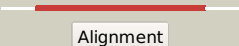



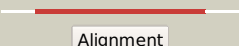





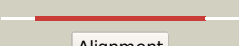













# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2990c_(-)_3346869_3347729
Date	Thu Aug 8 16:20:15 BST 2019
Unique Job ID	0d4edcd3b9df8cd5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ineB_</a>	 Alignment		98.5	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 caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
2	<a href="#">c4krhB_</a>	 Alignment		98.4	16	<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
3	<a href="#">d1nkva_</a>	 Alignment		98.3	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
4	<a href="#">c4pneA_</a>	 Alignment		98.2	13	<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
5	<a href="#">d1l1ea_</a>	 Alignment		98.2	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
6	<a href="#">c2fk8A_</a>	 Alignment		98.1	16	<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
7	<a href="#">c5gm2E_</a>	 Alignment		98.1	11	<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
8	<a href="#">c3g2qA_</a>	 Alignment		98.0	20	<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
9	<a href="#">d2o57a1</a>	 Alignment		98.0	10	<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
10	<a href="#">c5wp5A_</a>	 Alignment		98.0	14	<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
11	<a href="#">c3lccA_</a>	 Alignment		97.9	19	<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

12	<a href="#">c3mczB_</a>	Alignment		97.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
13	<a href="#">c3e7pA_</a>	Alignment		97.9	13	<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="#">c3dmgA_</a>	Alignment		97.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribosomal rna small subunit methyltransferase; <b>PDBTitle:</b> t. thermophilus 16s rna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
15	<a href="#">c5z9oA_</a>	Alignment		97.9	16	<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
16	<a href="#">d2fk8a1</a>	Alignment		97.9	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
17	<a href="#">d1kpga_</a>	Alignment		97.8	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
18	<a href="#">c3dp7B_</a>	Alignment		97.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
19	<a href="#">c3grzA_</a>	Alignment		97.8	21	<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 from2 lactobacillus delbrueckii subsp. bulgaricus
20	<a href="#">d2ex4a1</a>	Alignment		97.8	15	<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
21	<a href="#">d2nxca1</a>	Alignment	not modelled	97.8	29	<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
22	<a href="#">d1tpya_</a>	Alignment	not modelled	97.8	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
23	<a href="#">c5w7kA_</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
24	<a href="#">c3bkxB_</a>	Alignment	not modelled	97.7	11	<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
25	<a href="#">d1kpia_</a>	Alignment	not modelled	97.6	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
26	<a href="#">c2r3sA_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase (npun_r0239) from2 nostoc punctiforme pcc 73102 at 2.15 a resolution
27	<a href="#">c3f4kA_</a>	Alignment	not modelled	97.6	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.
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-

28	<a href="#">c3ujcA</a>	Alignment	not modelled	97.6	14	methyltransferase; <b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
29	<a href="#">d1r74a</a>	Alignment	not modelled	97.6	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
30	<a href="#">c3lpmA</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
31	<a href="#">c3busB</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
32	<a href="#">c3g2qB</a>	Alignment	not modelled	97.6	17	<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 mfa2 complexed with sinefungin
33	<a href="#">c3h2bB</a>	Alignment	not modelled	97.6	20	<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
34	<a href="#">d1zx0a1</a>	Alignment	not modelled	97.6	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
35	<a href="#">c3mtiA</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> the crystal structure of a rna methylase from streptococcus2 thermophilus to 1.95a
36	<a href="#">d1im8a</a>	Alignment	not modelled	97.5	17	<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)
37	<a href="#">d1xtpa</a>	Alignment	not modelled	97.5	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
38	<a href="#">c2iipD</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
39	<a href="#">c5ubbA</a>	Alignment	not modelled	97.5	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
40	<a href="#">c5i2hB</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase family 2; <b>PDBTitle:</b> crystal structure of o-methyltransferase family 2 protein plim_11472 from planctomyces limnophilus dsm 3776 complex with apigenin
41	<a href="#">d1xcla</a>	Alignment	not modelled	97.4	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
42	<a href="#">c6bqcA</a>	Alignment	not modelled	97.4	20	<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
43	<a href="#">c6clwA</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of tmh
44	<a href="#">d1dusa</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
45	<a href="#">c4kdcA</a>	Alignment	not modelled	97.4	12	<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
46	<a href="#">c1tw3A</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carminomycin 4-o-methyltransferase; <b>PDBTitle:</b> crystal structure of carminomycin-4-o-methyltransferase (dnrk) in2 complex with s-adenosyl-l-homocystein (sah) and 4-methoxy-e-3 rhodomycin t (m-et)
47	<a href="#">c2pjdA</a>	Alignment	not modelled	97.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase c; <b>PDBTitle:</b> crystal structure of 16s rna methyltransferase rsmc
48	<a href="#">c3ou7A</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
49	<a href="#">c3ofkA</a>	Alignment	not modelled	97.4	13	<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)
50	<a href="#">c6ectA</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
51	<a href="#">c3lbyA</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1697c; <b>PDBTitle:</b> crystal structure of smu.1697c, a putative methyltransferase from2 streptococcus mutans in complex with sah
52	<a href="#">c3p2kA</a>	Alignment	not modelled	97.3	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rna methylase;

						<b>PDBTitle:</b> structure of an antibiotic related methyltransferase
53	<a href="#">d2a14a1</a>	Alignment	not modelled	97.3	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
54	<a href="#">c4qnuH</a>	Alignment	not modelled	97.3	16	<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
55	<a href="#">c3mq2A</a>	Alignment	not modelled	97.3	15	<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
56	<a href="#">c4iv0B</a>	Alignment	not modelled	97.3	16	<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
57	<a href="#">d1yzha1</a>	Alignment	not modelled	97.3	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
58	<a href="#">c1vl5B</a>	Alignment	not modelled	97.3	14	<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
59	<a href="#">c1x1aA</a>	Alignment	not modelled	97.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> crtf-related protein; <b>PDBTitle:</b> crystal structure of bchu complexed with s-adenosyl-l-methionine
60	<a href="#">c4kwcA</a>	Alignment	not modelled	97.3	17	<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
61	<a href="#">c3vc2J</a>	Alignment	not modelled	97.3	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
62	<a href="#">c6c5bB</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure analysis of laphzm
63	<a href="#">d1vl5a</a>	Alignment	not modelled	97.2	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
64	<a href="#">d2bzga1</a>	Alignment	not modelled	97.2	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
65	<a href="#">d1xxla</a>	Alignment	not modelled	97.2	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
66	<a href="#">c2yvlB</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
67	<a href="#">c2gpyB</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of putative o-methyltransferase from bacillus2 halodurans
68	<a href="#">c4necC</a>	Alignment	not modelled	97.2	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
69	<a href="#">c6mroA</a>	Alignment	not modelled	97.2	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.
70	<a href="#">c4kvzA</a>	Alignment	not modelled	97.2	16	<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
71	<a href="#">c4iscA</a>	Alignment	not modelled	97.2	14	<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
72	<a href="#">c3ocjA</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> the crystal structure of a possible exported protein from bordetella2 parapertussis
73	<a href="#">d2fpoa1</a>	Alignment	not modelled	97.2	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
74	<a href="#">c3dtnA</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase mm_2633; <b>PDBTitle:</b> crystal structure of putative methyltransferase-mm_2633 from2 methanosarcina mazei .
75	<a href="#">c3tfwB</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
76	<a href="#">c3n8cA</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sam dependent methyltransferase;

76	<a href="#">c2e6sA</a>	Alignment	not modelled	97.1	19	<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
77	<a href="#">c4hgyC</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ccbaj; <b>PDBTitle:</b> structure of the ccbj methyltransferase from streptomyces caelestis
78	<a href="#">c4htfA</a>	Alignment	not modelled	97.1	14	<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.
79	<a href="#">c4dcmA</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase g; <b>PDBTitle:</b> crystal structure of methyltransferase rlmg modifying g1835 of 23s2 rrna in escherichia coli
80	<a href="#">c2ozvA</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0636; <b>PDBTitle:</b> crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
81	<a href="#">c2esrB</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> conserved hypothetical protein- streptococcus pyogenes
82	<a href="#">c3bgdB</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
83	<a href="#">c5lhmA</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of safc from myxococcus xanthus apo-form
84	<a href="#">c3hm2G</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> precocorrin-6y c5,15-methyltransferase; <b>PDBTitle:</b> crystal structure of putative precocorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
85	<a href="#">c5kn4B</a>	Alignment	not modelled	97.0	13	<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
86	<a href="#">c4rwzA</a>	Alignment	not modelled	97.0	16	<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
87	<a href="#">c5bp9A</a>	Alignment	not modelled	97.0	16	<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
88	<a href="#">c3e05B</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-6y c5,15-methyltransferase (decarboxylating); <b>PDBTitle:</b> crystal structure of precocorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
89	<a href="#">d2esra1</a>	Alignment	not modelled	97.0	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
90	<a href="#">d1p1ca</a>	Alignment	not modelled	97.0	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
91	<a href="#">c3merA</a>	Alignment	not modelled	97.0	13	<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
92	<a href="#">c3bgvC</a>	Alignment	not modelled	97.0	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
93	<a href="#">c3ccfB</a>	Alignment	not modelled	97.0	13	<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
94	<a href="#">c6ecvB</a>	Alignment	not modelled	97.0	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
95	<a href="#">c2ip2B</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable phenazine-specific methyltransferase; <b>PDBTitle:</b> structure of the pyocyanin biosynthetic protein phzm
96	<a href="#">c3lecA</a>	Alignment	not modelled	97.0	14	<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
97	<a href="#">c4qpnA</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-lysine methyltransferase mettl21b; <b>PDBTitle:</b> crystal structure of human methyltransferase-like protein 21b
98	<a href="#">c3m70A</a>	Alignment	not modelled	96.9	10	<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="#">c3m9gB</a>	Alignment	not modelled	96.9	10	<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
						<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases



100	<a href="#">d2g72a1</a>	Alignment	not modelled	96.9	15	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
101	<a href="#">c4oa8A</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase family protein; <b>PDBTitle:</b> x-ray crystal structure of o-methyltransferase from anaplasma2 phagocytophilum in apo form
102	<a href="#">c2yr0A</a>	Alignment	not modelled	96.9	14	<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 thermophilus hb8
103	<a href="#">d1qzza2</a>	Alignment	not modelled	96.9	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
104	<a href="#">c6gkvB</a>	Alignment	not modelled	96.9	20	<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
105	<a href="#">c5bxyB</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rna methyltransferase; <b>PDBTitle:</b> crystal structure of rna methyltransferase from salinibacter ruber in2 complex with s-adenosyl-l-homocysteine
106	<a href="#">c3i53A</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
107	<a href="#">c3cbgA</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> functional and structural characterization of a cationdependent o-2 methyltransferase from the cyanobacterium synechocystis sp. strain3 pcc 6803
108	<a href="#">c3ku1E</a>	Alignment	not modelled	96.9	16	<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
109	<a href="#">d1susa1</a>	Alignment	not modelled	96.9	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
110	<a href="#">c5egpB</a>	Alignment	not modelled	96.9	13	<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
111	<a href="#">c3cc8A</a>	Alignment	not modelled	96.9	17	<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
112	<a href="#">c3eeyL</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> putative rrna methylase; <b>PDBTitle:</b> crystal structure of putative rrna-methylase from clostridium2 thermocellum
113	<a href="#">c3p9nA</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible methyltransferase (methylase); <b>PDBTitle:</b> rv2966c of m. tuberculosis is a rsmd-like methyltransferase
114	<a href="#">c1z3cA</a>	Alignment	not modelled	96.8	16	<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 methyltransferasein complexed with azoadomet
115	<a href="#">d1wzna1</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
116	<a href="#">c4gekG</a>	Alignment	not modelled	96.8	14	<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
117	<a href="#">c5u18A</a>	Alignment	not modelled	96.8	14	<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
118	<a href="#">d1ri5a</a>	Alignment	not modelled	96.8	16	<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
119	<a href="#">c3l8dA</a>	Alignment	not modelled	96.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus thuringiensis
120	<a href="#">d1nv8a</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N5-glutamine methyltransferase, HemK