


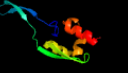

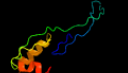

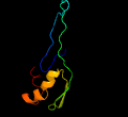

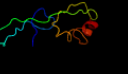


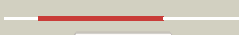
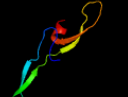
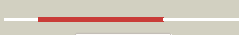
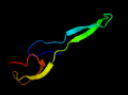

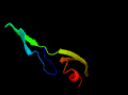

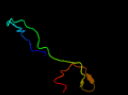

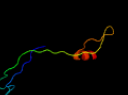

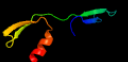






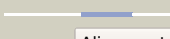
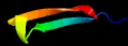

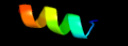

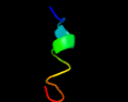






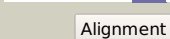
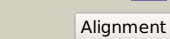
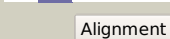

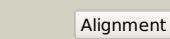



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0105c_rpmB_123977_124261
Date	Tue Jul 23 14:50:14 BST 2019
Unique Job ID	16db6609968d9fc6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vw4S_	 Alignment		100.0	26	PDB header: ribosome Chain: S; PDB Molecule: 54s ribosomal protein l24, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
2	c4v191_	 Alignment		100.0	19	PDB header: ribosome Chain: 1; PDB Molecule: mitoribosomal protein bl28m, mrpl28; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
3	d2qamz1	 Alignment		100.0	34	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
4	c6dzpy_	 Alignment		99.9	66	PDB header: ribosome Chain: Y; PDB Molecule: PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit
5	c3bboY_	 Alignment		99.9	28	PDB header: ribosome Chain: Y; PDB Molecule: ribosomal protein l28; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
6	d2jz6a1	 Alignment		99.9	29	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
7	c5o60Y_	 Alignment		99.9	43	PDB header: ribosome Chain: Y; PDB Molecule: 50s ribosomal protein l28; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
8	c6ddgl_	 Alignment		99.8	34	PDB header: ribosome/antibiotic Chain: J; PDB Molecule: 50s ribosomal protein l28; PDBTitle: structure of the 50s ribosomal subunit from methicillin resistant2 staphylococcus aureus in complex with the oxazolidinone antibiotic3 lzd-6
9	c2jl81_	 Alignment		99.7	23	PDB header: ribosome Chain: 1; PDB Molecule: 50s ribosomal protein l28; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
10	c4wfaU_	 Alignment		99.0	36	PDB header: ribosome Chain: U; PDB Molecule: 50s ribosomal protein l28; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with linezolid
11	d2zjru1	 Alignment		98.7	18	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28

12	c4ce41_	 Alignment		98.5	24	PDB header: ribosome Chain: 1: PDB Molecule: mrpl28; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
13	d2j0111	 Alignment		94.7	24	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
14	d2cu8a1	 Alignment		44.7	37	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
15	c4v19P_	 Alignment		35.1	21	PDB header: ribosome Chain: P: PDB Molecule: mitoribosomal protein ul15m, mrpl15; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
16	c2uz0B_	 Alignment		24.0	29	PDB header: hydrolase Chain: B: PDB Molecule: tributyrin esterase; PDBTitle: the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
17	c5o60M_	 Alignment		20.8	20	PDB header: ribosome Chain: M: PDB Molecule: 50s ribosomal protein l15; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
18	d2zjri1	 Alignment		20.4	33	Fold: Ribosomal proteins L15p and L18e Superfamily: Ribosomal proteins L15p and L18e Family: Ribosomal proteins L15p and L18e
19	c1vw4J_	 Alignment		19.8	40	PDB header: ribosome Chain: J: PDB Molecule: 54s ribosomal protein l10, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
20	c3j3vL_	 Alignment		15.8	20	PDB header: ribosome Chain: L: PDB Molecule: 50s ribosomal protein l15; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
21	c2zkro_	 Alignment	not modelled	15.6	31	PDB header: ribosomal protein/rna Chain: O: PDB Molecule: rna expansion segment es30; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
22	c4ce4P_	 Alignment	not modelled	15.0	29	PDB header: ribosome Chain: P: PDB Molecule: mrpl15; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
23	d1vqol1	 Alignment	not modelled	14.5	13	Fold: Ribosomal proteins L15p and L18e Superfamily: Ribosomal proteins L15p and L18e Family: Ribosomal proteins L15p and L18e
24	c3j21P_	 Alignment	not modelled	13.1	19	PDB header: ribosome Chain: P: PDB Molecule: 50s ribosomal protein l18e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
25	c4n0oC_	 Alignment	not modelled	12.8	36	PDB header: hydrolase/dna Chain: C: PDB Molecule: replicase polyprotein 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
26	c2jo5C_	 Alignment	not modelled	12.6	23	PDB header: de novo protein Chain: C: PDB Molecule: kia7f; PDBTitle: tetrameric structure of kia7f peptide
27	c2jo5B_	 Alignment	not modelled	12.6	23	PDB header: de novo protein Chain: B: PDB Molecule: kia7f; PDBTitle: tetrameric structure of kia7f peptide
28	c2jo5A_	 Alignment	not modelled	12.6	23	PDB header: de novo protein Chain: A: PDB Molecule: kia7f; PDBTitle: tetrameric structure of kia7f peptide

29	c2jo5D_	Alignment	not modelled	12.6	23	PDB header: de novo protein Chain: D: PDB Molecule: kia7f; PDBTitle: tetrameric structure of kia7f peptide
30	c2elrA_	Alignment	not modelled	12.5	29	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 15th c2h2 zinc finger of human2 zinc finger protein 406
31	c2zkrL_	Alignment	not modelled	12.3	20	PDB header: ribosomal protein/rna Chain: L: PDB Molecule: rna expansion segment es20; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
32	c4a1cK_	Alignment	not modelled	12.2	20	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l27a; 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.
33	d2j01p1	Alignment	not modelled	11.8	14	Fold: Ribosomal proteins L15p and L18e Superfamily: Ribosomal proteins L15p and L18e Family: Ribosomal proteins L15p and L18e
34	c3j39a_	Alignment	not modelled	11.7	20	PDB header: ribosome Chain: A: PDB Molecule: 60s ribosomal protein l8; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
35	d2yt9a2	Alignment	not modelled	11.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
36	c4zxsC_	Alignment	not modelled	11.2	8	PDB header: viral protein Chain: C: PDB Molecule: virion egress protein ul34; PDBTitle: hsv-1 nuclear egress complex
37	c3j21L_	Alignment	not modelled	11.0	20	PDB header: ribosome Chain: L: PDB Molecule: 50s ribosomal protein l15p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
38	c1xtaA_	Alignment	not modelled	10.5	16	PDB header: translation Chain: A: PDB Molecule: eukaryotic initiation factor 5a; PDBTitle: structural analysis of leishmania mexicana eukaryotic initiation2 factor 5a
39	c3zf7b_	Alignment	not modelled	10.4	33	PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
40	d2dmda2	Alignment	not modelled	10.0	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
41	c3iz5R_	Alignment	not modelled	9.6	19	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l18 (l18e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
42	c3izbP_	Alignment	not modelled	9.0	39	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein rps11 (s17p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
43	c3u5gL_	Alignment	not modelled	8.8	29	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s11-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
44	c2c4iA_	Alignment	not modelled	8.7	33	PDB header: glycoprotein Chain: A: PDB Molecule: avidin; PDBTitle: crystal structure of engineered avidin
45	c3iz6P_	Alignment	not modelled	8.6	35	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s11 (s17p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
46	c4a1aN_	Alignment	not modelled	8.4	19	PDB header: ribosome Chain: N: PDB Molecule: rpl18; 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 3.
47	c4qiWp_	Alignment	not modelled	8.2	27	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
48	c3er0A_	Alignment	not modelled	8.0	16	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 5a-2; PDBTitle: crystal structure of the full length eif5a from2 saccharomyces cerevisiae
49	c3hksB_	Alignment	not modelled	7.9	14	PDB header: translation, rna binding protein Chain: B: PDB Molecule: eukaryotic translation initiation factor 5a-2; PDBTitle: crystal structure of eukaryotic translation initiation2 factor eif-5a2 from arabidopsis thaliana
50	c3zf7I_	Alignment	not modelled	7.6	25	PDB header: ribosome Chain: l: PDB Molecule: 60s ribosomal protein l18; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
51	c2jtgA_	Alignment	not modelled	7.6	25	PDB header: metal binding protein Chain: A: PDB Molecule: thap domain-containing protein 1; PDBTitle: solution structure of the thap-zinc finger of thap1
52	c4z3uC_	Alignment	not modelled	7.6	14	PDB header: viral protein Chain: C: PDB Molecule: ul34 protein; PDBTitle: prv nuclear egress complex
						Fold: Glucocorticoid receptor-like (DNA-binding domain)

53	d2b8ta2	Alignment	not modelled	7.6	14	Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
54	c3j3bQ	Alignment	not modelled	7.3	17	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l18; PDBTitle: structure of the human 60s ribosomal proteins
55	c3iufA	Alignment	not modelled	6.9	23	PDB header: protein binding Chain: A: PDB Molecule: zinc finger protein ubi-d4; PDBTitle: crystal structure of the c2h2-type zinc finger domain of human ubi-d4
56	c2qm0B	Alignment	not modelled	6.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: bes; PDBTitle: crystal structure of bes protein from bacillus cereus
57	c3zeyE	Alignment	not modelled	6.8	20	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal proteins s11, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
58	c1wbiD	Alignment	not modelled	6.8	33	PDB header: avidin-related protein Chain: D: PDB Molecule: avidin-related protein 2; PDBTitle: avr2
59	d2csha2	Alignment	not modelled	6.6	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
60	d1dxga	Alignment	not modelled	6.6	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulfiredoxin
61	c3j20R	Alignment	not modelled	6.5	27	PDB header: ribosome Chain: R: PDB Molecule: 30s ribosomal protein s17p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
62	c3izcR	Alignment	not modelled	6.5	25	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein rpl18 (l18e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
63	c3j39Q	Alignment	not modelled	6.5	19	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l18; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
64	c3hi2C	Alignment	not modelled	6.3	13	PDB header: dna binding protein/toxin Chain: C: PDB Molecule: hth-type transcriptional regulator mqa(ygit); PDBTitle: structure of the n-terminal domain of the e. coli antitoxin mqa2 (ygit/b3021) in complex with the e. coli toxin mqs (ygiu/b3022)
65	d1ibia2	Alignment	not modelled	6.3	23	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
66	c5xyiL	Alignment	not modelled	6.1	35	PDB header: ribosome Chain: L: PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome
67	c4b6aQ	Alignment	not modelled	5.9	25	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l18-b; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
68	d1vzya2	Alignment	not modelled	5.8	17	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
69	d1vq0a2	Alignment	not modelled	5.7	17	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
70	c3jyvN	Alignment	not modelled	5.7	20	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s29(a); PDBTitle: structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
71	c2l8eA	Alignment	not modelled	5.6	29	PDB header: dna binding protein Chain: A: PDB Molecule: polyhomeotic-like protein 1; PDBTitle: solution nmr structure of fcs domain of human polyhomeotic homolog 12 (hph1)
72	c5z58w	Alignment	not modelled	5.5	26	PDB header: splicing Chain: W: PDB Molecule: PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
73	c5zwnY	Alignment	not modelled	5.5	29	PDB header: splicing Chain: Y: PDB Molecule: protein luc7; PDBTitle: cryo-em structure of the yeast pre-b complex at an average resolution2 of 3.3 angstrom (part ii: u1 snrnp region)
74	c3j20P	Alignment	not modelled	5.4	33	PDB header: ribosome Chain: P: PDB Molecule: 30s ribosomal protein s14p type z; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
75	c3j3aL	Alignment	not modelled	5.4	30	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s11; PDBTitle: structure of the human 40s ribosomal proteins
76	c4rgyA	Alignment	not modelled	5.4	5	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural and functional analysis of a low-temperature-active2 alkaline esterase from south china sea marine sediment microbial3 metagenomic library
77	c5xxud	Alignment	not modelled	5.3	20	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein us3; PDBTitle: small subunit of toxoplasma gondii ribosome
						PDB header: ribosome

78	c2xznN_	Alignment	not modelled	5.3	30	Chain: N; PDB Molecule: rps29e; 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
79	c6az1S_	Alignment	not modelled	5.2	22	PDB header: ribosome/antibiotic Chain: S; PDB Molecule: ribosomal protein s14; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
80	d1xjha_	Alignment	not modelled	5.1	25	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
81	c3zey8_	Alignment	not modelled	5.1	33	PDB header: ribosome Chain: 8; PDB Molecule: ribosomal protein s29, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome