



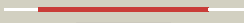




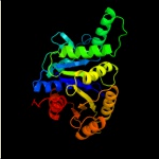








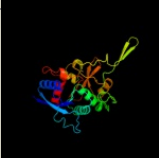













#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ad5B_	 Alignment		100.0	99	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
2	c3nvaB_	 Alignment		100.0	49	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
3	c1vcnA_	 Alignment		100.0	54	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
4	dlslma2	 Alignment		100.0	100	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
5	dlvcoa2	 Alignment		100.0	59	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
6	d2vo1a1	 Alignment		100.0	54	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
7	c2v4uA_	 Alignment		100.0	46	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
8	dlslma1	 Alignment		100.0	99	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
9	c2w7tA_	 Alignment		100.0	41	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
10	dlvcoa1	 Alignment		100.0	48	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
11	c3fijD_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909

12	d1a9xb2	Alignment		99.9	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
13	c1keeH_	Alignment		99.9	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
14	d2a9va1	Alignment		99.9	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
15	d1i7qb_	Alignment		99.9	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
16	c1gpmD_	Alignment		99.9	23	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
17	d1wl8a1	Alignment		99.9	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
18	d1gpm2	Alignment		99.9	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
19	d1qdlb_	Alignment		99.9	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
20	d1l9xa_	Alignment		99.9	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
21	c1l9xA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
22	c2ywcC_	Alignment	not modelled	99.9	24	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
23	d1i1qb_	Alignment	not modelled	99.9	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
24	d2nv0a1	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
25	c2vx0B_	Alignment	not modelled	99.9	24	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
26	c3uowB_	Alignment	not modelled	99.9	17	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
27	c2vpiA_	Alignment	not modelled	99.9	23	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
28	d1k9vf_	Alignment	not modelled	99.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
29	d1q7ra_	Alignment	not modelled	99.9	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like

						Family: Class I glutamine amidotransferases (GAT)
30	c1jvnB_	Alignment	not modelled	99.9	23	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
31	c3tqiB_	Alignment	not modelled	99.9	27	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
32	c2issF_	Alignment	not modelled	99.8	21	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
33	c2ywjA_	Alignment	not modelled	99.8	26	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
34	d1t3ta2	Alignment	not modelled	99.8	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	d2abwa1	Alignment	not modelled	99.8	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
36	c3d54D_	Alignment	not modelled	99.8	18	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: stucture of purlqs from thermotoga maritima
37	c3r74B_	Alignment	not modelled	99.8	20	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
38	d1jvna2	Alignment	not modelled	99.8	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
39	d1ka9h_	Alignment	not modelled	99.8	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
40	c2ywdA_	Alignment	not modelled	99.8	29	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
41	c3l7nA_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
42	c3l83A_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
43	d1o1ya_	Alignment	not modelled	99.7	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
44	d2ghra1	Alignment	not modelled	99.6	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
45	c2h2wA_	Alignment	not modelled	99.5	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
46	c1t3tA_	Alignment	not modelled	98.4	19	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
47	c3of5A_	Alignment	not modelled	97.4	15	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
48	d1byia_	Alignment	not modelled	97.3	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
49	c2qmoA_	Alignment	not modelled	96.9	16	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
50	c3l4eA_	Alignment	not modelled	96.9	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
51	c1sy7B_	Alignment	not modelled	96.5	14	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.
52	c3fmfA_	Alignment	not modelled	96.4	16	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
53	c3cioA_	Alignment	not modelled	96.1	20	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
54	c3uk7B_	Alignment	not modelled	96.1	24	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing

					PDBTitle: crystal structure of arabidopsis thaliana dj-1d
55	d1fyea_	Alignment	not modelled	96.1	19 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
56	d1p80a1	Alignment	not modelled	96.1	14 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
57	c3cneD_	Alignment	not modelled	95.9	15 PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
58	c3ibgF_	Alignment	not modelled	95.9	20 PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
59	d1p5fa_	Alignment	not modelled	95.7	10 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
60	d1sy7a1	Alignment	not modelled	95.6	12 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
61	c3n7tA_	Alignment	not modelled	95.6	17 PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
62	c3kkIA_	Alignment	not modelled	95.5	18 PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
63	c3l3bA_	Alignment	not modelled	95.4	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
64	d1vhqa_	Alignment	not modelled	95.4	24 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
65	d1iona_	Alignment	not modelled	95.4	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
66	d1qvwa_	Alignment	not modelled	95.3	11 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
67	c3nooB_	Alignment	not modelled	95.0	19 PDB header: lyase Chain: B: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
68	d1g2ia_	Alignment	not modelled	94.9	24 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
69	c3fseB_	Alignment	not modelled	94.7	24 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
70	c3graA_	Alignment	not modelled	94.5	13 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from2 pseudomonas putida
71	d1g3qa_	Alignment	not modelled	94.2	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
72	d1oi4a1	Alignment	not modelled	94.1	35 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
73	c2ph1A_	Alignment	not modelled	94.0	16 PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein; PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
74	c2j7pA_	Alignment	not modelled	94.0	22 PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
75	d1u9ca_	Alignment	not modelled	94.0	22 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
76	c1ii0A_	Alignment	not modelled	93.9	33 PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
77	c2wojD_	Alignment	not modelled	93.9	17 PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
78	d1n57a_	Alignment	not modelled	93.8	27 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
79	c3zq6D_	Alignment	not modelled	93.8	28 PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
					PDB header: hydrolase

80	c3ug7D_	Alignment	not modelled	93.7	38	Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
81	d1tjya_	Alignment	not modelled	93.5	19	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
82	c3f5dA_	Alignment	not modelled	93.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from2 bacillus subtilis
83	c3endA_	Alignment	not modelled	93.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the I protein of rhodobacter2 spheraoides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
84	c2an1D_	Alignment	not modelled	92.9	30	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
85	d2afhe1	Alignment	not modelled	92.9	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	c1hyqA_	Alignment	not modelled	92.8	33	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
87	d1hyqa_	Alignment	not modelled	92.8	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
88	c2bekB_	Alignment	not modelled	92.5	30	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein2 soj
89	c3k9cA_	Alignment	not modelled	92.4	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
90	c2wooc_	Alignment	not modelled	91.9	30	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
91	c3brsA_	Alignment	not modelled	91.7	12	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
92	c3er6D_	Alignment	not modelled	91.6	8	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
93	c3efeC_	Alignment	not modelled	91.5	16	PDB header: chaperone Chain: C: PDB Molecule: thij/pfpi family protein; PDBTitle: the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
94	d1xjca_	Alignment	not modelled	91.5	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
95	c3q9lB_	Alignment	not modelled	91.4	23	PDB header: cell cycle, hydrolase Chain: B: PDB Molecule: septum site-determining protein mind; PDBTitle: the structure of the dimeric e.coli mind-atp complex
96	c3bhnA_	Alignment	not modelled	91.4	19	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
97	c3k9gA_	Alignment	not modelled	91.3	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
98	d2ab0a1	Alignment	not modelled	91.2	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
99	d1cp2a_	Alignment	not modelled	90.8	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
100	c2xj9B_	Alignment	not modelled	90.6	25	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
101	d8abpa_	Alignment	not modelled	90.5	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
102	c1p81A_	Alignment	not modelled	90.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
103	c3ot1B_	Alignment	not modelled	90.2	17	PDB header: structural genomics Chain: B: PDB Molecule: 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate PDBTitle: crystal structure of vc2308 protein
104	c2qy9A_	Alignment	not modelled	90.0	24	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy

105	c3io3A_	Alignment	not modelled	89.8	30	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
106	c3dmdA_	Alignment	not modelled	89.7	31	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
107	d2fexa1	Alignment	not modelled	89.6	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
108	c3ewnA_	Alignment	not modelled	89.3	14	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
109	dlsq5a_	Alignment	not modelled	89.1	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
110	d1rz3a_	Alignment	not modelled	88.8	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
111	c2vedA_	Alignment	not modelled	88.7	24	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
112	c2og2A_	Alignment	not modelled	88.6	29	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
113	c3kigB_	Alignment	not modelled	88.3	32	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
114	c3lv8A_	Alignment	not modelled	88.3	19	PDB header: transferase Chain: A: PDB Molecule: thymidylate kinase; PDBTitle: 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tmk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp
115	dlihua2	Alignment	not modelled	88.3	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
116	c3en0A_	Alignment	not modelled	88.0	14	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
117	c2f1rA_	Alignment	not modelled	87.9	26	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobbb)
118	c3b9qA_	Alignment	not modelled	87.8	29	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts from arabidopsis thaliana
119	dlihua1	Alignment	not modelled	87.7	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
120	c1vmaA_	Alignment	not modelled	87.7	29	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution