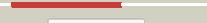
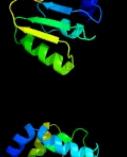
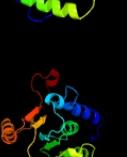


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD2954c_(-)_3306676_3307401
Date	Thu Aug 8 16:20:11 BST 2019
Unique Job ID	36db5ac973adaac2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4p7cB_</a>			99.9	26	<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
2	<a href="#">c5wp5A_</a>			99.9	12	<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
3	<a href="#">c4krhB_</a>			99.9	14	<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
4	<a href="#">c2yr0A_</a>			99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein ttha0223; <b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
5	<a href="#">c4ineB_</a>			99.9	13	<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 caenorhabditis elegans complexed with s-adenosyl homocysteine and3 phosphoethanolamine
6	<a href="#">c3vc2J_</a>			99.9	12	<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
7	<a href="#">d2o57a1</a>			99.9	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
8	<a href="#">c4gnuH_</a>			99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> H; <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of cmob bound with cx-sam in p21212
9	<a href="#">c1vl5B_</a>			99.9	20	<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
10	<a href="#">d1vl5a_</a>			99.9	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
11	<a href="#">c5kn4B_</a>			99.9	17	<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

12	<a href="#">c6g4wq</a>	Alignment		99.9	15	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 40s ribosomal protein s16; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state a
13	<a href="#">c4necC</a>	Alignment		99.9	17	<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
14	<a href="#">d1jqa</a>	Alignment		99.9	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
15	<a href="#">c6gkvB</a>	Alignment		99.9	16	<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
16	<a href="#">c5mgzA</a>	Alignment		99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-demethylnovobiocic acid c(8)-methyltransferase; <b>PDBTitle:</b> streptomyces sphaeroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah
17	<a href="#">c3g5tA</a>	Alignment		99.9	11	<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
18	<a href="#">c3bkxB</a>	Alignment		99.9	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
19	<a href="#">c5egpB</a>	Alignment		99.9	14	<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
20	<a href="#">c5w7kA</a>	Alignment		99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
21	<a href="#">d1ve3a1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
22	<a href="#">c4kdcA</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-demethylubiquinone-9 3-methyltransferase; <b>PDBTitle:</b> crystal structure of ubiq
23	<a href="#">d1xxla</a>	Alignment	not modelled	99.9	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
24	<a href="#">c3cc8A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution
25	<a href="#">d1nkva</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein YjhP
26	<a href="#">c6ectA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
27	<a href="#">c5fcda</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
28	<a href="#">c4htfA</a>	Alignment	not modelled	99.9	15	<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-

29	<a href="#">c4kvzA</a>	Alignment	not modelled	99.9	10	adenosylmethionine. <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
30	<a href="#">c3lccA</a>	Alignment	not modelled	99.9	15	<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 arabiadopsis2 thaliana
31	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
32	<a href="#">c3e7pA</a>	Alignment	not modelled	99.9	14	<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 vulgaris atcc 8482
33	<a href="#">c3egeA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase from antibiotic biosynthesis <b>PDBTitle:</b> crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution
34	<a href="#">c4pneA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of the [4+2]-cyclase snpf
35	<a href="#">c6f5zB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 24-sterol c-methyltransferase; <b>PDBTitle:</b> complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
36	<a href="#">c4iscA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase from pseudomonas2 syringae
37	<a href="#">c4krqB</a>	Alignment	not modelled	99.9	19	<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
38	<a href="#">c3bgvC</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> mrna cap guanine-n7 methyltransferase; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
39	<a href="#">c4rvgA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-mycarose 3-c-methyltransferase; <b>PDBTitle:</b> crystal structure of mtmc in complex with sam and tdp
40	<a href="#">c6ecvB</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
41	<a href="#">c6ec3C</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein; <b>PDBTitle:</b> crystal structure of evdmo1
42	<a href="#">c3f4kA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
43	<a href="#">c5t39A</a>	Alignment	not modelled	99.9	24	<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
44	<a href="#">d1xvaa</a>	Alignment	not modelled	99.9	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
45	<a href="#">d1r74a</a>	Alignment	not modelled	99.9	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
46	<a href="#">c3qnhA</a>	Alignment	not modelled	99.9	16	<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)
47	<a href="#">d2avna1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
48	<a href="#">c3ofkA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nodulation protein s; <b>PDBTitle:</b> crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wmp9 in complex with s-adenosyl-l-homocysteine (sah)
49	<a href="#">c5z9oA</a>	Alignment	not modelled	99.9	15	<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
50	<a href="#">c3g5IA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosylmethionine dependent methyltransferase; <b>PDBTitle:</b> crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
51	<a href="#">c4kwca</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bpuml; <b>PDBTitle:</b> structure of the plantazolicin methyltransferase bpuml in complex with2 sah
52	<a href="#">c5dnIR</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein lysine methyltransferase 2;

52	<a href="#">c0up10</a>	Alignment	not modelled	99.9	13	<b>PDBTitle:</b> the structure of pkmt2 from rickettsia typhi in complex with adohcy <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mRNA capping enzyme; <b>PDBTitle:</b> encephalitozoan cuniculi mRNA cap (guanine-n7)2 methyltransferase in complexed with azoadomet <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> mRNA cap (Guanine N-7) methyltransferase
53	<a href="#">c1z3cA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mRNA capping enzyme; <b>PDBTitle:</b> encephalitozoan cuniculi mRNA cap (guanine-n7)2 methyltransferase in complexed with azoadomet <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> mRNA cap (Guanine N-7) methyltransferase
54	<a href="#">d1ri5a</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus thuringiensis <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
55	<a href="#">c3l8dA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus thuringiensis <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
56	<a href="#">d1kpga</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> phosphoethanolamine n-methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Phosphoethanolamine methyltransferase
57	<a href="#">c3ujcA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase; <b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Phosphoethanolamine methyltransferase
58	<a href="#">c5je0B</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase; <b>PDBTitle:</b> crystal structure of burkholderia glumiae toxsa with bound s-2 adenylhomocysteine (sah) and 1,6-didemethylxoflavin <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Adenylylhomocysteine methyltransferase
59	<a href="#">c3mggB</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanoscarcina2 mazei <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Methyltransferase
60	<a href="#">c5evjA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenite methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of crarsm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
61	<a href="#">d2p7ia1</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative methyltransferase bud23; <b>PDBTitle:</b> structure of s. cerevisiae bud23-trm112 complex involved in formation of m7g1575 on 18s rrna (apo-form) <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Putative methyltransferase
62	<a href="#">c4qttB</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative methyltransferase bud23; <b>PDBTitle:</b> structure of s. cerevisiae bud23-trm112 complex involved in formation of m7g1575 on 18s rrna (apo-form) <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Putative methyltransferase
63	<a href="#">d2fk8a1</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative methyltransferase bud23; <b>PDBTitle:</b> structure of s. cerevisiae bud23-trm112 complex involved in formation of m7g1575 on 18s rrna (apo-form) <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Putative methyltransferase
64	<a href="#">c2fk8A</a>	Alignment	not modelled	99.9	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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Methoxy mycolic acid synthase
65	<a href="#">d1l1ea</a>	Alignment	not modelled	99.9	10	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein lysine methyltransferase
66	<a href="#">c5do0A</a>	Alignment	not modelled	99.9	14	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein lysine methyltransferase
67	<a href="#">d1pjza</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-L-methionine-dependent methyltransferases <b>PDBTitle:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
68	<a href="#">c3dlcA</a>	Alignment	not modelled	99.9	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosyl-L-methionine-dependent methyltransferase <b>PDBTitle:</b> crystal structure of a putative s-adenosyl-L-methionine-dependent2 methyltransferase (mmpl1179) from methanococcus maripaludis at 1.15 a3 resolution <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Putative s-adenosyl-L-methionine-dependent methyltransferase
69	<a href="#">c6d6yA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> apra methyltransferase 2; <b>PDBTitle:</b> apra methyltransferase 2 - gnat didomain in complex with sah <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Putative methyltransferase
70	<a href="#">c4x1oA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna (adenine(1408)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulispores acidiphilus
71	<a href="#">c2gs9A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tt1324; <b>PDBTitle:</b> crystal structure of tt1324 from thermus thermophilis hb8 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein tt1324
72	<a href="#">c3ndjA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> x-ray structure of a c-3'-methyltransferase in complex with s-2 adenyl-L-homocysteine and sugar product <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> c-3'-methyltransferase
73	<a href="#">c3m70A</a>	Alignment	not modelled	99.9	14	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Tellurite resistance protein tehb homolog
74	<a href="#">c5bp9A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase protein; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from bacteroides2 fragilis in complex with s-adenosyl-L-homocysteine <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Putative methyltransferase
75	<a href="#">d1xcla</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> Guanoacetate methyltransferase <b>PDBTitle:</b> Guanoacetate methyltransferase <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanoacetate methyltransferase
76	<a href="#">c6dcba</a>	Alignment	not modelled	99.9	19	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Methylphosphate capping enzyme methyltransferase

77	<a href="#">c2xvmB</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tellurite resistance protein tehb; <b>PDBTitle:</b> crystal structure of the tellurite detoxification protein2 tehb from e. coli in complex with sah
78	<a href="#">c5u18A</a>		Alignment	not modelled	99.9	15	<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
79	<a href="#">c4iv0B</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase, putative; <b>PDBTitle:</b> crystal structure of n-methyl transferase from plasmodium vivax2 complexed with s-adenosyl methionine and phosphate
80	<a href="#">c4xcxA</a>		Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> small rna 2'-o-methyltransferase; <b>PDBTitle:</b> methyltransferase domain of small rna 2'-o-methyltransferase
81	<a href="#">c2p7iB</a>		Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a sam dependent methyl-transferase type 12 family2 protein (eca1738) from pectobacterium atrosepticum scri1043 at 1.74 a3 resolution
82	<a href="#">c3ou7A</a>		Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
83	<a href="#">c4azwA</a>		Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wbdd; <b>PDBTitle:</b> crystal structure of monomeric wbdd.
84	<a href="#">c3opnA</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hemolysin; <b>PDBTitle:</b> the crystal structure of a putative hemolysin from lactococcus lactis <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
85	<a href="#">d1kpia</a>		Alignment	not modelled	99.9	10	<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
86	<a href="#">c6bqca</a>		Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citrinin polyketide synthase; <b>PDBTitle:</b> structure of the citrinin polyketide synthase cmet domain
87	<a href="#">c5mptA</a>		Alignment	not modelled	99.9	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
88	<a href="#">d1tpya</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
89	<a href="#">c3dlb</a>		Alignment	not modelled	99.9	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
90	<a href="#">d1zx0a1</a>		Alignment	not modelled	99.9	14	<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
91	<a href="#">d2ex4a1</a>		Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> crystal structure of putative methyltransferase (yp_321342.1) from2 anabaena variabilis atcc 29413 at 1.90 a resolution
92	<a href="#">c3ccfB</a>		Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
93	<a href="#">c3busB</a>		Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
94	<a href="#">c3fuxB</a>		Alignment	not modelled	99.9	17	<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
95	<a href="#">c6mroA</a>		Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyl transferase from methanoscincina acetivorans; <b>PDBTitle:</b> crystal structure of methyl transferase from methanoscincina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
96	<a href="#">c3e8sA</a>		Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sam dependent methyltransferase; <b>PDBTitle:</b> crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
97	<a href="#">c3h2bB</a>		Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of the sam-dependent methyltransferase cg3271 from2 corynebacterium glutamicum in complex with s-adenosyl-l-homocysteine3 and pyrophosphate. northeast structural genomics consortium target4 cgr113a
98	<a href="#">c3bkwB</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine dependent methyltransferase2 (np_104914.1) from mesorhizobium loti at 1.60 a resolution
99	<a href="#">c4azsA</a>		Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase wbdd;

					<b>PDBTitle:</b> high resolution (2.2 a) crystal structure of wbdd.
100	<a href="#">d1yzha1</a>	Alignment	not modelled	99.9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
101	<a href="#">d1p91a_</a>	Alignment	not modelled	99.9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA methyltransferase RlmA
102	<a href="#">c4hg2B_</a>	Alignment	not modelled	99.9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase type 11; <b>PDBTitle:</b> the structure of a putative type ii methyltransferase from2 anaeromyxobacter dehalogenans.
103	<a href="#">d1wzna1</a>	Alignment	not modelled	99.9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
104	<a href="#">c3jwhA_</a>	Alignment	not modelled	99.9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hen1; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of2 bacterial-avhen1-c
105	<a href="#">c4xrpF_</a>	Alignment	not modelled	99.9	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> hen1; <b>PDBTitle:</b> structure of the pnkp1/rnl/hen1 rna repair complex
106	<a href="#">d2bzga1</a>	Alignment	not modelled	99.9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
107	<a href="#">d1d2ha_</a>	Alignment	not modelled	99.9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
108	<a href="#">c3bgdB_</a>	Alignment	not modelled	99.8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
109	<a href="#">c3jwgA_</a>	Alignment	not modelled	99.8	<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
110	<a href="#">c2pxxA_</a>	Alignment	not modelled	99.8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mgc2408; <b>PDBTitle:</b> human putative methyltransferase mgc2408
111	<a href="#">c3ggdA_</a>	Alignment	not modelled	99.8	<b>PDB header:</b> transferase <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
112	<a href="#">c3merA_</a>	Alignment	not modelled	99.8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> slr1183 protein; <b>PDBTitle:</b> crystal structure of the methyltransferase slr1183 from synchocystis2 sp. pcc 6803, northeast structural genomics consortium target sgr145
113	<a href="#">c3tqsB_</a>	Alignment	not modelled	99.8	<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
114	<a href="#">c3cgkB_</a>	Alignment	not modelled	99.8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
115	<a href="#">c5gm2E_</a>	Alignment	not modelled	99.8	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase tld complexed with sah and2 teleocidin a1
116	<a href="#">c3e23A_</a>	Alignment	not modelled	99.8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rpa2492; <b>PDBTitle:</b> crystal structure of the rpa2492 protein in complex with sam from2 rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr299
117	<a href="#">c2p8jA_</a>	Alignment	not modelled	99.8	<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 (np_349143.1) from clostridium acetobutylicum at 2.0 a resolution
118	<a href="#">c4qdkB_</a>	Alignment	not modelled	99.8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> magnesium-protoporphyrin o-methyltransferase; <b>PDBTitle:</b> crystal structure of magnesium protoporphyrin ix methyltransferase2 (chl)m from synchocystis pcc 6803 with bound sah
119	<a href="#">d1xtpa_</a>	Alignment	not modelled	99.8	<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
120	<a href="#">c3mtiA_</a>	Alignment	not modelled	99.8	<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