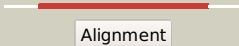
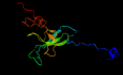

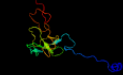
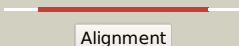
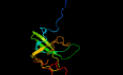
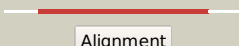
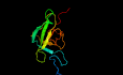
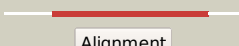
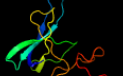
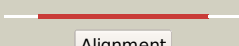

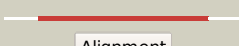
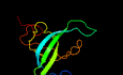

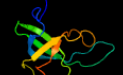



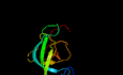

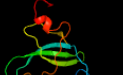
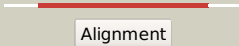
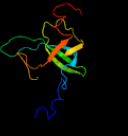






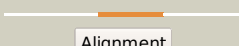
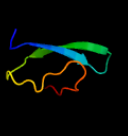
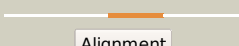
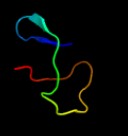
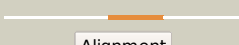

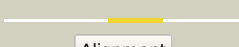


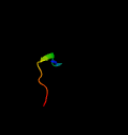
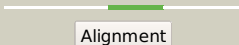
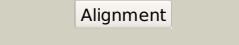

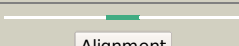

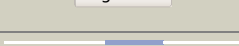
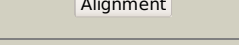
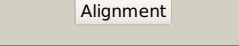


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0682_(rpsL)_781563_781937
Date	Fri Jul 26 01:50:25 BST 2019
Unique Job ID	6fc1ebfad0592c64

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i94l_	 Alignment		100.0	73	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
2	d2qall1	 Alignment		100.0	69	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
3	d2uubl1	 Alignment		100.0	74	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
4	c3j6vL_	 Alignment		100.0	50	PDB header: ribosome Chain: L: PDB Molecule: 28s ribosomal protein s12, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
5	c1zn1L_	 Alignment		100.0	76	PDB header: biosynthetic/structural protein/rna Chain: L: PDB Molecule: 30s ribosomal protein s12; PDBTitle: coordinates of rrf fitted into cryo-em map of the 70s post-termination2 complex
6	c2xzmL_	 Alignment		100.0	32	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s12; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
7	c2zkl_	 Alignment		100.0	30	PDB header: ribosomal protein/rna Chain: L: 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
8	c3u5gX_	 Alignment		100.0	35	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s23-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
9	c3zeyS_	 Alignment		100.0	36	PDB header: ribosome Chain: S: PDB Molecule: 40s ribosomal protein s23, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
10	c1s1hL_	 Alignment		100.0	34	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s23; 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.
11	c3j20N_	 Alignment		100.0	39	PDB header: ribosome Chain: N: PDB Molecule: 30s ribosomal protein s12p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)

12	c5xyiX_	 Alignment		100.0	32	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s23, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
13	c4ql5A_	 Alignment		88.7	20	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
14	c2nchA_	 Alignment		86.4	30	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: solution structure of translation initiation factor if1 from wolbachia2 endosymbiont strain trs of brugia malayi
15	c3i4oA_	 Alignment		86.1	27	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
16	c4dapA_	 Alignment		86.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: sugar fermentation stimulation protein a; PDBTitle: the structure of escherichia coli sfsa
17	d1ah9a_	 Alignment		86.0	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
18	c6c00A_	 Alignment		85.4	30	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: solution structure of translation initiation factor 1 from clostridium2 difficile
19	d1hr0w_	 Alignment		72.1	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
20	c4bpp0_	 Alignment		53.4	19	PDB header: ribosome Chain: 0: PDB Molecule: translation initiation factor eif-1a family protein; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 4
21	c3j81i_	 Alignment	not modelled	52.4	17	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
22	c4davA_	 Alignment	not modelled	50.7	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: sugar fermentation stimulation protein homolog; PDBTitle: the structure of pyrococcus furiosus sfsa in complex with dna
23	d1jt8a_	 Alignment	not modelled	47.6	31	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
24	c2oqkA_	 Alignment	not modelled	40.0	13	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
25	c2d1cB_	 Alignment	not modelled	29.4	33	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase; PDBTitle: crystal structure of tt0538 protein from thermus thermophilus hb8
26	d1d7qa_	 Alignment	not modelled	28.8	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
27	d2ix0a3	 Alignment	not modelled	25.7	34	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
28	c1y80A_	 Alignment	not modelled	23.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica

29	d1v7wa1	Alignment	not modelled	23.2	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
30	d1ju2a1	Alignment	not modelled	19.7	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
31	d1pb1a	Alignment	not modelled	16.9	33	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
32	d1eara1	Alignment	not modelled	16.9	5	Fold: Urease metallochaperone UreE, N-terminal domain Superfamily: Urease metallochaperone UreE, N-terminal domain Family: Urease metallochaperone UreE, N-terminal domain
33	c5y6rA	Alignment	not modelled	15.9	90	PDB header: transferase Chain: A: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of csfv ns5b
34	d1rutx4	Alignment	not modelled	15.5	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
35	c6ic4C	Alignment	not modelled	14.2	22	PDB header: protein transport Chain: C: PDB Molecule: toluene tolerance efflux transporter (abc superfamily, PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
36	d3bula2	Alignment	not modelled	13.9	29	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
37	d1o7ia	Alignment	not modelled	13.2	5	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
38	d1yrra1	Alignment	not modelled	12.1	25	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
39	d1dwna	Alignment	not modelled	11.6	28	Fold: RNA bacteriophage capsid protein Superfamily: RNA bacteriophage capsid protein Family: RNA bacteriophage capsid protein
40	c4c92D	Alignment	not modelled	11.5	10	PDB header: transcription Chain: D: PDB Molecule: u6 snrna-associated sm-like protein lsm4; PDBTitle: crystal structure of the yeast lsm1-7 complex
41	c4uqfB	Alignment	not modelled	10.8	33	PDB header: hydrolase Chain: B: PDB Molecule: gtp cyclohydrolase 1; PDBTitle: crystal structure of listeria monocytogenes gtp cyclohydrolase i
42	c3swnA	Alignment	not modelled	10.1	14	PDB header: rna binding protein Chain: A: PDB Molecule: u6 snrna-associated sm-like protein lsm5; PDBTitle: structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
43	d1hqsa	Alignment	not modelled	9.8	28	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
44	d1rxta1	Alignment	not modelled	9.1	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-myristoyl transferase, NMT
45	d1e32a1	Alignment	not modelled	8.6	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
46	c3n0vD	Alignment	not modelled	7.9	15	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
47	d2dipa1	Alignment	not modelled	7.8	17	Fold: RING/U-box Superfamily: RING/U-box Family: ZZ domain
48	c5w5cE	Alignment	not modelled	7.8	63	PDB header: exocytosis Chain: E: PDB Molecule: complexin-1; PDBTitle: crystal structure of the primed snare-complexin-synaptotagmin-1 c2ab2 complex
49	c2jx5A	Alignment	not modelled	7.6	26	PDB header: ribosomal protein Chain: A: PDB Molecule: glub(s27a); PDBTitle: solution structure of the ubiquitin domain n-terminal to2 the s27a ribosomal subunit of giardia lamblia
50	d1x7fa2	Alignment	not modelled	7.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
51	c3jcr3	Alignment	not modelled	6.9	18	PDB header: splicing Chain: 3: PDB Molecule: lsm3; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
52	d1ccwa	Alignment	not modelled	6.9	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
53	c2e0cA	Alignment	not modelled	6.9	39	PDB header: oxidoreductase Chain: A: PDB Molecule: 409aa long hypothetical nadp-dependent isocitrate PDBTitle: crystal structure of isocitrate dehydrogenase from sulfobolus tokodaii2 strain7 at 2.0 a resolution
54	d1w98b1	Alignment	not modelled	6.6	38	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
55	c3bw1A	Alignment	not modelled	6.6	14	PDB header: rna binding protein Chain: A: PDB Molecule: u6 snrna-associated sm-like protein lsm3; PDBTitle: crystal structure of homomeric yeast lsm3 exhibiting

						novel octameric2 ring organisation
56	d2vo1a1	Alignment	not modelled	6.4	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
57	c3hx6A	Alignment	not modelled	6.4	33	PDB header: cell adhesion Chain: A: PDB Molecule: type 4 fimbrial biogenesis protein pily1; PDBTitle: crystal structure of pseudomonas aeruginosa pily1 c-terminal2 domain
58	c3louB	Alignment	not modelled	6.3	16	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
59	c2r8cB	Alignment	not modelled	6.3	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
60	c3cw1D	Alignment	not modelled	6.2	5	PDB header: splicing Chain: D: PDB Molecule: small nuclear ribonucleoprotein sm d3; PDBTitle: crystal structure of human spliceosomal u1 snrnp
61	c1xyr6	Alignment	not modelled	6.1	55	PDB header: virus Chain: 6: PDB Molecule: genome polyprotein, coat protein vp3; PDB Fragment: residues 620-630 PDBTitle: poliovirus 135s cell entry intermediate
62	c5ol7A	Alignment	not modelled	6.1	15	PDB header: splicing Chain: A: PDB Molecule: dna-directed dna polymerase,dna-directed dna polymerase; PDBTitle: crystal structure of an inactivated npu siclpps intein with cfahpq2 extein
63	d1d3ba	Alignment	not modelled	6.1	5	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
64	c3nrbD	Alignment	not modelled	5.7	22	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
65	d1iica1	Alignment	not modelled	5.4	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-myristoyl transferase, NMT
66	c1x7fA	Alignment	not modelled	5.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
67	d2fcta1	Alignment	not modelled	5.3	24	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: PhyH-like
68	c2fwkB	Alignment	not modelled	5.2	9	PDB header: dna binding protein Chain: B: PDB Molecule: u6 snrna-associated sm-like protein lsm5; PDBTitle: crystal structure of cryptosporidium parvum u6 snrna-associated sm-2 like protein lsm5
69	c6f1ud	Alignment	not modelled	5.2	50	PDB header: motor protein Chain: D: PDB Molecule: arp1 actin related protein 1 homolog a; PDBTitle: n terminal region of dynein tail domains in complex with dynactin2 filament and bicdr-1