



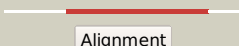

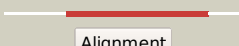

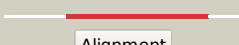

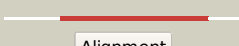







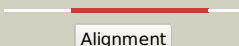





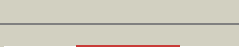


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2118c (-) _2377478_2378320
Date	Mon Aug 5 13:25:23 BST 2019
Unique Job ID	c8fab4b5272aa563

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1i9ga_</a>	Alignment		100.0	100	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
2	<a href="#">c5ergB_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (adenine(58)-n(1))-methyltransferase catalytic subunit <b>PDBTitle:</b> crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam
3	<a href="#">c5ccbA_</a>	Alignment		100.0	26	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna (adenine(58)-n(1))-methyltransferase catalytic subunit <b>PDBTitle:</b> crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
4	<a href="#">d1o54a_</a>	Alignment		100.0	29	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
5	<a href="#">c2pwyB_</a>	Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (adenine-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of a m1a58 trna methyltransferase
6	<a href="#">c3mb5A_</a>	Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of p. abyssi trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine
7	<a href="#">c2yvlB_</a>	Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
8	<a href="#">d2b25a1</a>	Alignment		100.0	34	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
9	<a href="#">c5cd1B_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna (adenine(58)-n(1))-methyltransferase non-catalytic <b>PDBTitle:</b> structure of an asymmetric tetramer of human trna m1a582 methyltransferase in a complex with sah and trna3lys
10	<a href="#">c5ergA_</a>	Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (adenine(58)-n(1))-methyltransferase non-catalytic <b>PDBTitle:</b> crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam
11	<a href="#">d1yb2a1</a>	Alignment		100.0	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like

12	<a href="#">c1yb2A</a>	 Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0852; <b>PDBTitle:</b> structure of a putative methyltransferase from thermoplasma2 acidophilum.
13	<a href="#">c5ccbB</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna (adenine(58)-n(1))-methyltransferase non-catalytic <b>PDBTitle:</b> crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
14	<a href="#">c3e05B</a>	 Alignment		99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase (decarboxylating); <b>PDBTitle:</b> crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
15	<a href="#">c2yxdA</a>	 Alignment		99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cobalt-precorrin-6y c(15)-methyltransferase <b>PDBTitle:</b> crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbit)
16	<a href="#">c3njrB</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y methylase; <b>PDBTitle:</b> crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
17	<a href="#">d1l3ia</a>	 Alignment		99.9	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Precorrin-6Y methyltransferase (CbIT)
18	<a href="#">c3id5F</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase/ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> fibrillar-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillar, l7ae and a split half c/d rna
19	<a href="#">d1l1na</a>	 Alignment		99.9	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
20	<a href="#">c1dl5A</a>	 Alignment		99.9	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> protein-l-isoaspartate o-methyltransferase
21	<a href="#">c3mtiA</a>	 Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
22	<a href="#">c2yxeB</a>	 Alignment	not modelled	99.8	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> crystal structure of l-isoaspartyl protein carboxyl methyltransferase
23	<a href="#">d1dl5a1</a>	 Alignment	not modelled	99.8	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
24	<a href="#">c4o29A</a>	 Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> protein-l-isoaspartate o-methyltransferase from pyrobaculum aerophilum2 in complex with s-adenosyl-l-homocysteine
25	<a href="#">c3eeyl</a>	 Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> putative rrna methylase; <b>PDBTitle:</b> crystal structure of putative rrna-methylase from clostridium2 thermocellum
26	<a href="#">c4df3B</a>	 Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fibrillar-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of aeropyrum pernix fibrillar in complex with2 natively bound s-adenosyl-l-methionine at 1.7a
27	<a href="#">c4krhB</a>	 Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 2; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-

						methyltransferase 22 in complex with s-adenosyl-l-methionine
28	<a href="#">c2ipxA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna 2'-o-methyltransferase fibrillarlin; <b>PDBTitle:</b> human fibrillarlin
29	<a href="#">c4ineB_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein pmt-2; <b>PDBTitle:</b> crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
30	<a href="#">d1jg1a_</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
31	<a href="#">c2yx1A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 450aa long hypothetical fmu protein; <b>PDBTitle:</b> crystal structure of ph0851
32	<a href="#">c5wp5A_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomethylethanolamine n-methyltransferase 2; <b>PDBTitle:</b> arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
33	<a href="#">c5zvdB_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> 389aa long hypothetical nucleolar protein; <b>PDBTitle:</b> the crystal structure of nsun6 from pyrococcus horikoshii
34	<a href="#">d1ixka_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
35	<a href="#">c3qnhA_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenic methyltransferase; <b>PDBTitle:</b> arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
36	<a href="#">c2pbfA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase beta-aspartate <b>PDBTitle:</b> crystal structure of a putative protein-l-isoaspartate o-2 methyltransferase beta-aspartate methyltransferase (pcmt) from3 plasmodium falciparum in complex with s-adenosyl-l-homocysteine
37	<a href="#">d1prya_</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarlin homologue
38	<a href="#">d1m6ya2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> MraW-like putative methyltransferases
39	<a href="#">d1r18a_</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
40	<a href="#">d1vbfa_</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
41	<a href="#">d1g8aa_</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarlin homologue
42	<a href="#">c3lbfC_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
43	<a href="#">c3a4tA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase mj0026; <b>PDBTitle:</b> crystal structure of atrm4 from m.jannaschii with sinefungin
44	<a href="#">c3hm2G_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase; <b>PDBTitle:</b> crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
45	<a href="#">c3tmaA_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of trmn from thermus thermophilus
46	<a href="#">c3g5tA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-aconitate 3-methyltransferase; <b>PDBTitle:</b> crystal structure of trans-aconitate 3-methyltransferase from yeast
47	<a href="#">c3bkxB_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution
48	<a href="#">c417vA_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> crystal structure of protein l-isoaspartyl-o-methyltransferase of2 vibrio cholerae
49	<a href="#">c5kn4B_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pavine n-methyltransferase; <b>PDBTitle:</b> pavine n-methyltransferase apoenzyme ph 6.0
50	<a href="#">c3lbyA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1697c; <b>PDBTitle:</b> crystal structure of smu.1697c, a putative methyltransferase from2 streptococcus mutans in complex with sah
51	<a href="#">d1nkyA_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent

51	<a href="#">c1tkvA_</a>	Alignment	not modelled	99.8	17	methyltransferases <b>Family:</b> Hypothetical Protein YjHP
52	<a href="#">c6gkvB_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> coclaurine n-methyltransferase; <b>PDBTitle:</b> crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah
53	<a href="#">c2ozvA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein atu0636; <b>PDBTitle:</b> crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
54	<a href="#">d1yzha1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
55	<a href="#">c3lecA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> nadb-rossmann superfamily protein; <b>PDBTitle:</b> the crystal structure of a protein in the nadb-rossmann superfamily2 from streptococcus agalactiae to 1.8a
56	<a href="#">c6h1dA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> hemk methyltransferase family member 2; <b>PDBTitle:</b> crystal structure of c21orf127-trmt112 in complex with sah
57	<a href="#">c3vc2I_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> J; <b>PDB Molecule:</b> geranyl diphosphate 2-c-methyltransferase; <b>PDBTitle:</b> crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine
58	<a href="#">c6em5q_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> 60s ribosomal protein l18-a; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
59	<a href="#">c1vl5B_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> unknown conserved protein bh2331; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution
60	<a href="#">d1vl5a_</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
61	<a href="#">c4ponB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> putative rna methylase; <b>PDBTitle:</b> the crystal structure of a putative sam-dependent methyltransferase,2 ytqb, from bacillus subtilis
62	<a href="#">d1g8sa_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
63	<a href="#">c3dlcA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative s-adenosyl-l-methionine-dependent <b>PDBTitle:</b> crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
64	<a href="#">c2fk8A_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methoxy mycolic acid synthase 4; <b>PDBTitle:</b> crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
65	<a href="#">c3dxyA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of ectrmb in complex with sam
66	<a href="#">c5evjA_</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> arsenite methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of crasm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii
67	<a href="#">c3evzA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
68	<a href="#">d1nt2a_</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
69	<a href="#">c5fcdA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
70	<a href="#">d1sqa2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
71	<a href="#">c3e7pA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
72	<a href="#">c3grzA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal protein l11 methyltransferase; <b>PDBTitle:</b> crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
73	<a href="#">d1dusa_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
74	<a href="#">c3m6wA_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
75	<a href="#">c2frxD_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> hypothetical protein yebu; <b>PDBTitle:</b> crystal structure of yebu, a m5c rna methyltransferase

						from e.coli
76	<a href="#">c5z9oA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus
77	<a href="#">c5e72A</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n2, n2-dimethylguanosine trna methyltransferase; <b>PDBTitle:</b> crystal structure of the archaeal trna m2g/m22g10 methyltransferase2 (atrm11) in complex with s-adenosyl-l-methionine (sam) from3 thermococcus kodakarensis
78	<a href="#">c5egpB</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ubie/coq5 family methyltransferase, putative; <b>PDBTitle:</b> crystal structure of the s-methyltransferase tmta
79	<a href="#">d1l1ea</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
80	<a href="#">c3ku1E</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae sp1610, a putative trna2 (m1a22) methyltransferase, in complex with s-adenosyl-l-methionine
81	<a href="#">c6ecvB</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
82	<a href="#">c3ujcA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase; <b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
83	<a href="#">c3bgvC</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> mrna cap guanine-n7 methyltransferase; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
84	<a href="#">d2o57a1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
85	<a href="#">c3gnlB</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmof2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (lmof2365_1472) from listeria2 monocytogenes serotype 4b
86	<a href="#">c5n5dA</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of the o-methyltransferase tomg from streptomyces2 achromogenes involved in tomaymycin synthesis in complex with sam
87	<a href="#">d2nxca1</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ribosomal protein L11 methyltransferase PrmA
88	<a href="#">c6ectA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
89	<a href="#">d2fk8a1</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
90	<a href="#">c4dcmA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase g; <b>PDBTitle:</b> crystal structure of methyltransferase rlmg modifying g1835 of 23s2 rna in escherichia coli
91	<a href="#">c1sqgA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sun protein; <b>PDBTitle:</b> the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
92	<a href="#">d1kpga</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
93	<a href="#">d1nv8a</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N5-glutamine methyltransferase, HemK
94	<a href="#">c3f4kA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
95	<a href="#">c3m4xA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> no11/hop2/sun family protein; <b>PDBTitle:</b> structure of a ribosomal methyltransferase
96	<a href="#">d2fcaa1</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
97	<a href="#">c3lpmA</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
98	<a href="#">c4pneA</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of the [4+2]-cyclase spnf
99	<a href="#">c4ottB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative methyltransferase bud23;

99	<a href="#">c4qtuB</a>	Alignment	not modelled	99.7	19	<b>PDBTitle:</b> structure of s. cerevisiae bud23-trm112 complex involved in formation2 of m7g1575 on 18s rrna (apo-form) <b>PDB header:</b> transferase
100	<a href="#">c4p7cB</a>	Alignment	not modelled	99.7	21	<b>Chain:</b> B: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
101	<a href="#">c5mgzA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-demethylnovobioc acid c(8)-methyltransferase; <b>PDBTitle:</b> streptomyces spheroides novo (8-demethylnovobioc acid2 methyltransferase) with sah
102	<a href="#">c5w7kA</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
103	<a href="#">d1kpia</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
104	<a href="#">d1xxla</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
105	<a href="#">d1xcla</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
106	<a href="#">c3c3yB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum
107	<a href="#">c3mggB</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 mazei
108	<a href="#">c5u18A</a>	Alignment	not modelled	99.7	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-3" methyltransferase; <b>PDBTitle:</b> crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin
109	<a href="#">d2b9ea1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
110	<a href="#">c4necC</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> C: <b>PDB Molecule:</b> putative sam-dependent methyltransferase; <b>PDBTitle:</b> conversion of a disulfide bond into a thioacetal group during2 echinomycin biosynthesis
111	<a href="#">c3egeA</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase from antibiotic biosynthesis <b>PDBTitle:</b> crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution
112	<a href="#">c4x1oA</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna (adenine(1408)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
113	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
114	<a href="#">d2avda1</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
115	<a href="#">c6bqcA</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> cyclopropane fatty acid synthase from e. coli
116	<a href="#">c3fpjA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of e81q mutant of mtas in complex with s-2 adenosylmethionine
117	<a href="#">c5bxyB</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rrna methyltransferase; <b>PDBTitle:</b> crystal structure of rna methyltransferase from salinibacter ruber in2 complex with s-adenosyl-l-homocysteine
118	<a href="#">c6q56C</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna (adenine(22)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the b. subtilis m1a22 trna methyltransferase trmk
119	<a href="#">c2yr0A</a>	Alignment	not modelled	99.7	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha0223; <b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
120	<a href="#">c4iv0B</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase, putative; <b>PDBTitle:</b> crystal structure of n-methyl transferase from plasmodium vivax2 complexed with s-adenosyl methionine and phosphate