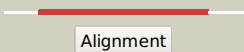

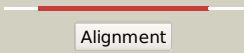



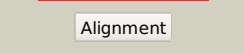



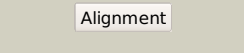

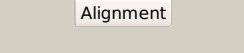


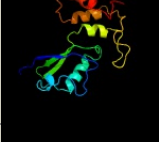
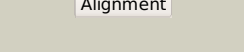
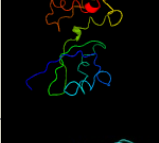
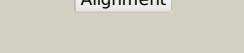
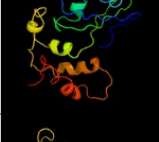
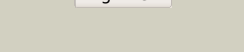


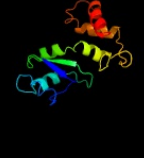

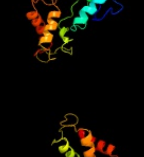
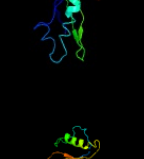



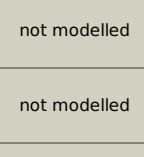


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0640_(rplK)_735025_735453
Date	Fri Jul 26 01:50:20 BST 2019
Unique Job ID	a0f211b45d080ed6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bboK_			100.0	63	PDB header: ribosome Chain: K; PDB Molecule: ribosomal protein l11; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
2	c5o60J_			100.0	95	PDB header: ribosome Chain: J; PDB Molecule: 50s ribosomal protein l11; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
3	c5colB_			100.0	35	PDB header: translation Chain: B; PDB Molecule: 50s ribosomal protein l11; PDBTitle: ribosomal protein l11 from methanococcus jannaschii
4	c1jqmA_			100.0	67	PDB header: ribosome Chain: A; PDB Molecule: 50s ribosomal protein l11; PDBTitle: fitting of l11 protein and elongation factor g (ef-g) in2 the cryo-em map of e. coli 70s ribosome bound with ef-g,3 gdp and fusicid acid
5	c2vhl_			100.0	62	PDB header: ribosome Chain: I; PDB Molecule: 50s ribosomal protein l11; PDBTitle: structure of pdf binding helix in complex with the ribosome2 (part 1 of 4)
6	c2ftcG_			100.0	40	PDB header: ribosome Chain: G; PDB Molecule: 39s ribosomal protein l11, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
7	c3j21H_			100.0	38	PDB header: ribosome Chain: H; PDB Molecule: 50s ribosomal protein l11p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
8	c3j39K_			100.0	19	PDB header: ribosome Chain: K; PDB Molecule: 60s ribosomal protein l12; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
9	c1vowJ_			100.0	66	PDB header: ribosome Chain: J; PDB Molecule: 50s ribosomal protein l11; PDBTitle: crystal structure of five 70s ribosomes from escherichia coli in2 complex with protein y. this file contains the 50s subunit of one 70s3 ribosome. the entire crystal structure contains five 70s ribosomes4 and is described in remark 400.
10	c5anbD_			100.0	22	PDB header: translation Chain: D; PDB Molecule: 60s ribosomal protein l12; PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit
11	c1s1iK_			100.0	17	PDB header: ribosome Chain: K; PDB Molecule: 60s ribosomal protein l12; 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, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.

12	c3zf7M_	Alignment		100.0	17	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l12, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
13	c3iz5J_	Alignment		100.0	24	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l12 (l11p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
14	c3cjqB_	Alignment		100.0	63	PDB header: transferase/ribosomal protein Chain: B: PDB Molecule: 50s ribosomal protein l11; PDBTitle: ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11 in space group p212121
15	c4hubl_	Alignment		100.0	39	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l11p; PDBTitle: the re-refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution: more complete structure3 of the l7/l12 and l1 stalk, l5 and lx proteins
16	c2qa4L_	Alignment		100.0	39	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l11p; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
17	d1wiba_	Alignment		100.0	21	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
18	c3cjtP_	Alignment		100.0	69	PDB header: transferase/ribosomal protein Chain: P: PDB Molecule: 50s ribosomal protein l11; PDBTitle: ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11
19	d3cjsb1	Alignment		100.0	68	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
20	d1hc8a_	Alignment		100.0	62	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein L11, C-terminal domain Family: Ribosomal protein L11, C-terminal domain
21	d1xbpg2	Alignment	not modelled	100.0	69	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
22	d1mmsa2	Alignment	not modelled	100.0	70	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
23	d2gycg2	Alignment	not modelled	100.0	70	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
24	c1vq8L_	Alignment	not modelled	99.9	44	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l11p; PDBTitle: the structure of ccca-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
25	d1mmsa1	Alignment	not modelled	99.9	64	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein L11, C-terminal domain Family: Ribosomal protein L11, C-terminal domain
26	d1vqoi1	Alignment	not modelled	99.9	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein L11, C-terminal domain Family: Ribosomal protein L11, C-terminal domain
27	d1xbpg1	Alignment	not modelled	99.9	63	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein L11, C-terminal domain Family: Ribosomal protein L11, C-terminal domain
28	c2zkri_	Alignment	not modelled	99.9	27	PDB header: ribosomal protein/rna Chain: I: PDB Molecule: rna expansion segment es15 part i; 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

29	d2gycg1	Alignment	not modelled	99.9	53	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein L11, C-terminal domain Family: Ribosomal protein L11, C-terminal domain
30	d3cjr1	Alignment	not modelled	99.5	50	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein L11, C-terminal domain Family: Ribosomal protein L11, C-terminal domain
31	c4iffC_	Alignment	not modelled	42.5	39	PDB header: cell cycle Chain: C: PDB Molecule: fusion of phage phi29 gp7 protein and cell division protein PDBTitle: structural organization of ftsb, a transmembrane protein of the 2 bacterial divisome
32	c2jwb_	Alignment	not modelled	22.7	14	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxs data
33	c4wv4A_	Alignment	not modelled	21.6	42	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 10; PDBTitle: heterodimer of taf8/taf10
34	c2mewA_	Alignment	not modelled	21.1	27	PDB header: structural protein Chain: A: PDB Molecule: 30s ribosomal protein s10; PDBTitle: solution structure of nuse (s10) from thermotoga maritima
35	c3r2cj_	Alignment	not modelled	20.3	23	PDB header: transcription/rna Chain: J: PDB Molecule: 30s ribosomal protein s10; PDBTitle: crystal structure of antitermination factors nusB and nusE in complex2 with boxA rna
36	c5wlgA_	Alignment	not modelled	18.5	43	PDB header: motor protein Chain: A: PDB Molecule: capsid assembly scaffolding protein,myosin-7,microtubule- PDBTitle: crystal structure of amino acids 1677-1755 of human beta cardiac2 myosin fused to gp7 and eb1
37	c2asbA_	Alignment	not modelled	15.8	12	PDB header: transcription/rna Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: structure of a mycobacterium tuberculosis nusa-rna complex
38	c1nohB_	Alignment	not modelled	14.9	43	PDB header: viral protein Chain: B: PDB Molecule: head morphogenesis protein; PDBTitle: the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
39	c5ejoA_	Alignment	not modelled	14.0	21	PDB header: nuclear protein Chain: A: PDB Molecule: chromatin assembly factor 1 subunit p90; PDBTitle: crystal structure of the winged helix domain in chromatin assembly2 factor 1 subunit p90
40	c5xyiU_	Alignment	not modelled	13.5	10	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein s10p/s20e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
41	c3zeyQ_	Alignment	not modelled	12.7	16	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein s20, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
42	d1hh2p2	Alignment	not modelled	11.8	29	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
43	c4dqyF_	Alignment	not modelled	11.3	23	PDB header: transferase/dna Chain: F: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: structure of human parp-1 bound to a dna double strand break
44	d1ny711	Alignment	not modelled	11.0	30	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
45	c1s1hj_	Alignment	not modelled	11.0	10	PDB header: ribosome Chain: J: PDB Molecule: 40s ribosomal protein s20; 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.
46	c3iz6J_	Alignment	not modelled	10.6	6	PDB header: ribosome Chain: J: PDB Molecule: 40s ribosomal protein s20 (s10p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
47	d2hfha_	Alignment	not modelled	10.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
48	c1lshB_	Alignment	not modelled	10.3	19	PDB header: lipid binding protein Chain: B: PDB Molecule: lipovitellin (lv-2); PDBTitle: lipid-protein interactions in lipovitellin
49	d1lshb_	Alignment	not modelled	10.3	19	Fold: Lipovitellin-phosvitin complex; beta-sheet shell regions Superfamily: Lipovitellin-phosvitin complex; beta-sheet shell regions Family: Lipovitellin-phosvitin complex; beta-sheet shell regions
50	c3bbnj_	Alignment	not modelled	10.3	21	PDB header: ribosome Chain: J: PDB Molecule: ribosomal protein s10; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
51	d1i94m_	Alignment	not modelled	10.2	20	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
52	c2zkqj_	Alignment	not modelled	10.1	10	PDB header: ribosomal protein/rna Chain: J: PDB Molecule: 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
53	c2a03A_	Alignment	not modelled	9.6	8	PDB header: oxidoreductase Chain: A: PDB Molecule: fe-superoxide dismutase homolog; PDBTitle: superoxide dismutase protein from plasmodium berghei
						Fold: Ferredoxin-like

54	d2qalj1	Alignment	not modelled	9.5	35	Superfamily: Ribosomal protein S10 Family: Ribosomal protein S10
55	c1l2fA	Alignment	not modelled	9.4	19	PDB header: transcription Chain: A: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
56	c1hh2P	Alignment	not modelled	8.9	19	PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima
57	c5o5ij	Alignment	not modelled	8.5	35	PDB header: ribosome Chain: J: PDB Molecule: 30s ribosomal protein s10; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
58	c2k29A	Alignment	not modelled	8.3	16	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
59	c5npxS	Alignment	not modelled	8.2	23	PDB header: virus Chain: S: PDB Molecule: polyprotein; PDBTitle: atomic structure of the broad bean stain virus (bbsv) by cryo-em
60	d1mnga2	Alignment	not modelled	8.0	14	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
61	c2k53A	Alignment	not modelled	8.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a3dk08 protein; PDBTitle: nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
62	d2uubj1	Alignment	not modelled	8.0	40	Fold: Ferredoxin-like Superfamily: Ribosomal protein S10 Family: Ribosomal protein S10
63	d1k1sa1	Alignment	not modelled	7.9	26	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
64	d1iwga2	Alignment	not modelled	7.9	17	Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
65	d2gy9m1	Alignment	not modelled	7.6	17	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
66	c6cfzH	Alignment	not modelled	7.5	33	PDB header: nuclear protein Chain: H: PDB Molecule: dam1; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
67	c4a18U	Alignment	not modelled	7.5	56	PDB header: ribosome Chain: U: PDB Molecule: rpl13; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
68	d2asba2	Alignment	not modelled	7.3	14	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
69	c3j20L	Alignment	not modelled	7.1	26	PDB header: ribosome Chain: L: PDB Molecule: 30s ribosomal protein s10p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
70	c3mtuE	Alignment	not modelled	6.7	43	PDB header: contractile protein Chain: E: PDB Molecule: capsid assembly scaffolding protein,tropomyosin alpha-1 PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle
71	d1pgl11	Alignment	not modelled	6.7	23	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
72	c3j3bL	Alignment	not modelled	6.7	56	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l13; PDBTitle: structure of the human 60s ribosomal proteins
73	d1kkca2	Alignment	not modelled	6.7	24	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
74	c2khvA	Alignment	not modelled	6.7	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phage integrase; PDBTitle: solution nmr structure of protein nmu_l_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
75	c3u5eL	Alignment	not modelled	6.6	56	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l13-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
76	c5jhoA	Alignment	not modelled	6.6	21	PDB header: transport protein Chain: A: PDB Molecule: electroneutral sodium bicarbonate exchanger 1; PDBTitle: crystal structure of the regulatory domain of the sodium driven2 chloride bicarbonate exchanger.
77	c2vohB	Alignment	not modelled	6.5	25	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2 homologous antagonist/killer; PDBTitle: structure of mouse a1 bound to the bak bh3-domain
78	c3j39L	Alignment	not modelled	6.5	44	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l13;

						PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
79	c3bboD_	Alignment	not modelled	6.2	33	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein l1; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
80	c1k0rB_	Alignment	not modelled	5.9	12	PDB header: transcription Chain: B: PDB Molecule: nusa; PDBTitle: crystal structure of mycobacterium tuberculosis nusa
81	c4q2uM_	Alignment	not modelled	5.8	9	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
82	c2k6xA_	Alignment	not modelled	5.7	11	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
83	c5mmjm_	Alignment	not modelled	5.7	10	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
84	c2kwyA_	Alignment	not modelled	5.6	43	PDB header: proton transport Chain: A: PDB Molecule: v-type proton atpase subunit g; PDBTitle: structure of g61-101
85	d2j01c1	Alignment	not modelled	5.6	36	Fold: Ribosomal protein L1 Superfamily: Ribosomal protein L1 Family: Ribosomal protein L1
86	c3zf7N_	Alignment	not modelled	5.5	56	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l13; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
87	c2k5eA_	Alignment	not modelled	5.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
88	c5m31A_	Alignment	not modelled	5.4	42	PDB header: antitoxin Chain: A: PDB Molecule: appr-1-p processing domain protein; PDBTitle: macrodomain of thermus aquaticus darg
89	c6flqF_	Alignment	not modelled	5.4	24	PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
90	c6emvA_	Alignment	not modelled	5.3	16	PDB header: rna binding protein Chain: A: PDB Molecule: trna (guanine(9)-/adenine(9)-n1)-methyltransferase; PDBTitle: crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis.
91	d2d9ra1	Alignment	not modelled	5.1	22	Fold: Double-split beta-barrel Superfamily: AF2212/PG0164-like Family: PG0164-like