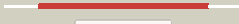



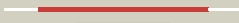




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1699_(pyrG)_1923836_1925596
Date	Fri Aug 2 13:30:30 BST 2019
Unique Job ID	c8c69d13db8fd0e0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zdiE_	 Alignment		100.0	100	PDB header: ligase Chain: E: PDB Molecule: ctp synthase; PDBTitle: crystal structure of the m. tuberculosis ctp synthase pyrG (apo form)
2	c5u03C_	 Alignment		100.0	47	PDB header: ligase, protein fibril Chain: C: PDB Molecule: ctp synthase 1; PDBTitle: cryo-em structure of the human ctp synthase filament
3	c2ad5B_	 Alignment		100.0	52	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.
4	c3nvaB_	 Alignment		100.0	49	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
5	c1vcnA_	 Alignment		100.0	56	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
6	d1vcoa2	 Alignment		100.0	58	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
7	d1s1ma2	 Alignment		100.0	62	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
8	d2vo1a1	 Alignment		100.0	52	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
9	c2v4uA_	 Alignment		100.0	42	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
10	c2w7tA_	 Alignment		100.0	40	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound acivicin
11	d1s1ma1	 Alignment		100.0	46	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

12	d1vcoa1	Alignment		100.0	56	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
13	c3fijD_	Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
14	d1a9xb2	Alignment		99.9	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
15	c4l8fA_	Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
16	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
17	d1l9xa_	Alignment		99.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
18	c1l9xA_	Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
19	d2a9va1	Alignment		99.9	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
20	d1i7qb_	Alignment		99.9	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
21	c6qurA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
22	d1wl8a1	Alignment	not modelled	99.9	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
23	c1gpmD_	Alignment	not modelled	99.9	20	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
24	d1gpmA2	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
25	c2ywcC_	Alignment	not modelled	99.9	21	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
26	c5tw7E_	Alignment	not modelled	99.9	20	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
27	d1qdlb_	Alignment	not modelled	99.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
28	d1l1qb_	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
						PDB header: ligase

29	c2lxnA	Alignment	not modelled	99.9	20	Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit a; PDBTitle: solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
30	c3uowB	Alignment	not modelled	99.9	16	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
31	c2vxoB	Alignment	not modelled	99.9	19	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
32	d1k9vf	Alignment	not modelled	99.8	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
33	d2nv0a1	Alignment	not modelled	99.8	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
34	c2vpiA	Alignment	not modelled	99.8	19	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
35	c3tqiB	Alignment	not modelled	99.8	20	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
36	c5dotA	Alignment	not modelled	99.8	24	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
37	c4gudA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
38	c5douC	Alignment	not modelled	99.8	22	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
39	d1q7ra	Alignment	not modelled	99.8	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
40	d1jvna2	Alignment	not modelled	99.8	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	c3d54D	Alignment	not modelled	99.8	17	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
42	c2ywjA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
43	c2issF	Alignment	not modelled	99.8	20	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
44	c3r74B	Alignment	not modelled	99.8	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
45	c1jvnB	Alignment	not modelled	99.8	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
46	c3l7nA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
47	d1ka9h	Alignment	not modelled	99.8	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
48	c2ywdA	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
49	d2abwa1	Alignment	not modelled	99.8	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
50	d1t3ta2	Alignment	not modelled	99.8	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
51	c3l83A	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
52	d1o1ya	Alignment	not modelled	99.7	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
53	d2ghra1	Alignment	not modelled	99.6	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like

54	c2h2wA	Alignment	not modelled	99.4	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
55	c6mtgB	Alignment	not modelled	99.2	15	PDB header: transferase Chain: B: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
56	c6fqbE	Alignment	not modelled	99.1	19	PDB header: ligase Chain: E: PDB Molecule: cobyrinic acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
57	c5n9mA	Alignment	not modelled	98.8	18	PDB header: transferase Chain: A: PDB Molecule: cobyrinic acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
58	c1t3tA	Alignment	not modelled	97.8	21	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
59	c3of5A	Alignment	not modelled	97.4	13	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
60	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
61	c6a4tB	Alignment	not modelled	96.6	22	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
62	c3fmfA	Alignment	not modelled	96.5	19	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
63	c2qmoA	Alignment	not modelled	96.4	16	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
64	c3ibgF	Alignment	not modelled	96.4	19	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
65	c3l4eA	Alignment	not modelled	96.2	12	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
66	c3zq6D	Alignment	not modelled	96.1	22	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
67	c3cneD	Alignment	not modelled	96.0	13	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
68	c3uk7B	Alignment	not modelled	95.7	20	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
69	c1sy7B	Alignment	not modelled	95.4	15	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.
70	c4pfsA	Alignment	not modelled	95.3	18	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
71	c3n7tA	Alignment	not modelled	95.3	18	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
72	c3kkIA	Alignment	not modelled	95.2	16	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
73	d1fyea	Alignment	not modelled	95.2	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
74	c3cioA	Alignment	not modelled	95.1	22	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
75	c1ii0A	Alignment	not modelled	95.1	28	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
76	d1p80a1	Alignment	not modelled	95.1	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
77	c2wojD	Alignment	not modelled	95.1	18	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
78	c4hcgA	Alignment	not modelled	94.9	17	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
79	d1qvwa	Alignment	not modelled	94.8	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like

						Family: DJ-1/Pfpl
80	c4iruA	Alignment	not modelled	94.7	16	PDB header: lyase Chain: A: PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from candida albicans
81	d1vhqa	Alignment	not modelled	94.6	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
82	c3l3bA	Alignment	not modelled	94.6	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
83	c6dspB	Alignment	not modelled	94.4	14	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrB; PDBTitle: lsrB from clostridium saccharobutylicum in complex with ai-2
84	c3n2aA	Alignment	not modelled	94.4	30	PDB header: ligase Chain: A: PDB Molecule: bifunctional folypolyglutamate synthase/dihydrofolate PDBTitle: crystal structure of bifunctional folypolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
85	c3graA	Alignment	not modelled	94.3	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from2 pseudomonas putida
86	c3ug7D	Alignment	not modelled	94.2	33	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
87	d1tjya	Alignment	not modelled	94.2	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
88	c5z6vA	Alignment	not modelled	94.2	22	PDB header: protein transport Chain: A: PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
89	c4pz0A	Alignment	not modelled	94.1	15	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar abc transporter, sugar-binding protein; PDBTitle: the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
90	c4p5pA	Alignment	not modelled	94.0	11	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi family protein; PDBTitle: x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
91	c5ulbA	Alignment	not modelled	93.9	15	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter from yersinia2 enterocolitica subsp. enterocolitica 8081
92	c4rxuA	Alignment	not modelled	93.9	16	PDB header: transport protein Chain: A: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
93	c3fseB	Alignment	not modelled	93.8	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 anaerobaculum variabilis3 atcc 29413 at 1.90 a resolution
94	c2bekB	Alignment	not modelled	93.6	25	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
95	d1oi4a1	Alignment	not modelled	93.5	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
96	c5dkvD	Alignment	not modelled	93.5	16	PDB header: sugar binding protein Chain: D: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein from2 agrobacterium vitis(avis_5339, target efi-511225) bound with alpha-d-3 tagatopyranose
97	c2vosA	Alignment	not modelled	93.4	25	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase protein folC; PDBTitle: mycobacterium tuberculosis folypolyglutamate synthase2 complexed with adp
98	d1iona	Alignment	not modelled	93.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
99	c3endA	Alignment	not modelled	93.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the I protein of rhodospirillum rubrum light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
100	c4i2nC	Alignment	not modelled	92.9	29	PDB header: hydrolase Chain: C: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
101	c1o5zA	Alignment	not modelled	92.8	24	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase/dihydrofolate synthase; PDBTitle: crystal structure of folypolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
						Fold: P-loop containing nucleoside triphosphate hydrolases

102	d2afhe1	Alignment	not modelled	92.8	27	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
103	c5l3qb	Alignment	not modelled	92.8	18	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
104	d1n57a	Alignment	not modelled	92.7	27	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
105	d1hyqa	Alignment	not modelled	92.6	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
106	c1hyqA	Alignment	not modelled	92.6	28	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
107	d1o5za2	Alignment	not modelled	92.6	27	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
108	d1u9ca	Alignment	not modelled	92.5	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
109	c5l3rC	Alignment	not modelled	92.5	18	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
110	d1p5fa	Alignment	not modelled	92.5	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
111	d1g3qa	Alignment	not modelled	92.4	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
112	c5bwkA	Alignment	not modelled	92.3	29	PDB header: hydrolase/transport Chain: A: PDB Molecule: atpase get3; PDBTitle: 6.0 a crystal structure of a get3-get4-get5 intermediate complex from2 s.cerevisiae
113	c5l3sF	Alignment	not modelled	92.3	18	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
114	c5zmfA	Alignment	not modelled	92.3	18	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
115	c4v02B	Alignment	not modelled	92.2	18	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
116	c6g2gA	Alignment	not modelled	92.2	21	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
117	c3k9gA	Alignment	not modelled	92.2	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
118	c5l1jA	Alignment	not modelled	92.2	22	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
119	c3io3A	Alignment	not modelled	92.2	30	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
120	c3f5dA	Alignment	not modelled	92.1	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from bacillus2 subtilis