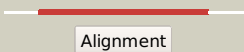

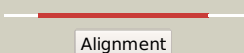

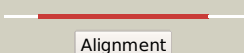

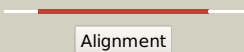

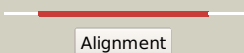

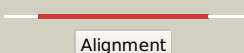

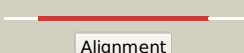





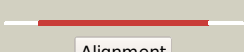

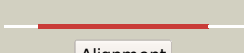





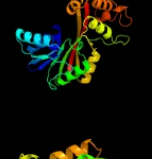


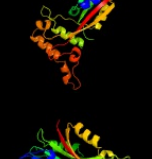



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1405c_(-)_1581151_1581975
Date	Wed Jul 31 22:05:51 BST 2019
Unique Job ID	5ed1567c4265bfe2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5egpB_</a>	 Alignment		100.0	20	<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
2	<a href="#">c5w7kA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
3	<a href="#">c5wp5A_</a>	 Alignment		100.0	17	<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
4	<a href="#">c2yr0A_</a>	 Alignment		100.0	20	<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="#">c3ccfB_</a>	 Alignment		99.9	14	<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 anaabaena variabilis atcc 29413 at 1.90 a resolution
6	<a href="#">c2p35A_</a>	 Alignment		99.9	13	<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
7	<a href="#">c3mggB_</a>	 Alignment		99.9	20	<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
8	<a href="#">c3bkbB_</a>	 Alignment		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
9	<a href="#">c4krhB_</a>	 Alignment		99.9	15	<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
10	<a href="#">c5z9oA_</a>	 Alignment		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
11	<a href="#">c4ineB_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein pmt-2; <b>PDBTitle:</b> crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine

12	<a href="#">d2o57a1</a>	Alignment		99.9	14	<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
13	<a href="#">c2fk8A</a>	Alignment		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
14	<a href="#">c3g5tA</a>	Alignment		99.9	14	<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="#">d1kpga</a>	Alignment		99.9	14	<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
16	<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
17	<a href="#">c3vc2j</a>	Alignment		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
18	<a href="#">c1vl5B</a>	Alignment		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
19	<a href="#">d1vl5a</a>	Alignment		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
20	<a href="#">d1nkva</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> Hypothetical Protein YjHP
21	<a href="#">d2fk8a1</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
22	<a href="#">c4pneA</a>	Alignment	not modelled	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
23	<a href="#">c3e7pA</a>	Alignment	not modelled	99.9	12	<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
24	<a href="#">d1kpia</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="#">c5gm2E</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
26	<a href="#">d1jqea</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> Histamine methyltransferase
27	<a href="#">d1tpya</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
28	<a href="#">c6bqcA</a>	Alignment	not modelled	99.9	12	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases

29	<a href="#">d1l1ea_</a>	Alignment	not modelled	99.9	12	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase <b>PDB header:</b> transferase
30	<a href="#">c3f4kA_</a>	Alignment	not modelled	99.9	15	<b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from <i>Bacteroides thetaiotaomicron</i> . northeast structural3 genomics target btr309.
31	<a href="#">c3busB_</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 rebm
32	<a href="#">c3ujcA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase; <b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from <i>Plasmodium falciparum</i> in complex with phosphocholine
33	<a href="#">c4iv0B_</a>	Alignment	not modelled	99.9	10	<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 <i>Plasmodium vivax</i> 2 complexed with s-adenosyl methionine and phosphate
34	<a href="#">c6f5zB_</a>	Alignment	not modelled	99.9	20	<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
35	<a href="#">c5kn4B_</a>	Alignment	not modelled	99.9	12	<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
36	<a href="#">c6gkvB_</a>	Alignment	not modelled	99.9	11	<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
37	<a href="#">c3egeA_</a>	Alignment	not modelled	99.9	20	<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 <i>Anabaena variabilis</i> atcc3 29413 at 2.40 a resolution
38	<a href="#">c4hg2B_</a>	Alignment	not modelled	99.9	16	<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 from <i>Mycobacterium anaeromyxobacter</i> dehalogenans.
39	<a href="#">c5fcdA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
40	<a href="#">c4p7cB_</a>	Alignment	not modelled	99.9	17	<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 <i>Pseudomonas syringae</i> pv. tomato
41	<a href="#">c3dlcA_</a>	Alignment	not modelled	99.9	16	<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 <i>Methanococcus marisaludis</i> at 1.15 a3 resolution
42	<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 ubig
43	<a href="#">c4necC_</a>	Alignment	not modelled	99.9	23	<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
44	<a href="#">c4qnuH_</a>	Alignment	not modelled	99.9	15	<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
45	<a href="#">c6g4wq_</a>	Alignment	not modelled	99.9	19	<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
46	<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 <i>Thermus thermophilus</i> hb8
47	<a href="#">d2gh1a1</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> BC2162-like
48	<a href="#">c3cc8A_</a>	Alignment	not modelled	99.9	12	<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) from <i>Bacillus cereus</i> atcc 10987 at 1.64 a resolution
49	<a href="#">c4qttB_</a>	Alignment	not modelled	99.9	20	<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 formation2 of m7g1575 on 18s rRNA (apo-form)
50	<a href="#">c4htfA_</a>	Alignment	not modelled	99.9	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 <i>Escherichia coli</i> in complex with s-adenosylmethionine.
51	<a href="#">c6ecvB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
						<b>PDB header:</b> transferase

52	<a href="#">c3ou7A_</a>	Alignment	not modelled	99.9	13	<b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
53	<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
54	<a href="#">c5mgzA_</a>	Alignment	not modelled	99.8	25	<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
55	<a href="#">c6ectA_</a>	Alignment	not modelled	99.8	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
56	<a href="#">c3qnhA_</a>	Alignment	not modelled	99.8	17	<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)
57	<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
58	<a href="#">c3bgvC_</a>	Alignment	not modelled	99.8	15	<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
59	<a href="#">c3dliB_</a>	Alignment	not modelled	99.8	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
60	<a href="#">c4kvzA_</a>	Alignment	not modelled	99.8	10	<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
61	<a href="#">d2ex4a1</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> AD-003 protein-like
62	<a href="#">c3e8sA_</a>	Alignment	not modelled	99.8	15	<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
63	<a href="#">c3l8dA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus thuringiensis
64	<a href="#">c4krqB_</a>	Alignment	not modelled	99.8	20	<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
65	<a href="#">d1ve3a1</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> CAC2371-like
66	<a href="#">c3e23A_</a>	Alignment	not modelled	99.8	21	<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
67	<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
68	<a href="#">c3lccA_</a>	Alignment	not modelled	99.8	14	<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
69	<a href="#">c4iscA_</a>	Alignment	not modelled	99.8	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
70	<a href="#">c5evjA_</a>	Alignment	not modelled	99.8	23	<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
71	<a href="#">d2p7ia1</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> UbiE/COQ5-like
72	<a href="#">d1vlma_</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> UbiE/COQ5-like
73	<a href="#">c4x1oA_</a>	Alignment	not modelled	99.8	20	<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 catenulisporales acidiphilia
74	<a href="#">d2avna1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
75	<a href="#">c3h2bB_</a>	Alignment	not modelled	99.8	13	<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
76	<a href="#">c6d6yA_</a>	Alignment	not modelled	99.8	11 <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
77	<a href="#">c5je0B_</a>	Alignment	not modelled	99.8	18 <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
78	<a href="#">c5t39A_</a>	Alignment	not modelled	99.8	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> evdmo1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of evdmo1 in the presence of sah and d-fucose
79	<a href="#">d1xcla_</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> Guanidinoacetate methyltransferase
80	<a href="#">c6ccaA_</a>	Alignment	not modelled	99.8	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> disa protein; <b>PDBTitle:</b> crystal structure of dsza carbon methyltransferase
81	<a href="#">c2p7iB_</a>	Alignment	not modelled	99.8	11 <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="#">c4qdkB_</a>	Alignment	not modelled	99.8	19 <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
83	<a href="#">c5u18A_</a>	Alignment	not modelled	99.8	22 <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
84	<a href="#">c6ec3C_</a>	Alignment	not modelled	99.8	19 <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
85	<a href="#">c3merA_</a>	Alignment	not modelled	99.8	16 <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 synechocystis2 sp. pcc 6803, northeast structural genomics consortium target sgr145
86	<a href="#">d1xtpa_</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> AD-003 protein-like
87	<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)
88	<a href="#">d1r74a_</a>	Alignment	not modelled	99.8	24 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
89	<a href="#">c6dcbA_</a>	Alignment	not modelled	99.8	17 <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
90	<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)
91	<a href="#">c3ocjA_</a>	Alignment	not modelled	99.8	16 <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 possible exported protein from bordetella2 parapertussis
92	<a href="#">d1pjza_</a>	Alignment	not modelled	99.8	15 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
93	<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
94	<a href="#">d1ri5a_</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> mRNA cap (Guanine N-7) methyltransferase
95	<a href="#">c5mptA_</a>	Alignment	not modelled	99.8	13 <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
96	<a href="#">d1p91a_</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> rRNA methyltransferase RlMA
97	<a href="#">d1wzna1</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> CAC2371-like
98	<a href="#">c3m70A_</a>	Alignment	not modelled	99.8	19 <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
99	<a href="#">c5ubbA_</a>	Alignment	not modelled	99.8	15 <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

100	<a href="#">c4obxD</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, <b>PDBTitle:</b> crystal structure of yeast coq5 in the apo form
101	<a href="#">d1xvaa</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> Glycine N-methyltransferase
102	<a href="#">c5thyB</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transferase,lyase <b>Chain:</b> B: <b>PDB Molecule:</b> curj; <b>PDBTitle:</b> crystal structure of semet-substituted curj carbon methyltransferase
103	<a href="#">c6mroA</a>	Alignment	not modelled	99.8	21	<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.
104	<a href="#">d1wg8a2</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> MraW-like putative methyltransferases
105	<a href="#">c5ufmB</a>	Alignment	not modelled	99.8	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
106	<a href="#">d1zx0a1</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> Guanidinoacetate methyltransferase
107	<a href="#">c2xvmB</a>	Alignment	not modelled	99.8	19	<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
108	<a href="#">d1m6ya2</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> MraW-like putative methyltransferases
109	<a href="#">d1dusa</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
110	<a href="#">c3dh0B</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam dependent methyltransferase; <b>PDBTitle:</b> crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
111	<a href="#">d1vbfA</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> Protein-L-isoaspartyl O-methyltransferase
112	<a href="#">c4xcxA</a>	Alignment	not modelled	99.8	10	<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
113	<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 methyltransferase2 bt9727_4108 from bacillus thuringiensis subsp. northeast3 structural genomics consortium target id bur219
114	<a href="#">c3mtiA</a>	Alignment	not modelled	99.8	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
115	<a href="#">c4hgyC</a>	Alignment	not modelled	99.8	19	<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
116	<a href="#">c5bp9A</a>	Alignment	not modelled	99.8	18	<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
117	<a href="#">c3mq2A</a>	Alignment	not modelled	99.8	19	<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
118	<a href="#">c3ggdA</a>	Alignment	not modelled	99.8	13	<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
119	<a href="#">d1p1ca</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> Guanidinoacetate methyltransferase
120	<a href="#">d2a14a1</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> Arylamine N-methyltransferase