

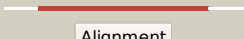

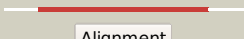



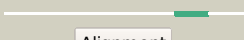


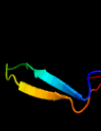

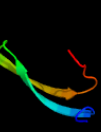





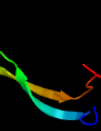




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1130_(-)_1254560_1256140
Date	Wed Jul 31 22:05:21 BST 2019
Unique Job ID	0b1a3e30140ffe89

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hp0A_	 Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: ids-epimerase; PDBTitle: crystal structure of iminodisuccinate epimerase
2	c5muxB_	 Alignment		100.0	21	PDB header: lyase Chain: B: PDB Molecule: 2-methylcitrate dehydratase; PDBTitle: crystal structure of 2-methylcitrate dehydratase (mmge) from bacillus2 subtilis.
3	d1szqa_	 Alignment		100.0	23	Fold: 2-methylcitrate dehydratase PrpD Superfamily: 2-methylcitrate dehydratase PrpD Family: 2-methylcitrate dehydratase PrpD
4	c4rqoB_	 Alignment		97.5	18	PDB header: lyase Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
5	d1i27a_	 Alignment		41.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of the rap74 subunit of TFIIF
6	c5gaon_	 Alignment		40.9	19	PDB header: transcription Chain: N: PDB Molecule: PDBTitle: head region of the yeast spliceosomal u4/u6.u5 tri-snrnp
7	c3jb9D_	 Alignment		40.3	19	PDB header: rna binding protein/rna Chain: D: PDB Molecule: small nuclear ribonucleoprotein sm d3; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
8	c3cw1D_	 Alignment		39.2	26	PDB header: splicing Chain: D: PDB Molecule: small nuclear ribonucleoprotein sm d3; PDBTitle: crystal structure of human spliceosomal u1 snrnp
9	c1b34A_	 Alignment		37.7	14	PDB header: rna binding protein Chain: A: PDB Molecule: protein (small nuclear ribonucleoprotein sm d1); PDBTitle: crystal structure of the d1d2 sub-complex from the human snrnp core2 domain
10	d1b34a_	 Alignment		37.7	14	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
11	d1d3ba_	 Alignment		33.9	26	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP

12	c4emhY_	Alignment		33.7	29	PDB header: rna binding protein Chain: Y; PDB Molecule: PDBTitle: crystal structure of splsm4
13	c6an0A_	Alignment		33.5	17	PDB header: oxidoreductase Chain: A; PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
14	c4c92D_	Alignment		32.3	30	PDB header: transcription Chain: D; PDB Molecule: u6 snrna-associated sm-like protein lsm4; PDBTitle: crystal structure of the yeast lsm1-7 complex
15	c3e21A_	Alignment		32.2	13	PDB header: apoptosis Chain: A; PDB Molecule: fas-associated factor 1; PDBTitle: crystal structure of faf-1 uba domain
16	c2fwkB_	Alignment		31.3	22	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
17	c3jcr3_	Alignment		30.9	14	PDB header: splicing Chain: 3; PDB Molecule: lsm3; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
18	c5mknK_	Alignment		30.7	26	PDB header: rna binding protein Chain: K; PDB Molecule: like-sm ribonucleoprotein core; PDBTitle: crystal structure of smap (lsm) protein from methanococcus vannielii
19	c3jb9b_	Alignment		30.5	27	PDB header: rna binding protein/rna Chain: B; PDB Molecule: pre-mrna-splicing factor cwf10; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
20	c5ganr_	Alignment		30.2	19	PDB header: transcription Chain: R; PDB Molecule: PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
21	d2c0ra1	Alignment	not modelled	29.9	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
22	c5gaol_	Alignment	not modelled	29.3	15	PDB header: transcription Chain: L; PDB Molecule: PDBTitle: head region of the yeast spliceosomal u4/u6.u5 tri-snrnp
23	c3pgwQ_	Alignment	not modelled	29.2	23	PDB header: splicing/dna/rna Chain: Q; PDB Molecule: sm b; PDBTitle: crystal structure of human u1 snrnp
24	c5vldC_	Alignment	not modelled	29.1	20	PDB header: oxidoreductase Chain: C; PDB Molecule: histidinol dehydrogenase, chloroplastic; PDBTitle: crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
25	c4c92B_	Alignment	not modelled	29.1	23	PDB header: transcription Chain: B; PDB Molecule: u6 snrna-associated sm-like protein lsm2; PDBTitle: crystal structure of the yeast lsm1-7 complex
26	c2e12B_	Alignment	not modelled	28.8	30	PDB header: translation Chain: B; PDB Molecule: hypothetical protein xcc3642; PDBTitle: the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif
27	c3jcr7_	Alignment	not modelled	28.1	19	PDB header: splicing Chain: 7; PDB Molecule: lsm7; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
28	c1vw4V_	Alignment	not modelled	27.7	15	PDB header: ribosome Chain: V; PDB Molecule: 54s ribosomal protein l36, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
						Fold: Sm-like fold

29	d1i8fa_	Alignment	not modelled	27.6	26	Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
30	c3bw1A_	Alignment	not modelled	27.6	25	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
31	c5uz5K_	Alignment	not modelled	27.5	21	PDB header: nuclear protein/rna Chain: K: PDB Molecule: small nuclear ribonucleoprotein-associated protein b; PDBTitle: s. cerevisiae u1 snrnp
32	c2koeA_	Alignment	not modelled	27.4	27	PDB header: membrane protein, signaling protein Chain: A: PDB Molecule: human cannabinoid receptor 1 - helix 7/8 peptide; PDBTitle: human cannabinoid receptor 1 - helix 7/8 peptide
33	c4c8qF_	Alignment	not modelled	27.2	26	PDB header: transcription Chain: F: PDB Molecule: u6 snrna-associated sm-like protein lsm6; PDBTitle: crystal structure of the yeast lsm1-7-pat1 complex
34	c5lopC_	Alignment	not modelled	26.9	29	PDB header: rna binding protein Chain: C: PDB Molecule: klla0a11308p; PDBTitle: structure of the active form of /k. lactis/ dcp1-dcp2-edc3 decapping2 complex bound to m7gdp
35	d1th7a1	Alignment	not modelled	26.1	19	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
36	c3cw1A_	Alignment	not modelled	25.9	19	PDB header: splicing Chain: A: PDB Molecule: small nuclear ribonucleoprotein-associated proteins b and PDBTitle: crystal structure of human spliceosomal u1 snrnp
37	d1i4k1_	Alignment	not modelled	25.4	22	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
38	c4xq3F_	Alignment	not modelled	25.0	21	PDB header: rna binding protein Chain: F: PDB Molecule: like-sm ribonucleoprotein core; PDBTitle: crystal structure of sso-smap2
39	c4m78H_	Alignment	not modelled	24.9	25	PDB header: rna binding protein Chain: H: PDB Molecule: u6 snrna-associated sm-like protein lsm8; PDBTitle: crystal structure of lsm2-8 complex, space group p21
40	d2fwka1	Alignment	not modelled	24.8	21	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
41	c3k8rA_	Alignment	not modelled	24.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution
42	c3pgwB_	Alignment	not modelled	24.3	19	PDB header: splicing/dna/rna Chain: B: PDB Molecule: sm b; PDBTitle: crystal structure of human u1 snrnp
43	c3cw15_	Alignment	not modelled	24.2	19	PDB header: splicing Chain: 5: PDB Molecule: small nuclear ribonucleoprotein g; PDB Fragment: residues 1-215; PDBTitle: crystal structure of human spliceosomal u1 snrnp
44	c5gank_	Alignment	not modelled	24.1	22	PDB header: transcription Chain: K: PDB Molecule: 13 kda ribonucleoprotein-associated protein; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
45	d1jw2a_	Alignment	not modelled	23.7	11	Fold: Open three-helical up-and-down bundle Superfamily: Hemolysin expression modulating protein HHA Family: Hemolysin expression modulating protein HHA
46	c3jcr4_	Alignment	not modelled	23.3	26	PDB header: splicing Chain: 4: PDB Molecule: lsm4; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
47	c3jb9E_	Alignment	not modelled	23.3	27	PDB header: rna binding protein/rna Chain: E: PDB Molecule: small nuclear ribonucleoprotein-associated protein b; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
48	c4c8qE_	Alignment	not modelled	23.2	19	PDB header: transcription Chain: E: PDB Molecule: u6 snrna-associated sm-like protein lsm5; PDBTitle: crystal structure of the yeast lsm1-7-pat1 complex
49	c5f8vH_	Alignment	not modelled	22.6	14	PDB header: transferase Chain: H: PDB Molecule: aminotransferase, class v family protein; PDBTitle: crystal structure of plp bound phosphoserine aminotransferase (psat)2 from trichomonas vaginalis
50	c6a19A_	Alignment	not modelled	22.6	6	PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of chorismate mutase from helicobacter pylori in2 complex with prephenate
51	c3jcr2_	Alignment	not modelled	22.5	24	PDB header: splicing Chain: 2: PDB Molecule: lsm2; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
52	d1d3bb_	Alignment	not modelled	22.2	19	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
53	c4a53A_	Alignment	not modelled	22.2	20	PDB header: rna binding protein Chain: A: PDB Molecule: edc3; PDBTitle: structural basis of the dcp1:dcp2 mrna decapping complex activation2 by edc3 and scd6
54	c3swnT_	Alignment	not modelled	22.1	26	PDB header: rna binding protein Chain: T: PDB Molecule: u6 snrna-associated sm-like protein lsm6; PDBTitle: structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings

55	d1b34b_	Alignment	not modelled	22.1	9	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
56	c1b34B_	Alignment	not modelled	22.1	9	PDB header: rna binding protein Chain: B: PDB Molecule: protein (small nuclear ribonucleoprotein sm d2); PDBTitle: crystal structure of the d1d2 sub-complex from the human snrnp core2 domain
57	c3kowH_	Alignment	not modelled	22.1	25	PDB header: metal binding protein Chain: H: PDB Molecule: d-ornithine aminomutase s component; PDBTitle: crystal structure of ornithine 4,5 aminomutase backsoaked complex
58	d1jbma_	Alignment	not modelled	22.0	15	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
59	d1mgqa_	Alignment	not modelled	21.6	15	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
60	d1h641_	Alignment	not modelled	21.3	22	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
61	d1d3bl_	Alignment	not modelled	21.1	19	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
62	d1j6ua3	Alignment	not modelled	20.8	14	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
63	c3swnA_	Alignment	not modelled	20.5	22	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
64	c3jb9l_	Alignment	not modelled	20.1	19	PDB header: rna binding protein/rna Chain: J: PDB Molecule: small nuclear ribonucleoprotein g; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
65	c4emgM_	Alignment	not modelled	19.9	19	PDB header: rna binding protein Chain: M: PDB Molecule: probable u6 snrna-associated sm-like protein lsm3; PDBTitle: crystal structure of splsm3
66	c4m77H_	Alignment	not modelled	19.4	22	PDB header: structural protein Chain: H: PDB Molecule: u6 snrna-associated sm-like protein lsm8; PDBTitle: crystal structure of lsm2-8 complex, space group i212121
67	c3cw1Z_	Alignment	not modelled	18.7	22	PDB header: splicing Chain: Z: PDB Molecule: small nuclear ribonucleoprotein f; PDBTitle: crystal structure of human spliceosomal u1 snrnp
68	c4qicB_	Alignment	not modelled	18.6	22	PDB header: oxidoreductase Chain: B: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
69	c3jcr5_	Alignment	not modelled	18.5	30	PDB header: splicing Chain: 5: PDB Molecule: lsm5; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
70	c4g07A_	Alignment	not modelled	18.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: the crystal structure of the c366s mutant of hdh from brucella suis
71	c4c8qA_	Alignment	not modelled	18.3	23	PDB header: transcription Chain: A: PDB Molecule: sm-like protein lsm1; PDBTitle: crystal structure of the yeast lsm1-7-pat1 complex
72	d1ni7a_	Alignment	not modelled	17.8	15	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
73	c3jcr8_	Alignment	not modelled	16.9	22	PDB header: splicing Chain: 8: PDB Molecule: lsm8; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
74	c3swnC_	Alignment	not modelled	16.5	22	PDB header: rna binding protein Chain: C: PDB Molecule: u6 snrna-associated sm-like protein lsm7; PDBTitle: structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
75	d2jfga3	Alignment	not modelled	15.9	14	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
76	d1m5q1_	Alignment	not modelled	15.8	33	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
77	c4c92G_	Alignment	not modelled	15.8	22	PDB header: transcription Chain: G: PDB Molecule: u6 snrna-associated sm-like protein lsm7; PDBTitle: crystal structure of the yeast lsm1-7 complex
78	c1y7JA_	Alignment	not modelled	15.8	67	PDB header: signaling protein Chain: A: PDB Molecule: agouti signaling protein; PDBTitle: nmr structure family of human agouti signalling protein (80-2 132: q115y, s124y)
79	c3jcr6_	Alignment	not modelled	15.4	30	PDB header: splicing Chain: 6: PDB Molecule: lsm6; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
80	d2bkwa1	Alignment	not modelled	15.4	9	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
81	d1mr0a_	Alignment	not modelled	15.1	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Agouti-related protein

						Family: Agouti-related protein
82	d1kn0a_	Alignment	not modelled	14.8	33	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: The homologous-pairing domain of Rad52 recombinase
83	c4lhdB_	Alignment	not modelled	14.8	9	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine dehydrogenase [decarboxylating]; PDBTitle: crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
84	c5kz5M_	Alignment	not modelled	14.3	16	PDB header: transferase/oxidoreductase Chain: M: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: architecture of the human mitochondrial iron-sulfur cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold
85	c4lqvA_	Alignment	not modelled	14.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium
86	d2fp1a1	Alignment	not modelled	13.6	20	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Secreted chorismate mutase-like
87	c2gbbA_	Alignment	not modelled	13.6	12	PDB header: isomerase Chain: A: PDB Molecule: putative chorismate mutase; PDBTitle: crystal structure of secreted chorismate mutase from yersinia pestis
88	d1dd4c_	Alignment	not modelled	13.5	12	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
89	c2x8nA_	Alignment	not modelled	13.5	10	PDB header: structural genomics Chain: A: PDB Molecule: cv0863; PDBTitle: solution nmr structure of uncharacterized protein cv0863 from2 chromobacterium violaceum. northeast structural genomics target3 (nesg) target cvt3. oesp target cv0863.
90	c2qtxL_	Alignment	not modelled	13.1	33	PDB header: rna binding protein Chain: L: PDB Molecule: uncharacterized protein mj1435; PDBTitle: crystal structure of an hfq-like protein from methanococcus jannaschii
91	c2kztA_	Alignment	not modelled	13.1	11	PDB header: apoptosis Chain: A: PDB Molecule: programmed cell death protein 4; PDBTitle: structure of the tandem ma-3 region of pdc4
92	c4c92A_	Alignment	not modelled	13.1	23	PDB header: transcription Chain: A: PDB Molecule: sm-like protein lsm1; PDBTitle: crystal structure of the yeast lsm1-7 complex
93	c1h2iG_	Alignment	not modelled	12.8	15	PDB header: dna binding protein Chain: G: PDB Molecule: dna repair protein rad52 homolog; PDBTitle: human rad52 protein, n-terminal domain
94	c2g40A_	Alignment	not modelled	12.6	17	PDB header: unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
95	d2g40a1	Alignment	not modelled	12.6	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: YkgG-like
96	d1vlfm2	Alignment	not modelled	12.3	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
97	c2ki9A_	Alignment	not modelled	12.0	45	PDB header: membrane protein Chain: A: PDB Molecule: cannabinoid receptor 2; PDBTitle: human cannabinoid receptor-2 helix 6
98	c5ig0A_	Alignment	not modelled	11.6	31	PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub
99	d1n9ra_	Alignment	not modelled	11.5	21	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP