



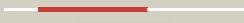




























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3lduA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methylase; <b>PDBTitle:</b> the crystal structure of a possible methylase from2 clostridium difficile 630.
2	<a href="#">c3k0bA_</a>	 Alignment		100.0	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted n6-adenine-specific dna methylase; <b>PDBTitle:</b> crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365
3	<a href="#">c3ldgA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.472; <b>PDBTitle:</b> crystal structure of smu.472, a putative methyltransferase complexed2 with sah
4	<a href="#">c2b78A_</a>	 Alignment		100.0	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein smu.776; <b>PDBTitle:</b> a putative sam-dependent methyltransferase from2 streptococcus mutans
5	<a href="#">d2b78a2</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> hypothetical RNA methyltransferase
6	<a href="#">c3c0kB_</a>	 Alignment		100.0	26	<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
7	<a href="#">d1wxxa2</a>	 Alignment		100.0	31	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
8	<a href="#">c2as0A_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1915; <b>PDBTitle:</b> crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
9	<a href="#">d2as0a2</a>	 Alignment		100.0	25	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
10	<a href="#">c1wxwA_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tth1280; <b>PDBTitle:</b> crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophilus hb8
11	<a href="#">d2igta1</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> hypothetical RNA methyltransferase

12	<a href="#">dlo9ga_</a>	Alignment		100.0	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA methyltransferase AviRa
13	<a href="#">c2yx1A_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mj0883; <b>PDBTitle:</b> crystal structure of m.jannaschii trna m1g37 methyltransferase
14	<a href="#">d2frna1</a>	Alignment		99.9	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Met-10+ protein-like
15	<a href="#">c3a26A_</a>	Alignment		99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0793; <b>PDBTitle:</b> crystal structure of p. horikoshii tyw2 in complex with mesado
16	<a href="#">d1nv8a_</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> N5-glutamine methyltransferase, HemK
17	<a href="#">c3axtA_</a>	Alignment		99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable n(2),n(2)-dimethylguanosine trna methyltransferase <b>PDBTitle:</b> complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
18	<a href="#">c3a27A_</a>	Alignment		99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj1557; <b>PDBTitle:</b> crystal structure of m. jannaschii tyw2 in complex with2 adomet
19	<a href="#">d1uwva2</a>	Alignment		99.8	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> (Uracil-5-)-methyltransferase
20	<a href="#">d2dula1</a>	Alignment		99.8	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TRM1-like
21	<a href="#">c3bt7A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna (uracil-5-)-methyltransferase; <b>PDBTitle:</b> structure of e. coli 5-methyluridine methyltransferase trma2 in complex with 19 nucleotide t-arm analogue
22	<a href="#">c1uwvA_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 23s rrna (uracil-5-)-methyltransferase ruma; <b>PDBTitle:</b> crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
23	<a href="#">d2ifta1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
24	<a href="#">d2fhpa1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
25	<a href="#">d2fpoa1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
26	<a href="#">c2vs1A_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rna methyltransferase pyrab10780; <b>PDBTitle:</b> the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine
27	<a href="#">c3a4tA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase mj0026; <b>PDBTitle:</b> crystal structure of atm4 from m.jannaschii with sinefungin

28	<a href="#">c3p9nA</a>	Alignment	not modelled	99.7	21	<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
29	<a href="#">d2b3ta1</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> N5-glutamine methyltransferase, HemK
30	<a href="#">d2esra1</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> YhhF-like
31	<a href="#">c2esrB</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> conserved hypothetical protein- streptococcus pyogenes
32	<a href="#">d1wy7a1</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> Ta1320-like
33	<a href="#">c3dmga</a>	Alignment	not modelled	99.7	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
34	<a href="#">d1sqga2</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> NOL1/NOP2/sun
35	<a href="#">c3c6kC</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> spermine synthase; <b>PDBTitle:</b> crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
36	<a href="#">d1ws6a1</a>	Alignment	not modelled	99.6	25	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
37	<a href="#">c3evzA</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal strucure of methyltransferase from pyrococcus furiosus
38	<a href="#">c3egiA</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine2 synthase tgs1 bound to m7gpppa (inactive form)
39	<a href="#">c3lpmA</a>	Alignment	not modelled	99.6	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
40	<a href="#">d2nxca1</a>	Alignment	not modelled	99.6	22	<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
41	<a href="#">c3grzA</a>	Alignment	not modelled	99.6	23	<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
42	<a href="#">d1dusa</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> Hypothetical protein MJ0882
43	<a href="#">c3gdhC</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine2 synthase 1 (tgs1) bound to m7gtp and adenosyl-homocysteine3 (active form)
44	<a href="#">c2r6za</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0341 protein in rsp 3' region; <b>PDBTitle:</b> crystal structure of the sam-dependent methyltransferase2 ngo1261 from neisseria gonorrhoeae, northeast structural3 genomics consortium target ngr48
45	<a href="#">c2yxlA</a>	Alignment	not modelled	99.5	13	<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
46	<a href="#">c3khkA</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system <b>PDBTitle:</b> crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazei.
47	<a href="#">d2ar0a1</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> N-6 DNA Methylase-like
48	<a href="#">d1ixka</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> NOL1/NOP2/sun
49	<a href="#">d2okca1</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> N-6 DNA Methylase-like
50	<a href="#">c3lkdB</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction-modification system <b>PDBTitle:</b> crystal structure of the type i restriction-modification2 system methyltransferase subunit from streptococcus3 thermophilus, northeast structural genomics consortium4 target sur80
51	<a href="#">c2ozvA</a>	Alignment	not modelled	99.5	17	<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.
						<b>PDB header:</b> transferase

52	<a href="#">c2pjdA_</a>	Alignment	not modelled	99.5	20	<b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase c; <b>PDBTitle:</b> crystal structure of 16s rrna methyltransferase rsmc
53	<a href="#">d1l3ia_</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> Precorin-6Y methyltransferase (CbiT)
54	<a href="#">c3q87B_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> transferase activator/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n6 adenine specific dna methylase; <b>PDBTitle:</b> structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
55	<a href="#">c1sqgA_</a>	Alignment	not modelled	99.4	18	<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
56	<a href="#">c3e05B_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorin-6y c5,15-methyltransferase (decarboxylating); <b>PDBTitle:</b> crystal structure of precorin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
57	<a href="#">c1aqjB_</a>	Alignment	not modelled	99.4	26	<b>PDB header:</b> methyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenine-n6-dna-methyltransferase taqi; <b>PDBTitle:</b> structure of adenine-n6-dna-methyltransferase taqi
58	<a href="#">c3eeyl_</a>	Alignment	not modelled	99.4	11	<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
59	<a href="#">c3m6wA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
60	<a href="#">d2f8la1</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N-6 DNA Methylase-like
61	<a href="#">c3mtiA_</a>	Alignment	not modelled	99.4	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
62	<a href="#">c1g38A_</a>	Alignment	not modelled	99.4	27	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> modification methylase taqi; <b>PDBTitle:</b> adenine-specific methyltransferase m. taqi i/dna complex
63	<a href="#">c3bzbA_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein cmq451c from the2 primitive red alga cyanidioschyzon merolae
64	<a href="#">c2gpyB_</a>	Alignment	not modelled	99.4	19	<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
65	<a href="#">c3ku1E_</a>	Alignment	not modelled	99.4	18	<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
66	<a href="#">d1o54a_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
67	<a href="#">c3hm2G_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> precorin-6y c5,15-methyltransferase; <b>PDBTitle:</b> crystal structure of putative precorin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
68	<a href="#">c3cbgA_</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> functional and structural characterization of a2 cation-dependent o-methyltransferase from the3 cyanobacterium synechocystis sp. strain pcc 6803
69	<a href="#">d2b9ea1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
70	<a href="#">d1susa1</a>	Alignment	not modelled	99.3	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
71	<a href="#">c2yxdA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cobalt-precorin-6y c(15)-methyltransferase <b>PDBTitle:</b> crystal structure of cobalamin biosynthesis precorin 8w decarboxylase2 (cbt)
72	<a href="#">d2fcaa1</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
73	<a href="#">d1oria_</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
74	<a href="#">c3c3yB_</a>	Alignment	not modelled	99.3	21	<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
75	<a href="#">d1yzha1</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
76	<a href="#">c3duwB_</a>	Alignment	not modelled	99.3	27	<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
77	<a href="#">c2frxD_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein yebu; <b>PDBTitle:</b> crystal structure of yebu, a m5c rna methyltransferase from e.coli
78	<a href="#">c3njrB_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-6y methylase; <b>PDBTitle:</b> crystal structure of c-terminal domain of precocorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
79	<a href="#">c2hncC_</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent o-methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent o-methyltransferase from2 pathogenic bacterium leptospira interrogans
80	<a href="#">c3m4xA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nol1/nop2/sun family protein; <b>PDBTitle:</b> structure of a ribosomal methyltransferase
81	<a href="#">dlzx0a1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
82	<a href="#">c3gnlB_</a>	Alignment	not modelled	99.3	14	<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
83	<a href="#">c3lecA_</a>	Alignment	not modelled	99.2	19	<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
84	<a href="#">c3tfwB_</a>	Alignment	not modelled	99.2	24	<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
85	<a href="#">d2avda1</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
86	<a href="#">c3tr6A_</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> structure of a o-methyltransferase from coxiella burnetii
87	<a href="#">dlg6q1_</a>	Alignment	not modelled	99.2	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
88	<a href="#">d2h00a1</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Methyltransferase 10 domain
89	<a href="#">c1orhA_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 1; <b>PDBTitle:</b> structure of the predominant protein arginine methyltransferase prmt1
90	<a href="#">dliy9a_</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
91	<a href="#">c2yvlB_</a>	Alignment	not modelled	99.2	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
92	<a href="#">d2fyta1</a>	Alignment	not modelled	99.2	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
93	<a href="#">d2ex4a1</a>	Alignment	not modelled	99.2	22	<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
94	<a href="#">d1ri5a_</a>	Alignment	not modelled	99.2	16	<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
95	<a href="#">c2hteB_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> the crystal structure of spermidine synthase from p. falciiparum in2 complex with 5'-methylthioadenosine
96	<a href="#">dlp1ca_</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
97	<a href="#">d1kpia_</a>	Alignment	not modelled	99.2	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
98	<a href="#">c1z3cA_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> encephalitozoan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
99	<a href="#">c3dxyA_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of ectrmb in complex with sam
100	<a href="#">c3mb5A_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of p. abyss trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine
101	<a href="#">d1ne2a_</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
102	<a href="#">c3pnaA_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hemolysin;



102	<a href="#">c3upnA_</a>	Alignment	not modelled	99.1	10	<b>PDBTitle:</b> the crystal structure of a putative hemolysin from lactococcus lactis <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
103	<a href="#">d1lnla_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase pg_1098 from2 porphyromonas gingivalis w83
104	<a href="#">c3ll7A_</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA adenine dimethylase-like
105	<a href="#">d1zq9a1</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein teh homolog; <b>PDBTitle:</b> crystal structure of teh from haemophilus influenzae
106	<a href="#">c3m70A_</a>	Alignment	not modelled	99.1	17	<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.
107	<a href="#">c1yb2A_</a>	Alignment	not modelled	99.1	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
108	<a href="#">d1yb2a1</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
109	<a href="#">d1xvaa_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
110	<a href="#">c3bgdB_</a>	Alignment	not modelled	99.1	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
111	<a href="#">d1l1ea_</a>	Alignment	not modelled	99.1	18	<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.
112	<a href="#">c3dr5A_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> restriction endonuclease bpusi; <b>PDBTitle:</b> characterization and crystal structure of the type iig restriction2 endonuclease bpusi
113	<a href="#">c3s1sA_</a>	Alignment	not modelled	99.1	24	<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
114	<a href="#">d1tpya_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mw1564 protein; <b>PDBTitle:</b> crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus
115	<a href="#">c3ntvB_</a>	Alignment	not modelled	99.1	21	<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
116	<a href="#">c3lccA_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase, sam-dependent; <b>PDBTitle:</b> crystal structure of o-methyltransferase from legionella pneumophila
117	<a href="#">c3r3hA_</a>	Alignment	not modelled	99.1	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
118	<a href="#">d2b2ca1</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-arginine methyltransferase carml1; <b>PDBTitle:</b> the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
119	<a href="#">c3b3jA_</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
120	<a href="#">d1r74a_</a>	Alignment	not modelled	99.1	20	