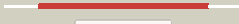



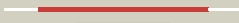












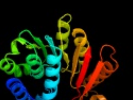






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0187 (- )_218703_219365
Date	Tue Jul 23 14:50:24 BST 2019
Unique Job ID	82ffc035364a92a9

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5n5dA_</a>	 Alignment		100.0	51	<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
2	<a href="#">c3tfwB_</a>	 Alignment		100.0	49	<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
3	<a href="#">c3tr6A_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> structure of a o-methyltransferase from coxiella burnetii
4	<a href="#">c3duwB_</a>	 Alignment		100.0	50	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> o-methyltransferase, putative; <b>PDBTitle:</b> crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah
5	<a href="#">c2hncC_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> sam-dependent o-methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent o-methyltransferase from pathogenic2 bacterium leptospira interrogans
6	<a href="#">c3c3yB_</a>	 Alignment		100.0	20	<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
7	<a href="#">c3cbgA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> functional and structural characterization of a cationdependent o-2 methyltransferase from the cyanobacterium synechocystis sp. strain3 pcc 6803
8	<a href="#">c3r3hA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase, sam-dependent; <b>PDBTitle:</b> crystal structure of o-methyltransferase from legionella pneumophila
9	<a href="#">d2avda1</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> COMT-like
10	<a href="#">c3dr5A_</a>	 Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of the q8nrd3_corgl protein from corynebacterium2 glutamicum. northeast structural genomics consortium target cgr117.
11	<a href="#">d1susa1</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> COMT-like

12	<a href="#">c4ymhB_</a>	Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sam-dependent o-methyltransferase; <b>PDBTitle:</b> crystal structure of sah-bound podospira anserina methyltransferase2 pamth1
13	<a href="#">c5lhmA_</a>	Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of safc from myxococcus xanthus apo-form
14	<a href="#">c3ntvB_</a>	Alignment		100.0	20	<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
15	<a href="#">d2cl5a1</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> COMT-like
16	<a href="#">c4oa8A_</a>	Alignment		100.0	28	<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
17	<a href="#">c5zy5B_</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable catechol o-methyltransferase 1; <b>PDBTitle:</b> spcomt apo structure
18	<a href="#">c3c3pC_</a>	Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a methyltransferase (np_951602.1) from geobacter2 sulfurreducens at 1.90 a resolution
19	<a href="#">c5zw3B_</a>	Alignment		100.0	24	<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
20	<a href="#">c5x7fA_</a>	Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase rv1220c; <b>PDBTitle:</b> structure of a o-methyltransferase from mycobacterium tuberculosis at2 2.0 resolution
21	<a href="#">c2gpyB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of putative o-methyltransferase from bacillus2 halodurans
22	<a href="#">c6g80C_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain protein; <b>PDBTitle:</b> structure of mycobacterium hassiacum met1 from orthorhombic crystals.
23	<a href="#">d2bm8a1</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> Cmcl-like
24	<a href="#">c1dl5A_</a>	Alignment	not modelled	99.8	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
25	<a href="#">d1yb2a1</a>	Alignment	not modelled	99.8	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
26	<a href="#">c1yb2A_</a>	Alignment	not modelled	99.8	16	<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.
27	<a href="#">d1o54a_</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> tRNA(1-methyladenosine) methyltransferase-like
28	<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
						<b>PDB header:</b> transferase

29	<a href="#">c3mb5A_</a>	Alignment	not modelled	99.8	24	<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
30	<a href="#">c5ccbA_</a>	Alignment	not modelled	99.8	21	<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
31	<a href="#">c4o29A_</a>	Alignment	not modelled	99.8	24	<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
32	<a href="#">d1i1na_</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> Protein-L-isoaspartyl O-methyltransferase
33	<a href="#">c2yxeB_</a>	Alignment	not modelled	99.7	25	<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
34	<a href="#">c2yxIA_</a>	Alignment	not modelled	99.7	18	<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
35	<a href="#">c4I7vA_</a>	Alignment	not modelled	99.7	23	<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
36	<a href="#">d1r18a_</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> Protein-L-isoaspartyl O-methyltransferase
37	<a href="#">d1i9ga_</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> tRNA(1-methyladenosine) methyltransferase-like
38	<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
39	<a href="#">c3e05B_</a>	Alignment	not modelled	99.7	23	<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
40	<a href="#">d2b25a1</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> tRNA(1-methyladenosine) methyltransferase-like
41	<a href="#">c3mtiA_</a>	Alignment	not modelled	99.7	15	<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
42	<a href="#">d1jg1a_</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> Protein-L-isoaspartyl O-methyltransferase
43	<a href="#">c2pbfA_</a>	Alignment	not modelled	99.7	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
44	<a href="#">c3lecA_</a>	Alignment	not modelled	99.7	16	<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
45	<a href="#">d1l3ia_</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> Precorrin-6Y methyltransferase (CbiT)
46	<a href="#">c4ce0A_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of sah-bound spinosyn rhamnosyl 4'-o-2 methyltransferase spnh from saccharopolyspora spinosa
47	<a href="#">c2yvlB_</a>	Alignment	not modelled	99.7	22	<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
48	<a href="#">c4xvzB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mycinamicin iii 3"-o-methyltransferase; <b>PDBTitle:</b> mycf mycinamicin iii 3'-o-methyltransferase in complex with mg
49	<a href="#">c3lpmA_</a>	Alignment	not modelled	99.7	15	<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
50	<a href="#">c6qmmA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyamine aminopropyltransferase; <b>PDBTitle:</b> crystal structure of synecochoccus spermidine synthase in complex with2 putrescine, spermidine and mta
51	<a href="#">c3lbfC_</a>	Alignment	not modelled	99.7	22	<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
52	<a href="#">c3eeyl_</a>	Alignment	not modelled	99.6	20	<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

53	<a href="#">c4krhB</a>	Alignment	not modelled	99.6	22	<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
54	<a href="#">c3gnlB</a>	Alignment	not modelled	99.6	10	<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
55	<a href="#">c5z9oA</a>	Alignment	not modelled	99.6	17	<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
56	<a href="#">c3bkbB</a>	Alignment	not modelled	99.6	18	<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
57	<a href="#">c3ku1E</a>	Alignment	not modelled	99.6	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
58	<a href="#">c4ineB</a>	Alignment	not modelled	99.6	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 and 3 phosphoethanolamine
59	<a href="#">c3vc2J</a>	Alignment	not modelled	99.6	17	<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
60	<a href="#">d1vbfA</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> Protein-L-isoaspartyl O-methyltransferase
61	<a href="#">c3e7pA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from bacteroides2 vulgatus atcc 8482
62	<a href="#">d1nv8a</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> N5- glutamine methyltransferase, HemK
63	<a href="#">c5ergB</a>	Alignment	not modelled	99.6	17	<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
64	<a href="#">c6ecvB</a>	Alignment	not modelled	99.6	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
65	<a href="#">d1inla</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> Spermidine synthase
66	<a href="#">c3qnhA</a>	Alignment	not modelled	99.6	19	<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)
67	<a href="#">c3g5tA</a>	Alignment	not modelled	99.6	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
68	<a href="#">c5evjA</a>	Alignment	not modelled	99.6	21	<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
69	<a href="#">d1zx0a1</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> Guanidinoacetate methyltransferase
70	<a href="#">c3njrB</a>	Alignment	not modelled	99.6	21	<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
71	<a href="#">c5kn4B</a>	Alignment	not modelled	99.6	11	<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
72	<a href="#">c5bxyB</a>	Alignment	not modelled	99.6	22	<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
73	<a href="#">c2fk8A</a>	Alignment	not modelled	99.6	14	<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
74	<a href="#">c1sqgA</a>	Alignment	not modelled	99.6	19	<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
75	<a href="#">d1r74a</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> Glycine N-methyltransferase
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;

76	<a href="#">c3f4kA_</a>	Alignment	not modelled	99.6	19	<b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
77	<a href="#">d1p1ca_</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> Guanidinoacetate methyltransferase
78	<a href="#">c6q56C_</a>	Alignment	not modelled	99.6	8	<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
79	<a href="#">d1l1ea_</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> Mycolic acid cyclopropane synthase
80	<a href="#">c3lccA_</a>	Alignment	not modelled	99.6	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
81	<a href="#">c5wp5A_</a>	Alignment	not modelled	99.6	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
82	<a href="#">d1lixka_</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> NOL1/NOP2/sun
83	<a href="#">d1xcla_</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
84	<a href="#">c3hm2G_</a>	Alignment	not modelled	99.6	20	<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
85	<a href="#">d1kpia_</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> Mycolic acid cyclopropane synthase
86	<a href="#">c6gkvB_</a>	Alignment	not modelled	99.6	14	<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
87	<a href="#">d1kpga_</a>	Alignment	not modelled	99.6	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
88	<a href="#">d2o07a1</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> Spermidine synthase
89	<a href="#">c5dplB_</a>	Alignment	not modelled	99.6	17	<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
90	<a href="#">c3axtA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable n(2),n(2)-dimethylguanosine trna methyltransferase <b>PDBTitle:</b> complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
91	<a href="#">c2hteB_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> the crystal structure of spermidine synthase from p. falciparum in2 complex with 5'-methylthioadenosine
92	<a href="#">d2as0a2</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
93	<a href="#">c3evzA_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
94	<a href="#">c6ectA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
95	<a href="#">c5zvdB_</a>	Alignment	not modelled	99.6	22	<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
96	<a href="#">c5do0A_</a>	Alignment	not modelled	99.6	17	<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
97	<a href="#">d1yzha1</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
98	<a href="#">d2fk8a1</a>	Alignment	not modelled	99.6	12	<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
99	<a href="#">d2o57a1</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> Mycolic acid cyclopropane synthase
100	<a href="#">c3jwgA_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c <b>PDB header:</b> transferase

101	<a href="#">c4ponB_</a>	Alignment	not modelled	99.5	18	<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
102	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
103	<a href="#">d1iy9a_</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
104	<a href="#">c2ozvA_</a>	Alignment	not modelled	99.5	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.
105	<a href="#">c3bwbA_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> crystal structure of the apo form of spermidine synthase from2 trypanosoma cruzi at 2.5 a resolution
106	<a href="#">c6em5q_</a>	Alignment	not modelled	99.5	18	<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
107	<a href="#">c6h1dA_</a>	Alignment	not modelled	99.5	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
108	<a href="#">c2b78A_</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein smu.776; <b>PDBTitle:</b> a putative sam-dependent methyltransferase from streptococcus mutans
109	<a href="#">c3c0kB_</a>	Alignment	not modelled	99.5	19	<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
110	<a href="#">d2igta1</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> hypothetical RNA methyltransferase
111	<a href="#">d1nkva_</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein YjhP
112	<a href="#">d2b2ca1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
113	<a href="#">c1wxwA_</a>	Alignment	not modelled	99.5	21	<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
114	<a href="#">d1tpya_</a>	Alignment	not modelled	99.5	13	<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
115	<a href="#">d2fcaa1</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
116	<a href="#">c3a4tA_</a>	Alignment	not modelled	99.5	18	<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
117	<a href="#">c3fpjA_</a>	Alignment	not modelled	99.5	23	<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
118	<a href="#">d1g8aa_</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarlin homologue
119	<a href="#">c4necC_</a>	Alignment	not modelled	99.5	28	<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
120	<a href="#">c2yxdA_</a>	Alignment	not modelled	99.5	20	<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)