

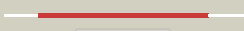








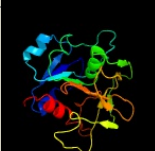


















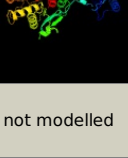


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1383_(carA)_1555977_1557107
Date	Wed Jul 31 22:05:49 BST 2019
Unique Job ID	5f61c3ac51f00879

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5dotA_	 Alignment		100.0	38	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
2	c5douC_	 Alignment		100.0	38	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
3	c1keeH_	 Alignment		100.0	46	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
4	d1a9xb1	 Alignment		100.0	48	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Carbamoyl phosphate synthetase, small subunit N-terminal domain Family: Carbamoyl phosphate synthetase, small subunit N-terminal domain
5	d1a9xb2	 Alignment		100.0	45	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
6	c2ywcC_	 Alignment		100.0	23	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermophilus in2 complex with xmp
7	c1gpmD_	 Alignment		100.0	20	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
8	c5tw7E_	 Alignment		100.0	19	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
9	c2vx0B_	 Alignment		100.0	21	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
10	c3tqiB_	 Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
11	c3r74B_	 Alignment		100.0	17	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383

12	d1gpma2	Alignment		100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
13	d1wl8a1	Alignment		100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
14	d1qddb_	Alignment		100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
15	d1i7qb_	Alignment		100.0	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
16	c6qurA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
17	d2a9va1	Alignment		100.0	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
18	c3uowB_	Alignment		100.0	19	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
19	c2vpiA_	Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
20	c1vcnA_	Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
21	d1i1qb_	Alignment	not modelled	100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
22	c2lxnA_	Alignment	not modelled	100.0	21	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
23	c5u03C_	Alignment	not modelled	100.0	18	PDB header: ligase, protein fibril Chain: C: PDB Molecule: ctp synthase 1; PDBTitle: cryo-em structure of the human ctp synthase filament
24	c1jvnB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
25	d1vcoa1	Alignment	not modelled	100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
26	c2ad5B_	Alignment	not modelled	100.0	18	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.
27	d1s1ma1	Alignment	not modelled	100.0	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
						PDB header: ligase

28	c2w7tA	Alignment	not modelled	100.0	23	Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound acivicin
29	c3nvaB	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
30	c4gudA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
31	c4zdiE	Alignment	not modelled	100.0	19	PDB header: ligase Chain: E: PDB Molecule: ctp synthase; PDBTitle: crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
32	d1ka9h	Alignment	not modelled	100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
33	c2v4uA	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with 2 5-oxo-l-norleucine
34	d1k9vf	Alignment	not modelled	100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	c3d54D	Alignment	not modelled	100.0	15	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
36	d1jvna2	Alignment	not modelled	100.0	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
37	c2issF	Alignment	not modelled	100.0	15	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
38	d2nv0a1	Alignment	not modelled	100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
39	c3fijD	Alignment	not modelled	100.0	22	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
40	d1q7ra	Alignment	not modelled	99.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	d1l9xa	Alignment	not modelled	99.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
42	c1l9xA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
43	c3l83A	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
44	c4l8fA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtb
45	c2ywjA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from 2 methanocaldococcus jannaschii
46	d1o1ya	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
47	c3l7nA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
48	c2ywdA	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
49	d1t3ta2	Alignment	not modelled	99.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
50	d2abwa1	Alignment	not modelled	99.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
51	d2ghra1	Alignment	not modelled	99.8	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
52	c2h2wA	Alignment	not modelled	99.7	17	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
53	c6mtgB	Alignment	not modelled	99.7	17	PDB header: transferase Chain: B: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
54	c6fahE	Alignment	not modelled	99.4	18	PDB header: ligase Chain: E: PDB Molecule: cobyrinic acid synthase;

54	c0lqeL	Alignment	not modelled	99.4	18	PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6 PDB header: transferase
55	c5n9mA	Alignment	not modelled	99.4	18	Chain: A; PDB Molecule: cobyrinic acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
56	c1t3tA	Alignment	not modelled	98.6	18	PDB header: ligase Chain: A; PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
57	c3uk7B	Alignment	not modelled	98.1	24	PDB header: transferase Chain: B; PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
58	c1sy7B	Alignment	not modelled	98.0	16	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.
59	d1vhqa	Alignment	not modelled	97.9	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
60	c3l3bA	Alignment	not modelled	97.9	16	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
61	d1sy7a1	Alignment	not modelled	97.8	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
62	c3fseB	Alignment	not modelled	97.7	18	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
63	c3cneD	Alignment	not modelled	97.6	18	PDB header: hydrolase Chain: D; PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
64	c6a4tB	Alignment	not modelled	97.6	21	PDB header: hydrolase Chain: B; PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
65	c4hcaA	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A; PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
66	d1p80a1	Alignment	not modelled	97.4	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
67	c3kklA	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: A; PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
68	d1n57a	Alignment	not modelled	97.4	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
69	d1p5fa	Alignment	not modelled	97.4	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
70	c3n7tA	Alignment	not modelled	97.3	18	PDB header: protein binding Chain: A; PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
71	c4e08B	Alignment	not modelled	97.3	22	PDB header: motor protein Chain: B; PDB Molecule: dj-1 beta; PDBTitle: crystal structure of drosophila melanogaster dj-1beta
72	c4lruA	Alignment	not modelled	97.3	19	PDB header: lyase Chain: A; PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from candida albicans
73	d1oi4a1	Alignment	not modelled	97.3	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
74	d1qvwa	Alignment	not modelled	97.2	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
75	d1g2ia	Alignment	not modelled	97.1	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
76	c4xllB	Alignment	not modelled	97.0	12	PDB header: unknown function Chain: B; PDB Molecule: dj-1 family protein; PDBTitle: toxoplasma gondii dj-1, oxidized
77	c3l4eA	Alignment	not modelled	97.0	17	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
78	c1p81A	Alignment	not modelled	96.9	17	PDB header: oxidoreductase Chain: A; PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
79	d1u9ca	Alignment	not modelled	96.9	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
						PDB header: hydrolase

80	c4p5pA	Alignment	not modelled	96.9	11	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
81	c3ot1B	Alignment	not modelled	96.7	15	PDB header: structural genomics Chain: B: PDB Molecule: 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate PDBTitle: crystal structure of vc2308 protein
82	c4y0nB	Alignment	not modelled	96.6	10	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein sav1875; PDBTitle: sav1875
83	d1fyea	Alignment	not modelled	96.5	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
84	c5xr2D	Alignment	not modelled	96.5	17	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase hcha; PDBTitle: sav0551
85	c4fxsA	Alignment	not modelled	96.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
86	c4i2nC	Alignment	not modelled	96.4	20	PDB header: hydrolase Chain: C: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
87	d2jfga1	Alignment	not modelled	96.4	22	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
88	c3ewnA	Alignment	not modelled	96.3	21	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
89	d2ab0a1	Alignment	not modelled	96.3	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
90	c3f5dA	Alignment	not modelled	96.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from bacillus2 subtilis
91	c2vrnA	Alignment	not modelled	95.7	12	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
92	c4k2hG	Alignment	not modelled	95.6	26	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
93	d1p3da1	Alignment	not modelled	95.3	12	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
94	c3efeC	Alignment	not modelled	95.2	12	PDB header: chaperone Chain: C: PDB Molecule: thij/pfpi family protein; PDBTitle: the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
95	d1j6ua1	Alignment	not modelled	95.0	11	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
96	d2fexa1	Alignment	not modelled	94.8	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
97	c2f00A	Alignment	not modelled	94.6	14	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
98	c1m6vE	Alignment	not modelled	94.5	28	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
99	c4rxuA	Alignment	not modelled	94.4	12	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
100	c6cauA	Alignment	not modelled	94.0	14	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with ampnp
101	c2an1D	Alignment	not modelled	93.7	18	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
102	d1a9xa4	Alignment	not modelled	93.6	26	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
103	c2yxba	Alignment	not modelled	93.5	22	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
104	c3graA	Alignment	not modelled	93.2	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from2 pseudomonas putida
105	c1j6uA	Alignment	not modelled	93.0	11	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase

					murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
106	c3nooB_	Alignment	not modelled	92.8	19 PDB header: lyase Chain: B: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
107	d1fmfa_	Alignment	not modelled	92.7	16 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
108	d1xi8a3	Alignment	not modelled	92.6	17 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
109	c3uagA_	Alignment	not modelled	92.3	21 PDB header: ligase Chain: A: PDB Molecule: protein (udp-n-acetylmuramoyl-l-alanine:d-alanine:d- PDBTitle: udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
110	c3bhnA_	Alignment	not modelled	92.2	12 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
111	c3r6mD_	Alignment	not modelled	91.9	17 PDB header: hydrolase Chain: D: PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz
112	c5dmxC_	Alignment	not modelled	91.7	19 PDB header: ligase Chain: C: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
113	c5t6oA_	Alignment	not modelled	91.6	18 PDB header: biosynthetic protein Chain: A: PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
114	c3tsdA_	Alignment	not modelled	91.5	16 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
115	c4yhsA_	Alignment	not modelled	91.4	17 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
116	c5xavB_	Alignment	not modelled	91.2	17 PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
117	d1t0ba_	Alignment	not modelled	90.4	15 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: ThuA-like
118	c4r3uD_	Alignment	not modelled	90.3	17 PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
119	c4eggD_	Alignment	not modelled	90.3	19 PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
120	c2dlnA_	Alignment	not modelled	90.1	18 PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution