










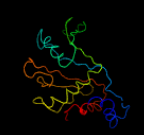
















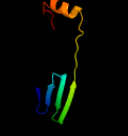
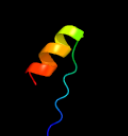



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0716_(rplE)_812062_812625
Date	Fri Jul 26 01:50:28 BST 2019
Unique Job ID	dee36a1ba296b7c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60F_	 Alignment		100.0	84	PDB header: ribosome Chain: F: PDB Molecule: 50s ribosomal protein l5; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	d1iq4a_	 Alignment		100.0	57	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
3	d1mjia_	 Alignment		100.0	58	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
4	d2zjrd1	 Alignment		100.0	54	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
5	c3bboH_	 Alignment		100.0	49	PDB header: ribosome Chain: H: PDB Molecule: ribosomal protein l5; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
6	d2gycd1	 Alignment		100.0	57	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
7	c1vw4E_	 Alignment		100.0	38	PDB header: ribosome Chain: E: PDB Molecule: 54s ribosomal protein l7, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
8	c3j21E_	 Alignment		100.0	30	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein l5p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
9	c4a1cD_	 Alignment		100.0	31	PDB header: ribosome Chain: D: PDB Molecule: 60s ribosomal protein l11; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
10	c3zf7L_	 Alignment		100.0	27	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l11, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
11	c1s1ij_	 Alignment		100.0	31	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l11; PDBTitle: structure of the ribosomal 80s-eeef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.

12	d1vqod1	Alignment		100.0	42	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
13	c4xeoB_	Alignment		63.8	22	PDB header: ligase Chain: B: PDB Molecule: alanine--trna ligase, cytoplasmic; PDBTitle: crystal structure of human alars catalytic domain with r329h mutation
14	c5knnG_	Alignment		57.0	22	PDB header: ligase Chain: G: PDB Molecule: alanine--trna ligase, cytoplasmic; PDBTitle: evolutionary gain of alanine mischarging to non-cognate trnas with a2 g4:u69 base pair
15	c3hxxA_	Alignment		26.6	22	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
16	c2rf4B_	Alignment		23.2	45	PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase i subunit rpa4; PDBTitle: crystal structure of the rna polymerase i subcomplex a14/43
17	c1yfsB_	Alignment		21.6	22	PDB header: ligase Chain: B: PDB Molecule: alanyl-trna synthetase; PDBTitle: the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
18	c5o8oA_	Alignment		18.2	23	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial import receptor subunit tom40; PDBTitle: n. crassa tom40 model based on cryo-em structure of the tom core2 complex at 6.8 a
19	c2jvfA_	Alignment		13.9	24	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
20	d3d37a1	Alignment		13.9	27	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
21	c1qysA_	Alignment	not modelled	13.6	19	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
22	c4whjA_	Alignment	not modelled	12.7	20	PDB header: antiviral protein, hydrolase Chain: A: PDB Molecule: interferon-induced gtp-binding protein mx2; PDBTitle: myxovirus resistance protein 2 (mx2)
23	d1riqa2	Alignment	not modelled	12.7	22	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
24	c4arjB_	Alignment	not modelled	12.5	40	PDB header: hydrolase Chain: B: PDB Molecule: pesticin, lysozyme; PDBTitle: crystal structure of a pesticin (translocation and receptor binding2 domain) from y. pestis and t4-lysozyme chimera
25	c1xtzA_	Alignment	not modelled	12.5	8	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
26	c4ky3A_	Alignment	not modelled	10.6	19	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
27	c4c8qA_	Alignment	not modelled	9.7	27	PDB header: transcription Chain: A: PDB Molecule: sm-like protein lsm1; PDBTitle: crystal structure of the yeast lsm1-7-pat1 complex
28	c3j3v5_	Alignment	not modelled	9.4	23	PDB header: ribosome Chain: 5: PDB Molecule: 50s ribosomal protein l1; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)

29	d1a8ya3	Alignment	not modelled	9.0	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Calsequestrin
30	d2b8ea1	Alignment	not modelled	8.5	17	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
31	d1wmxa_	Alignment	not modelled	7.8	16	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 30 carbohydrate binding module, CBM30 (PKD repeat)
32	d1j6xa_	Alignment	not modelled	7.7	9	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
33	c2ebba_	Alignment	not modelled	7.3	17	PDB header: lyase Chain: A: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
34	c5owga_	Alignment	not modelled	7.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: pcyx_ebk42635; PDBTitle: structure of pcyx_ebk42635
35	d1a62a2	Alignment	not modelled	6.6	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
36	c2xznH_	Alignment	not modelled	6.2	26	PDB header: ribosome Chain: H: PDB Molecule: ribosomal protein s8 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1, this file3 contains the 40s subunit and initiation factor for4 molecule 2
37	d1nt2b_	Alignment	not modelled	5.9	21	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
38	d1i6ua_	Alignment	not modelled	5.8	20	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
39	d3eipa_	Alignment	not modelled	5.8	50	Fold: FKBP-like Superfamily: Colicin E3 immunity protein Family: Colicin E3 immunity protein
40	c2x9oA_	Alignment	not modelled	5.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 15,16-dihydrobiliverdin-ferredoxin oxidoreductase; PDBTitle: structure of 15, 16- dihydrobiliverdin:ferredoxin2 oxidoreductase (peba)
41	c2x6vB_	Alignment	not modelled	5.7	18	PDB header: transcription/dna Chain: B: PDB Molecule: t-box transcription factor tbx5; PDBTitle: crystal structure of human tbx5 in the dna-bound and dna-2 free form
42	c5el3D_	Alignment	not modelled	5.4	11	PDB header: rna binding protein Chain: D: PDB Molecule: kh domain-containing, rna-binding, signal transduction- PDBTitle: structure of the kh domain of t-star
43	d3cjsb1	Alignment	not modelled	5.4	27	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
44	c6em5j_	Alignment	not modelled	5.4	35	PDB header: ribosome Chain: J: PDB Molecule: rrna-processing protein ebp2; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
45	c2g18K_	Alignment	not modelled	5.3	15	PDB header: oxidoreductase Chain: K: PDB Molecule: phycocyanobilin:ferredoxin oxidoreductase; PDBTitle: crystal structure of nostoc sp. 7120 phycocyanobilin:ferredoxin2 oxidoreductase (pcya) apoprotein
46	c4waaA_	Alignment	not modelled	5.3	22	PDB header: protein binding/rna Chain: A: PDB Molecule: branchpoint-bridging protein; PDBTitle: crystal structure of selenomethionine msl5 protein in complex with rna2 at 2.2 a
47	d1k1ga_	Alignment	not modelled	5.2	22	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
48	d1mmsa2	Alignment	not modelled	5.2	27	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain