

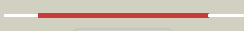





















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3713_(cobQ2)_4158405_4159100
Date	Fri Aug 9 18:20:41 BST 2019
Unique Job ID	4a544ecb5537a230

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fqbE_	 Alignment		100.0	30	PDB header: ligase Chain: E: PDB Molecule: cobyric acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
2	c5n9mA_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: cobyric acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
3	d1q7ra_	 Alignment		100.0	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
4	d2nv0a1	 Alignment		99.9	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
5	c2ywdA_	 Alignment		99.9	20	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
6	d2abwa1	 Alignment		99.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
7	c2issF_	 Alignment		99.9	21	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
8	c1jvnB_	 Alignment		99.9	16	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hish1f; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
9	d1k9vf_	 Alignment		99.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
10	c2ywjA_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
11	d1ka9h_	 Alignment		99.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

12	c3l7nA_	Alignment		99.8	17	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
13	d1o1ya_	Alignment		99.8	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
14	d1jvna2	Alignment		99.8	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
15	c3l83A_	Alignment		99.8	15	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
16	d2a9va1	Alignment		99.8	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
17	c2ywcC_	Alignment		99.7	18	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
18	c4gudA_	Alignment		99.7	20	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
19	c1gpmD_	Alignment		99.7	15	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
20	d1wl8a1	Alignment		99.7	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
21	d1i7qb_	Alignment	not modelled	99.7	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
22	c3tqiB_	Alignment	not modelled	99.7	16	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
23	c5tw7E_	Alignment	not modelled	99.7	15	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
24	c3d54D_	Alignment	not modelled	99.7	16	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
25	d1gpma2	Alignment	not modelled	99.7	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
26	d1qd1b_	Alignment	not modelled	99.7	10	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
27	c3r74B_	Alignment	not modelled	99.7	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
28	d1t3ta2	Alignment	not modelled	99.7	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

29	c3uowB_	Alignment	not modelled	99.7	12	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
30	c6qurA_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
31	c2vpiA_	Alignment	not modelled	99.6	17	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
32	c2vxob_	Alignment	not modelled	99.6	17	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
33	c2lxnA_	Alignment	not modelled	99.6	14	PDB header: ligase 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
34	d1i1qb_	Alignment	not modelled	99.6	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	d1s1ma1	Alignment	not modelled	99.6	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
36	c3fijD_	Alignment	not modelled	99.5	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
37	d1a9xb2	Alignment	not modelled	99.5	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
38	c1vcnA_	Alignment	not modelled	99.5	15	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
39	c1keeH_	Alignment	not modelled	99.5	18	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
40	d1vcoa1	Alignment	not modelled	99.5	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	c2w7tA_	Alignment	not modelled	99.3	11	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound acivicin
42	c5u03C_	Alignment	not modelled	99.3	18	PDB header: ligase, protein fibril Chain: C: PDB Molecule: ctp synthase 1; PDBTitle: cryo-em structure of the human ctp synthase filament
43	c3nvaB_	Alignment	not modelled	99.3	18	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
44	c2ad5B_	Alignment	not modelled	99.3	19	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.
45	c4zdiE_	Alignment	not modelled	99.2	18	PDB header: ligase Chain: E: PDB Molecule: ctp synthase; PDBTitle: crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
46	c5dotA_	Alignment	not modelled	99.2	16	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
47	c5douC_	Alignment	not modelled	99.2	16	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
48	d2ghra1	Alignment	not modelled	99.1	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
49	c4l8fA_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
50	c2v4uA_	Alignment	not modelled	99.1	14	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	d1l9xa_	Alignment	not modelled	99.0	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
52	c1l9xA_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
53	c3l4eA_	Alignment	not modelled	98.9	12	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e

54	d1fyea_	Alignment	not modelled	98.6	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
55	c6a4tB_	Alignment	not modelled	98.6	20	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
56	c2h2wA_	Alignment	not modelled	98.3	11	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
57	c3uk7B_	Alignment	not modelled	98.2	23	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
58	d1sy7a1	Alignment	not modelled	98.2	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
59	c1sy7B_	Alignment	not modelled	98.1	12	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.
60	c6mtgB_	Alignment	not modelled	98.1	12	PDB header: transferase Chain: B: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
61	c4lruA_	Alignment	not modelled	98.0	18	PDB header: lyase Chain: A: PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from candida albicans
62	c3l3bA_	Alignment	not modelled	98.0	14	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
63	d1qvwa_	Alignment	not modelled	98.0	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
64	c4xllB_	Alignment	not modelled	97.8	15	PDB header: unknown function Chain: B: PDB Molecule: dj-1 family protein; PDBTitle: toxoplasma gondii dj-1, oxidized
65	d1p80a1	Alignment	not modelled	97.8	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
66	c3kklA_	Alignment	not modelled	97.7	12	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
67	c3fseB_	Alignment	not modelled	97.7	16	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
68	d1oi4a1	Alignment	not modelled	97.7	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
69	d1p5fa_	Alignment	not modelled	97.6	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
70	c3n7tA_	Alignment	not modelled	97.6	15	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
71	c4p5pA_	Alignment	not modelled	97.6	13	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
72	d1g2ia_	Alignment	not modelled	97.5	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
73	c4e08B_	Alignment	not modelled	97.5	20	PDB header: motor protein Chain: B: PDB Molecule: dj-1 beta; PDBTitle: crystal structure of drosophila melanogaster dj-1beta
74	c3cneD_	Alignment	not modelled	97.5	13	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
75	d1vhqa_	Alignment	not modelled	97.4	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
76	c4hclA_	Alignment	not modelled	97.4	8	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
77	c3f5dA_	Alignment	not modelled	97.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from bacillus2 subtilis
78	d2fexa1	Alignment	not modelled	97.2	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
79	c4y0nB_	Alignment	not modelled	97.2	13	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein sav1875;

						PDBTitle: sav1875
80	d1u9ca_	Alignment	not modelled	97.2	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
81	c3ot1B_	Alignment	not modelled	97.0	14	PDB header: structural genomics Chain: B: PDB Molecule: 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate PDBTitle: crystal structure of vc2308 protein
82	c3er6D_	Alignment	not modelled	97.0	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative transcriptional regulator protein; PDBTitle: crystal structure of a putative transcriptional regulator protein from2 vibrio parahaemolyticus
83	c4k2hG_	Alignment	not modelled	96.9	15	PDB header: unknown function Chain: G: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of c103a mutant of dj-1 superfamily protein stm19312 from salmonella typhimurium
84	c2vrnA_	Alignment	not modelled	96.9	13	PDB header: hydrolase Chain: A: PDB Molecule: protease i; PDBTitle: the structure of the stress response protein dr1199 from deinococcus2 radiodurans: a member of the dj-1 superfamily
85	c3en0A_	Alignment	not modelled	96.9	13	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
86	c3nooB_	Alignment	not modelled	96.9	16	PDB header: lyase Chain: B: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
87	c3mgkA_	Alignment	not modelled	96.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: intracellular protease/amidase related enzyme (thij) PDBTitle: crystal structure of probable protease/amidase from clostridium2 acetobutylicum atcc 824
88	c1t3tA_	Alignment	not modelled	96.8	20	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
89	c3ewnA_	Alignment	not modelled	96.6	17	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
90	c1p81A_	Alignment	not modelled	96.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
91	d2ab0a1	Alignment	not modelled	96.5	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
92	c4ge0C_	Alignment	not modelled	96.5	10	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein c22e12.03c; PDBTitle: schizosaccharomyces pombe dj-1 t114p mutant
93	c3efeC_	Alignment	not modelled	96.3	27	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	c3graA_	Alignment	not modelled	96.3	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from2 pseudomonas putida
95	c4i2nC_	Alignment	not modelled	96.3	14	PDB header: hydrolase Chain: C: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
96	c5xr2D_	Alignment	not modelled	96.3	12	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase hcha; PDBTitle: sav0551
97	d1n57a_	Alignment	not modelled	96.3	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
98	c3bhnA_	Alignment	not modelled	94.6	16	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
99	c3ej6D_	Alignment	not modelled	92.5	21	PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: neurospora crassa catalase-3 crystal structure
100	c5fmsA_	Alignment	not modelled	91.7	14	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 52 homolog; PDBTitle: mmift52 n-terminal domain
101	c4rxuA_	Alignment	not modelled	90.7	15	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
102	c3o1hB_	Alignment	not modelled	90.1	12	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
103	c5vymB_	Alignment	not modelled	89.7	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase bgab; PDBTitle: crystal structure of beta-galactosidase from bifidobacterium2 adolescentis
104	c5widB_	Alignment	not modelled	89.4	11	PDB header: flavoprotein Chain: B: PDB Molecule: flavodoxin; PDBTitle: structure of a flavodoxin from the domain archaea
						Fold: Flavodoxin-like

105	d1ydga_	Alignment	not modelled	88.0	14	Superfamily: Flavoproteins Family: WrbA-like
106	d1kwga3	Alignment	not modelled	87.9	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: A4 beta-galactosidase middle domain
107	c5f4bB_	Alignment	not modelled	86.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
108	d1e5da1	Alignment	not modelled	85.2	5	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
109	c2zkih_	Alignment	not modelled	83.6	22	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
110	c6hyhA_	Alignment	not modelled	83.6	12	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose
111	c1gshA_	Alignment	not modelled	83.5	18	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
112	c5vegC_	Alignment	not modelled	82.8	16	PDB header: electron transport Chain: C: PDB Molecule: flavodoxin; PDBTitle: structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment
113	d1gsaa1	Alignment	not modelled	82.8	12	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Prokaryotic glutathione synthetase, N-terminal domain
114	c2an1D_	Alignment	not modelled	82.6	16	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
115	c6dspB_	Alignment	not modelled	80.9	13	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2
116	c4h2dB_	Alignment	not modelled	78.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
117	c5z6vA_	Alignment	not modelled	78.4	19	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
118	c4yhsA_	Alignment	not modelled	77.3	16	PDB header: solute-binding protein Chain: A: PDB Molecule: monosaccharide abc transporter substrate-binding protein, PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from bradyrhizobium sp. bta1 (bbta_2440, target efi-3 511490) with bound bis-tris
119	d1z0sa1	Alignment	not modelled	77.1	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
120	c1z0zC_	Alignment	not modelled	77.1	18	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad