














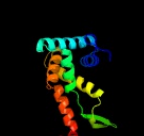











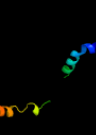
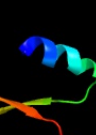




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0683_(rpsG_781937_782407)
 Date Fri Jul 26 01:50:25 BST 2019
 Unique Job ID 8b0188d933d1a6db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o5jG_	 Alignment		100.0	96	PDB header: ribosome Chain: G; PDB Molecule: 30s ribosomal protein s7; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	c3j0xl_	 Alignment		100.0	53	PDB header: ribosome Chain: J; PDB Molecule: 30s ribosomal protein s7; PDBTitle: structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes)
3	c3gtyS_	 Alignment		100.0	56	PDB header: chaperone/ribosomal protein Chain: S; PDB Molecule: 30s ribosomal protein s7; PDBTitle: promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
4	c3bbnG_	 Alignment		100.0	45	PDB header: ribosome Chain: G; PDB Molecule: ribosomal protein s7; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
5	d2qalg1	 Alignment		100.0	51	Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7
6	c3j6vG_	 Alignment		100.0	32	PDB header: ribosome Chain: G; PDB Molecule: 28s ribosomal protein s7, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
7	c1vs5G_	 Alignment		100.0	51	PDB header: ribosome Chain: G; PDB Molecule: 30s ribosomal protein s7; PDBTitle: crystal structure of the bacterial ribosome from escherichia coli in2 complex with the antibiotic kasugamycin at 3.5a resolution. this file3 contains the 30s subunit of one 70s ribosome. the entire crystal4 structure contains two 70s ribosomes and is described in remark 400.
8	d1rssa_	 Alignment		100.0	54	Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7
9	d1husa_	 Alignment		100.0	62	Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7
10	c2xzmG_	 Alignment		100.0	25	PDB header: ribosome Chain: G; PDB Molecule: ribosomal protein s7 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 1
11	c3zey2_	 Alignment		100.0	30	PDB header: ribosome Chain: 2; PDB Molecule: 40s ribosomal protein s5, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

12	d1iqva_	Alignment		100.0	30	Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7
13	c1s1hG_	Alignment		100.0	28	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s5; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
14	c3izbF_	Alignment		100.0	28	PDB header: ribosome Chain: F: PDB Molecule: 40s ribosomal protein rps5 (s7p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
15	c2zkgg_	Alignment		100.0	29	PDB header: ribosomal protein/rna Chain: G: PDB Molecule: rna helix; PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
16	c5xyiF_	Alignment		100.0	28	PDB header: ribosome Chain: F: PDB Molecule: 40s ribosomal protein s5-b, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
17	c2kn8A_	Alignment		39.2	22	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: dna cleavage and packaging protein large subunit, ul89; PDBTitle: nmr structure of the c-terminal domain of pul89
18	d1u5ta1	Alignment		23.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
19	c2hv8D_	Alignment		10.4	31	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
20	d1o7fa1	Alignment		10.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
21	c5kevA_	Alignment	not modelled	9.6	18	PDB header: signaling protein Chain: A: PDB Molecule: vtra protein; PDBTitle: vibrio parahaemolyticus vtra/vtrc complex
22	c6hv8A_	Alignment	not modelled	8.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: cryo-em structure of s. cerevisiae polymerase epsilon delcatcat mutant
23	c3u6xU_	Alignment	not modelled	8.0	50	PDB header: viral protein Chain: U: PDB Molecule: orf48; PDBTitle: phage tp901-1 baseplate tripod
24	c1u5ta_	Alignment	not modelled	7.8	23	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
25	c5yrzC_	Alignment	not modelled	7.7	20	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
26	c1w7pD_	Alignment	not modelled	7.1	12	PDB header: protein transport Chain: D: PDB Molecule: vps36p, ylr417w; PDBTitle: the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
27	c4ioxB_	Alignment	not modelled	7.0	27	PDB header: viral protein Chain: B: PDB Molecule: tripartite terminase subunit ul15; PDBTitle: the structure of the herpes simplex virus dna-packaging motor pul15 c-2 terminal nuclease domain provides insights into cleavage of3 concatemeric viral genome precursors
28	c3kmpA_	Alignment	not modelled	6.6	20	PDB header: transcription regulator/dna Chain: A: PDB Molecule: smad1-mh1; PDBTitle: crystal structure of smad1-mh1/dna complex

29	c3g36D_	Alignment	not modelled	6.0	18	PDB header: nuclear protein Chain: D: PDB Molecule: protein dpy-30 homolog; PDBTitle: crystal structure of the human dpy-30-like c-terminal domain
30	c6rrkC_	Alignment	not modelled	5.9	15	PDB header: gene regulation Chain: C: PDB Molecule: double-strand-break repair protein rad21 homolog; PDBTitle: crystal structure of the central region of human cohesin subunit stag12 in complex with rad21 peptide
31	c2lurA_	Alignment	not modelled	5.8	75	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
32	d3bula1	Alignment	not modelled	5.8	21	Fold: Methionine synthase domain-like Superfamily: Methionine synthase domain Family: Methionine synthase domain
33	d1n8va_	Alignment	not modelled	5.5	28	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
34	d1kx9b_	Alignment	not modelled	5.3	28	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2