

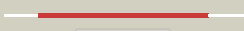




















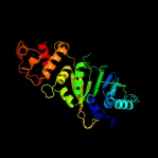


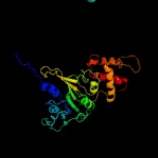
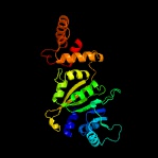


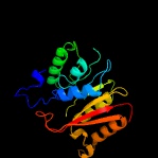


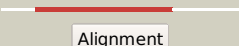


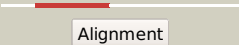


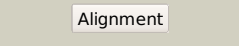

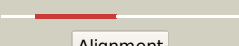
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1010_(ksgA)_1129156_1130109
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	ab059ae2c6b5ae73

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4gc5A_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dimethyladenosine transferase 1, mitochondrial; <b>PDBTitle:</b> crystal structure of murine tfb1m
2	<a href="#">c3fuxB_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> dimethyladenosine transferase; <b>PDBTitle:</b> t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
3	<a href="#">c6ifsB_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a; <b>PDBTitle:</b> ksga from bacillus subtilis 168
4	<a href="#">c3uzuA_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a; <b>PDBTitle:</b> the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
5	<a href="#">c3tqsB_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a; <b>PDBTitle:</b> structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
6	<a href="#">d1qyra_</a>	 Alignment		100.0	35	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA adenine dimethylase-like
7	<a href="#">c4jxiA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a; <b>PDBTitle:</b> crystal structure of ribosomal rna small subunit methyltransferase a2 from rickettsia bellii determined by iodide sad phasing
8	<a href="#">c2h1rA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dimethyladenosine transferase, putative; <b>PDBTitle:</b> crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
9	<a href="#">d1zq9a1</a>	 Alignment		100.0	33	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA adenine dimethylase-like
10	<a href="#">c3grrA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
11	<a href="#">c3fydA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi

12	<a href="#">c3fteA</a>	Alignment		100.0	32	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of a. aeolicus ksga in complex with rna
13	<a href="#">c1i4wA</a>	Alignment		100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial replication protein mtf1; <b>PDBTitle:</b> the crystal structure of the transcription factor sc-mtffb2 offers intriguing insights into mitochondrial transcription
14	<a href="#">d1i4wa</a>	Alignment		100.0	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA adenine dimethylase-like
15	<a href="#">c6erpj</a>	Alignment		100.0	25	<b>PDB header:</b> transcription <b>Chain:</b> J: <b>PDB Molecule:</b> dimethyladenosine transferase 2, mitochondrial; <b>PDBTitle:</b> structure of the human mitochondrial transcription initiation complex2 at the lsp promoter
16	<a href="#">d1yuba</a>	Alignment		100.0	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA adenine dimethylase-like
17	<a href="#">d1qama</a>	Alignment		100.0	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA adenine dimethylase-like
18	<a href="#">c6rbdy</a>	Alignment		100.0	24	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 40s ribosomal protein s24-a; <b>PDBTitle:</b> state 1 of yeast tsr1-tap rps20-delta loop pre-40s particles
19	<a href="#">d1wy7a1</a>	Alignment		99.6	25	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
20	<a href="#">c5ybbA</a>	Alignment		99.6	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> structural basis underlying complex assembly and conformational2 transition of the type i r-m system
21	<a href="#">d2okca1</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N-6 DNA Methylase-like
22	<a href="#">c3ufbA</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> crystal structure of a modification subunit of a putative type i2 restriction enzyme from vibrio vulnificus yj016
23	<a href="#">d1uwva2</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> (Uracil-5-)-methyltransferase
24	<a href="#">c3lkdB</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> crystal structure of the type i restriction-modification system2 methyltransferase subunit from streptococcus thermophilus, northeast3 structural genomics consortium target sur80
25	<a href="#">d2ar0a1</a>	Alignment	not modelled	99.5	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N-6 DNA Methylase-like
26	<a href="#">d1vbfa</a>	Alignment	not modelled	99.4	18	<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
27	<a href="#">c2ozvA</a>	Alignment	not modelled	99.4	17	<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.

28	<a href="#">c3khkA</a>	 Alignment	not modelled	99.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methylation subunit; <b>PDBTitle:</b> crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazei.
29	<a href="#">c2yxdA</a>	 Alignment	not modelled	99.4	13	<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)
30	<a href="#">c6q56C</a>	 Alignment	not modelled	99.4	11	<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
31	<a href="#">d2fpoa1</a>	 Alignment	not modelled	99.4	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
32	<a href="#">d1nv8a</a>	 Alignment	not modelled	99.4	17	<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
33	<a href="#">c5ccbA</a>	 Alignment	not modelled	99.4	18	<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
34	<a href="#">d1dusa</a>	 Alignment	not modelled	99.4	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
35	<a href="#">c3gdhC</a>	 Alignment	not modelled	99.4	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine synthase 1 (tgs1)2 bound to m7gtp and adenosyl-homocysteine (active form)
36	<a href="#">c3lbfC</a>	 Alignment	not modelled	99.4	21	<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
37	<a href="#">c3egiA</a>	 Alignment	not modelled	99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine synthase tgs12 bound to m7gpppa (inactive form)
38	<a href="#">c5e72A</a>	 Alignment	not modelled	99.3	16	<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
39	<a href="#">c5ergB</a>	 Alignment	not modelled	99.3	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
40	<a href="#">d1ne2a</a>	 Alignment	not modelled	99.3	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
41	<a href="#">c1uwvA</a>	 Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 23s rna (uracil-5-)-methyltransferase ruma; <b>PDBTitle:</b> crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
42	<a href="#">c3lpmA</a>	 Alignment	not modelled	99.3	17	<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
43	<a href="#">c4krhB</a>	 Alignment	not modelled	99.3	17	<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
44	<a href="#">d1m6ya2</a>	 Alignment	not modelled	99.3	17	<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
45	<a href="#">c5hjmA</a>	 Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(37)-n1)-methyltransferase trm5a; <b>PDBTitle:</b> crystal structure of pyrococcus abyssi trm5a complexed with mta
46	<a href="#">c4i7vA</a>	 Alignment	not modelled	99.3	16	<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
47	<a href="#">c2yxeB</a>	 Alignment	not modelled	99.3	19	<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
48	<a href="#">d2f8la1</a>	 Alignment	not modelled	99.3	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N-6 DNA Methylase-like
49	<a href="#">c4ineB</a>	 Alignment	not modelled	99.3	18	<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

50	<a href="#">c5u18A</a>	Alignment	not modelled	99.3	20	<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
51	<a href="#">c3e05B</a>	Alignment	not modelled	99.3	11	<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
52	<a href="#">c3mtiA</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> the crystal structure of a rna methylase from streptococcus2 thermophilus to 1.95a
53	<a href="#">d1l3ia</a>	Alignment	not modelled	99.3	16	<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)
54	<a href="#">c3mb5A</a>	Alignment	not modelled	99.3	24	<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
55	<a href="#">c5xj2C</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized rna methyltransferase sp_1029; <b>PDBTitle:</b> structure of sprlmcld with u747 rna
56	<a href="#">c6h1dA</a>	Alignment	not modelled	99.3	26	<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="#">d1i9ga</a>	Alignment	not modelled	99.3	23	<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
58	<a href="#">c3evzA</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
59	<a href="#">c1dl5A</a>	Alignment	not modelled	99.3	15	<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
60	<a href="#">c2yvlB</a>	Alignment	not modelled	99.3	15	<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
61	<a href="#">d1o54a</a>	Alignment	not modelled	99.3	17	<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
62	<a href="#">c5bxyB</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rna methyltransferase; <b>PDBTitle:</b> crystal structure of rna methyltransferase from salinibacter ruber in2 complex with s-adenosyl-l-homocysteine
63	<a href="#">c3lecA</a>	Alignment	not modelled	99.3	17	<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
64	<a href="#">c3p9nA</a>	Alignment	not modelled	99.3	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible methyltransferase (methylase); <b>PDBTitle:</b> rv2966c of m. tuberculosis is a rsm-d-like methyltransferase
65	<a href="#">c3tm4A</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine n2-)-methyltransferase trm14; <b>PDBTitle:</b> crystal structure of trm14 from pyrococcus furiosus in complex with s-2 adenosylmethionine
66	<a href="#">c3ku1E</a>	Alignment	not modelled	99.3	19	<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
67	<a href="#">d1jg1a</a>	Alignment	not modelled	99.2	18	<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
68	<a href="#">c3gnlB</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmf2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (lmo2365_1472) from listeria2 monocytogenes serotype 4b
69	<a href="#">d1dl5a1</a>	Alignment	not modelled	99.2	15	<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
70	<a href="#">c3tmaA</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of trmn from thermus thermophilus
71	<a href="#">d2fhp1</a>	Alignment	not modelled	99.2	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
72	<a href="#">c4dcmA</a>	Alignment	not modelled	99.2	20	<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 rrna in escherichia coli
73	<a href="#">c3lbyA</a>	Alignment	not modelled	99.2	14	<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

74	<a href="#">c3bt7A_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna (uracil-5-)-methyltransferase; <b>PDBTitle:</b> structure of e. coli 5-methyluridine methyltransferase trma in complex2 with 19 nucleotide t-arm analogue
75	<a href="#">d2esra1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
76	<a href="#">c3njrB_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-6y methylase; <b>PDBTitle:</b> crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
77	<a href="#">d1i1na_</a>	Alignment	not modelled	99.2	16	<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
78	<a href="#">c2esrB_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> conserved hypothetical protein- streptococcus pyogenes
79	<a href="#">d2h00a1</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Methyltransferase 10 domain
80	<a href="#">c4o29A_</a>	Alignment	not modelled	99.2	20	<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
81	<a href="#">c1yb2A_</a>	Alignment	not modelled	99.2	24	<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.
82	<a href="#">d1yb2a1</a>	Alignment	not modelled	99.2	24	<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
83	<a href="#">c4ponB_</a>	Alignment	not modelled	99.2	17	<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
84	<a href="#">c2pwyB_</a>	Alignment	not modelled	99.2	22	<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
85	<a href="#">c6qe6A_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (adenine(22)-n(1))-methyltransferase; <b>PDBTitle:</b> structure of m. capricolum trmk in complex with the natural cofactor2 product s-adenosyl-homocysteine (sah)
86	<a href="#">c5yacA_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(37)-n1)-methyltransferase trm5b; <b>PDBTitle:</b> crystal structure of wt trm5b from pyrococcus abyssi
87	<a href="#">c3eeyl_</a>	Alignment	not modelled	99.2	17	<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
88	<a href="#">d1ws6a1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
89	<a href="#">c4dmgA_</a>	Alignment	not modelled	99.2	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1493; <b>PDBTitle:</b> thermus thermophilus m5c1942 methyltransferase rimo
90	<a href="#">c5wp5A_</a>	Alignment	not modelled	99.2	13	<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
91	<a href="#">d1r18a_</a>	Alignment	not modelled	99.2	17	<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
92	<a href="#">c2pbfA_</a>	Alignment	not modelled	99.2	13	<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
93	<a href="#">c6j27D_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n(4)-bis(aminopropyl)spermidine synthase; <b>PDBTitle:</b> crystal structure of the branched-chain polyamine synthase from2 thermus thermophilus (tth-bpsa) in complex with n4-3 aminopropylspermidine and 5'-methylthioadenosine
94	<a href="#">c1aqjB_</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> methyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenine-n6-dna-methyltransferase taqi; <b>PDBTitle:</b> structure of adenine-n6-dna-methyltransferase taqi
95	<a href="#">c1g38A_</a>	Alignment	not modelled	99.2	22	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> modification methylase taqi; <b>PDBTitle:</b> adenine-specific methyltransferase m. taqi i/dna complex
96	<a href="#">d2b25a1</a>	Alignment	not modelled	99.1	16	<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
97	<a href="#">c2pjdA_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase c; <b>PDBTitle:</b> crystal structure of 16s rrna methyltransferase rsmc
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-



98	<a href="#">c4krkB</a>	Alignment	not modelled	99.1	16	methyltransferase 1; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine
99	<a href="#">c3lduA</a>	Alignment	not modelled	99.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methylase; <b>PDBTitle:</b> the crystal structure of a possible methylase from2 clostridium difficile 630.
100	<a href="#">c5fcdA</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
101	<a href="#">c1m6yA</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-methyltransferase mraw; <b>PDBTitle:</b> crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah
102	<a href="#">c6gkvB</a>	Alignment	not modelled	99.1	18	<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
103	<a href="#">c3dmgA</a>	Alignment	not modelled	99.1	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribosomal rna small subunit methyltransferase; <b>PDBTitle:</b> t. thermophilus 16s rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
104	<a href="#">d2ifta1</a>	Alignment	not modelled	99.1	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
105	<a href="#">c3vseA</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of methyltransferase
106	<a href="#">c5kn4B</a>	Alignment	not modelled	99.1	18	<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
107	<a href="#">c3a26A</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0793; <b>PDBTitle:</b> crystal structure of p. horikoshii tyw2 in complex with2 mesado
108	<a href="#">d2nxca1</a>	Alignment	not modelled	99.1	17	<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
109	<a href="#">c1wxwA</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1280; <b>PDBTitle:</b> crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophilus hb8
110	<a href="#">c2vs1A</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rna methyltransferase pyrab10780; <b>PDBTitle:</b> the crystal structure of pyrococcus abyssi trna (uracil-54, c5)-2 methyltransferase in complex with s-adenosyl-l-homocysteine
111	<a href="#">c3c0kB</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0064 protein yccw; <b>PDBTitle:</b> crystal structure of a ribosomal rna methyltransferase
112	<a href="#">c5z9oA</a>	Alignment	not modelled	99.1	19	<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
113	<a href="#">c3g5tA</a>	Alignment	not modelled	99.1	9	<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
114	<a href="#">c6b92A</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> u6 small nuclear rna (adenine-(43)-n(6))-methyltransferase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of human mettl16 in complex2 with sah
115	<a href="#">d2b3ta1</a>	Alignment	not modelled	99.1	22	<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
116	<a href="#">d1wg8a2</a>	Alignment	not modelled	99.1	16	<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
117	<a href="#">c3grzA</a>	Alignment	not modelled	99.1	20	<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
118	<a href="#">c4m38A</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> transferase/transferase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 7; <b>PDBTitle:</b> crystal structure of trypanosoma brucei protein arginine2 methyltransferase 7 complex with adohcy and histone h4 peptide
119	<a href="#">c2fk8A</a>	Alignment	not modelled	99.1	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
120	<a href="#">d2frna1</a>	Alignment	not modelled	99.1	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Met-10+ protein-like