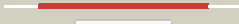



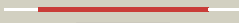





















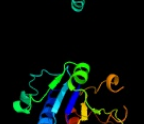


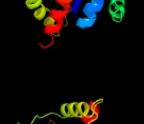



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1644_(tsnR)_1853613_1854395
Date	Fri Aug 2 13:30:24 BST 2019
Unique Job ID	c976588e64144116

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ipaA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: rna 2'-o-ribose methyltransferase; PDBTitle: crystal structure of rna 2'-o ribose methyltransferase
2	c4x3mB_	 Alignment		100.0	36	PDB header: transferase Chain: B: PDB Molecule: rna 2'-o ribose methyltransferase; PDBTitle: crystal structure of ttha0275 from thermus thermophilus (hb8) in2 complex with adenosine in space group p212121
3	c5kzkA_	 Alignment		100.0	32	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna methyltransferase, trmh family; PDBTitle: crystal structure of rna methyltransferase from sinorhizobium2 meliloti
4	c2i6dA_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: rna methyltransferase, trmh family; PDBTitle: the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
5	c3gyqB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: rrna (adenosine-2'-o-)-methyltransferase; PDBTitle: structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
6	c1x7pB_	 Alignment		100.0	34	PDB header: transferase Chain: B: PDB Molecule: rrna methyltransferase; PDBTitle: crystal structure of the spoU methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
7	c1gz0H_	 Alignment		100.0	23	PDB header: transferase Chain: H: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rlmb
8	c1gz0G_	 Alignment		100.0	23	PDB header: transferase Chain: G: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rlmb
9	d1gz0a1	 Alignment		100.0	23	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
10	c5co4A_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: putative trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structural insights into the 2-oh methylation of c/u34 on trna
11	d1ipaa1	 Alignment		100.0	38	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase

12	c1zjrA	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: trna (guanosine-2'-o-)-methyltransferase; PDBTitle: crystal structure of a. aeolicus trmh/spou trna modifying enzyme
13	d1v2xa	Alignment		100.0	33	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
14	c2ha8A	Alignment		100.0	23	PDB header: rna binding protein Chain: A: PDB Molecule: tar (hiv-1) rna loop binding protein; PDBTitle: methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
15	c4pzka	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: crystal structure of putative rna methyltransferase from bacillus2 anthracis.
16	d1mxia	Alignment		100.0	21	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
17	c3onpA	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: trna/rrna methyltransferase (spou); PDBTitle: crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
18	c3ic6A	Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methylase family protein; PDBTitle: crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
19	c5gm8A	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o-)-methyltransferase trmj; PDBTitle: methylation at position 32 of trna catalyzed by trmj alters oxidative2 stress response in pseudomonas aeruginosa
20	c4cngB	Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: spou rrna methylase; PDBTitle: crystal structure of sulfobolus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
21	c3e5yB	Alignment	not modelled	100.0	27	PDB header: transferase Chain: B: PDB Molecule: trmh family rna methyltransferase; PDBTitle: crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
22	c3l8uA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: putative rrna methylase; PDBTitle: crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
23	c5graA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o-)-methyltransferase trmj; PDBTitle: crystal structure of trmj from z. mobilis zm4
24	c3ktyA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase; PDBTitle: crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
25	c4xboA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o-)-methyltransferase trmj; PDBTitle: crystal structure of full length e.coli trmj in complex with sah
26	c4cndB	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B: PDB Molecule: trna (cytidine/uridine-2'-o-)-methyltransferase trmj; PDBTitle: crystal structure of e.coli trmj
27	c3ilkB	Alignment	not modelled	100.0	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized trna/rrna methyltransferase hi0380; PDBTitle: the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20
						PDB header: transferase Chain: X: PDB Molecule: uncharacterized protein tm_1570;

28	c3dcmX_	Alignment	not modelled	99.9	17	PDBTitle: crystal structure of the thermotoga maritima spout family rna-2 methyltransferase protein tm1570 in complex with s-adenosyl-l-3 methionine
29	d1ipaa2	Alignment	not modelled	99.9	27	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
30	c6ahwB_	Alignment	not modelled	99.9	27	PDB header: transferase Chain: B: PDB Molecule: circular-permuted trna (cytidine(34)-2'-o)- PDBTitle: crystal structure of circular-permuted yibk methyltransferase from2 haemophilus influenzae
31	d1gz0a2	Alignment	not modelled	98.5	21	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
32	d1gz0f2	Alignment	not modelled	98.4	22	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
33	c2yy8B_	Alignment	not modelled	97.1	25	PDB header: transferase Chain: B: PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
34	d1vhka2	Alignment	not modelled	96.9	13	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
35	c1vhkA_	Alignment	not modelled	96.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yqeu; PDBTitle: crystal structure of an hypothetical protein
36	c4l69A_	Alignment	not modelled	95.8	18	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: rv2372c of mycobacterium tuberculosis is rsme like methyltransferase
37	c5vm8A_	Alignment	not modelled	95.7	14	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of a ribosomal rna small subunit methyltransferase e2 from neisseria gonorrhoeae bound to s-adenosyl methionine
38	c3ai9X_	Alignment	not modelled	95.5	16	PDB header: transferase Chain: X: PDB Molecule: upf0217 protein mj1640; PDBTitle: crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
39	c1vhyB_	Alignment	not modelled	94.7	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein hi0303; PDBTitle: crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
40	d2o3aa1	Alignment	not modelled	94.1	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF0751-like
41	c3kw2A_	Alignment	not modelled	93.7	12	PDB header: transferase Chain: A: PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
42	c5o96F_	Alignment	not modelled	93.5	17	PDB header: transferase Chain: F: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: structure of the putative methyltransferase lpg2936 from legionella2 pneumophila in complex with the bound cofactor sam
43	d1nxza2	Alignment	not modelled	93.5	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
44	c2zkr6_	Alignment	not modelled	91.4	9	PDB header: ribosomal protein/rna Chain: 6: PDB Molecule: 60s ribosomal protein l30e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
45	c2cx8B_	Alignment	not modelled	88.7	23	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
46	d2vgna3	Alignment	not modelled	86.6	12	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
47	c2vgmA_	Alignment	not modelled	85.4	14	PDB header: cell cycle Chain: A: PDB Molecule: dom34; PDBTitle: structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
48	c3zf7g_	Alignment	not modelled	84.7	11	PDB header: ribosome Chain: G: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
49	c4j3cB_	Alignment	not modelled	84.3	17	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s ribosomal rna methyltransferase rsme
50	c1z85B_	Alignment	not modelled	82.5	20	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein tm1380; PDBTitle: crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
51	d1x52a1	Alignment	not modelled	82.1	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
52	d1t0kb_	Alignment	not modelled	81.1	12	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins

53	c4e8bA	Alignment	not modelled	81.0	20	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s rrna methyltransferase rsme from e.coli
54	c4a1dG	Alignment	not modelled	80.4	14	PDB header: ribosome Chain: G: PDB Molecule: rpl30; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
55	d2qwva1	Alignment	not modelled	80.2	13	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
56	c3cpqB	Alignment	not modelled	79.6	14	PDB header: ribosomal protein Chain: B: PDB Molecule: 50s ribosomal protein l30e; PDBTitle: crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
57	c2cx8A	Alignment	not modelled	78.5	25	PDB header: transferase Chain: A: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
58	d1dt9a2	Alignment	not modelled	78.2	18	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
59	d2bo1a1	Alignment	not modelled	78.2	12	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
60	c3e20C	Alignment	not modelled	77.8	18	PDB header: translation Chain: C: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
61	d2qi2a3	Alignment	not modelled	77.3	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
62	c3j21Z	Alignment	not modelled	76.9	13	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l30e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
63	c3agjD	Alignment	not modelled	76.6	21	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
64	d1v6za2	Alignment	not modelled	74.3	23	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
65	d1vqof1	Alignment	not modelled	74.3	19	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
66	c2ktvA	Alignment	not modelled	74.3	16	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: human erf1 c-domain, "open" conformer
67	c3agiB	Alignment	not modelled	73.9	21	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
68	c2egwB	Alignment	not modelled	73.2	14	PDB header: rna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rrna methyltransferase with sah ligand
69	c3mcaB	Alignment	not modelled	72.5	18	PDB header: translation regulation/hydrolase Chain: B: PDB Molecule: protein dom34; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
70	d1jj2f	Alignment	not modelled	71.9	20	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
71	c3e20H	Alignment	not modelled	69.5	18	PDB header: translation Chain: H: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
72	c3ir9A	Alignment	not modelled	68.8	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: c-terminal domain of peptide chain release factor from methanosarcina2 mazei.
73	c1dt9A	Alignment	not modelled	66.9	18	PDB header: translation Chain: A: PDB Molecule: protein (eukaryotic peptide chain release factor) PDBTitle: the crystal structure of human eukaryotic release factor2 erf1-mechanism of stop codon recognition and peptidyl-trna3 hydrolysis
74	d2qmma1	Alignment	not modelled	65.8	19	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
75	d2fc3a1	Alignment	not modelled	64.7	29	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
76	d1rlga	Alignment	not modelled	64.7	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
77	c1t9hA	Alignment	not modelled	61.2	15	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase.
						PDB header: translation

78	c3agkA	Alignment	not modelled	56.8	25	Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: crystal structure of archaeal translation termination factor, arf1
79	c3obyB	Alignment	not modelled	56.8	12	PDB header: hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
80	dlw41a1	Alignment	not modelled	56.5	16	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
81	c3v7qB	Alignment	not modelled	54.3	15	PDB header: rna binding protein Chain: B: PDB Molecule: probable ribosomal protein ylqx; PDBTitle: crystal structure of b. subtilis ylqx at 1.55 a resolution
82	d2czwa1	Alignment	not modelled	53.2	22	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
83	dljvna2	Alignment	not modelled	52.8	10	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
84	d2aifa1	Alignment	not modelled	49.8	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
85	d1k3ra2	Alignment	not modelled	49.6	19	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
86	c1k3rA	Alignment	not modelled	48.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
87	c2qi2A	Alignment	not modelled	47.6	13	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein pelota related protein; PDBTitle: crystal structure of the thermoplasma acidophilum pelota2 protein
88	c2lbwA	Alignment	not modelled	47.2	17	PDB header: rna binding protein Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 2; PDBTitle: solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
89	d2ozba1	Alignment	not modelled	45.4	18	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
90	c3obwA	Alignment	not modelled	44.2	24	PDB header: hydrolase Chain: A: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
91	c4rg1A	Alignment	not modelled	43.5	12	PDB header: transferase Chain: A: PDB Molecule: c9orf114; PDBTitle: methyltransferase domain of c9orf114
92	c4af1A	Alignment	not modelled	43.3	16	PDB header: hydrolase Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: archeal release factor arf1
93	c2yv5A	Alignment	not modelled	43.1	16	PDB header: hydrolase Chain: A: PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus
94	c5ewrA	Alignment	not modelled	42.2	19	PDB header: rna binding protein Chain: A: PDB Molecule: box c/d snrnp and u4 snrnp component snu13p; PDBTitle: c merolae u4 snrnp protein snu13
95	c3on1A	Alignment	not modelled	38.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2414 protein; PDBTitle: the structure of a protein with unknown function from bacillus2 halodurans c
96	c3o85A	Alignment	not modelled	27.7	17	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosomal protein l7ae; PDBTitle: giardia lamblia 15.5kd rna binding protein
97	c4crnX	Alignment	not modelled	26.3	28	PDB header: translation Chain: X: PDB Molecule: erf1 in ribosome-bound erf1-erf3-gdnpn complex; PDBTitle: cryo-em of a pretermination complex with erf1 and erf3
98	c2v3jA	Alignment	not modelled	25.9	13	PDB header: ribosomal protein Chain: A: PDB Molecule: essential for mitotic growth 1; PDBTitle: the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
99	d1o6da	Alignment	not modelled	25.9	31	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
100	c3e1yD	Alignment	not modelled	25.8	18	PDB header: translation Chain: D: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of human erf1/erf3 complex
101	c4a2iV	Alignment	not modelled	23.1	15	PDB header: ribosome/hydrolase Chain: V: PDB Molecule: putative ribosome biogenesis gtpase rsga; PDBTitle: cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
102	c2rcnA	Alignment	not modelled	22.5	16	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
103	c5xyiM	Alignment	not modelled	21.6	16	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein l7ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
104	c2y0fD	Alignment	not modelled	20.6	35	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase;

