



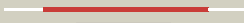




























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2h00a1</a>	 Alignment		100.0	32	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Methyltransferase 10 domain
2	<a href="#">c3evzA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal strucure of methyltransferase from pyrococcus furiosus
3	<a href="#">d2b3ta1</a>	 Alignment		99.9	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N5-glutamine methyltransferase, HemK
4	<a href="#">d1nv8a_</a>	 Alignment		99.9	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
5	<a href="#">c2ozvA_</a>	 Alignment		99.7	15	<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.
6	<a href="#">c2pjdA_</a>	 Alignment		99.7	20	<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
7	<a href="#">c3lpmA_</a>	 Alignment		99.7	21	<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
8	<a href="#">c3eqiA_</a>	 Alignment		99.7	13	<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)
9	<a href="#">c3gdhC_</a>	 Alignment		99.7	14	<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)
10	<a href="#">c3ocjA_</a>	 Alignment		99.6	13	<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
11	<a href="#">c3ku1E_</a>	 Alignment		99.6	16	<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

12	<a href="#">d2fhpA1</a>	Alignment		99.6	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
13	<a href="#">c3gnlB_</a>	Alignment		99.6	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, Imof2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (Imof2365_1472) from2 listeria monocytogenes serotype 4b
14	<a href="#">d1dusa_</a>	Alignment		99.6	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
15	<a href="#">c2esrB_</a>	Alignment		99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> conserved hypothetical protein- streptococcus pyogenes
16	<a href="#">d2fpoa1</a>	Alignment		99.6	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
17	<a href="#">d1wy7a1</a>	Alignment		99.6	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
18	<a href="#">c3p9nA_</a>	Alignment		99.6	17	<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
19	<a href="#">c3q87B_</a>	Alignment		99.6	22	<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
20	<a href="#">c3lecA_</a>	Alignment		99.6	17	<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 ph1915 (apc 5817): a hypothetical rna2 superfamily from streptococcus agalactiae to 1.8a
21	<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
22	<a href="#">c2as0A_</a>	Alignment	not modelled	99.6	13	<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
23	<a href="#">c3c0kB_</a>	Alignment	not modelled	99.5	16	<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
24	<a href="#">d2as0a2</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
25	<a href="#">d1l3ia_</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> Precorrin-6Y methyltransferase (CbiT)
26	<a href="#">c2b78A_</a>	Alignment	not modelled	99.5	12	<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
27	<a href="#">d2esra1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
28	<a href="#">c1wxwA_</a>	Alignment	not modelled	99.5	16	<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

29	<a href="#">c3eeyl_</a>	Alignment	not modelled	99.5	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
30	<a href="#">c3grzA_</a>	Alignment	not modelled	99.5	13	<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
31	<a href="#">d1o54a_</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
32	<a href="#">d1uwva2</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> (Uracil-5-)-methyltransferase
33	<a href="#">d2ifta1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
34	<a href="#">d1ws6a1</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> YhhF-like
35	<a href="#">dlyzha1</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
36	<a href="#">d2b78a2</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
37	<a href="#">c3dlcA_</a>	Alignment	not modelled	99.5	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
38	<a href="#">c3e05B_</a>	Alignment	not modelled	99.5	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
39	<a href="#">d2nxca1</a>	Alignment	not modelled	99.4	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
40	<a href="#">d1yb2a1</a>	Alignment	not modelled	99.4	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
41	<a href="#">c1yb2A_</a>	Alignment	not modelled	99.4	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.
42	<a href="#">d1m6ya2</a>	Alignment	not modelled	99.4	19	<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
43	<a href="#">d2frna1</a>	Alignment	not modelled	99.4	12	<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
44	<a href="#">d1wxxa2</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
45	<a href="#">d1xdza_</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> Glucose-inhibited division protein B (GidB)
46	<a href="#">c3m33B_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein from2 deinococcus radiodurans r1
47	<a href="#">d1ne2a_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
48	<a href="#">d1im8a_</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein HI0319 (YecO)
49	<a href="#">c3bt7A_</a>	Alignment	not modelled	99.4	18	<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 trm2 in complex with 19 nucleotide t-arm analogue
50	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
51	<a href="#">d1zq9a1</a>	Alignment	not modelled	99.4	10	<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
52	<a href="#">c1uwvA_</a>	Alignment	not modelled	99.4	12	<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
53	<a href="#">d2icta1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent

53	<a href="#">c2tgaA</a>	Alignment	not modelled	99.4	10	methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
54	<a href="#">c3g8aF</a>	Alignment	not modelled	99.3	19	<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
55	<a href="#">c2pwyB</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (adenine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of a mla58 trna methyltransferase
56	<a href="#">d1jsxa</a>	Alignment	not modelled	99.3	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glucose-inhibited division protein B (GidB)
57	<a href="#">c3g5tA</a>	Alignment	not modelled	99.3	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
58	<a href="#">c3mb5A</a>	Alignment	not modelled	99.3	19	<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 mla58 methyltransferase in complex2 with s-adenosyl-l-methionine
59	<a href="#">d2fcaa1</a>	Alignment	not modelled	99.3	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
60	<a href="#">c3fzgA</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methylase; <b>PDBTitle:</b> structure of the 16s rrna methylase arma
61	<a href="#">c3a26A</a>	Alignment	not modelled	99.3	12	<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 with2 mesado
62	<a href="#">c3fpjA</a>	Alignment	not modelled	99.3	18	<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 mtas in complex with s-2 adenosylmethionine
63	<a href="#">c2yx1A</a>	Alignment	not modelled	99.3	13	<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
64	<a href="#">d1ri5a</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> mRNA cap (Guanine N-7) methyltransferase
65	<a href="#">c1z3cA</a>	Alignment	not modelled	99.3	14	<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
66	<a href="#">c3lkdB</a>	Alignment	not modelled	99.3	13	<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
67	<a href="#">c3lcvB</a>	Alignment	not modelled	99.3	14	<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
68	<a href="#">d1sqa2</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> NOL1/NOP2/sun
69	<a href="#">c3fuxB</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dimethyladenosine transferase; <b>PDBTitle:</b> t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksqa) in2 complex with 5'-methylthioadenosine in space group p212121
70	<a href="#">c3mtiA</a>	Alignment	not modelled	99.3	12	<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
71	<a href="#">c3g07C</a>	Alignment	not modelled	99.3	16	<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)
72	<a href="#">c3fydA</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
73	<a href="#">c3e7pA</a>	Alignment	not modelled	99.3	12	<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
74	<a href="#">d2fk8a1</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> Mycolic acid cyclopropane synthase
75	<a href="#">c3grrA</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
76	<a href="#">c3lduA</a>	Alignment	not modelled	99.2	16	<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.
77	<a href="#">c2yxdA</a>	Alignment	not modelled	99.2	10	<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)

78	<a href="#">c3f4kA</a>	Alignment	not modelled	99.2	10	<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.
79	<a href="#">dli1na</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> Protein-L-isoaspartyl O-methyltransferase
80	<a href="#">dlqama</a>	Alignment	not modelled	99.2	12	<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
81	<a href="#">c2vs1A</a>	Alignment	not modelled	99.2	13	<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
82	<a href="#">c2fk8A</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methoxy mycolic acid synthase 4; <b>PDBTitle:</b> crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
83	<a href="#">c3njrB</a>	Alignment	not modelled	99.2	18	<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
84	<a href="#">c3a27A</a>	Alignment	not modelled	99.2	8	<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
85	<a href="#">dljqea</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> Histamine methyltransferase
86	<a href="#">dlve3a1</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
87	<a href="#">c3k0bA</a>	Alignment	not modelled	99.2	25	<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
88	<a href="#">dlg6q1</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> Arginine methyltransferase
89	<a href="#">c3p2kA</a>	Alignment	not modelled	99.2	15	<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
90	<a href="#">dl1lea</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
91	<a href="#">dlkpga</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> Mycolic acid cyclopropane synthase
92	<a href="#">d2o57a1</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
93	<a href="#">dlxvaa</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> Glycine N-methyltransferase
94	<a href="#">dlnkva</a>	Alignment	not modelled	99.2	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein YjHP
95	<a href="#">d2b25a1</a>	Alignment	not modelled	99.2	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
96	<a href="#">c3m70A</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein tehb homolog; <b>PDBTitle:</b> crystal structure of tehb from haemophilus influenzae
97	<a href="#">c3lccA</a>	Alignment	not modelled	99.2	15	<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
98	<a href="#">c3b3jA</a>	Alignment	not modelled	99.2	24	<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(carml1:28-507,3 residues 28-146 and 479-507 not ordered)
99	<a href="#">c2vduE</a>	Alignment	not modelled	99.2	15	<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
100	<a href="#">dlr18a</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
101	<a href="#">dltpya</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
						<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases



102	<a href="#">d2f8la1</a>	Alignment	not modelled	99.2	14	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N-6 DNA Methylase-like
103	<a href="#">c2yr0A</a>	Alignment	not modelled	99.2	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
104	<a href="#">d1kpia</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> Mycolic acid cyclopropane synthase
105	<a href="#">c2pbfA</a>	Alignment	not modelled	99.2	11	<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
106	<a href="#">c3khkA</a>	Alignment	not modelled	99.2	15	<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 maezi.
107	<a href="#">c3dxyA</a>	Alignment	not modelled	99.2	17	<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
108	<a href="#">c2yxeB</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> crystal structure of l-isoaspartyl protein carboxyl methyltransferase
109	<a href="#">d1d2ha</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> Glycine N-methyltransferase
110	<a href="#">d2ex4a1</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> AD-003 protein-like
111	<a href="#">d1dl5a1</a>	Alignment	not modelled	99.1	11	<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
112	<a href="#">d1g8sa</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
113	<a href="#">d1i9ga</a>	Alignment	not modelled	99.1	15	<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
114	<a href="#">c3tqsB</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a; <b>PDBTitle:</b> structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
115	<a href="#">d1nt2a</a>	Alignment	not modelled	99.1	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
116	<a href="#">c3bgvC</a>	Alignment	not modelled	99.1	10	<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
117	<a href="#">c3axtA</a>	Alignment	not modelled	99.1	10	<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
118	<a href="#">c1vl5B</a>	Alignment	not modelled	99.1	17	<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
119	<a href="#">d1vl5a</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> UbiE/COQ5-like
120	<a href="#">d1f3la</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> Arginine methyltransferase