




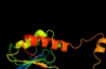



























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2gs9A_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tt1324; <b>PDBTitle:</b> crystal structure of tt1324 from thermus thermophilis hb8
2	<a href="#">d1vlma_</a>	 Alignment		99.9	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
3	<a href="#">c2yr0A_</a>	 Alignment		99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha0223; <b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
4	<a href="#">c3cc8A_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution
5	<a href="#">c3l8dA_</a>	 Alignment		99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus2 thuringiensis
6	<a href="#">c3dliB_</a>	 Alignment		99.8	17	<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
7	<a href="#">d1vl5a_</a>	 Alignment		99.8	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
8	<a href="#">c3g5lA_</a>	 Alignment		99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosylmethionine dependent <b>PDBTitle:</b> crystal structure of putative s-adenosylmethionine2 dependent methyltransferase from listeria monocytogenes
9	<a href="#">c1vl5B_</a>	 Alignment		99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> unknown conserved protein bh2331; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution
10	<a href="#">c3bkxB_</a>	 Alignment		99.8	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
11	<a href="#">d2p7ia1</a>	 Alignment		99.8	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

12	<a href="#">d2o57a1</a>	Alignment		99.8	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
13	<a href="#">c2zfuA</a>	Alignment		99.8	24	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> cerebral protein 1; <b>PDBTitle:</b> structure of the methyltransferase-like domain of nucleomethilin
14	<a href="#">c3bkwB</a>	Alignment		99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine dependent methyltransferase2 (np_104914.1) from mesorhizobium loti at 1.60 a resolution
15	<a href="#">c3f4kA</a>	Alignment		99.8	13	<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.
16	<a href="#">d1jqea</a>	Alignment		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
17	<a href="#">c3ndjA</a>	Alignment		99.8	13	<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
18	<a href="#">c2p7iB</a>	Alignment		99.8	15	<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
19	<a href="#">d2a14a1</a>	Alignment		99.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
20	<a href="#">c3e7pA</a>	Alignment		99.8	10	<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
21	<a href="#">d1nkva</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> Hypothetical Protein Yjhp
22	<a href="#">d1xxla</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> UbiE/COQ5-like
23	<a href="#">d2gh1a1</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> BC2162-like
24	<a href="#">c3h2bB</a>	Alignment	not modelled	99.8	17	<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 methyltransferase2 cg3271 from corynebacterium glutamicum in complex with s-3 adenosyl-l-homocysteine and pyrophosphate. northeast4 structural genomics consortium target cgr113a
25	<a href="#">c3mggB</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 mazei
26	<a href="#">d2avna1</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> UbiE/COQ5-like
27	<a href="#">c3ou7A</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase from

28	<a href="#">c3egeA</a>	Alignment	not modelled	99.7	12	antibiotic biosynthesis <b>PDBTitle:</b> crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution
29	<a href="#">c3dlcA</a>	Alignment	not modelled	99.7	15	<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
30	<a href="#">d2ex4a1</a>	Alignment	not modelled	99.7	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
31	<a href="#">c3ujcA</a>	Alignment	not modelled	99.7	14	<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
32	<a href="#">c3dh0B</a>	Alignment	not modelled	99.7	18	<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
33	<a href="#">d1p91a</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA methyltransferase R1mA
34	<a href="#">d1kpga</a>	Alignment	not modelled	99.7	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
35	<a href="#">c3e8sA</a>	Alignment	not modelled	99.7	13	<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
36	<a href="#">d1kpia</a>	Alignment	not modelled	99.7	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
37	<a href="#">c3busB</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
38	<a href="#">c3merA</a>	Alignment	not modelled	99.7	14	<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 from2 synechocystis sp. pcc 6803, northeast structural genomics3 consortium target sgr145
39	<a href="#">c2fk8A</a>	Alignment	not modelled	99.7	10	<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
40	<a href="#">c3ccfB</a>	Alignment	not modelled	99.7	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 anabaena variabilis atcc 29413 at 1.90 a resolution
41	<a href="#">d1l1ea</a>	Alignment	not modelled	99.7	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
42	<a href="#">c2p35A</a>	Alignment	not modelled	99.7	10	<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
43	<a href="#">d1r74a</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
44	<a href="#">d2g72a1</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
45	<a href="#">d2fk8a1</a>	Alignment	not modelled	99.7	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
46	<a href="#">c3ofkA</a>	Alignment	not modelled	99.7	14	<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)
47	<a href="#">c3bgvC</a>	Alignment	not modelled	99.7	11	<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
48	<a href="#">c3e23A</a>	Alignment	not modelled	99.7	15	<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 with2 sam from rhodopseudomonas palustris, northeast structural3 genomics consortium target rpr299
49	<a href="#">c3lccA</a>	Alignment	not modelled	99.7	11	<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
50	<a href="#">d1tpya</a>	Alignment	not modelled	99.7	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
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylethanolamine n-

51	<a href="#">c2g8nB_</a>	Alignment	not modelled	99.7	17	methyltransferase; <b>PDBTitle:</b> structure of hpnmt with inhibitor 3-hydroxymethyl-7-(n-4-2 chlorophenylaminosulfonyl)-thiq and adohcy
52	<a href="#">d1xtpa_</a>	Alignment	not modelled	99.7	10	<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
53	<a href="#">c2iipD_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
54	<a href="#">d1y8ca_</a>	Alignment	not modelled	99.6	11	<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="#">c3ocjA_</a>	Alignment	not modelled	99.6	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 possilbe exported protein from bordetella2 parapertussis
56	<a href="#">c3hnrA_</a>	Alignment	not modelled	99.6	13	<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
57	<a href="#">d1ve3a1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
58	<a href="#">c3mq2A_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methyltransferase; <b>PDBTitle:</b> crystal structure of 16s rrna methyltranferase kamb
59	<a href="#">c3d2lC_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exigubacterium sp. 255-15 at 1.90 a resolution
60	<a href="#">c3dtnA_</a>	Alignment	not modelled	99.6	13	<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 26332 from methanosarcina mazel .
61	<a href="#">c3sm3A_</a>	Alignment	not modelled	99.6	21	<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 mazel. northeast structural genomics consortium3 target mar262.
62	<a href="#">d1xvaa_</a>	Alignment	not modelled	99.6	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
63	<a href="#">c3jwgA_</a>	Alignment	not modelled	99.6	7	<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 domain2 of bacterial-cthen1-c
64	<a href="#">c3ggdA_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anabaena variabilis atcc 29413 at 2.11 a resolution
65	<a href="#">c3pfhD_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n
66	<a href="#">c3g2qA_</a>	Alignment	not modelled	99.6	12	<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 mtfa2 complexed with sinefungin
67	<a href="#">c3g5tA_</a>	Alignment	not modelled	99.6	17	<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-methyltransferase2 from yeast
68	<a href="#">d1im8a_</a>	Alignment	not modelled	99.6	13	<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)
69	<a href="#">c3gwzB_</a>	Alignment	not modelled	99.6	13	<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
70	<a href="#">c3e05B_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase (decarboxylating); <b>PDBTitle:</b> crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
71	<a href="#">c3opnA_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hemolysin; <b>PDBTitle:</b> the crystal structure of a putative hemolysin from lactococcus lactis
72	<a href="#">c3i9fB_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative type 11 methyltransferase; <b>PDBTitle:</b> crystal structure of a putative type 11 methyltransferase2 from sulfolobus solfataricus
73	<a href="#">d1xcla_</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
74	<a href="#">c3m70A_</a>	Alignment	not modelled	99.5	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
75	<a href="#">d1ri5a_</a>	Alignment	not modelled	99.5	13	<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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
76	<a href="#">d1wzna1</a>	Alignment	not modelled	99.5	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> encephalitozoon cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
77	<a href="#">c1z3cA_</a>	Alignment	not modelled	99.5	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mgc2408; <b>PDBTitle:</b> human putative methyltransferase mgc2408
78	<a href="#">c2pxxA_</a>	Alignment	not modelled	99.5	21 <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
79	<a href="#">c2ip2B_</a>	Alignment	not modelled	99.5	21 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
80	<a href="#">d2bzga1</a>	Alignment	not modelled	99.5	11 <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
81	<a href="#">d1fp1d2</a>	Alignment	not modelled	99.5	15 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
82	<a href="#">d1d2ha_</a>	Alignment	not modelled	99.5	14 <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
83	<a href="#">c2r3sA_</a>	Alignment	not modelled	99.5	16 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
84	<a href="#">d1zx0a1</a>	Alignment	not modelled	99.5	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 (np_349143.1) from clostridium acetobutylicum at 2.00 a resolution
85	<a href="#">c2p8iA_</a>	Alignment	not modelled	99.5	18 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 7sk snrna methylphosphate capping enzyme; <b>PDBTitle:</b> methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
86	<a href="#">c3g07C_</a>	Alignment	not modelled	99.5	17 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
87	<a href="#">c3cggB_</a>	Alignment	not modelled	99.5	19 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hen1; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain2 of bacterial-avhen1-c
88	<a href="#">c3jwhA_</a>	Alignment	not modelled	99.5	7 <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.
89	<a href="#">c3mczB_</a>	Alignment	not modelled	99.5	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethyltransferase; <b>PDBTitle:</b> crystal structure of streptomyces venezuelae desvi
90	<a href="#">c3bxoA_</a>	Alignment	not modelled	99.5	10 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methylase; <b>PDBTitle:</b> structure of an antibiotic related methyltransferase
91	<a href="#">c3p2kA_</a>	Alignment	not modelled	99.5	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
92	<a href="#">c3bgdB_</a>	Alignment	not modelled	99.5	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
93	<a href="#">d1qzza2</a>	Alignment	not modelled	99.5	12 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
94	<a href="#">d1yzha1</a>	Alignment	not modelled	99.4	13 <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
95	<a href="#">d1kyza2</a>	Alignment	not modelled	99.4	9 <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
96	<a href="#">c3mtiA_</a>	Alignment	not modelled	99.4	9 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
97	<a href="#">d1dusa_</a>	Alignment	not modelled	99.4	13 <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
98	<a href="#">c3lstB_</a>	Alignment	not modelled	99.4	11 <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)
99	<a href="#">c3i53A_</a>	Alignment	not modelled	99.4	13 <b>PDB header:</b> transferase



100	<a href="#">c3dp7B_</a>	Alignment	not modelled	99.4	13	<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
101	<a href="#">c3p9kD_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> caffeic acid o-methyltransferase; <b>PDBTitle:</b> crystal structure of perennial ryegrass lpomt1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
102	<a href="#">c1kyzC_</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> caffeic acid 3-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of caffeic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex
103	<a href="#">d1tw3a2</a>	Alignment	not modelled	99.4	11	<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="#">d1wg8a2</a>	Alignment	not modelled	99.4	20	<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="#">c1yb2A_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0852; <b>PDBTitle:</b> structure of a putative methyltransferase from thermoplasma2 acidophilum.
106	<a href="#">d1yb2a1</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
107	<a href="#">c2pwyB_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (adenine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of a mla58 trna methyltransferase
108	<a href="#">c2yvlB_</a>	Alignment	not modelled	99.4	13	<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
109	<a href="#">c3dxyA_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of ectrmb in complex with sam
110	<a href="#">d2nxc1</a>	Alignment	not modelled	99.4	15	<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
111	<a href="#">c3dmgA_</a>	Alignment	not modelled	99.4	10	<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 rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
112	<a href="#">d1vbfa_</a>	Alignment	not modelled	99.4	13	<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
113	<a href="#">c1xdUa_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein rdmb; <b>PDBTitle:</b> crystal structure of aclacinomycin-10-hydroxylase (rdmb) in complex2 with sinefungin (sfg)
114	<a href="#">d1p1ca_</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
115	<a href="#">c3giwA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function duf574; <b>PDBTitle:</b> crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
116	<a href="#">d1m6ya2</a>	Alignment	not modelled	99.3	12	<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
117	<a href="#">d2i6ga1</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TehB-like
118	<a href="#">d1o54a_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
119	<a href="#">c3lecA_</a>	Alignment	not modelled	99.3	15	<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-rossmann2 superfamily from streptococcus agalactiae to 1.8a
120	<a href="#">c1fpqA_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoliquiritigenin 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase