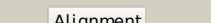
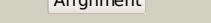
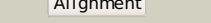
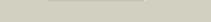
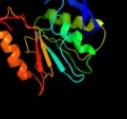
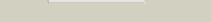
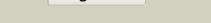
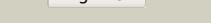
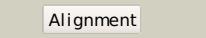
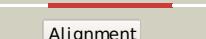
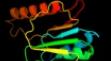
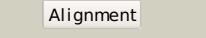
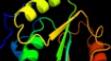
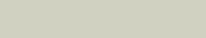
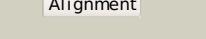
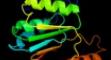
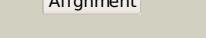
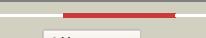
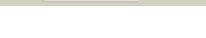


# Phyre<sup>2</sup>

Email	I.a.kelley@imperial.ac.uk
Description	P39199
Date	Thu Jan 5 11:58:28 GMT 2012
Unique Job ID	a057197707c028ab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2b3ta1	 Alignment		100.0	28	<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
2	d1nv8a_	 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> N5-glutamine methyltransferase, HemK
3	c3evzA_	 Alignment		100.0	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
4	d2h00a1	 Alignment		100.0	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Methyltransferase 10 domain
5	c3ocjA_	 Alignment		99.9	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
6	c3dmgA_	 Alignment		99.9	20	<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
7	c2pjda_	 Alignment		99.9	22	<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
8	d1dusa_	 Alignment		99.9	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
9	d2fhpa1	 Alignment		99.9	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
10	c3q87B_	 Alignment		99.9	19	<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
11	d2nxca1	 Alignment		99.9	24	<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

12	<a href="#">c3p9nA</a>			99.9	23	<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
13	<a href="#">d2as0a2</a>			99.9	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
14	<a href="#">c3grzA</a>			99.9	22	<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
15	<a href="#">c2ozvA</a>			99.9	25	<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.
16	<a href="#">d1yzha1</a>			99.9	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
17	<a href="#">c3e05B</a>			99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase (decarboxylating); <b>PDBTitle:</b> crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
18	<a href="#">c3lpmA</a>			99.8	23	<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
19	<a href="#">c2as0A</a>			99.8	25	<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
20	<a href="#">d2fpoa1</a>			99.8	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
21	<a href="#">d1sqga2</a>		not modelled	99.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
22	<a href="#">d1ws6a1</a>		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 <b>PDB header:</b> transferase
23	<a href="#">c3ku1E</a>		not modelled	99.8	23	<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="#">d1o54a</a>		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> tRNA(1-methyladenosine) methyltransferase-like
25	<a href="#">d2igta1</a>		not modelled	99.8	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
26	<a href="#">c3lecA</a>		not modelled	99.8	18	<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
27	<a href="#">d2fcaa1</a>		not modelled	99.8	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
28	<a href="#">c3eeyl</a>		not modelled	99.8	19	<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
29	c3c0kB_	Alignment	not modelled	99.8	22	<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
30	c3egiA_	Alignment	not modelled	99.8	26	<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)
31	c1wxwA_	Alignment	not modelled	99.8	27	<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 <i>thermus thermophilus</i> hb8
32	d2frna1	Alignment	not modelled	99.8	17	<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
33	c3mb5A_	Alignment	not modelled	99.8	17	<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
34	d1m6ya2	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> MraW-like putative methyltransferases
35	c2b78A_	Alignment	not modelled	99.8	17	<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
36	c2esrB_	Alignment	not modelled	99.8	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> conserved hypothetical protein- <i>streptococcus pyogenes</i>
37	c3lduA_	Alignment	not modelled	99.8	19	<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.
38	d1l3ia_	Alignment	not modelled	99.8	28	<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) <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmo2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (lmo2365_1472) from2 <i>listeria monocytogenes</i> serotype 4b
39	c3gnlB_	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> Mycolic acid cyclopropane synthase
40	d2fk8a1	Alignment	not modelled	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 <i>thermoplasma2 acidophilum</i> .
41	c1yb2A_	Alignment	not modelled	99.8	23	<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
42	d1yb2a1	Alignment	not modelled	99.8	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
43	d2b78a2	Alignment	not modelled	99.8	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
44	d1wxxa2	Alignment	not modelled	99.8	28	<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	d2esra1	Alignment	not modelled	99.8	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
46	c3a26A_	Alignment	not modelled	99.8	18	<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
47	c3gdhC_	Alignment	not modelled	99.8	22	<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)
48	c3p2kA_	Alignment	not modelled	99.8	20	<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
49	c3k0bA_	Alignment	not modelled	99.8	18	<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 <i>listeria monocytogenes</i> str. 4b f2365
50	c2yxdA_	Alignment	not modelled	99.8	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)
51	d1l1ea_	Alignment	not modelled	99.8	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
52	c2fk8A_	Alignment	not modelled	99.8	15	<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 (mma4) from <i>mycobacterium tuberculosis2</i> complexed with s-adenosyl methionine
53	c2pwvB_	Alignment	not modelled	99.8	22	<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
54	<a href="#">d1kpia</a>	Alignment	not modelled	99.8	<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
55	<a href="#">d1nkva</a>	Alignment	not modelled	99.8	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein YjhP
56	<a href="#">d1kpga</a>	Alignment	not modelled	99.8	<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
57	<a href="#">d1xvaa</a>	Alignment	not modelled	99.8	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
58	<a href="#">c2yx1A</a>	Alignment	not modelled	99.8	<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
59	<a href="#">c2pbfa</a>	Alignment	not modelled	99.8	<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) from <i>Plasmodium falciparum</i> in complex with S-adenosyl-L-homocysteine
60	<a href="#">c3ldgA</a>	Alignment	not modelled	99.8	<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
61	<a href="#">c3dxyA</a>	Alignment	not modelled	99.8	<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
62	<a href="#">c2gpyB</a>	Alignment	not modelled	99.8	<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 <i>Bacillus2 halodurans</i>
63	<a href="#">d1r74a</a>	Alignment	not modelled	99.8	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
64	<a href="#">c3g5tA</a>	Alignment	not modelled	99.8	<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
65	<a href="#">c3m70A</a>	Alignment	not modelled	99.8	<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 <i>haemophilus influenzae</i>
66	<a href="#">d1tpya</a>	Alignment	not modelled	99.8	<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
67	<a href="#">c3m33B</a>	Alignment	not modelled	99.8	<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 from <i>Deinococcus radiodurans</i> r1
68	<a href="#">c2yx1A</a>	Alignment	not modelled	99.8	<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
69	<a href="#">c3dlcA</a>	Alignment	not modelled	99.8	<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 <i>Methanococcus maripaludis</i> at 1.15 a3 resolution
70	<a href="#">c3e7pA</a>	Alignment	not modelled	99.8	<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 <i>bacteroides2 vulgatus</i> atcc 8482
71	<a href="#">d2b25a1</a>	Alignment	not modelled	99.8	<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
72	<a href="#">c3njrb</a>	Alignment	not modelled	99.8	<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 methyl transferase from <i>Rhodobacter capsulatus</i>
73	<a href="#">d2ifta1</a>	Alignment	not modelled	99.7	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Yhhf-like
74	<a href="#">c3mtiA</a>	Alignment	not modelled	99.7	<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 <i>streptococcus2 thermophilus</i> to 1.95a
75	<a href="#">d1zx0a1</a>	Alignment	not modelled	99.7	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
76	<a href="#">c1z3ca</a>	Alignment	not modelled	99.7	<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 methyltransferase in complexed with azoadomet
77	<a href="#">d1jsxa</a>	Alignment	not modelled	99.7	<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) <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases

78	<a href="#">d1wy7a1</a>	Alignment	not modelled	99.7	17	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
79	<a href="#">d1ri5a_</a>	Alignment	not modelled	99.7	20	<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
80	<a href="#">c1sqgA_</a>	Alignment	not modelled	99.7	19	<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
81	<a href="#">c3f4kA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetalotaomicron. northeast structural3 genomics target btr309.
82	<a href="#">c3bgvC_</a>	Alignment	not modelled	99.7	19	<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
83	<a href="#">c3lccA_</a>	Alignment	not modelled	99.7	23	<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
84	<a href="#">c3lcvB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sisomicin-gentamicin resistance methylase sgm; <b>PDBTitle:</b> crystal structure of antibiotic related methyltransferase
85	<a href="#">c2yxeB_</a>	Alignment	not modelled	99.7	24	<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
86	<a href="#">d1i1na_</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> Protein-L-isoaspartyl O-methyltransferase
87	<a href="#">d1uwva2</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> (Uracil-5-)methyltransferase
88	<a href="#">d2o57a1</a>	Alignment	not modelled	99.7	20	<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
89	<a href="#">d2gh1a1</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> BC2162-like
90	<a href="#">c3bkxB_</a>	Alignment	not modelled	99.7	18	<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
91	<a href="#">d1dl5a1</a>	Alignment	not modelled	99.7	25	<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
92	<a href="#">c2vdvE_</a>	Alignment	not modelled	99.7	20	<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
93	<a href="#">d1o9ga_</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA methyltransferase AviRa
94	<a href="#">d1xcla_</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
95	<a href="#">d1xdza_</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)
96	<a href="#">c3g07C_</a>	Alignment	not modelled	99.7	19	<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)
97	<a href="#">d1plca_</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> Guanidinoacetate methyltransferase
98	<a href="#">c1vl5B_</a>	Alignment	not modelled	99.7	22	<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
99	<a href="#">c3mggB_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanoscarcina2 mazei
100	<a href="#">d1vl5a_</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
101	<a href="#">d1xxla_</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> UbiE/COQ5-like
102	<a href="#">c2yvlB_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of tRNA (m1a58) methyltransferase trm1 from aquifex2 aeolicus

103	<a href="#">c3a27A</a>	Alignment	not modelled	99.7	19	<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
104	<a href="#">d1d2ha</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> Glycine N-methyltransferase
105	<a href="#">d1ixka</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
106	<a href="#">c3cbgA</a>	Alignment	not modelled	99.7	18	<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
107	<a href="#">d1r18a</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> Protein-L-isoaspartyl O-methyltransferase
108	<a href="#">c2hnkC</a>	Alignment	not modelled	99.7	21	<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
109	<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> rRNA(1-methyladenosine) methyltransferase-like
110	<a href="#">c3ntvB</a>	Alignment	not modelled	99.7	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
111	<a href="#">c3lbfC</a>	Alignment	not modelled	99.7	22	<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
112	<a href="#">c3hm2G</a>	Alignment	not modelled	99.7	20	<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
113	<a href="#">d2f8la1</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> N-6 DNA Methylase-like
114	<a href="#">d2ex4a1</a>	Alignment	not modelled	99.7	24	<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
115	<a href="#">c3g8aF</a>	Alignment	not modelled	99.7	20	<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
116	<a href="#">c2yr0A</a>	Alignment	not modelled	99.7	19	<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
117	<a href="#">c1uwvA</a>	Alignment	not modelled	99.7	23	<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
118	<a href="#">c3mq2A</a>	Alignment	not modelled	99.7	17	<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
119	<a href="#">d1wg8a2</a>	Alignment	not modelled	99.7	22	<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
120	<a href="#">c3fpjA</a>	Alignment	not modelled	99.7	19	<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 mtnas in complex with s-2 adenylmethionine