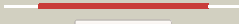



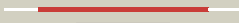

















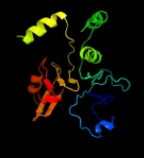
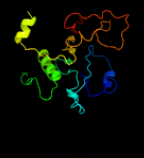

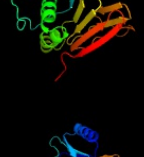
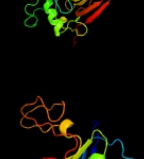
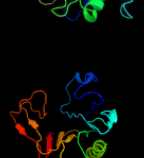


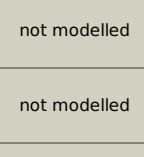


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3702c_(-)_4145091_4145792
Date	Fri Aug 9 18:20:39 BST 2019
Unique Job ID	4ca5e2e17697b9a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zfb_	 Alignment		100.0	73	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase egtc; PDBTitle: ergothioneine-biosynthetic ntn hydrolase egtc, apo form
2	c3mdnD_	 Alignment		100.0	25	PDB header: transferase Chain: D: PDB Molecule: glutamine aminotransferase class-ii domain protein; PDBTitle: structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
3	dlte5a_	 Alignment		100.0	24	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
4	dlcfa2	 Alignment		100.0	24	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
5	clecb_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
6	clgph1_	 Alignment		100.0	21	PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
7	dlgph12	 Alignment		100.0	21	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
8	dlxf_a_	 Alignment		100.0	18	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
9	cljxaA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
10	dlct9a2	 Alignment		99.9	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
11	clct9D_	 Alignment		99.9	17	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli

12	d1ofda3	Alignment		99.8	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
13	d1ea0a3	Alignment		99.8	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
14	d1jgta2	Alignment		99.7	15	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
15	c1m1zB_	Alignment		99.7	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
16	c1q15A_	Alignment		99.4	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
17	d1q15a2	Alignment		99.3	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
18	c2vdcF_	Alignment		99.1	18	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadh] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
19	c1lm1A_	Alignment		99.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
20	c5vrvA_	Alignment		26.9	9	PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: protein regulated by acid ph; PDBTitle: 2.05 angstrom resolution crystal structure of c-terminal domain2 (duf2156) of putative lysylphosphatidylglycerol synthetase from3 agrobacterium fabrum.
21	d1nm8a2	Alignment	not modelled	20.5	24	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
22	d1t1ua2	Alignment	not modelled	19.1	20	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
23	d1ndba2	Alignment	not modelled	14.8	22	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
24	c2je2A_	Alignment	not modelled	13.1	10	PDB header: metal binding protein Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cytochrome p460 from nitrosomonas europaea - probable2 nonphysiological oxidized form
25	d2ot2a1	Alignment	not modelled	12.1	20	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
26	c2oqbA_	Alignment	not modelled	11.9	11	PDB header: transferase, gene regulation Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: crystal structure of the n-terminal domain of coactivator-associated2 methyltransferase 1 (carm1)
27	d1xl7a2	Alignment	not modelled	11.3	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
28	c3nh8A_	Alignment	not modelled	10.8	10	PDB header: hydrolase Chain: A: PDB Molecule: histone-arginine methyltransferase 2; PDBTitle: crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
29	c1v8aA_	Alignment	not modelled	10.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437;

29	c1y8aA	Alignment	not modelled	10.0	12	PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus PDB header: transferase
30	c4v36B	Alignment	not modelled	9.7	10	Chain: B: PDB Molecule: lysyl-trna-dependent l-ysyl-phosphatidylglycerol synthase; PDBTitle: the structure of l-pgs from bacillus licheniformis
31	c4v34A	Alignment	not modelled	9.4	10	PDB header: transferase Chain: A: PDB Molecule: alanyl-trna-dependent l-alanyl-phosphatidylglycerol PDBTitle: the structure of a-pgs from pseudomonas aeruginosa (semet derivative)
32	c6dnmA	Alignment	not modelled	9.3	17	PDB header: chaperone Chain: A: PDB Molecule: export chaperone sats; PDBTitle: the crystal structure of sats c-terminal domain
33	d1kwga1	Alignment	not modelled	8.8	40	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
34	c3zmnA	Alignment	not modelled	8.6	18	PDB header: viral protein Chain: A: PDB Molecule: vp17; PDBTitle: vp17, a capsid protein of bacteriophage p23-77
35	c2a8vA	Alignment	not modelled	8.3	20	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
36	d1pj5a3	Alignment	not modelled	8.0	10	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
37	c3bbo1	Alignment	not modelled	7.4	27	PDB header: ribosome Chain: 1: PDB Molecule: ribosomal protein l31; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
38	d1a62a2	Alignment	not modelled	7.3	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
39	c2j034	Alignment	not modelled	7.2	40	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
40	d2j0141	Alignment	not modelled	7.2	40	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
41	d2z1ca1	Alignment	not modelled	7.0	40	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
42	c2rprA	Alignment	not modelled	6.9	27	PDB header: metal binding protein Chain: A: PDB Molecule: flywch-type zinc finger-containing protein 1; PDBTitle: solution structure of the fifth flywch domain of flywch-type2 zinc finger-containing protein 1
43	c6hihB	Alignment	not modelled	6.9	38	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: cytochrome c prime beta from methylococcus capsulatus (bath)
44	c2idrA	Alignment	not modelled	6.9	24	PDB header: translation regulator Chain: A: PDB Molecule: eukaryotic translation initiation factor 4e-1; PDBTitle: crystal structure of translation initiation factor eif4e from wheat
45	c3d3rA	Alignment	not modelled	6.7	40	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
46	d1ewqa3	Alignment	not modelled	6.6	60	Fold: Ribonuclease H-like motif Superfamily: DNA repair protein MutS, domain II Family: DNA repair protein MutS, domain II
47	c2vldA	Alignment	not modelled	6.5	11	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease nucs; PDBTitle: crystal structure of a repair endonuclease from pyrococcus abyssi
48	d3d3ra1	Alignment	not modelled	6.5	40	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
49	c2b664	Alignment	not modelled	6.3	40	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
50	c5o60g	Alignment	not modelled	6.3	40	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
51	c2h4tB	Alignment	not modelled	6.2	14	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii
52	c2ql0A	Alignment	not modelled	6.2	23	PDB header: transferase Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: structure of pae2307 in complex with adenosine
53	c1v06A	Alignment	not modelled	6.1	21	PDB header: dna-binding protein Chain: A: PDB Molecule: hmg box-containing protein 1; PDBTitle: axh domain of the transcription factor hbp1 from m.musculus
						PDB header: ribosome

54	c2hgz3	Alignment	not modelled	6.0	40	Chain: 3; PDB Molecule: 50s ribosomal protein l31; PDBTitle: crystal structure of the 70s thermus thermophilus ribosome showing how2 the 16s 3'-end mimicks mrna e and p codons. this entry 2hgz contains3 50s ribosomal subunit. the 30s ribosomal subunit can be found in pdb4 entry 2hgi.
55	c3hxiA	Alignment	not modelled	5.9	24	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation 4e; PDBTitle: crystal structure of schistosoma eif4e complexed with2 m7gpppg and 4e-bp
56	d1vs6z1	Alignment	not modelled	5.9	40	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
57	c2v8wA	Alignment	not modelled	5.8	19	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 4e; PDBTitle: crystallographic and mass spectrometric characterisation of2 eif4e with n7-cap derivatives
58	c2fyoA	Alignment	not modelled	5.6	14	PDB header: transferase Chain: A; PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
59	d1dcsa	Alignment	not modelled	5.5	22	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
60	d1vi4a	Alignment	not modelled	5.3	25	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
61	c2fy2A	Alignment	not modelled	5.3	14	PDB header: transferase Chain: A; PDB Molecule: choline o-acetyltransferase; PDBTitle: structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
62	c2gpgA	Alignment	not modelled	5.3	19	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 4e; PDBTitle: cap-free structure of eif4e suggests basis for its2 allosteric regulation
63	c6fbzA	Alignment	not modelled	5.2	14	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 4e-like protein, PDBTitle: crystal structure of the eif4e-eif4g complex from chaetomium2 thermophilum in the cap-bound state
64	c2yueA	Alignment	not modelled	5.2	14	PDB header: rna binding protein Chain: A; PDB Molecule: protein neuralized; PDBTitle: solution structure of the neu2 (nhr) domain in neuralized2 from drosophila melanogaster
65	c1t7qA	Alignment	not modelled	5.2	19	PDB header: transferase Chain: A; PDB Molecule: carnitine acetyltransferase; PDBTitle: crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
66	c2d16B	Alignment	not modelled	5.1	16	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein ph1918; PDBTitle: crystal structure of ph1918 protein from pyrococcus horikoshii ot3
67	c2ekmC	Alignment	not modelled	5.1	15	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: hypothetical protein st1511; PDBTitle: structure of st1219 protein from sulfolobus tokodaii