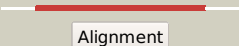



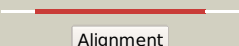




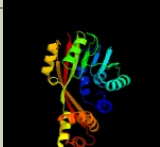
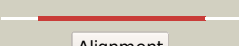




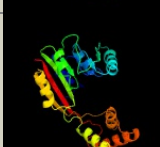








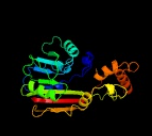





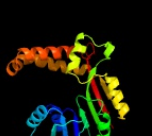


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1597_(-)_1798301_1799059
Date	Fri Aug 2 13:30:19 BST 2019
Unique Job ID	bf83cdf383c6d76d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ineB_</a>	 Alignment		100.0	16	<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
2	<a href="#">c1vl5B_</a>	 Alignment		100.0	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
3	<a href="#">d1vl5a_</a>	 Alignment		100.0	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
4	<a href="#">c4krhB_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 2; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine
5	<a href="#">c5egpB_</a>	 Alignment		100.0	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
6	<a href="#">c5w7kA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
7	<a href="#">c4htfA_</a>	 Alignment		100.0	17	<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.
8	<a href="#">c3ccfB_</a>	 Alignment		99.9	16	<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
9	<a href="#">c5wp5A_</a>	 Alignment		99.9	15	<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
10	<a href="#">c2yr0A_</a>	 Alignment		99.9	17	<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
11	<a href="#">d2o57a1</a>	 Alignment		99.9	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

12	<a href="#">d1xxla_</a>	Alignment		99.9	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
13	<a href="#">c3e7pA_</a>	Alignment		99.9	16	<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
14	<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
15	<a href="#">c4pneA_</a>	Alignment		99.9	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of the [4+2]-cyclase spnf
16	<a href="#">c3f4kA_</a>	Alignment		99.9	14	<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.
17	<a href="#">c5gm2E_</a>	Alignment		99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase tied complexed with sah and2 teleocidin a1
18	<a href="#">c2fk8A_</a>	Alignment		99.9	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
19	<a href="#">c3mggB_</a>	Alignment		99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 mazei
20	<a href="#">c3ujcA_</a>	Alignment		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
21	<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
22	<a href="#">d2fk8a1</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> Mycolic acid cyclopropane synthase
23	<a href="#">c3cc8A_</a>	Alignment	not modelled	99.9	18	<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
24	<a href="#">d1l1ea_</a>	Alignment	not modelled	99.9	15	<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
25	<a href="#">c5z9oA_</a>	Alignment	not modelled	99.9	11	<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
26	<a href="#">c3vc2J_</a>	Alignment	not modelled	99.9	15	<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
27	<a href="#">c3dliB_</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
28	<a href="#">c4qnuH</a>	Alignment	not modelled	99.9	17	<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
29	<a href="#">c4necC</a>	Alignment	not modelled	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
30	<a href="#">c3busB</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
31	<a href="#">d1p91a</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> rRNA methyltransferase RlmA
32	<a href="#">c4p7cB</a>	Alignment	not modelled	99.9	14	<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
33	<a href="#">d1kpga</a>	Alignment	not modelled	99.9	15	<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
34	<a href="#">c6ec3C</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein; <b>PDBTitle:</b> crystal structure of evdm1
35	<a href="#">c5fcdA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
36	<a href="#">d1tpya</a>	Alignment	not modelled	99.9	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
37	<a href="#">c2p35A</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-aconitate 2-methyltransferase; <b>PDBTitle:</b> crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
38	<a href="#">d1jqea</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
39	<a href="#">d1kpia</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> Mycolic acid cyclopropane synthase
40	<a href="#">c5t39A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> evdm1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of evdm1 in the presence2 of sah and d-fucose
41	<a href="#">c3lccA</a>	Alignment	not modelled	99.9	12	<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
42	<a href="#">c4hg2B</a>	Alignment	not modelled	99.9	17	<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.
43	<a href="#">d1nkva</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> Hypothetical Protein Yjhp
44	<a href="#">c3e23A</a>	Alignment	not modelled	99.9	19	<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 rhodospseudomonas palustris, northeast structural genomics consortium3 target rpr299
45	<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
46	<a href="#">c3ocjA</a>	Alignment	not modelled	99.9	15	<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
47	<a href="#">c3e8sA</a>	Alignment	not modelled	99.9	16	<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
48	<a href="#">c4kdcA</a>	Alignment	not modelled	99.9	13	<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
49	<a href="#">d1xtpa</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> AD-003 protein-like
50	<a href="#">d2avna1</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> UbiE/COQ5-like
51	<a href="#">c3qnhA</a>	Alignment	not modelled	99.9	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)
52	<a href="#">c2gs9A</a>	Alignment	not modelled	99.9	20	<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
53	<a href="#">c5evjA_</a>	Alignment	not modelled	99.9	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
54	<a href="#">c3bkxB_</a>	Alignment	not modelled	99.9	15	<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
55	<a href="#">c3h2bB_</a>	Alignment	not modelled	99.9	11	<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
56	<a href="#">d2p7ia1</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> UbiE/COQ5-like
57	<a href="#">c5ufmB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase domain protein; <b>PDBTitle:</b> crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine
58	<a href="#">c4x1oA_</a>	Alignment	not modelled	99.9	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
59	<a href="#">d2ex4a1</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> AD-003 protein-like
60	<a href="#">c3g2qA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.24; <b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
61	<a href="#">c2p7iB_</a>	Alignment	not modelled	99.9	14	<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
62	<a href="#">c3g5IA_</a>	Alignment	not modelled	99.9	20	<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
63	<a href="#">c4rvqA_</a>	Alignment	not modelled	99.8	12	<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
64	<a href="#">c6g4wq_</a>	Alignment	not modelled	99.8	18	<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
65	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.8	8	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
66	<a href="#">c5mptA_</a>	Alignment	not modelled	99.8	19	<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
67	<a href="#">c3bgvC_</a>	Alignment	not modelled	99.8	13	<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
68	<a href="#">c1z3cA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <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
69	<a href="#">c3dlcA_</a>	Alignment	not modelled	99.8	13	<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
70	<a href="#">c6f5zB_</a>	Alignment	not modelled	99.8	21	<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
71	<a href="#">c5ubbA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha n-terminal protein methyltransferase 1b; <b>PDBTitle:</b> crystal structure of human alpha n-terminal protein methyltransferase2 1b
72	<a href="#">c5bp9A_</a>	Alignment	not modelled	99.8	12	<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
73	<a href="#">d1ri5a_</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> mRNA cap (Guanine N-7) methyltransferase
74	<a href="#">c5je0B_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase; <b>PDBTitle:</b> crystal structure of burkholderia glumae toxa with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethyltoxoflavin
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferases;

75	<a href="#">c3sm3A_</a>	Alignment	not modelled	99.8	21	<b>PDBTitle:</b> crystal structure of sam-dependent methyltransferases q8puk2_metma2 from methanosarcina mazei. northeast structural genomics consortium3 target mar262.
76	<a href="#">c6dcbA_</a>	Alignment	not modelled	99.8	14	<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
77	<a href="#">c4krqB_</a>	Alignment	not modelled	99.8	15	<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
78	<a href="#">c6ecvB_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
79	<a href="#">d1ve3a1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
80	<a href="#">d1im8a_</a>	Alignment	not modelled	99.8	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein HI0319 (YecO)
81	<a href="#">d1xcla_</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
82	<a href="#">d2nxca1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ribosomal protein L11 methyltransferase PrmA
83	<a href="#">d1yzha1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
84	<a href="#">d1r74a_</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> Glycine N-methyltransferase
85	<a href="#">c6ectA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
86	<a href="#">d2a14a1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
87	<a href="#">c3ndjA_</a>	Alignment	not modelled	99.8	11	<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 adenosyl-l-homocysteine and sugar product
88	<a href="#">d1zx0a1</a>	Alignment	not modelled	99.8	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
89	<a href="#">c3ou7A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
90	<a href="#">c3opnA_</a>	Alignment	not modelled	99.8	11	<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
91	<a href="#">c5mgzA_</a>	Alignment	not modelled	99.8	16	<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
92	<a href="#">c3lecA_</a>	Alignment	not modelled	99.8	13	<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
93	<a href="#">c3ofkA_</a>	Alignment	not modelled	99.8	18	<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 wm9 in complex with s-adenosyl-l-homocysteine (sah)
94	<a href="#">c6mroA_</a>	Alignment	not modelled	99.8	16	<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.
95	<a href="#">c2pxxA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mgc2408; <b>PDBTitle:</b> human putative methyltransferase mgc2408
96	<a href="#">c4qdkB_</a>	Alignment	not modelled	99.8	12	<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 (chlm) from synechocystis pcc 6803 with bound sah
97	<a href="#">c3d2lC_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exiguobacterium sp. 255-15 at 1.90 a resolution
98	<a href="#">c6bqcA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase;

99	<a href="#">c4rwzA_</a>	Alignment	not modelled	99.8	17	<b>PDBTitle:</b> cyclopropane fatty acid synthase from e. coli <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative rRNA methyltransferase; <b>PDBTitle:</b> crystal structure of the antibiotic-resistance methyltransferase kmr
100	<a href="#">c6d6yA_</a>	Alignment	not modelled	99.8	16	<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
101	<a href="#">c3mq2A_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rRNA methyltransferase; <b>PDBTitle:</b> crystal structure of 16s rRNA methyltransferase kamb
102	<a href="#">c4hgyC_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ccbJ; <b>PDBTitle:</b> structure of the ccbJ methyltransferase from streptomyces caelestis
103	<a href="#">c3grzA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein l11 methyltransferase; <b>PDBTitle:</b> crystal structure of ribosomal protein l11 methylase from <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>
104	<a href="#">c4qttB_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative methyltransferase bud23; <b>PDBTitle:</b> structure of <i>S. cerevisiae</i> bud23-trm112 complex involved in formation of m7g1575 on 18s rRNA (apo-form)
105	<a href="#">d1vbfA_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
106	<a href="#">d1xvaa_</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> Glycine N-methyltransferase
107	<a href="#">c4iscA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase from <i>Pseudomonas</i> <i>syringae</i>
108	<a href="#">c4obxD_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-methoxy-6-polypropenyl-1,4-benzoquinol methylase, <b>PDBTitle:</b> crystal structure of yeast coq5 in the apo form
109	<a href="#">c3ggdA_</a>	Alignment	not modelled	99.8	11	<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) <sub>2</sub> from <i>Anabaena variabilis</i> atcc 29413 at 2.11 Å resolution
110	<a href="#">d1d2ha_</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> Glycine N-methyltransferase
111	<a href="#">c4kvzA_</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bamI; <b>PDBTitle:</b> crystal structure of the plantazolin methyltransferase bamI in 2 complex with sah
112	<a href="#">c3hnrA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable methyltransferase bt9727_4108; <b>PDBTitle:</b> crystal structure of a probable methyltransferase bt9727_4108 from <i>Bacillus thuringiensis</i> subsp. <i>northeast3</i> structural genomics consortium target id bur219
113	<a href="#">c3g2qB_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pcza361.24; <b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mtfA2 complexed with sinefungin
114	<a href="#">c3ku1E_</a>	Alignment	not modelled	99.8	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
115	<a href="#">c5u18A_</a>	Alignment	not modelled	99.8	13	<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 biosynthesis of gentamicin in complex with the geneticin
116	<a href="#">c3pfdD_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of the n,n-dimethyltransferase tylm1 from <i>Streptomyces fradiae</i> in complex with sah and dtdp-quip3n
117	<a href="#">d1y8ca_</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
118	<a href="#">c5hijA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine sarcosine n-methyltransferase; <b>PDBTitle:</b> crystal structure of glycine sarcosine n-methyltransferase from <i>Methanohalophilus portucalensis</i> in complex with betaine
119	<a href="#">d2fcaa1</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> TrmB-like
120	<a href="#">c4gekG_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> trna (cmo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of wild-type cmoA from e.coli