







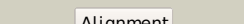

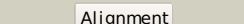

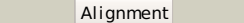
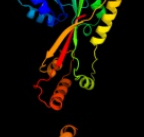
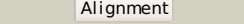

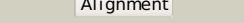

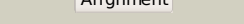

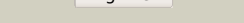





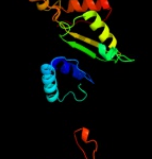
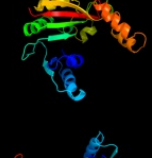
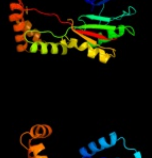
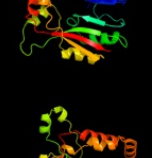
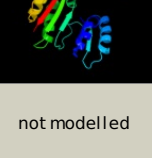


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1vl5a_</a>	 Alignment		100.0	30	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
2	<a href="#">c1vl5B_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> unknown conserved protein bh2331; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution
3	<a href="#">d1xxla_</a>	 Alignment		100.0	33	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
4	<a href="#">d2o57a1</a>	 Alignment		99.9	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
5	<a href="#">c3mggB_</a>	 Alignment		99.9	18	<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
6	<a href="#">c3ccfB_</a>	 Alignment		99.9	17	<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
7	<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
8	<a href="#">c3e7pA_</a>	 Alignment		99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
9	<a href="#">c3ujcA_</a>	 Alignment		99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase; <b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
10	<a href="#">c2fk8A_</a>	 Alignment		99.8	11	<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
11	<a href="#">c3f4kA_</a>	 Alignment		99.8	12	<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.

12	<a href="#">c3g5tA_</a>	Alignment		99.8	20	<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
13	<a href="#">d1kpia_</a>	Alignment		99.8	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
14	<a href="#">c3cc8A_</a>	Alignment		99.8	16	<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
15	<a href="#">c3busB_</a>	Alignment		99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
16	<a href="#">d1jqea_</a>	Alignment		99.8	9	<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="#">c2p7iB_</a>	Alignment		99.8	16	<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
18	<a href="#">d2gh1a1</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> BC2162-like
19	<a href="#">d1kpga_</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> Mycolic acid cyclopropane synthase
20	<a href="#">d2fk8a1</a>	Alignment		99.8	11	<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
21	<a href="#">d2p7ia1</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> UbiE/COQ5-like
22	<a href="#">c2p35A_</a>	Alignment	not modelled	99.8	16	<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
23	<a href="#">d1nkva_</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> Hypothetical Protein YjHP
24	<a href="#">d2ex4a1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> AD-003 protein-like
25	<a href="#">d1tpya_</a>	Alignment	not modelled	99.8	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
26	<a href="#">c3dliB_</a>	Alignment	not modelled	99.8	10	<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 archaeglobus fulgidus
27	<a href="#">d1l1ea_</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> Mycolic acid cyclopropane synthase
28	<a href="#">c3bkxB_</a>	Alignment	not modelled	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
29	<a href="#">c3lccA</a>	Alignment	not modelled	99.8	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyl chloride transferase; <b>PDBTitle:</b> structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
30	<a href="#">c3h2bB</a>	Alignment	not modelled	99.8	16 <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
31	<a href="#">c3ociA</a>	Alignment	not modelled	99.8	17 <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
32	<a href="#">c3l8dA</a>	Alignment	not modelled	99.8	19 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus2 thuringiensis
33	<a href="#">c3dlcA</a>	Alignment	not modelled	99.8	23 <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
34	<a href="#">dlr74a</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> Glycine N-methyltransferase
35	<a href="#">dlxtpa</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
36	<a href="#">c3g2qA</a>	Alignment	not modelled	99.7	21 <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
37	<a href="#">dlyzha1</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> TrmB-like
38	<a href="#">dlim8a</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> Hypothetical protein HI0319 (YecO)
39	<a href="#">dlxvaa</a>	Alignment	not modelled	99.7	23 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
40	<a href="#">d2a14a1</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> Arylamine N-methyltransferase
41	<a href="#">c3mq2A</a>	Alignment	not modelled	99.7	19 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methyltransferase; <b>PDBTitle:</b> crystal structure of 16s rrna methyltransferase kamb
42	<a href="#">c3bgvC</a>	Alignment	not modelled	99.7	18 <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
43	<a href="#">d2avna1</a>	Alignment	not modelled	99.7	17 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
44	<a href="#">d2fcaa1</a>	Alignment	not modelled	99.7	13 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
45	<a href="#">c2gs9A</a>	Alignment	not modelled	99.7	21 <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
46	<a href="#">dlri5a</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> mRNA cap (Guanine N-7) methyltransferase
47	<a href="#">c3sm3A</a>	Alignment	not modelled	99.7	19 <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.
48	<a href="#">c3e23A</a>	Alignment	not modelled	99.7	12 <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="#">clz3cA</a>	Alignment	not modelled	99.7	15 <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
50	<a href="#">c3m70A</a>	Alignment	not modelled	99.7	16 <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
51	<a href="#">c3e8sA</a>	Alignment	not modelled	99.7	17 <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
52	<a href="#">dlve3a1</a>	Alignment	not modelled	99.7	29 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases

						<b>Family:</b> CAC2371-like
53	<a href="#">c3ou7A_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
54	<a href="#">c3ku1E_</a>	Alignment	not modelled	99.7	14	<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, a2 putative trna (m1a22) methyltransferase, in complex with s-3 adenosyl-l-methionine
55	<a href="#">c3lecA_</a>	Alignment	not modelled	99.7	11	<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
56	<a href="#">d1d2ha_</a>	Alignment	not modelled	99.7	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
57	<a href="#">c2iipD_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
58	<a href="#">c3hnrA_</a>	Alignment	not modelled	99.7	17	<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
59	<a href="#">c3mtiA_</a>	Alignment	not modelled	99.7	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
60	<a href="#">c3g07C_</a>	Alignment	not modelled	99.7	15	<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)
61	<a href="#">c3g5lA_</a>	Alignment	not modelled	99.6	18	<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
62	<a href="#">d1pjza_</a>	Alignment	not modelled	99.6	5	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
63	<a href="#">d1xcla_</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> Guanidinoacetate methyltransferase
64	<a href="#">c3ofkA_</a>	Alignment	not modelled	99.6	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)
65	<a href="#">c3dtnA_</a>	Alignment	not modelled	99.6	17	<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 .
66	<a href="#">d2bzga1</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> Thiopurine S-methyltransferase
67	<a href="#">c3gnlB_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmof2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (lmof2365_1472) from2 listeria monocytogenes serotype 4b
68	<a href="#">c3merA_</a>	Alignment	not modelled	99.6	19	<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
69	<a href="#">c3bgdB_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
70	<a href="#">c3ndjA_</a>	Alignment	not modelled	99.6	12	<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
71	<a href="#">d1y8ca_</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
72	<a href="#">c3ggdA_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anabaena variabilis atcc 29413 at 2.11 a resolution
73	<a href="#">d1zx0a1</a>	Alignment	not modelled	99.6	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="#">c3dxyA_</a>	Alignment	not modelled	99.6	15	<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
75	<a href="#">c2p8jA_</a>	Alignment	not modelled	99.6	22	<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

76	<a href="#">c3pfhD</a>	Alignment	not modelled	99.6	17	<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
77	<a href="#">c3egeA</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase from antibiotic biosynthesis <b>PDBTitle:</b> crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution
78	<a href="#">c3opnA</a>	Alignment	not modelled	99.6	16	<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
79	<a href="#">c3cggB</a>	Alignment	not modelled	99.6	20	<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
80	<a href="#">c3bxoA</a>	Alignment	not modelled	99.6	20	<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
81	<a href="#">c2pxxA</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mgc2408; <b>PDBTitle:</b> human putative methyltransferase mgc2408
82	<a href="#">c3m33B</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein from2 deinococcus radiodurans r1
83	<a href="#">d1dusa</a>	Alignment	not modelled	99.6	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
84	<a href="#">c3jwgA</a>	Alignment	not modelled	99.6	15	<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
85	<a href="#">d1p91a</a>	Alignment	not modelled	99.6	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
86	<a href="#">c3dh0B</a>	Alignment	not modelled	99.6	20	<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
87	<a href="#">d1wzna1</a>	Alignment	not modelled	99.6	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
88	<a href="#">c3grzA</a>	Alignment	not modelled	99.6	18	<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
89	<a href="#">d1vlma</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
90	<a href="#">c3bkWB</a>	Alignment	not modelled	99.5	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
91	<a href="#">c3d21C</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exiguobacterium sp. 255-15 at 1.90 a resolution
92	<a href="#">c3eeyL</a>	Alignment	not modelled	99.5	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
93	<a href="#">c3p2kA</a>	Alignment	not modelled	99.5	19	<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
94	<a href="#">d1p1ca</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
95	<a href="#">d1yb2a1</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> tRNA(1-methyladenosine) methyltransferase-like
96	<a href="#">c1yb2A</a>	Alignment	not modelled	99.5	16	<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.
97	<a href="#">d2g72a1</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> Arylamine N-methyltransferase
98	<a href="#">d1af7a2</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> Chemotaxis receptor methyltransferase CheR, C-terminal domain
99	<a href="#">c3ckkA</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of human methyltransferase-like protein 1
						<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases

100	<a href="#">d2nxca1</a>	Alignment	not modelled	99.5	18	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ribosomal protein L11 methyltransferase PrmA
101	<a href="#">d1l3ia</a>	Alignment	not modelled	99.5	25	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Precorrin-6Y methyltransferase (CbiT)
102	<a href="#">c2g8nB</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylethanolamine n-methyltransferase; <b>PDBTitle:</b> structure of hpnmt with inhibitor 3-hydroxymethyl-7-(n-4-2 chlorophenylaminosulfonyl)-thiq and adohcy
103	<a href="#">c3e05B</a>	Alignment	not modelled	99.5	16	<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
104	<a href="#">c2vduE</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> structure of trm8-trm82, the yeast trna m7g methylation2 complex
105	<a href="#">d1m6ya2</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> MraW-like putative methyltransferases
106	<a href="#">c2yvlB</a>	Alignment	not modelled	99.5	12	<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
107	<a href="#">d2i6ga1</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TehB-like
108	<a href="#">d1vbfA</a>	Alignment	not modelled	99.5	19	<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
109	<a href="#">c3lbfC</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
110	<a href="#">d2b3ta1</a>	Alignment	not modelled	99.5	18	<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
111	<a href="#">c3dmgA</a>	Alignment	not modelled	99.5	17	<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="#">c3lpmA</a>	Alignment	not modelled	99.5	16	<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
113	<a href="#">c2ip2B</a>	Alignment	not modelled	99.5	11	<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
114	<a href="#">d2igta1</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> hypothetical RNA methyltransferase
115	<a href="#">c3gwzB</a>	Alignment	not modelled	99.5	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
116	<a href="#">d1g8sa</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> Fibrillarin homologue
117	<a href="#">c3evzA</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
118	<a href="#">d1jg1a</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
119	<a href="#">c3i9fB</a>	Alignment	not modelled	99.4	20	<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
120	<a href="#">d1dl5a1</a>	Alignment	not modelled	99.4	18	<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