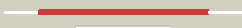












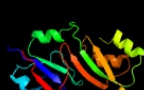







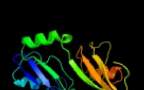




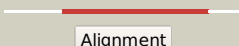

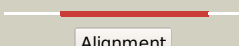
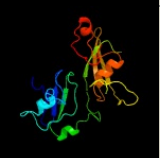
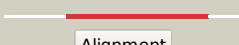
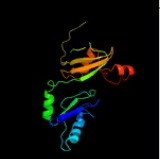
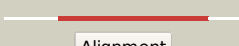

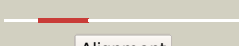
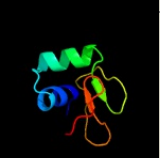

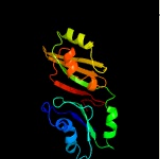

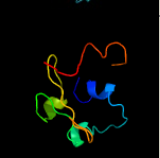

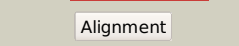





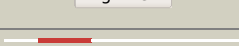


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1711 (-)_1938845_1939609
Date	Fri Aug 2 13:30:31 BST 2019
Unique Job ID	1ed5425839be8d2a

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dh3C_	 Alignment		100.0	33	PDB header: isomerase/rna Chain: C: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of rluf in complex with a 22 nucleotide rna2 substrate
2	c4lgtA_	 Alignment		100.0	40	PDB header: isomerase/rna Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase b; PDBTitle: crystal structure of the catalytic domain of rlub in complex with a2 21-nucleotide rna substrate
3	c1kskA_	 Alignment		100.0	35	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
4	c1vioA_	 Alignment		100.0	32	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridylylase
5	c2istA_	 Alignment		100.0	24	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of rlud from e. coli
6	c2gmlA_	 Alignment		100.0	35	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of catalytic domain of e.coli rluf
7	c2omlA_	 Alignment		100.0	33	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlue
8	c2olwB_	 Alignment		100.0	35	PDB header: isomerase Chain: B: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlue
9	d1kska4	 Alignment		100.0	36	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RLuD
10	d1vioa1	 Alignment		100.0	36	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RLuD
11	c1v9fA_	 Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli

12	d1v9fa_	 Alignment		100.0	21	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RLuD
13	c1qyuA_	 Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
14	d1v9ka_	 Alignment		100.0	26	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RLuD
15	c2i82D_	 Alignment		100.0	23	PDB header: lyase/rna Chain: D: PDB Molecule: ribosomal large subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
16	c5ubaA_	 Alignment		100.0	21	PDB header: rna binding protein Chain: A: PDB Molecule: rna pseudouridylate synthase domain-containing protein 4; PDBTitle: human rna pseudouridylate synthase domain containing 4
17	c5vbbA_	 Alignment		100.0	21	PDB header: rna binding protein Chain: A: PDB Molecule: rna pseudouridylate synthase domain-containing protein 1; PDBTitle: human rna pseudouridylate synthase domain containing 1
18	d1vioa2	 Alignment		99.1	18	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
19	d2apoa2	 Alignment		99.0	20	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
20	c2k6pA_	 Alignment		99.0	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
21	c3bbnD_	 Alignment	not modelled	98.9	20	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
22	d2ey4a2	 Alignment	not modelled	98.9	24	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
23	c5z81A_	 Alignment	not modelled	98.9	23	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 15; PDBTitle: trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
24	d1dm9a_	 Alignment	not modelled	98.9	24	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kD
25	c1dm9A_	 Alignment	not modelled	98.9	24	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
26	c2apoA_	 Alignment	not modelled	98.9	20	PDB header: isomerase/rna binding protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of the methanococcus jannaschii cbf52 nop10 complex
27	d1r3ea2	 Alignment	not modelled	98.8	24	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
28	d1p9ka_	 Alignment	not modelled	98.8	26	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ybcj-like
						PDB header: rna binding protein

29	c2cqjA_	Alignment	not modelled	98.8	30	Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein PDBTitle: solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
30	c2ey4A_	Alignment	not modelled	98.8	25	PDB header: isomerase/biosynthetic protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of a cbf5-nop10-gar1 complex
31	d1k8wa5	Alignment	not modelled	98.7	21	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
32	c3uiaiA_	Alignment	not modelled	98.6	22	PDB header: isomerase/chaperone Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 4; PDBTitle: structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
33	d1sgva2	Alignment	not modelled	98.6	24	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
34	c1sgvA_	Alignment	not modelled	98.6	23	PDB header: lyase Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: structure of trna psi55 pseudouridine synthase (trub)
35	c5o5jD_	Alignment	not modelled	98.5	31	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
36	c1k8wA_	Alignment	not modelled	98.5	20	PDB header: lyase/rna Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
37	d1c06a_	Alignment	not modelled	98.5	31	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
38	c3j20D_	Alignment	not modelled	98.5	21	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
39	d2uubd1	Alignment	not modelled	98.5	33	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
40	d2gy9d1	Alignment	not modelled	98.3	28	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
41	c6nd4Z_	Alignment	not modelled	98.1	24	PDB header: ribosome Chain: Z: PDB Molecule: imp3; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
42	c3hp7A_	Alignment	not modelled	97.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
43	c5jppb_	Alignment	not modelled	97.9	28	PDB header: ribosome Chain: B: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
44	c5xyij_	Alignment	not modelled	97.9	19	PDB header: ribosome Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome
45	c3zey6_	Alignment	not modelled	97.7	23	PDB header: ribosome Chain: 6: PDB Molecule: 40s ribosomal protein s9, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
46	d1h3fa2	Alignment	not modelled	97.6	22	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
47	d1kska3	Alignment	not modelled	97.5	33	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
48	c1s1hD_	Alignment	not modelled	97.5	20	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein s9-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, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
49	c2xzmD_	Alignment	not modelled	97.5	15	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4 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
50	d1jh3a_	Alignment	not modelled	97.3	28	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
51	c1ze2B_	Alignment	not modelled	97.3	24	PDB header: lyase/rna Chain: B: PDB Molecule: trna pseudouridine synthase b; PDBTitle: conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
52	c5wxmA_	Alignment	not modelled	97.3	26	PDB header: ribosomal protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein imp3; PDBTitle: crystal structure of the imp3 and mpp10 complex
53	c1h3eA_	Alignment	not modelled	97.1	22	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-tRNA synthetase; PDBTitle: tyrosyl-tRNA synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol
54	c4ouidA_	Alignment	not modelled	96.7	10	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-tRNA synthetase;

54	c800A	Alignment	not modelled	90.7	19	PDBTitle: engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine PDB header: ligase
55	c2janD	Alignment	not modelled	96.6	22	Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state PDB header: ligase
56	c6otjA	Alignment	not modelled	96.6	20	Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosyl-trna synthetase from neisseria2 gonorrhoeae with bound l-tyr PDB header: ribosome
57	c3j20E	Alignment	not modelled	95.5	20	Chain: E: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) PDB header: ribosome
58	c5xyiE	Alignment	not modelled	94.6	12	Chain: E: PDB Molecule: 40s ribosomal protein s4; PDBTitle: small subunit of trichomonas vaginalis ribosome PDB header: ribosome
59	c5xxuE	Alignment	not modelled	93.8	14	Chain: E: PDB Molecule: ribosomal protein es4; PDBTitle: small subunit of toxoplasma gondii ribosome PDB header: ribosome
60	c3kbgA	Alignment	not modelled	93.5	17	Chain: A: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: crystal structure of the 30s ribosomal protein s4e from thermoplasma2 acidophilum. northeast structural genomics consortium target tar28. PDB header: ribosome
61	c3zey1	Alignment	not modelled	93.5	14	Chain: 1: PDB Molecule: 40s ribosomal protein s4, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome PDB header: ribosome
62	c3iz6C	Alignment	not modelled	93.1	20	Chain: C: PDB Molecule: 40s ribosomal protein s9 (s4p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome PDB header: ribosome
63	c3u5cE	Alignment	not modelled	93.0	15	Chain: E: PDB Molecule: 40s ribosomal protein s4-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a PDB header: ribosome
64	c2xzmW	Alignment	not modelled	93.0	16	Chain: W: PDB Molecule: 40s ribosomal protein s4; 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 PDB header: ribosome
65	c3izbC	Alignment	not modelled	88.1	20	Chain: C: PDB Molecule: 40s ribosomal protein rps9 (s4p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome PDB header: ribosome
66	c3iz6D	Alignment	not modelled	87.5	18	Chain: D: PDB Molecule: 40s ribosomal protein s4 (s4e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome PDB header: ribosome
67	c3izbD	Alignment	not modelled	83.4	15	Chain: D: PDB Molecule: 40s ribosomal protein rps4 (s4e); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome PDB header: ribosome
68	c6jzbD	Alignment	not modelled	27.2	11	PDB header: transferase Chain: D: PDB Molecule: moad/this family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
69	d2hzb1	Alignment	not modelled	26.0	17	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
70	c6jc0A	Alignment	not modelled	24.3	11	PDB header: transferase Chain: A: PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
71	c4o1sB	Alignment	not modelled	17.5	18	PDB header: splicing Chain: B: PDB Molecule: v-type atp synthase alpha chain; PDBTitle: crystal structure of tvovma intein
72	d1v54d	Alignment	not modelled	17.2	29	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
73	c2y69Q	Alignment	not modelled	17.1	29	PDB header: electron transport Chain: Q: PDB Molecule: cytochrome c oxidase subunit 4 isoform 1; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
74	d2hzaa1	Alignment	not modelled	16.0	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
75	c3rpfC	Alignment	not modelled	14.1	11	PDB header: transferase Chain: C: PDB Molecule: molybdopterin converting factor, subunit 1 (moad); PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
76	d1nka1	Alignment	not modelled	13.1	21	Fold: Prealbumin-like Superfamily: Starch-binding domain-like Family: Rhamnogalacturonase B, RhgB, middle domain
77	c5fmmA	Alignment	not modelled	12.9	21	PDB header: viral protein Chain: A: PDB Molecule: influenza a pb2 subunit; PDBTitle: crystal structure of the mid, cap-binding, mid-link and 627 domains2 from avian influenza a virus polymerase pb2 subunit bound to m7gtp
78	d1x6oa1	Alignment	not modelled	12.6	17	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain

						Family: eIF5a N-terminal domain-like
79	d1khia1	Alignment	not modelled	12.1	17	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
80	d1rwsa_	Alignment	not modelled	12.0	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
81	c5w10A_	Alignment	not modelled	11.6	21	PDB header: viral protein/inhibitor Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: co-crystal structure of influenza a h3n2 pb2 (241-741) bound to vx-787
82	c4wfwA_	Alignment	not modelled	11.5	14	PDB header: structural protein Chain: A: PDB Molecule: general secretion pathway protein b; PDBTitle: the crystal structure of dickeya dadantii gspb from the type 22 secretion system
83	c4j2nA_	Alignment	not modelled	11.2	14	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
84	c4j2nB_	Alignment	not modelled	11.2	14	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
85	d1k4ta3	Alignment	not modelled	10.1	27	Fold: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Superfamily: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Family: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
86	c4jmrA_	Alignment	not modelled	9.6	35	PDB header: viral protein/peptide Chain: A: PDB Molecule: gag protein; PDBTitle: a unique spumavirus gag n-terminal domain with functional properties2 of orthoretroviral matrix and capsid
87	d1n1ta1	Alignment	not modelled	9.2	35	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Trypanosoma sialidase, C-terminal domain
88	d1i5za1	Alignment	not modelled	9.0	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
89	d1nrza_	Alignment	not modelled	8.9	14	Fold: PTS IIb component Superfamily: PTS IIb component Family: PTS IIb component
90	c4onqA_	Alignment	not modelled	8.5	25	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: dna methyltransferase; PDBTitle: crystal structure of ntdrm e283s/r309s/f310s/y590s/d591s mutant
91	c2in0A_	Alignment	not modelled	8.5	18	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease pi-mtui; PDBTitle: crystal structure of mtu reca intein splicing domain
92	c1q5vB_	Alignment	not modelled	7.9	17	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
93	c1mzwB_	Alignment	not modelled	7.8	38	PDB header: isomerase Chain: B: PDB Molecule: u4/u6 snrnp 60kda protein; PDBTitle: crystal structure of a u4/u6 snrnp complex between human2 spliceosomal cyclophilin h and a u4/u6-60k peptide
94	c5o9jB_	Alignment	not modelled	7.7	7	PDB header: hydrolase Chain: B: PDB Molecule: transcription initiation factor iib,transcription PDBTitle: crystal structure of transcription factor iib mja mini-intein
95	c5mpaL_	Alignment	not modelled	7.7	9	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
96	c5fmzF_	Alignment	not modelled	7.4	33	PDB header: transcription Chain: F: PDB Molecule: polymerase basic protein 2; PDBTitle: crystal structure of influenza b polymerase with bound 5' vrna
97	d1oisa_	Alignment	not modelled	7.3	19	Fold: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Superfamily: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Family: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
98	c4wsaC_	Alignment	not modelled	7.2	33	PDB header: transferase/rna Chain: C: PDB Molecule: pb2; PDBTitle: crystal structure of influenza b polymerase bound to the vrna promoter2 (flub1 form)
99	c4egxA_	Alignment	not modelled	7.1	23	PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a cc1-fha tandem