

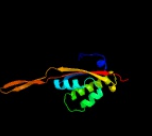

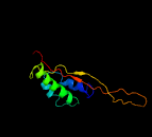

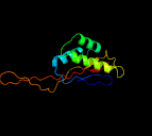
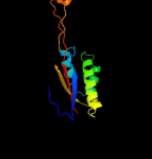
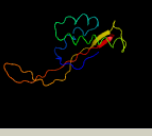


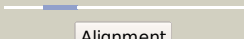
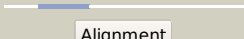
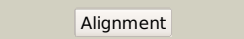
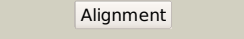
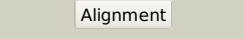
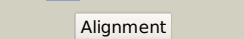
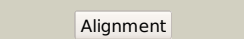
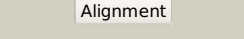
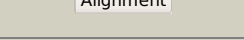




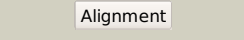
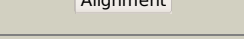
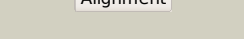
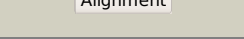
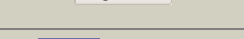

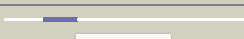
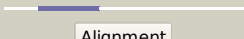
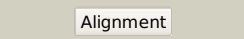

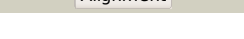

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0706_(rpIV)_803692_804285
Date	Fri Jul 26 01:50:27 BST 2019
Unique Job ID	a850578317b374ee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60T_	Alignment		100.0	88	PDB header: ribosome Chain: T: PDB Molecule: 50s ribosomal protein l22; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	d2zjrp1	Alignment		100.0	50	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
3	c4v19W_	Alignment		100.0	21	PDB header: ribosome Chain: W: PDB Molecule: mitoribosomal protein ul22m, mrpl22; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
4	c5mlcU_	Alignment		100.0	34	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l22, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
5	c1vw4O_	Alignment		100.0	21	PDB header: ribosome Chain: O: PDB Molecule: 54s ribosomal protein l22, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
6	c3j3wS_	Alignment		100.0	51	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l22; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
7	c4ce4W_	Alignment		100.0	23	PDB header: ribosome Chain: W: PDB Molecule: mrpl22; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
8	d1i4ja_	Alignment		100.0	50	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
9	c3bboU_	Alignment		100.0	39	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein l22; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
10	d1vqor1	Alignment		100.0	23	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
11	c3u5eP_	Alignment		100.0	30	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a

12	c3iz5V_	Alignment		100.0	27	PDB header: ribosome Chain: V: PDB Molecule: 60s ribosomal protein I17 (I22p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
13	c3j39P_	Alignment		100.0	22	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein I17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
14	c4a17Q_	Alignment		100.0	22	PDB header: ribosome Chain: Q: PDB Molecule: rpl17; 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 2.
15	c3zf7R_	Alignment		100.0	27	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein I17, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
16	c2ftcM_	Alignment		100.0	24	PDB header: ribosome Chain: M: PDB Molecule: mitochondrial ribosomal protein I22 isoform a; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
17	c3j21S_	Alignment		100.0	38	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein I22p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
18	c3jywN_	Alignment		100.0	33	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein I17(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
19	c2zkrr_	Alignment		100.0	23	PDB header: ribosomal protein/rna Chain: R: PDB Molecule: rna expansion segment es39 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
20	d2gycq1	Alignment		100.0	54	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
21	c1s1iN_	Alignment	not modelled	100.0	34	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein I17-a; 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.
22	d1r9pa_	Alignment	not modelled	85.7	24	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
23	c2z7eB_	Alignment	not modelled	78.0	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: nifu-like protein; PDBTitle: crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
24	d1wfza_	Alignment	not modelled	74.3	23	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
25	c4eb5C_	Alignment	not modelled	66.8	26	PDB header: transferase/metal binding protein Chain: C: PDB Molecule: nifu protein (nifu-1); PDBTitle: a. fulgidus iscs-iscu complex structure
26	c5uftA_	Alignment	not modelled	66.3	16	PDB header: metal binding protein Chain: A: PDB Molecule: nitrogen-fixing nifu-like, n-terminal; PDBTitle: crystal structure of a nitrogen-fixing nifu-like protein (n-terminal)2 from brucella abortus
27	d1xjsa_	Alignment	not modelled	40.2	17	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
28	d1fs1b1	Alignment	not modelled	31.1	13	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like

29	c3ka5A	 Alignment	not modelled	28.1	13	PDB header: chaperone Chain: A: PDB Molecule: ribosome-associated protein y (psrp-1); PDBTitle: crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
30	d2oux1	 Alignment	not modelled	24.1	14	Fold: alpha-alpha superhelix Superfamily: MgtE N-terminal domain-like Family: MgtE N-terminal domain-like
31	c2i88A	 Alignment	not modelled	22.3	20	PDB header: membrane protein Chain: A: PDB Molecule: colicin-e1; PDBTitle: crystal structure of the channel-forming domain of colicin e1
32	c1rh1A	 Alignment	not modelled	22.2	19	PDB header: antibiotic Chain: A: PDB Molecule: colicin b; PDBTitle: crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
33	c3lyvF	 Alignment	not modelled	22.1	13	PDB header: chaperone Chain: F: PDB Molecule: ribosome-associated factor y; PDBTitle: crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
34	c3k2tA	 Alignment	not modelled	21.7	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
35	d1dwka1	 Alignment	not modelled	21.4	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
36	d1cia1	 Alignment	not modelled	19.5	20	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
37	c3fewX	 Alignment	not modelled	19.3	27	PDB header: immune system Chain: X: PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a duplicated2 receptor binding domain
38	d2crna1	 Alignment	not modelled	17.3	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
39	c2crnA	 Alignment	not modelled	16.4	14	PDB header: immune system Chain: A: PDB Molecule: ubash3a protein; PDBTitle: solution structure of the uba domain of human ubash3a2 protein
40	c2cpwA	 Alignment	not modelled	16.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cb1-interacting protein sts-1 variant; PDBTitle: solution structure of rsgi ruh-031, a uba domain from human2 cdna
41	d1whca	 Alignment	not modelled	15.8	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
42	c1a87A	 Alignment	not modelled	14.7	25	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
43	d1a87a	 Alignment	not modelled	14.7	25	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
44	d1su0b	 Alignment	not modelled	14.0	21	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
45	c2qq4A	 Alignment	not modelled	13.9	33	PDB header: metal binding protein Chain: A: PDB Molecule: iron-sulfur cluster biosynthesis protein iscu; PDBTitle: crystal structure of iron-sulfur cluster biosynthesis protein iscu2 (ttha1736) from thermus thermophilus hb8
46	c5z08A	 Alignment	not modelled	13.5	18	PDB header: cell cycle Chain: A: PDB Molecule: cenp-i; PDBTitle: the crystal structure of kinetochore subunits cenp-h/i/k triple2 complex
47	d1pyya2	 Alignment	not modelled	13.0	19	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
48	d1cola	 Alignment	not modelled	12.4	25	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
49	d1rp5a2	 Alignment	not modelled	12.1	19	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
50	c2zqeA	 Alignment	not modelled	11.8	36	PDB header: dna binding protein Chain: A: PDB Molecule: smuts2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus muts2
51	d1rh1a2	 Alignment	not modelled	11.4	20	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
52	d1r4va	 Alignment	not modelled	11.3	28	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
53	d1fs2b1	 Alignment	not modelled	11.0	10	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
54	d1k25a2	Alignment	not modelled	10.4	19	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain

						Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
55	d2ovra1	Alignment	not modelled	8.9	10	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
56	c3ouvA	Alignment	not modelled	8.8	29	PDB header: transferase Chain: A; PDB Molecule: serine/threonine protein kinase; PDBTitle: semet derivative of I512m mutant of pasta domain 3 of mycobacterium2 tuberculosis pknb
57	d1nexa1	Alignment	not modelled	8.7	25	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
58	d1v95a	Alignment	not modelled	8.3	23	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
59	c2p1nD	Alignment	not modelled	8.0	20	PDB header: signaling protein Chain: D; PDB Molecule: skp1-like protein 1a; PDBTitle: mechanism of auxin perception by the tir1 ubiquitin ligase
60	c4qmfB	Alignment	not modelled	7.5	33	PDB header: rna binding protein Chain: B; PDB Molecule: krr1 small subunit processome component; PDBTitle: structure of the krr1 and faf1 complex from saccharomyces cerevisiae
61	c5ipmF	Alignment	not modelled	7.5	18	PDB header: transcription, transferase/dna/rna Chain: F; PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
62	c4ochA	Alignment	not modelled	7.5	50	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease muts2; PDBTitle: apo structure of smr domain of muts2 from deinococcus radiodurans
63	d1myla	Alignment	not modelled	6.4	53	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
64	d2yvxa1	Alignment	not modelled	5.8	14	Fold: alpha-alpha superhelix Superfamily: MgtE N-terminal domain-like Family: MgtE N-terminal domain-like
65	d1wwia1	Alignment	not modelled	5.5	33	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
66	c2w1oA	Alignment	not modelled	5.3	28	PDB header: translation Chain: A; PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: nmr structure of dimerization domain of human ribosomal2 protein p2
67	c2qdoC	Alignment	not modelled	5.2	23	PDB header: photosynthesis Chain: C; PDB Molecule: nbla protein; PDBTitle: nbla protein from t. vulcanus
68	d1b28a	Alignment	not modelled	5.2	53	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors