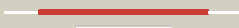



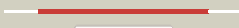





























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dxyA_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of ectrmB in complex with sam
2	<a href="#">dlyzha1</a>	 Alignment		100.0	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
3	<a href="#">d2fcaa1</a>	 Alignment		100.0	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
4	<a href="#">c3ckkA_</a>	 Alignment		100.0	18	<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
5	<a href="#">c2vduE_</a>	 Alignment		100.0	23	<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
6	<a href="#">c3p2kA_</a>	 Alignment		99.9	14	<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
7	<a href="#">d1yb2a1</a>	 Alignment		99.8	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
8	<a href="#">c1yb2A_</a>	 Alignment		99.8	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.
9	<a href="#">c3g5tA_</a>	 Alignment		99.8	12	<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
10	<a href="#">c3mq2A_</a>	 Alignment		99.8	20	<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
11	<a href="#">c3e05B_</a>	 Alignment		99.8	13	<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

12	<a href="#">c3mtiA_</a>	Alignment		99.8	13	<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
13	<a href="#">d1o54a_</a>	Alignment		99.8	17	<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
14	<a href="#">d1m6ya2</a>	Alignment		99.8	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
15	<a href="#">c2fk8A_</a>	Alignment		99.8	12	<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
16	<a href="#">c3eeyl_</a>	Alignment		99.7	12	<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
17	<a href="#">c3mb5A_</a>	Alignment		99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of p. abyssi trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine
18	<a href="#">c3mggB_</a>	Alignment		99.7	22	<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
19	<a href="#">c3e7pA_</a>	Alignment		99.7	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
20	<a href="#">c2pwyB_</a>	Alignment		99.7	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 m1a58 trna methyltransferase
21	<a href="#">d1xvaa_</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> Glycine N-methyltransferase
22	<a href="#">c3bkxB_</a>	Alignment	not modelled	99.7	22	<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
23	<a href="#">c3ku1E_</a>	Alignment	not modelled	99.7	10	<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
24	<a href="#">d1r74a_</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> Glycine N-methyltransferase
25	<a href="#">c3gnlB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmf2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (lmf2365_1472) from2 listeria monocytogenes serotype 4b
26	<a href="#">c2gpyB_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of putative o-methyltransferase from bacillus2 halodurans
27	<a href="#">d2b3ta1</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> N5-glutamine methyltransferase, HemK <b>PDB header:</b> structure genomics, unknown function

28	<a href="#">c3lecA</a>	Alignment	not modelled	99.7	12	<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
29	<a href="#">d1kpga</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> Mycolic acid cyclopropane synthase
30	<a href="#">c2yvlB</a>	Alignment	not modelled	99.7	16	<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
31	<a href="#">d1zx0a1</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> Guanidinoacetate methyltransferase
32	<a href="#">d1l1ea</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> Mycolic acid cyclopropane synthase
33	<a href="#">c3f4kA</a>	Alignment	not modelled	99.7	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.
34	<a href="#">d2fk8a1</a>	Alignment	not modelled	99.7	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
35	<a href="#">d2o57a1</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> Mycolic acid cyclopropane synthase
36	<a href="#">c2ozvA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0636; <b>PDBTitle:</b> crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
37	<a href="#">d1i9ga</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> tRNA(1-methyladenosine) methyltransferase-like
38	<a href="#">c1vl5B</a>	Alignment	not modelled	99.7	12	<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="#">d1vl5a</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> UbiE/COQ5-like
40	<a href="#">c3g8aF</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase g; <b>PDBTitle:</b> t. thermophilus 16s rrna g527 methyltransferase in complex with adohcy2 in space group p61
41	<a href="#">d1ri5a</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> mRNA cap (Guanine N-7) methyltransferase
42	<a href="#">d1tpya</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
43	<a href="#">c1z3cA</a>	Alignment	not modelled	99.7	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
44	<a href="#">d1xdza</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> Glucose-inhibited division protein B (GidB)
45	<a href="#">d1p91a</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA methyltransferase R1mA
46	<a href="#">c2pjda</a>	Alignment	not modelled	99.7	18	<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
47	<a href="#">d1l3ia</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> Precorrin-6Y methyltransferase (CbiT)
48	<a href="#">c3hm2G</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase; <b>PDBTitle:</b> crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
49	<a href="#">d1xcla</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> Guanidinoacetate methyltransferase
50	<a href="#">d1kpia</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> Mycolic acid cyclopropane synthase
51	<a href="#">d1xxla</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> UbiE/COQ5-like
52	<a href="#">c2yr0A</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha0223; <b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
						<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases

53	<a href="#">d1d2ha_</a>	Alignment	not modelled	99.7	10	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
54	<a href="#">d1jsxa_</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> Glucose-inhibited division protein B (GidB)
55	<a href="#">d2ex4a1</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> AD-003 protein-like
56	<a href="#">d1dl5a1</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> Protein-L-isoaspartyl O-methyltransferase
57	<a href="#">d1dusa_</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> Hypothetical protein MJ0882
58	<a href="#">c2yxdA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cobalt-precorrin-6y c(15)-methyltransferase <b>PDBTitle:</b> crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbt)
59	<a href="#">c3lpmA_</a>	Alignment	not modelled	99.7	13	<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
60	<a href="#">d1p1ca_</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> Guanidinoacetate methyltransferase
61	<a href="#">c3ocjA_</a>	Alignment	not modelled	99.7	15	<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
62	<a href="#">c3evzA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal strucure of methyltransferase from pyrococcus furiosus
63	<a href="#">c3bgvC_</a>	Alignment	not modelled	99.7	13	<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
64	<a href="#">d1nt2a_</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> Fibrillarin homologue
65	<a href="#">c3njrB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y methylase; <b>PDBTitle:</b> crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
66	<a href="#">c3lccA_</a>	Alignment	not modelled	99.6	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
67	<a href="#">c3g07C_</a>	Alignment	not modelled	99.6	12	<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)
68	<a href="#">d2gh1a1</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> BC2162-like
69	<a href="#">c3ggdA_</a>	Alignment	not modelled	99.6	9	<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="#">d2bzga1</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> Thiopurine S-methyltransferase
71	<a href="#">d1g8sa_</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> Fibrillarin homologue
72	<a href="#">c2yxlA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 450aa long hypothetical fmu protein; <b>PDBTitle:</b> crystal structure of ph0851
73	<a href="#">d1nkva_</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein Yjhp
74	<a href="#">c2ipxA_</a>	Alignment		99.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna 2'-o-methyltransferase fibrillarin; <b>PDBTitle:</b> human fibrillarin
75	<a href="#">d1susa1</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
76	<a href="#">c3c3yB_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum
						<b>PDB header:</b> transferase

77	<a href="#">c2yxeB_</a>	Alignment	not modelled	99.6	21	<b>Chain:</b> B: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> crystal structure of l-isoaspartyl protein carboxyl methyltransferase
78	<a href="#">c3m70A_</a>	Alignment	not modelled	99.6	13	<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
79	<a href="#">dljqea_</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> Histamine methyltransferase
80	<a href="#">c3dmgA_</a>	Alignment	not modelled	99.6	18	<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
81	<a href="#">c3tfwB_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
82	<a href="#">c3dlcA_</a>	Alignment	not modelled	99.6	16	<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
83	<a href="#">d2b25a1</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> tRNA(1-methyladenosine) methyltransferase-like
84	<a href="#">dlpjza_</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
85	<a href="#">c3grzA_</a>	Alignment	not modelled	99.6	11	<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
86	<a href="#">dlnv8a_</a>	Alignment	not modelled	99.6	20	<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
87	<a href="#">c3fpjA_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of e81q mutant of mnas in complex with s-2 adenosylmethionine
88	<a href="#">c3cc8A_</a>	Alignment	not modelled	99.6	12	<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
89	<a href="#">c3ntvB_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nw1564 protein; <b>PDBTitle:</b> crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus
90	<a href="#">c3lbfC_</a>	Alignment	not modelled	99.6	17	<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
91	<a href="#">c3id5F_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase/ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> fibrillarin-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of sulfobolus solfataricus c/d rnp assembled with2 nop5, fibrillarin, l7ae and a split half c/d rna
92	<a href="#">c3gvyA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> crystal structure of a probable spermidine synthase from2 corynebacterium glutamicum atcc 13032
93	<a href="#">c1wxwA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1280; <b>PDBTitle:</b> crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophilus hb8
94	<a href="#">dljgla_</a>	Alignment	not modelled	99.6	20	<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
95	<a href="#">dlve3a1</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
96	<a href="#">dlvbfa_</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> Protein-L-isoaspartyl O-methyltransferase
97	<a href="#">d2as0a2</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> hypothetical RNA methyltransferase
98	<a href="#">c3jwgA_</a>	Alignment	not modelled	99.6	13	<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
99	<a href="#">c3cggB_</a>	Alignment	not modelled	99.6	11	<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
100	<a href="#">dlsgqa2</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> NOL1/NOP2/sun
						<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases



101	<a href="#">d2igta1</a>	Alignment	not modelled	99.6	11	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
102	<a href="#">c1dl5A</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> protein-l-isoaspartate o-methyltransferase
103	<a href="#">c3p9nA</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible methyltransferase (methylase); <b>PDBTitle:</b> rv2966c of m. tuberculosis is a rsmd-like methyltransferase
104	<a href="#">d1wxxa2</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> hypothetical RNA methyltransferase
105	<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
106	<a href="#">d1l1na</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> Protein-L-isoaspartyl O-methyltransferase
107	<a href="#">c3ujcA</a>	Alignment	not modelled	99.6	15	<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
108	<a href="#">d1g8aa</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> Fibrillarin homologue
109	<a href="#">d1prya</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> Fibrillarin homologue
110	<a href="#">c2pbfA</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase beta-aspartate <b>PDBTitle:</b> crystal structure of a putative protein-l-isoaspartate o-2 methyltransferase beta-aspartate methyltransferase (pcmt) from3 plasmodium falciparum in complex with s-adenosyl-l-homocysteine
111	<a href="#">c3e23A</a>	Alignment	not modelled	99.6	13	<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
112	<a href="#">c3c0kB</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0064 protein yccw; <b>PDBTitle:</b> crystal structure of a ribosomal rna methyltransferase
113	<a href="#">c3ofkA</a>	Alignment	not modelled	99.6	15	<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)
114	<a href="#">c3duwB</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase, putative; <b>PDBTitle:</b> crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah
115	<a href="#">c1sqgA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sun protein; <b>PDBTitle:</b> the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
116	<a href="#">c3lcvB</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sisomicin-gentamicin resistance methylase sgml; <b>PDBTitle:</b> crystal structure of antibiotic related methyltransferase
117	<a href="#">c3cbgA</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> functional and structural characterization of a2 cationdependent o-methyltransferase from the3 cyanobacterium synechocystis sp. strain pcc 6803
118	<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 mazei .
119	<a href="#">c3dr5A</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of the q8nrd3_corgl protein from2 corynebacterium glutamicum. northeast structural genomics3 consortium target cgr117.
120	<a href="#">d2nxca1</a>	Alignment	not modelled	99.5	20	<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