	d1clib1	Alignment	not modelled	99.2	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
44	d1q7ra_	Alignment	not modelled	99.2	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
45	d1k9vf_	Alignment	not modelled	99.2	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
46	c2issF_	Alignment	not modelled	99.2	20	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
47	c3kizA_	Alignment	not modelled	99.1	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of putative phosphoribosylformylglycinamidine cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
48	c2ywjA_	Alignment	not modelled	99.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
49	c3uowB_	Alignment	not modelled	99.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
50	c2ywdA_	Alignment	not modelled	99.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of glutamine amidotransferase
51	d1wl8a1	Alignment	not modelled	99.0	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
52	d1clia1	Alignment	not modelled	98.9	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
53	d2a9va1	Alignment	not modelled	98.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)

54	d1gpma2	Alignment	not modelled	98.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
55	d1i7qb_	Alignment	not modelled	98.9	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
56	d1vcoa1	Alignment	not modelled	98.9	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
57	d2zaua1	Alignment	not modelled	98.8	30	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
58	c1gpmD_	Alignment	not modelled	98.8	18	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
59	d2zoda1	Alignment	not modelled	98.8	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
60	c2ad5B_	Alignment	not modelled	98.8	22	**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.
61	c3l7nA_	Alignment	not modelled	98.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
62	c1keeH_	Alignment	not modelled	98.7	11	**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
63	d1o1ya_	Alignment	not modelled	98.7	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
64	c1l9xA_	Alignment	not modelled	98.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
65	d1l9xa_	Alignment	not modelled	98.7	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
66	c2vpiA_	Alignment	not modelled	98.6	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
67	d1i1qb_	Alignment	not modelled	98.6	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
68	d3c9ua1	Alignment	not modelled	98.6	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
69	d1a9xb2	Alignment	not modelled	98.6	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
70	c3nvaB_	Alignment	not modelled	98.6	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
71	c1vcnA_	Alignment	not modelled	98.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
72	c3tqiB_	Alignment	not modelled	98.6	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
73	c2ywcC_	Alignment	not modelled	98.5	22	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
74	d1s1ma1	Alignment	not modelled	98.5	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
75	c3l83A_	Alignment	not modelled	98.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
76	c3cneD_	Alignment	not modelled	98.4	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative protease i; **PDBTitle:** crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
77	d2z1ea1	Alignment	not modelled	98.4	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
78	c2vxoB_	Alignment	not modelled	98.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
79	d1sy7a1	Alignment	not modelled	98.3	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
80	c1sy7B_	Alignment	not modelled	98.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1;

80	c1sy7B_	Alignment	not modelled	98.5	14	**PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
81	c3fseB_	Alignment	not modelled	98.2	25	**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
82	d1oi4a1	Alignment	not modelled	98.1	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
83	c2w7tA_	Alignment	not modelled	98.1	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
84	d1p80a1	Alignment	not modelled	98.0	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
85	d1g2ia_	Alignment	not modelled	98.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
86	d1p5fa_	Alignment	not modelled	97.8	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
87	c2v4uA_	Alignment	not modelled	97.8	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
88	c3uk7B_	Alignment	not modelled	97.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
89	d2ghra1	Alignment	not modelled	97.7	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
90	d1vhqa_	Alignment	not modelled	97.6	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
91	c3ot1B_	Alignment	not modelled	97.6	21	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**4-methyl-5(b-hydroxyethyl)-thiazole monophosphate **PDBTitle:** crystal structure of vc2308 protein
92	c3kklA_	Alignment	not modelled	97.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
93	c3ewnA_	Alignment	not modelled	97.4	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
94	c3nooB_	Alignment	not modelled	97.4	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
95	d2ab0a1	Alignment	not modelled	97.3	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
96	c3n7tA_	Alignment	not modelled	97.3	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**macrophage binding protein; **PDBTitle:** crystal structure of a macrophage binding protein from coccidioides2 immitis
97	c3r74B_	Alignment	not modelled	97.3	12	**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
98	c3f5dA_	Alignment	not modelled	97.2	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis
99	d2fexa1	Alignment	not modelled	97.1	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
100	d1qvwa_	Alignment	not modelled	97.1	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
101	c3l3bA_	Alignment	not modelled	97.0	20	**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
102	c2vrnA_	Alignment	not modelled	96.8	20	**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
103	c2h2wA_	Alignment	not modelled	96.8	15	**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
104	c3efeC_	Alignment	not modelled	96.8	22	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
105	c3mgkA_	Alignment	not modelled	96.6	15	**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
106	c2yx5A_	Alignment	not modelled	96.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
107	d1vq3a_	Alignment	not modelled	96.2	17	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
108	c3bhnA_	Alignment	not modelled	96.1	13	**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
109	c2zw2B_	Alignment	not modelled	95.9	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
110	d1n57a_	Alignment	not modelled	95.9	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
111	d1t4aa_	Alignment	not modelled	95.8	14	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
112	c1p81A_	Alignment	not modelled	95.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli
113	c3er6D_	Alignment	not modelled	95.7	16	**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
114	d1u9ca_	Alignment	not modelled	95.6	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
115	d1gtda_	Alignment	not modelled	95.4	13	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
116	c2dgbA_	Alignment	not modelled	95.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
117	c3graA_	Alignment	not modelled	94.6	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, arac family; **PDBTitle:** crystal structure of arac family transcriptional regulator from2 pseudomonas putida
118	c3l4eA_	Alignment	not modelled	93.3	14	**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
119	d1fyea_	Alignment	not modelled	75.6	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
120	d1sgva1	Alignment	not modelled	73.3	25	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain