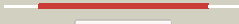
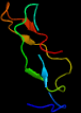


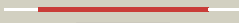








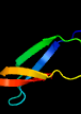





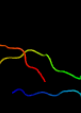


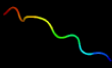
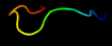

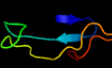


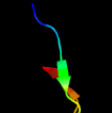




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2057c_(rpmG)_2314669_2314833
Date	Mon Aug 5 13:25:16 BST 2019
Unique Job ID	f56531daae4a7762

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2zjr11	 Alignment		99.9	55	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L33p
2	c2b9n6_	 Alignment		99.9	55	PDB header: ribosome Chain: 6; PDB Molecule: 50s ribosomal protein l33; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf2,2 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.
3	d2gyc11	 Alignment		99.9	49	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L33p
4	c2ftcP_	 Alignment		99.8	36	PDB header: ribosome Chain: P; PDB Molecule: mitochondrial ribosomal protein l33 isoform a; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
5	c1vw4X_	 Alignment		99.8	33	PDB header: ribosome Chain: X; PDB Molecule: 54s ribosomal protein l39, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
6	c5xym1_	 Alignment		99.7	89	PDB header: ribosome Chain: 1; PDB Molecule: 50s ribosomal protein l33 2; PDBTitle: large subunit of mycobacterium smegmatis
7	c5o60c_	 Alignment		99.5	41	PDB header: ribosome Chain: C; PDB Molecule: 50s ribosomal protein l2; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
8	c3bbo3_	 Alignment		99.4	41	PDB header: ribosome Chain: 3; PDB Molecule: ribosomal protein l33; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
9	c6hma1_	 Alignment		98.0	38	PDB header: ribosome Chain: 1; PDB Molecule: 50s ribosomal protein l33; PDBTitle: improved model derived from cryo-em map of staphylococcus aureus large2 ribosomal subunit
10	c3d5d6_	 Alignment		97.7	55	PDB header: ribosome Chain: 6; PDB Molecule: 50s ribosomal protein l33; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of the second 70s ribosome. the entire3 crystal structure contains two 70s ribosomes as described in remark4 400.
11	c2mewA_	 Alignment		21.0	38	PDB header: structural protein Chain: A; PDB Molecule: 30s ribosomal protein s10; PDBTitle: solution structure of nuse (s10) from thermotoga maritima

12	d1yfba1	Alignment		19.8	50	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
13	c3pnrB_	Alignment		16.9	38	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: pbicp-c; PDBTitle: structure of pbicp-c in complex with falcipain-2
14	d2fy9a1	Alignment		14.7	60	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
15	d1v7wa2	Alignment		14.0	14	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Glycosyltransferase family 36 N-terminal domain
16	c2mfkA_	Alignment		13.7	55	PDB header: allergen Chain: A: PDB Molecule: blo 1 12; PDBTitle: nmr solution structure of chitin-binding domain from dust mite group2 xii allergen blo t 12
17	c2ro5B_	Alignment		13.6	60	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: rdc-refined solution structure of the n-terminal dna recognition2 domain of the bacillus subtilis transition-state regulator spovt
18	d1fs1b2	Alignment		12.5	38	Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain
19	d1a9xa1	Alignment		12.5	40	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
20	c5xcoB_	Alignment		9.8	45	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: ace-arg-arg-arg-arg-cys-pro-leu-tyr-ile-ser-tyr-asp-pro- PDBTitle: crystal structure of human k-ras g12d mutant in complex with gdp and2 cyclic inhibitory peptide
21	d1u0a1	Alignment	not modelled	9.5	5	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
22	c2w9jB_	Alignment	not modelled	9.4	43	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle subunit srp14; PDBTitle: the crystal structure of srp14 from the schizosaccharomyces2 pombe signal recognition particle
23	c3f1zF_	Alignment	not modelled	9.4	32	PDB header: dna binding protein Chain: F: PDB Molecule: putative nucleic acid-binding lipoprotein; PDBTitle: crystal structure of putative nucleic acid-binding lipoprotein2 (yp_001337197.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.46 a resolution
24	c2ls4A_	Alignment	not modelled	8.5	83	PDB header: metal transport Chain: A: PDB Molecule: high affinity copper uptake protein 1; PDBTitle: 1h chemical shift assignments for the third transmembrane domain from2 the human copper transport 1
25	d1t9ha1	Alignment	not modelled	7.6	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
26	c5in3A_	Alignment	not modelled	7.3	29	PDB header: transferase Chain: A: PDB Molecule: galactose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of glucose-1-phosphate bound nucleotidylated human2 galactose-1-phosphate uridylyltransferase
27	d2c9wc1	Alignment	not modelled	7.0	42	Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain
28	c1v7wA_	Alignment	not modelled	6.6	14	PDB header: transferase Chain: A: PDB Molecule: chitobiose phosphorylase; PDBTitle: crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac

29	d1nexa2	Alignment	not modelled	6.4	36	Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain
30	c4bq3A_	Alignment	not modelled	6.4	42	PDB header: hydrolase Chain: A: PDB Molecule: b-agarase; PDBTitle: structural analysis of an exo-beta-agarase
31	c2hfgR_	Alignment	not modelled	5.9	44	PDB header: immune system Chain: R: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of hbr3 bound to cb3s-fab
32	c3m86B_	Alignment	not modelled	5.7	25	PDB header: protein binding Chain: B: PDB Molecule: amoebiasin-2; PDBTitle: crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica
33	d1m06g_	Alignment	not modelled	5.6	30	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
34	c5z6pB_	Alignment	not modelled	5.2	25	PDB header: hydrolase Chain: B: PDB Molecule: b-agarase; PDBTitle: the crystal structure of an agarase, agwh50c