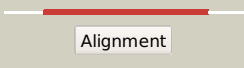

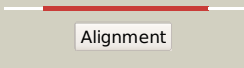

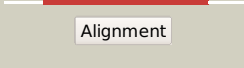

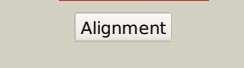

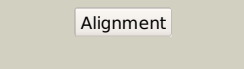

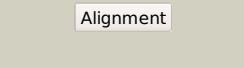

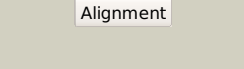

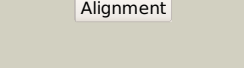

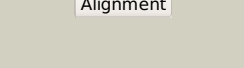

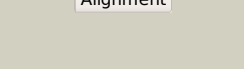

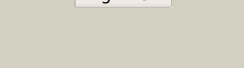



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0208c_trmB_248115_248906
Date	Tue Jul 23 14:50:26 BST 2019
Unique Job ID	d1887e0a07450d15

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dxyA_</a>	 Alignment		100.0	36	<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
2	<a href="#">d1yzha1</a>	 Alignment		100.0	25	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
3	<a href="#">d2fcaa1</a>	 Alignment		100.0	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
4	<a href="#">c3ckkA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of human methyltransferase-like protein 1
5	<a href="#">c2vduE_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> structure of trm8-trm82, the yeast trna m7g methylation2 complex
6	<a href="#">c3p2kA_</a>	 Alignment		99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rna methylase; <b>PDBTitle:</b> structure of an antibiotic related methyltransferase
7	<a href="#">c1yb2A_</a>	 Alignment		99.8	19	<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.
8	<a href="#">d1yb2a1</a>	 Alignment		99.8	19	<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="#">c4x1oA_</a>	 Alignment		99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rna (adenine(1408)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the 16s rna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
10	<a href="#">c3g5tA_</a>	 Alignment		99.8	13	<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
11	<a href="#">c4ineB_</a>	 Alignment		99.8	15	<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

12	<a href="#">c4krhB_</a>	Alignment		99.8	21	<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
13	<a href="#">d1o54a_</a>	Alignment		99.8	14	<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
14	<a href="#">c3vc2j_</a>	Alignment		99.7	14	<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
15	<a href="#">c5dplB_</a>	Alignment		99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein lysine methyltransferase 2; <b>PDBTitle:</b> the structure of pkmt2 from rickettsia typhi in complex with adohcy
16	<a href="#">c2fk8A_</a>	Alignment		99.7	17	<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
17	<a href="#">c3e05B_</a>	Alignment		99.7	15	<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
18	<a href="#">c6gkvB_</a>	Alignment		99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> coclairine n-methyltransferase; <b>PDBTitle:</b> crystal structure of coclairine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah
19	<a href="#">c5do0A_</a>	Alignment		99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein lysine methyltransferase 1; <b>PDBTitle:</b> the structure of pkmt1 from rickettsia prowazekii
20	<a href="#">c5evjA_</a>	Alignment		99.7	22	<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
21	<a href="#">c3mq2A_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rna methyltransferase; <b>PDBTitle:</b> crystal structure of 16s rna methyltransferase kamb
22	<a href="#">c4rwzA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative rna methyltransferase; <b>PDBTitle:</b> crystal structure of the antibiotic-resistance methyltransferase kmr
23	<a href="#">c5kn4B_</a>	Alignment	not modelled	99.7	14	<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
24	<a href="#">c5mgzA_</a>	Alignment	not modelled	99.7	15	<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
25	<a href="#">c2pwyB_</a>	Alignment	not modelled	99.7	21	<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
26	<a href="#">c5egpB_</a>	Alignment	not modelled	99.7	16	<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
27	<a href="#">c5wp5A_</a>	Alignment	not modelled	99.7	16	<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
28	<a href="#">c6ecvB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
						<b>PDB header:</b> transferase

29	<a href="#">c4dcmA</a>	Alignment	not modelled	99.7	15	<b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase g; <b>PDBTitle:</b> crystal structure of methyltransferase rimg modifying g1835 of 23s2 rrna in escherichia coli
30	<a href="#">c3mb5A</a>	Alignment	not modelled	99.7	15	<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
31	<a href="#">c3bkxB</a>	Alignment	not modelled	99.7	17	<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
32	<a href="#">c6ectA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
33	<a href="#">c5w7kA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
34	<a href="#">c3e7pA</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 of putative methyltransferase from bacteroides2 vulgatus atcc 8482
35	<a href="#">c4necC</a>	Alignment	not modelled	99.7	16	<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
36	<a href="#">d2fk8a1</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
37	<a href="#">c5ccbA</a>	Alignment	not modelled	99.7	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
38	<a href="#">c4p7cB</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
39	<a href="#">d1zx0a1</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> Guanidinoacetate methyltransferase
40	<a href="#">c3eeyL</a>	Alignment	not modelled	99.7	14	<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
41	<a href="#">d1kpga</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
42	<a href="#">d1m6ya2</a>	Alignment	not modelled	99.7	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
43	<a href="#">c3lccA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyl chloride transferase; <b>PDBTitle:</b> structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
44	<a href="#">d1xvaa</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> Glycine N-methyltransferase
45	<a href="#">c5z9oA</a>	Alignment	not modelled	99.7	18	<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
46	<a href="#">c4kvzA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> baml; <b>PDBTitle:</b> crystal structure of the plantazolicin methyltransferase baml in2 complex with sah
47	<a href="#">c3qnhA</a>	Alignment	not modelled	99.7	21	<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)
48	<a href="#">d1r74a</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> Glycine N-methyltransferase
49	<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
50	<a href="#">c2yvlB</a>	Alignment	not modelled	99.7	14	<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
51	<a href="#">c3ku1E</a>	Alignment	not modelled	99.7	12	<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
52	<a href="#">d1xcla</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> Guanidinoacetate methyltransferase <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;

53	<a href="#">c3f4kA_</a>	Alignment	not modelled	99.7	16	<b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309. <b>PDB header:</b> transferase
54	<a href="#">c5u18A_</a>	Alignment	not modelled	99.7	18	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
55	<a href="#">d2o57a1</a>	Alignment	not modelled	99.7	15	<b>Family:</b> Mycolic acid cyclopropane synthase <b>PDB header:</b> transferase
56	<a href="#">c3mtiA_</a>	Alignment	not modelled	99.7	19	<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 <b>PDB header:</b> structural genomics, unknown function
57	<a href="#">c3gnlB_</a>	Alignment	not modelled	99.7	14	<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 <b>PDB header:</b> structure genomics, unknown function
58	<a href="#">c3lecA_</a>	Alignment	not modelled	99.7	13	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
59	<a href="#">d1ri5a_</a>	Alignment	not modelled	99.7	14	<b>Family:</b> mRNA cap (Guanine N-7) methyltransferase <b>PDB header:</b> transferase
60	<a href="#">c4qnuH_</a>	Alignment	not modelled	99.7	21	<b>Chain:</b> H: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of cmob bound with cx-sam in p21212 <b>PDB header:</b> transferase
61	<a href="#">c3mggB_</a>	Alignment	not modelled	99.7	21	<b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 mazei <b>PDB header:</b> transferase
62	<a href="#">c4kwcA_</a>	Alignment	not modelled	99.7	12	<b>Chain:</b> A: <b>PDB Molecule:</b> bpuml; <b>PDBTitle:</b> structure of the plantazolicin methyltransferase bpuml in complex with2 sah <b>PDB header:</b> transferase
63	<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
64	<a href="#">c1z3cA_</a>	Alignment	not modelled	99.7	14	<b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet <b>PDB header:</b> transferase
65	<a href="#">c2pjdA_</a>	Alignment	not modelled	99.7	13	<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>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
66	<a href="#">d1i9ga_</a>	Alignment	not modelled	99.7	21	<b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like <b>PDB header:</b> transferase
67	<a href="#">c3lbyA_</a>	Alignment	not modelled	99.6	14	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
68	<a href="#">d1p1ca_</a>	Alignment	not modelled	99.6	14	<b>Family:</b> Guanidinoacetate methyltransferase <b>PDB header:</b> transferase
69	<a href="#">c4pneA_</a>	Alignment	not modelled	99.6	14	<b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of the [4+2]-cyclase spnf <b>PDB header:</b> transferase
70	<a href="#">c2ozvA_</a>	Alignment	not modelled	99.6	16	<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. <b>PDB header:</b> structural genomics, unknown function
71	<a href="#">c2gpyB_</a>	Alignment	not modelled	99.6	17	<b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of putative o-methyltransferase from bacillus2 halodurans <b>PDB header:</b> transferase
72	<a href="#">c2yr0A_</a>	Alignment	not modelled	99.6	25	<b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha0223; <b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
73	<a href="#">d1tpya_</a>	Alignment	not modelled	99.6	17	<b>Family:</b> Mycolic acid cyclopropane synthase <b>PDB header:</b> transferase
74	<a href="#">c5ergB_</a>	Alignment	not modelled	99.6	16	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
75	<a href="#">d1l3ia_</a>	Alignment	not modelled	99.6	19	<b>Family:</b> Precorrin-6Y methyltransferase (CbiT) <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
76	<a href="#">d1p91a_</a>	Alignment	not modelled	99.6	21	<b>Family:</b> rRNA methyltransferase RlMA <b>PDB header:</b> rna binding protein
77	<a href="#">c6q56C_</a>	Alignment	not modelled	99.6	15	<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 <b>PDB header:</b> transferase

78	<a href="#">c3ggdA</a>	Alignment	not modelled	99.6	16	<b>Chain:</b> A; <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anabaena variabilis atcc 29413 at 2.11 a resolution
79	<a href="#">c3evzA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
80	<a href="#">c4kdcA</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-demethylubiquinone-9 3-methyltransferase; <b>PDBTitle:</b> crystal structure of ubig
81	<a href="#">d1dusa</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
82	<a href="#">c5fcdA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
83	<a href="#">c3lpmA</a>	Alignment	not modelled	99.6	13	<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
84	<a href="#">d1vl5a</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
85	<a href="#">c3njrB</a>	Alignment	not modelled	99.6	17	<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
86	<a href="#">c1vl5B</a>	Alignment	not modelled	99.6	16	<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
87	<a href="#">c3hm2G</a>	Alignment	not modelled	99.6	17	<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
88	<a href="#">c3ocjA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> the crystal structure of a possilbe exported protein from bordetella2 parapertussis
89	<a href="#">d2b3ta1</a>	Alignment	not modelled	99.6	16	<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
90	<a href="#">d1d2ha</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
91	<a href="#">c6h1dA</a>	Alignment	not modelled	99.6	18	<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
92	<a href="#">d1nkva</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein YjHP
93	<a href="#">d1xxla</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
94	<a href="#">c4ponB</a>	Alignment	not modelled	99.6	11	<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 ytbq, from bacillus subtilis
95	<a href="#">c3c3yB</a>	Alignment	not modelled	99.6	22	<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
96	<a href="#">c6mroA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methyl transferase from methanosarcina acetivorans; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
97	<a href="#">d2b25a1</a>	Alignment	not modelled	99.6	19	<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
98	<a href="#">c2yxdA</a>	Alignment	not modelled	99.6	19	<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 (cbt)
99	<a href="#">c3dlcA</a>	Alignment	not modelled	99.6	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
100	<a href="#">c6dcbA</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transferase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> 7sk snrna methylphosphate capping enzyme; <b>PDBTitle:</b> structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna
101	<a href="#">c3dmgA</a>	Alignment	not modelled	99.6	19	<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
102	<a href="#">c4oa8A_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase family protein; <b>PDBTitle:</b> x-ray crystal structure of o-methyltransferase from anaplasma2 phagocytophilum in apo form
103	<a href="#">d2bzga1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
104	<a href="#">d1nt2a_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarlin homologue
105	<a href="#">c5t39A_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> evdmo1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of evdmo1 in the presence2 of sah and d-fucose
106	<a href="#">c6bqcA_</a>	Alignment	not modelled	99.6	18	<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
107	<a href="#">c5zw3B_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> putative o-methyltransferase yrrm; <b>PDBTitle:</b> crystal structure of trmr from b. subtilis
108	<a href="#">d1dl5a1</a>	Alignment	not modelled	99.6	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
109	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
110	<a href="#">c4krqB_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 1; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine
111	<a href="#">d2ex4a1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> AD-003 protein-like
112	<a href="#">d1xdza_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glucose-inhibited division protein B (GidB)
113	<a href="#">d1jqea_</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
114	<a href="#">c3tfwB_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
115	<a href="#">c4htfA_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> s-adenosylmethionine-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 from escherichia coli in complex with s-adenosylmethionine.
116	<a href="#">c3g07C_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> 7sk srna methylphosphate capping enzyme; <b>PDBTitle:</b> methyltransferase domain of human bicoid-interacting protein 3 homolog2 (drosophila)
117	<a href="#">c3bgdB_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
118	<a href="#">c3ntvB_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> mw1564 protein; <b>PDBTitle:</b> crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus
119	<a href="#">c3m70A_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> tellurite resistance protein tehb homolog; <b>PDBTitle:</b> crystal structure of tehb from haemophilus influenzae
120	<a href="#">d2as0a2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase