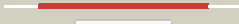



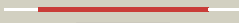


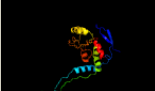



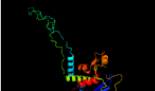



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0702_(rpID)_801465_802136
Date	Fri Jul 26 01:50:27 BST 2019
Unique Job ID	ab2ec221c8c6f28b



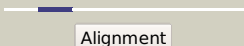
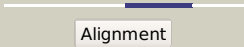
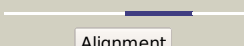


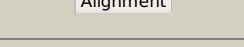
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60E_	 Alignment		100.0	87	PDB header: ribosome Chain: E; PDB Molecule: 50s ribosomal protein l4; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	c4v19F_	 Alignment		100.0	28	PDB header: ribosome Chain: F; PDB Molecule: mitoribosomal protein ul4m, mrpl4; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
3	c3j3vE_	 Alignment		100.0	40	PDB header: ribosome Chain: E; PDB Molecule: 50s ribosomal protein l4; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
4	c3bboG_	 Alignment		100.0	32	PDB header: ribosome Chain: G; PDB Molecule: ribosomal protein l4; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
5	c4wf9C_	 Alignment		100.0	43	PDB header: ribosome Chain: C; PDB Molecule: 50s ribosomal protein l4; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with telithromycin
6	c1vw3D_	 Alignment		100.0	23	PDB header: ribosome Chain: D; PDB Molecule: 54s ribosomal protein yml6, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
7	c4ce4F_	 Alignment		100.0	28	PDB header: ribosome Chain: F; PDB Molecule: mrpl4; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
8	d2j01f1	 Alignment		100.0	38	Fold: Ribosomal protein L4 Superfamily: Ribosomal protein L4 Family: Ribosomal protein L4
9	d2gycc1	 Alignment		100.0	36	Fold: Ribosomal protein L4 Superfamily: Ribosomal protein L4 Family: Ribosomal protein L4
10	d2zjrc1	 Alignment		100.0	35	Fold: Ribosomal protein L4 Superfamily: Ribosomal protein L4 Family: Ribosomal protein L4
11	c3j21D_	 Alignment		100.0	26	PDB header: ribosome Chain: D; PDB Molecule: 50s ribosomal protein l4p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)

12	c5tqbA_	Alignment		100.0	18	PDB header: ribosomal protein Chain: A; PDB Molecule: 60s ribosomal protein l4-like protein; PDBTitle: crystal structure of assembly chaperone of ribosomal protein l4 (acl4)2 in complex with ribosomal protein l4 (rpl4)
13	c3jywD_	Alignment		100.0	22	PDB header: ribosome Chain: D; PDB Molecule: 60s ribosomal protein l4(b); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
14	d1vqoc1	Alignment		100.0	23	Fold: Ribosomal protein L4 Superfamily: Ribosomal protein L4 Family: Ribosomal protein L4
15	c2zkrC_	Alignment		100.0	24	PDB header: ribosomal protein/rna Chain: C; PDB Molecule: rna expansion segment es5; 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
16	c1s1iD_	Alignment		100.0	22	PDB header: ribosome Chain: D; PDB Molecule: 60s ribosomal protein l4-b; 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.
17	c3j39C_	Alignment		100.0	27	PDB header: ribosome Chain: C; PDB Molecule: 60s ribosomal protein l4; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
18	c4b6aC_	Alignment		100.0	26	PDB header: ribosome Chain: C; PDB Molecule: 60s ribosomal protein l4-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
19	c2ftcD_	Alignment		100.0	32	PDB header: ribosome Chain: D; PDB Molecule: mitochondrial ribosomal protein l4 isoform a; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
20	c3iz5D_	Alignment		100.0	28	PDB header: ribosome Chain: D; PDB Molecule: 60s ribosomal protein l4 (l4p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
21	c3j3bC_	Alignment	not modelled	100.0	26	PDB header: ribosome Chain: C; PDB Molecule: 60s ribosomal protein l4; PDBTitle: structure of the human 60s ribosomal proteins
22	c3zf7r_	Alignment	not modelled	100.0	21	PDB header: ribosome Chain: R; PDB Molecule: 60s ribosomal protein l17, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
23	c4a1aC_	Alignment	not modelled	100.0	28	PDB header: ribosome Chain: C; PDB Molecule: rpl4; 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.
24	d1dmga_	Alignment	not modelled	100.0	30	Fold: Ribosomal protein L4 Superfamily: Ribosomal protein L4 Family: Ribosomal protein L4
25	c2d3wB_	Alignment	not modelled	37.6	8	PDB header: biosynthetic protein Chain: B; PDB Molecule: probable atp-dependent transporter sufC; PDBTitle: crystal structure of escherichia coli sufC, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
26	c1f2uD_	Alignment	not modelled	21.9	9	PDB header: replication Chain: D; PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
27	c6bzaA_	Alignment	not modelled	17.6	26	PDB header: transport protein Chain: A; PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd2 in adp-bound state
28	c2ehjA_	Alignment	not modelled	17.6	13	PDB header: transferase Chain: A; PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase

29	d1fsga_	Alignment	not modelled	17.1	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
30	c5xjyA_	Alignment	not modelled	16.8	15	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
31	d2pmka1	Alignment	not modelled	16.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
32	c5a5uB_	Alignment	not modelled	15.4	9	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: structure of mammalian eif3 in the context of the 43s preinitiation2 complex
33	c5kapA_	Alignment	not modelled	15.4	24	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: trypanosome brucei hypoxanthine-guanine phosphoribosyltransferase in2 complex with a 9-(4-(phosphonobutil)hypoxanthine
34	d2gycj1	Alignment	not modelled	15.0	39	Fold: Ribosomal proteins L15p and L18e Superfamily: Ribosomal proteins L15p and L18e Family: Ribosomal proteins L15p and L18e
35	c6n9lA_	Alignment	not modelled	13.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp
36	d1cjba_	Alignment	not modelled	13.2	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
37	c5t5dA_	Alignment	not modelled	13.1	12	PDB header: transport protein Chain: A: PDB Molecule: pts system, iib component; PDBTitle: crystal structure of the pts iib protein associated with the fucose2 utilization operon from streptococcus pneumoniae
38	c1x37A_	Alignment	not modelled	12.6	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease la 1; PDBTitle: structure of bacillus subtilis lon protease ssd domain
39	d1pf4a1	Alignment	not modelled	12.3	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
40	c1gpjA_	Alignment	not modelled	12.3	16	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
41	c3nvbA_	Alignment	not modelled	12.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
42	d1tc1a_	Alignment	not modelled	12.1	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
43	c4qitA_	Alignment	not modelled	12.0	25	PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of alpha sub-domain of lon protease from2 brevibacillus thermoruber
44	c5xeiA_	Alignment	not modelled	11.9	17	PDB header: dna binding protein, cell cycle Chain: A: PDB Molecule: chromosome partition protein smc; PDBTitle: crystal structure of the smc head domain with a coiled coil and joint2 derived from pyrococcus yayanosii
45	c3ozxA_	Alignment	not modelled	11.6	11	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase i inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
46	c3h0gE_	Alignment	not modelled	11.4	10	PDB header: transcription Chain: E: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc1; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
47	c5ipfA_	Alignment	not modelled	11.3	22	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase (hgprt); PDBTitle: crystal structure of hypoxanthine-guanine phosphoribosyltransferase2 from schistosoma mansoni in complex with imp
48	c3zqjF_	Alignment	not modelled	11.1	12	PDB header: dna binding protein Chain: F: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
49	d1qzma_	Alignment	not modelled	10.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
50	d2hyda1	Alignment	not modelled	10.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
51	c2wc1A_	Alignment	not modelled	9.4	11	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
52	c4gu0F_	Alignment	not modelled	9.4	35	PDB header: oxidoreductase Chain: F: PDB Molecule: histone h3.3; PDBTitle: crystal structure of lsd2 with h3
53	c4hsuC_	Alignment	not modelled	9.4	35	PDB header: oxidoreductase Chain: C: PDB Molecule: histone h3; PDBTitle: crystal structure of lsd2-npac with h3(1-26)in space group p21
						PDB header: oxidoreductase

54	c4gu0E_	Alignment	not modelled	9.4	35	Chain: E; PDB Molecule: histone h3.3; PDBTitle: crystal structure of lsd2 with h3
55	c3j3bq_	Alignment	not modelled	9.2	14	PDB header: ribosome Chain: Q; PDB Molecule: 60s ribosomal protein l18; PDBTitle: structure of the human 60s ribosomal proteins
56	c4mrnB_	Alignment	not modelled	8.5	13	PDB header: transport protein Chain: B; PDB Molecule: abc transporter related protein; PDBTitle: structure of a bacterial atm1-family abc transporter
57	c5idvA_	Alignment	not modelled	8.5	13	PDB header: transport protein Chain: A; PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: structure of the nucleotide binding domain of an abc transporter msba2 from acinetobacter baumannii
58	d1mv5a_	Alignment	not modelled	8.4	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
59	c1xxiF_	Alignment	not modelled	8.3	13	PDB header: transferase Chain: F; PDB Molecule: dna polymerase iii, delta subunit; PDBTitle: adp bound e. coli clamp loader complex
60	c2hydB_	Alignment	not modelled	8.3	15	PDB header: transport protein Chain: B; PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
61	c5tz8C_	Alignment	not modelled	8.2	16	PDB header: transferase Chain: C; PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
62	c3if4C_	Alignment	not modelled	8.0	50	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: integron cassette protein hfx_cass5; PDBTitle: structure from the mobile metagenome of north west arm sewage outfall:2 integron cassette protein hfx_cass5
63	c5vykC_	Alignment	not modelled	7.8	12	PDB header: signaling protein Chain: C; PDB Molecule: chimera protein of brs domain of braf and cc-sam domain of PDBTitle: crystal structure of the brs domain of braf in complex with the cc-sam2 domain of ksr1
64	d3b60a1	Alignment	not modelled	7.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
65	d1z7ga1	Alignment	not modelled	7.4	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
66	d1uhwa_	Alignment	not modelled	7.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
67	c3qf4A_	Alignment	not modelled	6.9	13	PDB header: transport protein Chain: A; PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
68	c2kftB_	Alignment	not modelled	6.8	37	PDB header: transcription/protein binding Chain: B; PDB Molecule: histone h3; PDBTitle: nmr solution structure of the first phd finger domain of2 human autoimmune regulator (aire) in complex with histone3 h3(1-20cys) peptide
69	c3iz5s_	Alignment	not modelled	6.7	22	PDB header: ribosome Chain: S; PDB Molecule: 60s ribosomal protein l18a (l18ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
70	c3izcs_	Alignment	not modelled	6.7	17	PDB header: ribosome Chain: S; PDB Molecule: 60s ribosomal protein rpl20 (l18ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
71	c2vf7B_	Alignment	not modelled	6.5	17	PDB header: dna binding protein Chain: B; PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
72	c3kb8A_	Alignment	not modelled	6.3	26	PDB header: transferase Chain: A; PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
73	c2v3jA_	Alignment	not modelled	6.1	18	PDB header: ribosomal protein Chain: A; PDB Molecule: essential for mitotic growth 1; PDBTitle: the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
74	c4pl0B_	Alignment	not modelled	6.0	11	PDB header: transport protein Chain: B; PDB Molecule: microcin-j25 export atp-binding/permease protein mcjd; PDBTitle: crystal structure of the antibacterial peptide abc transporter mcjd in2 an outward occluded state
75	d1oeyj_	Alignment	not modelled	5.8	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
76	c5ochF_	Alignment	not modelled	5.8	17	PDB header: hydrolase Chain: F; PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state
77	d1v2ya_	Alignment	not modelled	5.8	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
78	c3htrB_	Alignment	not modelled	5.7	43	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized prc-barrel domain protein; PDBTitle: crystal structure of prc-barrel domain protein from2 rhodospseudomonas palustris

79	c5e38D_	 Alignment	not modelled	5.6	10	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structural basis of mapping the spontaneous mutations with 5-2 flourouracil in uracil phosphoribosyltransferase from mycobacterium3 tuberculosis
80	c5mvrA_	 Alignment	not modelled	5.5	15	PDB header: transferase Chain: A: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsae; PDBTitle: crystal structure of bacillus subtilus ydib
81	d2v3ka1	 Alignment	not modelled	5.4	18	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: EMG1/NEP1-like
82	d1oxk2	 Alignment	not modelled	5.4	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
83	c4fwiB_	 Alignment	not modelled	5.3	13	PDB header: transport protein Chain: B: PDB Molecule: abc-type dipeptide/oligopeptide/nickel transport system, PDBTitle: crystal structure of the nucleotide-binding domain of a dipeptide abc2 transporter
84	c1pzmB_	 Alignment	not modelled	5.2	20	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
85	c4u02C_	 Alignment	not modelled	5.2	14	PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein; PDBTitle: crystal structure of apo-ttha1159
86	d1y0ja1	 Alignment	not modelled	5.0	27	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1