











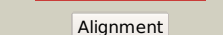

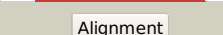





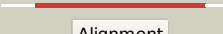












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0644c_(mmaA2)_738300_739163
Date	Fri Jul 26 01:50:21 BST 2019
Unique Job ID	dae56424c982a189

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1tpya_</a>	 Alignment		100.0	100	<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
2	<a href="#">d1kpga_</a>	 Alignment		100.0	72	<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
3	<a href="#">c5z9oA_</a>	 Alignment		100.0	35	<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
4	<a href="#">c6bqcA_</a>	 Alignment		100.0	36	<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
5	<a href="#">d1kpia_</a>	 Alignment		100.0	57	<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		100.0	57	<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="#">d1l1ea_</a>	 Alignment		100.0	73	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
8	<a href="#">d2fk8a1</a>	 Alignment		100.0	57	<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
9	<a href="#">c6gkvB_</a>	 Alignment		100.0	22	<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
10	<a href="#">c5kn4B_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> pavine n-methyltransferase; <b>PDBTitle:</b> pavine n-methyltransferase apoenzyme ph 6.0
11	<a href="#">c5gm2E_</a>	 Alignment		100.0	20	<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

12	<a href="#">c4pneA</a>	Alignment		100.0	17	<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
13	<a href="#">d2o57a1</a>	Alignment		100.0	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
14	<a href="#">c5wp5A</a>	Alignment		100.0	21	<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
15	<a href="#">c4krhB</a>	Alignment		100.0	18	<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
16	<a href="#">c4ineB</a>	Alignment		100.0	21	<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
17	<a href="#">c3ujcA</a>	Alignment		100.0	16	<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
18	<a href="#">c4iv0B</a>	Alignment		100.0	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
19	<a href="#">c3busB</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
20	<a href="#">c3vc2J</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> geranyl diphosphate 2-c-methyltransferase; <b>PDBTitle:</b> crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine
21	<a href="#">c6ectA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
22	<a href="#">c3e7pA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from bacteroides2 vulgatus atcc 8482
23	<a href="#">d1nkva</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein Yjhp
24	<a href="#">c3f4kA</a>	Alignment	not modelled	100.0	15	<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.
25	<a href="#">c6ecvB</a>	Alignment	not modelled	99.9	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
26	<a href="#">c3bkxB</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 cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution
27	<a href="#">c4qnuH</a>	Alignment	not modelled	99.9	21	<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
28	<a href="#">c5fcdA</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein

29	<a href="#">c3ocjA_</a>	Alignment	not modelled	99.9	14	<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
30	<a href="#">c2yr0A_</a>	Alignment	not modelled	99.9	18	<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
31	<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
32	<a href="#">c5egpB_</a>	Alignment	not modelled	99.9	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
33	<a href="#">c4p7cB_</a>	Alignment	not modelled	99.9	19	<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
34	<a href="#">c3mggB_</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 methyl transferase from methanosarcina2 mazei
35	<a href="#">d1xtpa_</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> AD-003 protein-like
36	<a href="#">d2ex4a1</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> AD-003 protein-like
37	<a href="#">d1vl5a_</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> UbiE/COQ5-like
38	<a href="#">c5w7kA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
39	<a href="#">c3bgvC_</a>	Alignment	not modelled	99.9	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
40	<a href="#">c1vl5B_</a>	Alignment	not modelled	99.9	13	<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
41	<a href="#">c6f5zB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 24-sterol c-methyltransferase; <b>PDBTitle:</b> complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
42	<a href="#">d1im8a_</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> Hypothetical protein HI0319 (YecO)
43	<a href="#">c3lccA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyl chloride transferase; <b>PDBTitle:</b> structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
44	<a href="#">c5je0B_</a>	Alignment	not modelled	99.9	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
45	<a href="#">d1xxla_</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> UbiE/COQ5-like
46	<a href="#">c4necC_</a>	Alignment	not modelled	99.9	22	<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
47	<a href="#">d1ri5a_</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> mRNA cap (Guanine N-7) methyltransferase
48	<a href="#">c1z3cA_</a>	Alignment	not modelled	99.9	14	<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
49	<a href="#">c3ccfB_</a>	Alignment	not modelled	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 anaabaena variabilis atcc 29413 at 1.90 a resolution
50	<a href="#">c5bp9A_</a>	Alignment	not modelled	99.9	14	<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
51	<a href="#">c4obxD_</a>	Alignment	not modelled	99.9	18	<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
52	<a href="#">c3mq2A_</a>	Alignment	not modelled	99.9	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
53	<a href="#">c5ubbA_</a>	Alignment	not modelled	99.9	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
54	<a href="#">d1wzna1</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> CAC2371-like
55	<a href="#">c3ou7A</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
56	<a href="#">c3qnhA</a>	Alignment	not modelled	99.9	25	<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="#">c4qdkB</a>	Alignment	not modelled	99.9	14	<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
58	<a href="#">c3dlcA</a>	Alignment	not modelled	99.9	14	<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
59	<a href="#">c3h2bB</a>	Alignment	not modelled	99.9	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
60	<a href="#">c4qttB</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative methyltransferase bud23; <b>PDBTitle:</b> structure of s. cerevisiae bud23-trm112 complex involved in formation2 of m7g1575 on 18s rrna (apo-form)
61	<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
62	<a href="#">c4htfA</a>	Alignment	not modelled	99.9	16	<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.
63	<a href="#">c5evjA</a>	Alignment	not modelled	99.9	17	<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
64	<a href="#">c3gwzB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mmcr; <b>PDBTitle:</b> structure of the mitomycin 7-o-methyltransferase mmcr
65	<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
66	<a href="#">c4x1oA</a>	Alignment	not modelled	99.9	13	<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
67	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.9	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
68	<a href="#">c3lstB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calo1 methyltransferase; <b>PDBTitle:</b> crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
69	<a href="#">c3dtnA</a>	Alignment	not modelled	99.9	14	<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 .
70	<a href="#">d1r74a</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> Glycine N-methyltransferase
71	<a href="#">d1jqea</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> Histamine methyltransferase
72	<a href="#">c3e23A</a>	Alignment	not modelled	99.8	20	<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
73	<a href="#">c4rvgA</a>	Alignment	not modelled	99.8	13	<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
74	<a href="#">c3dliB</a>	Alignment	not modelled	99.8	12	<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
75	<a href="#">d1pjza</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> Thiopurine S-methyltransferase <b>PDB header:</b> ribosome

76	<a href="#">c6g4wq_</a>	Alignment	not modelled	99.8	24	<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
77	<a href="#">d1qzza2</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> Plant O-methyltransferase, C-terminal domain
78	<a href="#">d1ve3a1</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> CAC2371-like
79	<a href="#">c5mgzA_</a>	Alignment	not modelled	99.8	22	<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
80	<a href="#">c3lecA_</a>	Alignment	not modelled	99.8	17	<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
81	<a href="#">c3g2qA_</a>	Alignment	not modelled	99.8	14	<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 mtf2 complexed with sinefungin
82	<a href="#">d1xvaa_</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> Glycine N-methyltransferase
83	<a href="#">c5ufmB_</a>	Alignment	not modelled	99.8	20	<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
84	<a href="#">c3cc8A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution
85	<a href="#">c6clwA_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of tnmh
86	<a href="#">c2p35A_</a>	Alignment	not modelled	99.8	12	<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
87	<a href="#">c4gekG_</a>	Alignment	not modelled	99.8	15	<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
88	<a href="#">d2a14a1</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> Arylamine N-methyltransferase
89	<a href="#">c3hnrA_</a>	Alignment	not modelled	99.8	16	<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
90	<a href="#">c3g5tA_</a>	Alignment	not modelled	99.8	16	<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
91	<a href="#">c6c5bB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure analysis of laphzm
92	<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
93	<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
94	<a href="#">c5t39A_</a>	Alignment	not modelled	99.8	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> evdmo1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of evdmo1 in the presence2 of sah and d-fucose
95	<a href="#">c4hgyC_</a>	Alignment	not modelled	99.8	17	<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
96	<a href="#">d1tw3a2</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> Plant O-methyltransferase, C-terminal domain
97	<a href="#">c6mroA_</a>	Alignment	not modelled	99.8	18	<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 (nesh) target mvr53.
98	<a href="#">c3ndjA_</a>	Alignment	not modelled	99.8	18	<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
99	<a href="#">c1tw3A_</a>	Alignment	not modelled	99.8	17	<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)
100	<a href="#">c5bxyB_</a>	Alignment	not modelled	99.8	14	<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
101	<a href="#">c3sm3A_</a>	Alignment	not modelled	99.8	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferases; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferases q8puk2_metma2 from methanosarcina mazei. northeast structural genomics consortium3 target mar262.
102	<a href="#">c5i2hB_</a>	Alignment	not modelled	99.8	17 <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
103	<a href="#">d1zx0a1</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> Guanidinoacetate methyltransferase
104	<a href="#">c4krqB_</a>	Alignment	not modelled	99.8	14 <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
105	<a href="#">c3ofkA_</a>	Alignment	not modelled	99.8	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nodulation protein s; <b>PDBTitle:</b> crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah)
106	<a href="#">c3jwgA_</a>	Alignment	not modelled	99.8	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c
107	<a href="#">c3dp7B_</a>	Alignment	not modelled	99.8	14 <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
108	<a href="#">c3g5lA_</a>	Alignment	not modelled	99.8	14 <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
109	<a href="#">c5hijA_</a>	Alignment	not modelled	99.8	15 <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 from2 methanohalophilus portucalensis in complex with betaine
110	<a href="#">c3m70A_</a>	Alignment	not modelled	99.8	15 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein teh homolog; <b>PDBTitle:</b> crystal structure of teh from haemophilus influenzae
111	<a href="#">d1yzha1</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
112	<a href="#">c5mptA_</a>	Alignment	not modelled	99.8	18 <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
113	<a href="#">c2xvmB_</a>	Alignment	not modelled	99.8	16 <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 teh from e. coli in complex with sah
114	<a href="#">c5do0A_</a>	Alignment	not modelled	99.8	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein lysine methyltransferase 1; <b>PDBTitle:</b> the structure of pkmt1 from rickettsia prowazekii
115	<a href="#">c6dcbA_</a>	Alignment	not modelled	99.8	15 <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
116	<a href="#">d2bzga1</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
117	<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
118	<a href="#">c3mczB_</a>	Alignment	not modelled	99.8	13 <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.
119	<a href="#">c2r3sA_</a>	Alignment	not modelled	99.8	12 <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
120	<a href="#">c3ggdA_</a>	Alignment	not modelled	99.8	15 <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