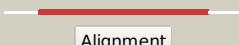
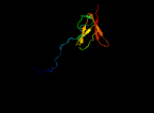

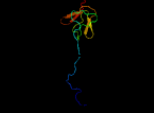
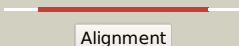
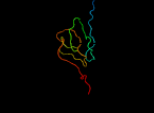
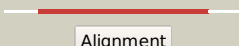
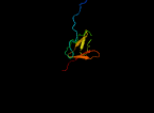
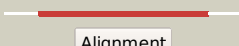
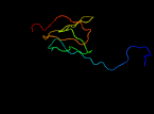
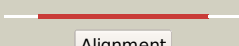
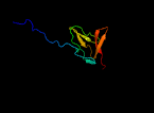
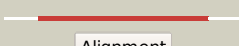
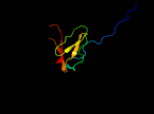

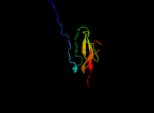

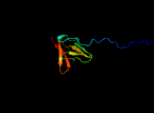

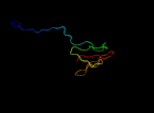

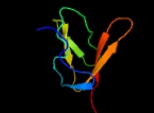



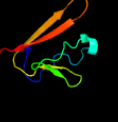









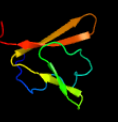



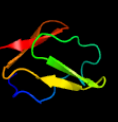
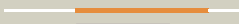
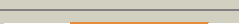

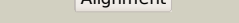
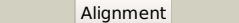
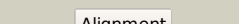

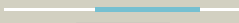


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2441c_rpmA_2739782_2740042
Date	Wed Aug 7 12:50:06 BST 2019
Unique Job ID	87075e3fb477bdf2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fin0_	 Alignment		100.0	63	PDB header: ribosome Chain: 0; PDB Molecule: 50s ribosomal protein l27; PDBTitle: t. thermophilus 70s ribosome in complex with mrna, trnas and ef-2 tu.gdp.kirromycin ternary complex, fitted to a 6.4 a cryo-em map.3 this file contains the 50s subunit.
2	d2zjt1	 Alignment		100.0	59	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein
3	c3bboX_	 Alignment		100.0	56	PDB header: ribosome Chain: X; PDB Molecule: ribosomal protein l27; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
4	c5mlcX_	 Alignment		100.0	58	PDB header: ribosome Chain: X; PDB Molecule: 50s ribosomal protein l27, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
5	d2gycu1	 Alignment		100.0	63	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein
6	c5o60X_	 Alignment		100.0	86	PDB header: ribosome Chain: X; PDB Molecule: 50s ribosomal protein l27; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
7	c1vw4R_	 Alignment		100.0	48	PDB header: ribosome Chain: R; PDB Molecule: 54s ribosomal protein l2, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
8	c4wf9T_	 Alignment		100.0	61	PDB header: ribosome Chain: T; PDB Molecule: 50s ribosomal protein l27; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with telithromycin
9	c4v190_	 Alignment		100.0	36	PDB header: ribosome Chain: 0; PDB Molecule: mitoribosomal protein bl27m, mrpl27; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
10	c2ftcO_	 Alignment		100.0	41	PDB header: ribosome Chain: O; PDB Molecule: mitochondrial 39s ribosomal protein l27; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
11	d1v8qa_	 Alignment		100.0	60	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein

12	d2ba0a2	 Alignment		95.5	17	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
13	d2je6i2	 Alignment		95.3	14	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
14	d2nn6h2	 Alignment		94.4	28	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
15	c4ifdl_	 Alignment		93.9	25	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
16	c6d6rH_	 Alignment		93.0	28	PDB header: hydrolase Chain: H: PDB Molecule: exosome complex component rrp4; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
17	d2nn6i2	 Alignment		91.5	18	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
18	c4ifdH_	 Alignment		91.3	19	PDB header: hydrolase/rna Chain: H: PDB Molecule: exosome complex component rrp4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
19	c2ba1B_	 Alignment		91.1	20	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
20	c2nn6H_	 Alignment		90.4	28	PDB header: hydrolase/transferase Chain: H: PDB Molecule: exosome complex exonuclease rrp4; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
21	c2nn6l_	 Alignment	not modelled	85.8	22	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
22	c2nn6G_	 Alignment	not modelled	84.2	23	PDB header: hydrolase/transferase Chain: G: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
23	c2ba0A_	 Alignment	not modelled	81.5	17	PDB header: rna binding protein Chain: A: PDB Molecule: archaeal exosome rna binding protein rrp4; PDBTitle: archaeal exosome core
24	c4ifdG_	 Alignment	not modelled	61.2	18	PDB header: hydrolase/rna Chain: G: PDB Molecule: exosome complex component rrp40; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
25	c2aukA_	 Alignment	not modelled	42.8	25	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
26	c5j1mD_	 Alignment	not modelled	35.5	16	PDB header: hydrolase Chain: D: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer ii
27	c2b44A_	 Alignment	not modelled	35.0	24	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
28	d1qwya_	 Alignment	not modelled	33.9	24	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM PDB header: metal binding protein

29	c5b0hB_	Alignment	not modelled	33.7	29	Chain: B; PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2
30	c3sluB_	Alignment	not modelled	31.5	19	PDB header: hydrolase Chain: B; PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
31	c2je6I_	Alignment	not modelled	26.9	9	PDB header: hydrolase Chain: I; PDB Molecule: exosome complex rna-binding protein 1; PDBTitle: structure of a 9-subunit archaeal exosome
32	c5j1IA_	Alignment	not modelled	24.5	18	PDB header: hydrolase Chain: A; PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer i
33	c4bh5B_	Alignment	not modelled	23.6	21	PDB header: cell cycle Chain: B; PDB Molecule: murein hydrolase activator envc; PDBTitle: lytm domain of envc, an activator of cell wall amidases in2 escherichia coli
34	c4aq2I_	Alignment	not modelled	23.2	45	PDB header: oxidoreductase Chain: I; PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: resting state of homogentisate 1,2-dioxygenase
35	c1ey2A_	Alignment	not modelled	22.9	45	PDB header: oxidoreductase Chain: A; PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: human homogentisate dioxygenase with fe(ii)
36	d1eyba_	Alignment	not modelled	22.9	45	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Homogentisate dioxygenase
37	c4iqzD_	Alignment	not modelled	19.9	31	PDB header: unknown function Chain: D; PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: the crystal structure of a large insert in rna polymerase (rroc)2 subunit from e. coli
38	c2lmcB_	Alignment	not modelled	18.9	26	PDB header: transcription Chain: B; PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
39	c4lxcA_	Alignment	not modelled	16.6	20	PDB header: hydrolase Chain: A; PDB Molecule: lysostaphin; PDBTitle: the antimicrobial peptidase lysostaphin from staphylococcus simulans
40	c2dn8A_	Alignment	not modelled	13.9	25	PDB header: ligase Chain: A; PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
41	c2yyoA_	Alignment	not modelled	13.2	23	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: spry domain-containing protein 3; PDBTitle: crystal structure of human spry domain
42	c3c8vA_	Alignment	not modelled	13.1	21	PDB header: transferase Chain: A; PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
43	c4rnzA_	Alignment	not modelled	12.3	23	PDB header: hydrolase Chain: A; PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd3 from the hexagonal crystal
44	c4qpbB_	Alignment	not modelled	11.9	17	PDB header: hydrolase Chain: B; PDB Molecule: lysostaphin; PDBTitle: catalytic domain of the antimicrobial peptidase lysostaphin from2 staphylococcus simulans crystallized in the absence of phosphate
45	c6hq9A_	Alignment	not modelled	11.0	38	PDB header: hydrolase Chain: A; PDB Molecule: dna excision repair protein ercc-6-like 2; PDBTitle: crystal structure of the tudor domain of human ercc6-12
46	c2cupA_	Alignment	not modelled	11.0	30	PDB header: metal binding protein Chain: A; PDB Molecule: skeletal muscle lim-protein 1; PDBTitle: solution structure of the skeletal muscle lim-protein 1
47	d1qpoa2	Alignment	not modelled	10.7	25	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
48	c5gt1A_	Alignment	not modelled	9.5	17	PDB header: choline-binding protein Chain: A; PDB Molecule: choline binding protein a; PDBTitle: crystal structure of cbpa from I. salivarius ren
49	d1o4ua2	Alignment	not modelled	9.0	10	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
50	d1a6ca3	Alignment	not modelled	8.9	21	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
51	c4lqeA_	Alignment	not modelled	8.8	25	PDB header: dna binding protein Chain: A; PDB Molecule: mepb; PDBTitle: crystal structure of mepb
52	c2kyaA_	Alignment	not modelled	8.7	29	PDB header: hydrolase Chain: A; PDB Molecule: group xvi phospholipase a2; PDBTitle: solution structure of the h-rev107 n-terminal domain
53	d1x3ha1	Alignment	not modelled	8.2	21	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
54	d2fsqa1	Alignment	not modelled	7.7	23	Fold: LigT-like Superfamily: LigT-like Family: Atu0111-like
						PDB header: hydrolase Chain: A; PDB Molecule: putative glycyl-glycine endopeptidase

55	c3nyyA_	Alignment	not modelled	7.6	21	lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
56	d2incc1	Alignment	not modelled	7.4	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: TmoB-like Family: TmoB-like
57	c2lktA_	Alignment	not modelled	7.4	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
58	c2l1sA_	Alignment	not modelled	6.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yohn; PDBTitle: yp_001336205.1
59	d1qapa2	Alignment	not modelled	6.8	19	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
60	c3es1A_	Alignment	not modelled	6.6	48	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of protein with a cupin-like fold and unknown2 function (yp_001165807.1) from novosphingobium aromaticivorans dsm3 12444 at 1.91 a resolution
61	c2nasA_	Alignment	not modelled	6.4	21	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a pwwp doamin from trypanosoma brucei
62	c2mbvA_	Alignment	not modelled	6.4	35	PDB header: transcription Chain: A: PDB Molecule: fusion protein of lim domain transcription factor lmo4 (77- PDBTitle: lmo4-lim2 in complex with deaf1 (404-418)
63	c1t5eB_	Alignment	not modelled	6.3	46	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
64	c3h41A_	Alignment	not modelled	6.3	18	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60 family protein; PDBTitle: crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
65	c3tbiB_	Alignment	not modelled	6.0	55	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
66	d1n27a_	Alignment	not modelled	6.0	14	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
67	c2rtyA_	Alignment	not modelled	5.9	23	PDB header: toxin Chain: A: PDB Molecule: navitoxin; PDBTitle: solution structure of navitoxin
68	d2nlua1	Alignment	not modelled	5.7	15	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
69	c5c22A_	Alignment	not modelled	5.6	24	PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli
70	c4x2oB_	Alignment	not modelled	5.6	24	PDB header: transport protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: sac3n peptide bound to mex67:mtr2