


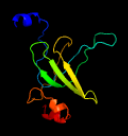



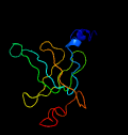

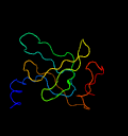



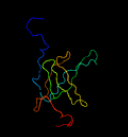





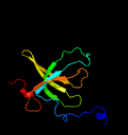



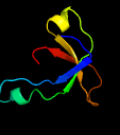




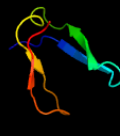




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2904c_(rplS)_3213922_3214263
Date	Thu Aug 8 16:20:06 BST 2019
Unique Job ID	b1f0a8ded0309013

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60Q_	 Alignment		100.0	90	PDB header: ribosome Chain: Q; PDB Molecule: 50s ribosomal protein l19; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	d2j01t1	 Alignment		100.0	50	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19
3	d2gycn1	 Alignment		100.0	53	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19
4	c1nwxN_	 Alignment		100.0	54	PDB header: ribosome Chain: N; PDB Molecule: ribosomal protein l19; PDBTitle: complex of the large ribosomal subunit from deinococcus2 radiodurans with abt-773
5	c3j3vP_	 Alignment		100.0	70	PDB header: ribosome Chain: P; PDB Molecule: 50s ribosomal protein l19; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
6	d2zjrm1	 Alignment		100.0	53	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19
7	c3bboR_	 Alignment		100.0	40	PDB header: ribosome Chain: R; PDB Molecule: ribosomal protein l19; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
8	c4v19T_	 Alignment		100.0	27	PDB header: ribosome Chain: T; PDB Molecule: mitoribosomal protein bl19m, mrpl19; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
9	c2ftcK_	 Alignment		100.0	29	PDB header: ribosome Chain: K; PDB Molecule: 39s ribosomal protein l19, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
10	c1vw4M_	 Alignment		100.0	23	PDB header: ribosome Chain: M; PDB Molecule: 54s ribosomal protein img1, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
11	dlzqla1	 Alignment		67.4	25	Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like

12	d1jb7a1	Alignment		66.6	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
13	c2e6zA_	Alignment		62.0	27	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5
14	c1zq1B_	Alignment		61.8	24	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
15	c3zf7Z_	Alignment		59.3	17	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein l26, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
16	c3iz5Y_	Alignment		55.3	17	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l26 (l24p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
17	d1vqot1	Alignment		52.7	18	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
18	c4he5A_	Alignment		49.6	24	PDB header: unknown function Chain: A: PDB Molecule: peptidase family u32; PDBTitle: crystal structure of the selenomethionine variant of the c-terminal2 domain of geobacillus thermoleovorans putative u32 peptidase
19	c2kvaG_	Alignment		49.0	33	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
20	c2jvvA_	Alignment		49.0	33	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
21	c3j21U_	Alignment	not modelled	48.1	17	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l24p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
22	d1nppa2	Alignment	not modelled	45.9	33	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
23	c2f1IA_	Alignment	not modelled	42.4	18	PDB header: unknown function Chain: A: PDB Molecule: 16s rna processing protein; PDBTitle: crystal structure of a putative 16s ribosomal rna processing protein2 rimm (pa3744) from pseudomonas aeruginosa at 2.46 a resolution
24	c4r80A_	Alignment	not modelled	41.3	35	PDB header: de novo protein Chain: A: PDB Molecule: or486; PDBTitle: crystal structure of a de novo designed beta sheet protein, cystatin2 fold, northeast structural genomics consortium (nesg) target or486
25	d1nz9a_	Alignment	not modelled	38.1	31	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
26	c4yt1B_	Alignment	not modelled	37.7	21	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
27	c4a1cS_	Alignment	not modelled	37.2	13	PDB header: ribosome Chain: S: PDB Molecule: rpl26; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 4. PDB header: ligase/rna

28	c2d6fA_	Alignment	not modelled	36.6	25	Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
29	c2dxcG_	Alignment	not modelled	36.2	36	PDB header: hydrolase Chain: G: PDB Molecule: thiocyanate hydrolase subunit alpha; PDBTitle: recombinant thiocyanate hydrolase, fully-matured form
30	c2mi6A_	Alignment	not modelled	33.5	14	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusg; PDBTitle: solution structure of the carboxy terminal domain of nusg from2 mycobacterium tuberculosis
31	c1jb7A_	Alignment	not modelled	32.5	21	PDB header: dna-binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
32	c1ph4A_	Alignment	not modelled	32.5	21	PDB header: dna binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggttttgccg
33	c1k8gC_	Alignment	not modelled	32.2	18	PDB header: dna binding protein/dna Chain: C: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the n-terminal domain of oxytricha2 nova telomere end binding protein alpha subunit both3 uncomplexed and complexed with telomeric ssdna
34	c3p8bB_	Alignment	not modelled	30.2	19	PDB header: transferase/transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
35	d1ugpb_	Alignment	not modelled	28.7	36	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
36	d2d6fa1	Alignment	not modelled	28.2	26	Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like
37	c3qz9D_	Alignment	not modelled	27.1	36	PDB header: lyase Chain: D: PDB Molecule: co-type nitrile hydratase beta subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
38	c5u9jB_	Alignment	not modelled	27.0	25	PDB header: signaling protein Chain: B: PDB Molecule: aryl hydrocarbon receptor-interacting protein-like 1 PDBTitle: crystal structure of the fkbp domain of human aryl hydrocarbon2 receptor-interacting protein-like 1 (aip1) complexed with geranyl3 geranyl pyrophosphate
39	c4ql5A_	Alignment	not modelled	26.9	17	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor if-1 from2 streptococcus pneumoniae tigr4
40	d1hr0w_	Alignment	not modelled	25.9	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
41	d1v29b_	Alignment	not modelled	25.7	36	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
42	c6c00A_	Alignment	not modelled	24.6	25	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: solution structure of translation initiation factor 1 from clostridium2 difficile
43	d2bi0a2	Alignment	not modelled	23.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
44	c4ljoA_	Alignment	not modelled	22.3	38	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase rnf31; PDBTitle: structure of an active ligase (hoip)/ubiquitin transfer complex
45	c4fm4D_	Alignment	not modelled	22.0	27	PDB header: lyase Chain: D: PDB Molecule: nitrile hydratase beta subunit; PDBTitle: wild type fe-type nitrile hydratase from comamonas testosteroni ni1
46	d2qdyb1	Alignment	not modelled	21.6	27	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
47	c2eifA_	Alignment	not modelled	21.5	17	PDB header: gene regulation Chain: A: PDB Molecule: protein (eukaryotic translation initiation factor 5a); PDBTitle: eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
48	c2lktA_	Alignment	not modelled	21.4	25	PDB header: hydrolase Chain: A: PDB Molecule: retinoic acid receptor responder protein 3; PDBTitle: solution structure of n-terminal domain of human tig3 in 2 m urea
49	d1ah9a_	Alignment	not modelled	21.4	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
50	c2bi0A_	Alignment	not modelled	20.7	19	PDB header: hypothetical protein Chain: A: PDB Molecule: hypothetical protein rv0216; PDBTitle: rv0216, a conserved hypothetical protein from mycobacterium2 tuberculosis that is essential for bacterial survival3 during infection, has a double hotdogfold
51	c3l53F_	Alignment	not modelled	20.7	27	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative fumarylacetoacetate isomerase/hydrolase; PDBTitle: crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
52	c2fhda_	Alignment	not modelled	20.5	20	PDB header: cell cycle Chain: A: PDB Molecule: dna repair protein rhp9/crb2;

						PDBTitle: crystal structure of crb2 tandem tudor domains
53	c3i4oA_	Alignment	not modelled	20.5	17	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
54	c5waiC_	Alignment	not modelled	20.4	18	PDB header: transcription Chain: C: PDB Molecule: zinc finger protein aebp2; PDBTitle: crystal structure of a suz12-rbbp4-jarid2-aebp2 heterotetrameric2 complex
55	d1je3a_	Alignment	not modelled	20.3	15	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
56	c1m1gB_	Alignment	not modelled	20.2	35	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
57	c4tkoB_	Alignment	not modelled	19.7	18	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
58	c2kyaA_	Alignment	not modelled	19.6	44	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution structure of the h-rev107 n-terminal domain
59	d1y14b1	Alignment	not modelled	19.5	8	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
60	c3zey0_	Alignment	not modelled	18.9	16	PDB header: ribosome Chain: 0: PDB Molecule: 40s ribosomal protein s3a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
61	d1kl9a2	Alignment	not modelled	18.7	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
62	c3e0eA_	Alignment	not modelled	18.5	29	PDB header: replication Chain: A: PDB Molecule: replication protein a; PDBTitle: crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
63	c2v43A_	Alignment	not modelled	17.6	16	PDB header: regulator Chain: A: PDB Molecule: sigma-e factor regulatory protein rseb; PDBTitle: crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
64	c5xyiB_	Alignment	not modelled	17.6	8	PDB header: ribosome Chain: B: PDB Molecule: ribosomal protein s3ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
65	c2l66B_	Alignment	not modelled	17.3	29	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, abrb family; PDBTitle: the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
66	d2bi0a1	Alignment	not modelled	16.9	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
67	d1e9ya1	Alignment	not modelled	16.8	32	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
68	c2equA_	Alignment	not modelled	16.5	13	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1
69	d1ejxb_	Alignment	not modelled	16.3	32	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
70	d4ubpb_	Alignment	not modelled	15.9	24	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
71	c2rm4A_	Alignment	not modelled	15.5	19	PDB header: protein binding Chain: A: PDB Molecule: cg6311-pb; PDBTitle: solution structure of the lsm domain of dm edc3 (enhancer2 of decapping 3)
72	c2wknE_	Alignment	not modelled	15.4	31	PDB header: hydrolase Chain: E: PDB Molecule: formamidase; PDBTitle: gamma lactamase from delftia acidovorans
73	c4z42B_	Alignment	not modelled	15.3	35	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of urease from yersinia enterocolitica
74	c2ldmA_	Alignment	not modelled	15.2	13	PDB header: transcription/protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
75	d2nn6i1	Alignment	not modelled	15.1	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
76	d2ifra1	Alignment	not modelled	14.6	31	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Peptidase A4
77	c3u5gB_	Alignment	not modelled	14.1	13	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s1-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
78	c2lknA_	Alignment	not modelled	13.4	25	PDB header: protein binding Chain: A: PDB Molecule: ah receptor-interacting protein; PDBTitle: solution structure of the ppiase domain of human aryl-hydrocarbon2 receptor-interacting protein (aip)

79	d1is3a_	Alignment	not modelled	13.2	30	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
80	d2asba1	Alignment	not modelled	13.1	6	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
81	d1hh2p1	Alignment	not modelled	13.1	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
82	d2hbba1	Alignment	not modelled	13.0	25	Fold: Mbth/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
83	d1cqua_	Alignment	not modelled	13.0	25	Fold: Mbth/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
84	c2dbkA_	Alignment	not modelled	12.7	35	PDB header: signaling protein Chain: A: PDB Molecule: crk-like protein; PDBTitle: solution structures of the sh3 domain of human crk-like2 protein
85	d1bf2a1	Alignment	not modelled	12.6	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
86	c4ifdl_	Alignment	not modelled	12.4	27	PDB header: hydrolase/rna Chain: I: PDB Molecule: exosome complex component csl4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
87	d1xjva1	Alignment	not modelled	12.4	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
88	d1vyva1	Alignment	not modelled	12.3	30	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
89	d2do3a1	Alignment	not modelled	12.2	44	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
90	d1t0ha_	Alignment	not modelled	12.1	35	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
91	c2nn6l_	Alignment	not modelled	11.8	19	PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
92	c3j3aB_	Alignment	not modelled	11.8	17	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s3a; PDBTitle: structure of the human 40s ribosomal proteins
93	c1vw4G_	Alignment	not modelled	11.5	35	PDB header: ribosome Chain: G: PDB Molecule: 54s ribosomal protein l50, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
94	d2ahob2	Alignment	not modelled	11.3	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
95	c1e9zA_	Alignment	not modelled	11.2	32	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
96	c2lq8A_	Alignment	not modelled	11.2	20	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: domain interaction in thermotoga maritima nusg
97	c2khjA_	Alignment	not modelled	11.1	9	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
98	d2vv5a1	Alignment	not modelled	11.0	18	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
99	d1t3la1	Alignment	not modelled	11.0	35	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain