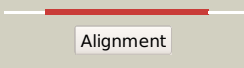

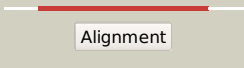

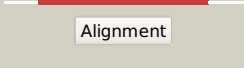

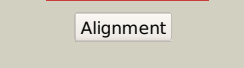

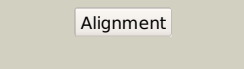

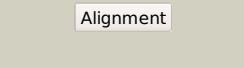

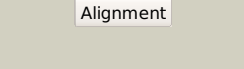

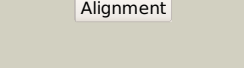

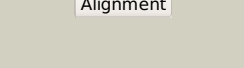

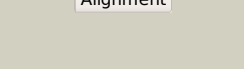

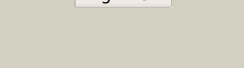









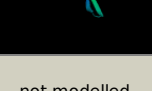


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0721_(rpsE)_814331_814993
Date	Fri Jul 26 01:50:29 BST 2019
Unique Job ID	5d9c42a61a5091b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o5jE_			100.0	96	PDB header: ribosome Chain: E; PDB Molecule: 30s ribosomal protein s5; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	c3j6vE_			100.0	21	PDB header: ribosome Chain: E; PDB Molecule: 28s ribosomal protein s5, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
3	c5mmje_			100.0	42	PDB header: ribosome Chain: E; PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
4	c3bbnE_			100.0	48	PDB header: ribosome Chain: E; PDB Molecule: ribosomal protein s5; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
5	c1p6gE_			100.0	60	PDB header: ribosome Chain: E; PDB Molecule: 30s ribosomal protein s5; PDBTitle: real space refined coordinates of the 30s subunit fitted into the low2 resolution cryo-em map of the ef-g.gtp state of e. coli 70s ribosome
6	c2ow8f_			100.0	49	PDB header: ribosome Chain: F; PDB Molecule: PDBTitle: crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
7	c2xzmE_			100.0	31	PDB header: ribosome Chain: E; PDB Molecule: ribosomal protein s5 containing protein; 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
8	c1eg0B_			100.0	60	PDB header: ribosome PDB COMPND:
9	c3zeyP_			100.0	32	PDB header: ribosome Chain: P; PDB Molecule: 40s ribosomal protein s2, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
10	c4kzzC_			100.0	31	PDB header: ribosome Chain: C; PDB Molecule: 40s ribosomal protein s2; PDBTitle: rabbit 40s ribosomal subunit in complex with mrna, initiator trna and2 eif1a
11	c5xyiC_			100.0	31	PDB header: ribosome Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome

12	c3j20F_	Alignment		100.0	29	PDB header: ribosome Chain: F; PDB Molecule: 30s ribosomal protein s5p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
13	c2zkqe_	Alignment		100.0	32	PDB header: ribosomal protein/rna Chain: E; PDB Molecule: rna expansion segment es6 part ii; 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
14	c1s1hE_	Alignment		100.0	34	PDB header: ribosome Chain: E; PDB Molecule: 40s ribosomal protein s2; 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.
15	c3izbE_	Alignment		100.0	32	PDB header: ribosome Chain: E; PDB Molecule: 40s ribosomal protein rps2 (s5p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
16	c3iz6E_	Alignment		100.0	33	PDB header: ribosome Chain: E; PDB Molecule: 40s ribosomal protein s2 (s5p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
17	d2qale1	Alignment		100.0	58	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
18	d2uube1	Alignment		100.0	52	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
19	d1pkpa1	Alignment		99.9	60	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
20	d2uube2	Alignment		99.9	46	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
21	d2qale2	Alignment	not modelled	99.9	62	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
22	d1pkpa2	Alignment	not modelled	99.9	62	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
23	c1vw45_	Alignment	not modelled	68.8	14	PDB header: ribosome Chain: 5; PDB Molecule: 54s ribosomal protein l3, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
24	d2b7ta1	Alignment	not modelled	55.6	22	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
25	d1p42a1	Alignment	not modelled	55.5	27	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
26	d2nuga2	Alignment	not modelled	52.0	19	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
27	c4oogC_	Alignment	not modelled	51.5	21	PDB header: hydrolase/rna Chain: C; PDB Molecule: ribonuclease 3; PDBTitle: crystal structure of yeast rnaase iii (rnt1p) complexed with the2 product of dsrna processing
28	c2go4A_	Alignment	not modelled	51.1	27	PDB header: hydrolase Chain: A; PDB Molecule: udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine PDBTitle: crystal structure of aquifex aeolicus lpxc complexed with tu-514
						PDB header: hydrolase Chain: B; PDB Molecule: udp-3-o-[3-hydroxymyristoyl] n-

29	c3nzkB	Alignment	not modelled	48.6	47	acetylglucosamine PDBTitle: structure of lpzc from yersinia enterocolitica complexed with chir0902 inhibitor
30	c2vesA	Alignment	not modelled	47.2	33	PDB header: hydrolase Chain: A: PDB Molecule: udp-3-o-acyl-n-acetylglucosamine deacetylase; PDBTitle: crystal structure of lpzc from pseudomonas aeruginosa complexed with2 the potent bb-78485 inhibitor
31	d1bf4a	Alignment	not modelled	46.8	31	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: "Histone-like" proteins from archaea
32	c2mdrA	Alignment	not modelled	43.3	10	PDB header: hydrolase Chain: A: PDB Molecule: double-stranded rna-specific adenosine deaminase; PDBTitle: solution structure of the third double-stranded rna-binding domain2 (dsrbd3) of human adenosine-deaminase adar1
33	c2zqeA	Alignment	not modelled	43.0	37	PDB header: dna binding protein Chain: A: PDB Molecule: muts2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus muts2
34	c6htuA	Alignment	not modelled	42.6	20	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein staufen homolog 1; PDBTitle: structure of hstau1 dsrbd3-4 in complex with arf1 rna
35	c3adjA	Alignment	not modelled	41.7	21	PDB header: gene regulation Chain: A: PDB Molecule: f21m12.9 protein; PDBTitle: structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
36	c2ljhA	Alignment	not modelled	41.1	19	PDB header: hydrolase Chain: A: PDB Molecule: double-stranded rna-specific editase adar; PDBTitle: nmr structure of double-stranded rna-specific editase adar
37	d2b7va1	Alignment	not modelled	39.1	23	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
38	d2vapa2	Alignment	not modelled	38.9	20	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
39	d2pifa1	Alignment	not modelled	38.7	19	Fold: PSTPO5379-like Superfamily: PSTPO5379-like Family: PSTPO5379-like
40	d1stua	Alignment	not modelled	38.2	20	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
41	d1sr9a3	Alignment	not modelled	37.5	18	Fold: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Superfamily: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Family: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
42	d1w5fa2	Alignment	not modelled	36.5	28	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
43	d1o0wa2	Alignment	not modelled	36.5	20	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
44	c5npgA	Alignment	not modelled	35.6	10	PDB header: rna binding protein Chain: A: PDB Molecule: loquacious, isoform f; PDBTitle: solution structure of drosophila melanogaster loquacious dsrbd1
45	d1ofua2	Alignment	not modelled	35.6	19	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
46	d1rq2a2	Alignment	not modelled	34.0	20	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
47	d1x47a1	Alignment	not modelled	33.6	22	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
48	c4gisB	Alignment	not modelled	33.2	18	PDB header: lyase Chain: B: PDB Molecule: enolase; PDBTitle: crystal structure of an enolase family member from vibrio harveyi2 (efi-target 501692) with homology to mannonate dehydratase, with mg,3 glycerol and dicarboxylates bound (mixed loops, space group i4122)
49	d1qu6a2	Alignment	not modelled	32.3	14	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
50	c2ltrA	Alignment	not modelled	32.1	25	PDB header: rna binding protein Chain: A: PDB Molecule: protein rde-4; PDBTitle: solution structure of rde-4(32-136)
51	c3adiC	Alignment	not modelled	31.1	15	PDB header: gene regulation/rna Chain: C: PDB Molecule: f21m12.9 protein; PDBTitle: structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
52	d1tzza2	Alignment	not modelled	29.2	32	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
53	d1uila	Alignment	not modelled	29.1	8	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
54	c2l3A	Alignment	not modelled	25.4	27	PDB header: hydrolase/rna Chain: A: PDB Molecule: double-stranded rna-specific editase 1;

54	c2bJA_	Alignment	not modelled	23.4	27	PDBTitle: the solution structure of the adar2 dsrbm-rna complex reveals a2 sequence-specific read out of the minor groove
55	d1t4oa_	Alignment	not modelled	23.4	23	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
56	c1t4oA_	Alignment	not modelled	23.4	23	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of rnt1p dsrbd
57	d2dixa1	Alignment	not modelled	22.3	22	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
58	c2fkpC_	Alignment	not modelled	22.3	21	PDB header: isomerase Chain: C: PDB Molecule: n-acylamino acid racemase; PDBTitle: the mutant g127c-t313c of deinococcus radiodurans n-2 acylamino acid racemase
59	d1jpdx2	Alignment	not modelled	21.7	18	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
60	c3c4tA_	Alignment	not modelled	19.8	20	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease dicer; PDBTitle: structure of rnaseiib and dsrna binding domains of mouse dicer
61	c2n3hA_	Alignment	not modelled	19.8	21	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein 4; PDBTitle: solution structure of drb4 dsrbd2 (viz. drb4(81-151))
62	c5b16A_	Alignment	not modelled	19.5	21	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease 3,drosha,ribonuclease 3,drosha,ribonuclease 3; PDBTitle: x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
63	d1r0ma2	Alignment	not modelled	19.3	19	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
64	d2f1da2	Alignment	not modelled	18.3	15	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
65	d1jdfa2	Alignment	not modelled	17.5	22	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
66	d1x48a1	Alignment	not modelled	17.4	28	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
67	d1bqga2	Alignment	not modelled	17.1	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
68	c5n8lA_	Alignment	not modelled	16.5	20	PDB header: rna binding protein Chain: A: PDB Molecule: crisc-loading complex subunit tarbp2; PDBTitle: structure of trbp dsrbd 1 and 2 in complex with a 19 bp sirna (complex2 b)
69	d1azpa_	Alignment	not modelled	16.0	30	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: "Histone-like" proteins from archaea
70	d1kn0a_	Alignment	not modelled	15.4	22	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: The homologous-pairing domain of Rad52 recombinase
71	d1znna1	Alignment	not modelled	15.1	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
72	c1znnF_	Alignment	not modelled	15.1	21	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
73	c2n3gA_	Alignment	not modelled	15.1	12	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein 4; PDBTitle: solution structure of drb4 dsrbd1 (viz. drb4(1-72))
74	c1yywB_	Alignment	not modelled	14.9	23	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of rnase iii from aquifex aeolicus2 complexed with double stranded rna at 2.8-angstrom3 resolution
75	d1l0oc_	Alignment	not modelled	14.7	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
76	c1l0oC_	Alignment	not modelled	14.7	21	PDB header: protein binding Chain: C: PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
77	c3adlA_	Alignment	not modelled	14.7	15	PDB header: gene regulation/rna Chain: A: PDB Molecule: crisc-loading complex subunit tarbp2; PDBTitle: structure of trbp2 and its molecule implications for mirna processing
78	d2dmya1	Alignment	not modelled	14.0	11	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
79	d1u7na_	Alignment	not modelled	13.7	13	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PlsX-like
80	d1di2a_	Alignment	not modelled	13.4	21	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
						PDB header: lyase

81	c6ezmL	Alignment	not modelled	13.4	15	Chain: L; PDB Molecule: imidazoleglycerol-phosphate dehydratase; PDBTitle: imidazoleglycerol-phosphate dehydratase from saccharomyces cerevisiae
82	d1t4na	Alignment	not modelled	13.0	23	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
83	c1h2iG	Alignment	not modelled	12.8	22	PDB header: dna binding protein Chain: G; PDB Molecule: dna repair protein rad52 homolog; PDBTitle: human rad52 protein, n-terminal domain
84	d1t4lb	Alignment	not modelled	12.5	25	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
85	d1uhza	Alignment	not modelled	12.4	21	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
86	c6ci7A	Alignment	not modelled	11.7	14	PDB header: biosynthetic protein Chain: A; PDB Molecule: ycao; PDBTitle: the structure of ycao from methanopyrus kandleri bound with amppcp and 2 mg2+
87	c2n5lA	Alignment	not modelled	11.7	25	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 c-terminal domain
88	c1w5fA	Alignment	not modelled	11.4	28	PDB header: cell division Chain: A; PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
89	c2gezE	Alignment	not modelled	11.4	13	PDB header: hydrolase Chain: E; PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
90	d1x49a1	Alignment	not modelled	11.2	13	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
91	c3rv0B	Alignment	not modelled	11.2	14	PDB header: rna binding protein Chain: B; PDB Molecule: k. polysporus dcr1; PDBTitle: crystal structure of k. polysporus dcr1 without the c-terminal dsrbd
92	d1tifa	Alignment	not modelled	11.0	53	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
93	c3u4fC	Alignment	not modelled	10.9	13	PDB header: isomerase Chain: C; PDB Molecule: mandelate racemase/muconate lactonizing enzyme family PDBTitle: crystal structure of a mandelate racemase (muconate lactonizing enzyme2 family protein) from roseovarius nubinhibens
94	d1txga1	Alignment	not modelled	10.8	25	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Glycerol-3-phosphate dehydrogenase
95	c6o6dA	Alignment	not modelled	10.8	18	PDB header: ligase Chain: A; PDB Molecule: translation initiation factor if-3; PDBTitle: n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori
96	c4v1ah	Alignment	not modelled	10.7	10	PDB header: ribosome Chain: H; PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
97	c1jpdX	Alignment	not modelled	10.3	17	PDB header: isomerase Chain: X; PDB Molecule: l-ala-d/l-glu epimerase; PDBTitle: l-ala-d/l-glu epimerase
98	c3llhB	Alignment	not modelled	10.2	34	PDB header: rna binding protein Chain: B; PDB Molecule: risc-loading complex subunit tarbp2; PDBTitle: crystal structure of the first dsrbd of tar rna-binding protein 2
99	c2l2nA	Alignment	not modelled	10.2	15	PDB header: rna binding protein, plant protein Chain: A; PDB Molecule: hyponastic leave 1; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for the first2 dsrbd of protein hyl1