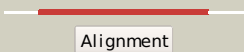

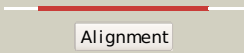







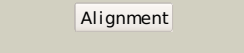

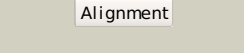

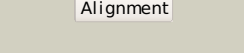



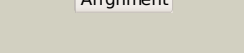

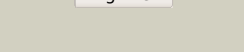












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3lccA_</a>	 Alignment		98.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyl chloride transferase; <b>PDBTitle:</b> structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
2	<a href="#">c3ou7A_</a>	 Alignment		98.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
3	<a href="#">c3d2lC_</a>	 Alignment		98.3	13	<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
4	<a href="#">c3l8dA_</a>	 Alignment		98.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus2 thuringiensis
5	<a href="#">c3ofkA_</a>	 Alignment		98.2	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)
6	<a href="#">d1wzna1</a>	 Alignment		98.2	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
7	<a href="#">d1tpya_</a>	 Alignment		98.1	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
8	<a href="#">d2a14a1</a>	 Alignment		98.1	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
9	<a href="#">c1z3cA_</a>	 Alignment		98.1	17	<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
10	<a href="#">c3h2bB_</a>	 Alignment		98.1	15	<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
11	<a href="#">d1ri5a_</a>	 Alignment		98.0	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> mRNA cap (Guanine N-7) methyltransferase

12	<a href="#">d1pjza_</a>	Alignment		98.0	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
13	<a href="#">d1kpga_</a>	Alignment		98.0	19	<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="#">c3g2qA_</a>	Alignment		98.0	13	<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
15	<a href="#">c3ccfB_</a>	Alignment		98.0	18	<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
16	<a href="#">c3bxoA_</a>	Alignment		97.9	15	<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
17	<a href="#">c3e23A_</a>	Alignment		97.9	18	<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
18	<a href="#">d2o57a1</a>	Alignment		97.9	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
19	<a href="#">c3m70A_</a>	Alignment		97.9	26	<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 homolog from haemophilus influenzae
20	<a href="#">c3bgvC_</a>	Alignment		97.9	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
21	<a href="#">d2ex4a1</a>	Alignment	not modelled	97.9	23	<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
22	<a href="#">d1kpia_</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
23	<a href="#">d1y8ca_</a>	Alignment	not modelled	97.8	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
24	<a href="#">c3jwgA_</a>	Alignment	not modelled	97.8	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 domain2 of bacterial-cthen1-c
25	<a href="#">c3bgdB_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
26	<a href="#">d1xtpa_</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> AD-003 protein-like
27	<a href="#">c3dtnA_</a>	Alignment	not modelled	97.8	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 mazei .
28	<a href="#">d2i6ga1</a>	Alignment	not modelled	97.7	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TehB-like
						<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases

29	<a href="#">d2bzga1</a>	Alignment	not modelled	97.7	13	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
30	<a href="#">c3cc8A_</a>	Alignment	not modelled	97.7	14	<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
31	<a href="#">c2fk8A_</a>	Alignment	not modelled	97.7	14	<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
32	<a href="#">d1xxla_</a>	Alignment	not modelled	97.7	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
33	<a href="#">d2fk8a1</a>	Alignment	not modelled	97.7	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
34	<a href="#">c3dh0B_</a>	Alignment	not modelled	97.7	14	<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
35	<a href="#">c1x1aA_</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> crtf-related protein; <b>PDBTitle:</b> crystal structure of bchu complexed with s-adenosyl-l-methionine
36	<a href="#">d1vl5a_</a>	Alignment	not modelled	97.7	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
37	<a href="#">c2q8nB_</a>	Alignment	not modelled	97.6	23	<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
38	<a href="#">c1vl5B_</a>	Alignment	not modelled	97.6	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
39	<a href="#">c3merA_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> slr1183 protein; <b>PDBTitle:</b> crystal structure of the methyltransferase slr1183 from2 synechocystis sp. pcc 6803, northeast structural genomics3 consortium target sgr145
40	<a href="#">c2p8jA_</a>	Alignment	not modelled	97.6	13	<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
41	<a href="#">c3ndjA_</a>	Alignment	not modelled	97.6	14	<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
42	<a href="#">c3sm3A_</a>	Alignment	not modelled	97.6	18	<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.
43	<a href="#">c3lstB_</a>	Alignment	not modelled	97.6	12	<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
44	<a href="#">c3i9fB_</a>	Alignment	not modelled	97.5	22	<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 sulfobolus solfataricus
45	<a href="#">d1im8a_</a>	Alignment	not modelled	97.5	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein HI0319 (YecO)
46	<a href="#">c2yr0A_</a>	Alignment	not modelled	97.5	15	<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
47	<a href="#">c3dp7B_</a>	Alignment	not modelled	97.5	11	<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
48	<a href="#">c3pfhD_</a>	Alignment	not modelled	97.5	13	<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
49	<a href="#">c3dliB_</a>	Alignment	not modelled	97.5	16	<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
50	<a href="#">c2gs9A_</a>	Alignment	not modelled	97.4	13	<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 thermophilus hb8
51	<a href="#">c2pxxA_</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mgc2408; <b>PDBTitle:</b> human putative methyltransferase mgc2408
52	<a href="#">d1jqea_</a>	Alignment	not modelled	97.4	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
53	<a href="#">c3i53A_</a>	Alignment	not modelled	97.4	16	<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)
54	<a href="#">c3hnrA</a>	Alignment	not modelled	97.4	14	<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
55	<a href="#">c3bkxB</a>	Alignment	not modelled	97.4	10	<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
56	<a href="#">c3ujcA</a>	Alignment	not modelled	97.4	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
57	<a href="#">d2g72a1</a>	Alignment	not modelled	97.4	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
58	<a href="#">c3ocjA</a>	Alignment	not modelled	97.4	12	<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
59	<a href="#">d1vlma</a>	Alignment	not modelled	97.4	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
60	<a href="#">c2iipD</a>	Alignment	not modelled	97.3	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
61	<a href="#">d2p7ia1</a>	Alignment	not modelled	97.3	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
62	<a href="#">d2avna1</a>	Alignment	not modelled	97.3	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
63	<a href="#">c3gwzB</a>	Alignment	not modelled	97.3	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
64	<a href="#">d1r74a</a>	Alignment	not modelled	97.3	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
65	<a href="#">c2vdwA</a>	Alignment	not modelled	97.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vaccinia virus capping enzyme d1 subunit; <b>PDBTitle:</b> guanosine n7 methyl-transferase sub-complex (d1-d12) of the2 vaccinia virus mrna capping enzyme
66	<a href="#">d1ve3a1</a>	Alignment	not modelled	97.2	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
67	<a href="#">c2p7iB</a>	Alignment	not modelled	97.2	13	<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
68	<a href="#">d1nkva</a>	Alignment	not modelled	97.1	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
69	<a href="#">c3ggdA</a>	Alignment	not modelled	97.1	17	<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
70	<a href="#">c3e8sA</a>	Alignment	not modelled	97.1	18	<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
71	<a href="#">d1d2ha</a>	Alignment	not modelled	97.1	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
72	<a href="#">d1l1ea</a>	Alignment	not modelled	97.0	19	<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
73	<a href="#">d1qzza2</a>	Alignment	not modelled	97.0	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
74	<a href="#">c1kyzC</a>	Alignment	not modelled	97.0	13	<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
75	<a href="#">d2gh1a1</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
76	<a href="#">c3e7pA</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482

77	<a href="#">c3busB_</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
78	<a href="#">c3mczB_</a>	Alignment	not modelled	96.9	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.
79	<a href="#">d1xvaa_</a>	Alignment	not modelled	96.9	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
80	<a href="#">c3cggB_</a>	Alignment	not modelled	96.7	19	<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
81	<a href="#">c3mtiA_</a>	Alignment	not modelled	96.7	13	<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
82	<a href="#">d2nxca1</a>	Alignment	not modelled	96.7	16	<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
83	<a href="#">c3g5lA_</a>	Alignment	not modelled	96.6	16	<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
84	<a href="#">c2p35A_</a>	Alignment	not modelled	96.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-aconitate 2-methyltransferase; <b>PDBTitle:</b> crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
85	<a href="#">c3dlcA_</a>	Alignment	not modelled	96.5	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
86	<a href="#">c1xdUA_</a>	Alignment	not modelled	96.5	16	<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)
87	<a href="#">c2ip2B_</a>	Alignment	not modelled	96.4	8	<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
88	<a href="#">c3p9kD_</a>	Alignment	not modelled	96.4	15	<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
89	<a href="#">c3mggB_</a>	Alignment	not modelled	96.3	19	<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
90	<a href="#">c3opnA_</a>	Alignment	not modelled	96.3	20	<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
91	<a href="#">c2r3sA_</a>	Alignment	not modelled	96.2	11	<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
92	<a href="#">c3bkwB_</a>	Alignment	not modelled	96.2	13	<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
93	<a href="#">c2zfuA_</a>	Alignment	not modelled	96.1	20	<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
94	<a href="#">c3f4kA_</a>	Alignment	not modelled	96.0	16	<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.
95	<a href="#">d1kyza2</a>	Alignment	not modelled	95.9	12	<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
96	<a href="#">c2pjda_</a>	Alignment	not modelled	95.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase c; <b>PDBTitle:</b> crystal structure of 16s rrna methyltransferase rsmc
97	<a href="#">d1fp1d2</a>	Alignment	not modelled	95.8	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
98	<a href="#">d1dusa_</a>	Alignment	not modelled	95.7	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
99	<a href="#">d1af7a2</a>	Alignment	not modelled	95.6	16	<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
100	<a href="#">d1p91a_</a>	Alignment	not modelled	95.6	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases



						<b>Family:</b> rRNA methyltransferase RlMA
101	<a href="#">c3jwhA_</a>	Alignment	not modelled	95.6	8	<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
102	<a href="#">d1tw3a2</a>	Alignment	not modelled	95.5	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
103	<a href="#">c3ku1E_</a>	Alignment	not modelled	95.3	13	<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
104	<a href="#">c1tw3A_</a>	Alignment	not modelled	95.2	19	<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-methyltransferase2 (dnrk) in complex with s-adenosyl-l-homocystein (sah) and3 4-methoxy-e-rhodomycin t (m-et)
105	<a href="#">d1fp2a2</a>	Alignment	not modelled	95.2	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
106	<a href="#">c3lecA_</a>	Alignment	not modelled	95.2	9	<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
107	<a href="#">c1fpqA_</a>	Alignment	not modelled	95.2	17	<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
108	<a href="#">c3egeA_</a>	Alignment	not modelled	95.2	18	<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
109	<a href="#">d1wg8a2</a>	Alignment	not modelled	95.1	14	<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
110	<a href="#">c3dmgA_</a>	Alignment	not modelled	95.1	19	<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
111	<a href="#">c3ckkA_</a>	Alignment	not modelled	94.9	12	<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
112	<a href="#">c3dxyA_</a>	Alignment	not modelled	94.9	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
113	<a href="#">c3g07C_</a>	Alignment	not modelled	94.9	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)
114	<a href="#">c3mq2A_</a>	Alignment	not modelled	94.9	9	<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
115	<a href="#">c3gnlB_</a>	Alignment	not modelled	94.7	10	<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
116	<a href="#">d1yzha1</a>	Alignment	not modelled	94.7	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
117	<a href="#">c3grzA_</a>	Alignment	not modelled	94.7	12	<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
118	<a href="#">d1ilna_</a>	Alignment	not modelled	94.5	23	<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="#">d1zx0a1</a>	Alignment	not modelled	94.4	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
120	<a href="#">d1m6ya2</a>	Alignment	not modelled	93.9	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> MraW-like putative methyltransferases