

# Phyre<sup>2</sup>

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Description	RVBD2756c_(hsdM)_3068471_3070093
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lkdB_	Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> crystal structure of the type i restriction-modification system2 methyltransferase subunit from streptococcus thermophilus, northeast3 structural genomics consortium target sur80
2	c3khkA_	Alignment		100.0	50	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methylation subunit; <b>PDBTitle:</b> crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosaarchina mazei.
3	c5ybbA_	Alignment		100.0	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> structural basis underlying complex assembly andconformational2 transition of the type i r-m system
4	d2okca1	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> N-6 DNA Methylase-like
5	d2ar0a1	Alignment		100.0	24	<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
6	c3ufbA_	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> crystal structure of a modification subunit of a putative type i2 restriction enzyme from vibrio vulnificus yj016
7	d2f8la1	Alignment		100.0	17	<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
8	c3s1sA_	Alignment		100.0	15	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> restriction endonuclease bpu51; <b>PDBTitle:</b> characterization and crystal structure of the type iig restriction2 endonuclease bpu51
9	c5hr4J_	Alignment		100.0	15	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> J: <b>PDB Molecule:</b> mmeI; <b>PDBTitle:</b> structure of type iii restriction-modification enzyme mmeI in complex2 with dna has implications for engineering of new specificities
10	c1aqjB_	Alignment		100.0	20	<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
11	c1g38A_	Alignment		100.0	18	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> modification methylase taqI; <b>PDBTitle:</b> adenine-specific methyltransferase m. taq I/dna complex

12	<a href="#">d2ih2a1</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> DNA methylase Taql, N-terminal domain
13	<a href="#">c4xqkB</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> llabibii; <b>PDBTitle:</b> atp-dependent type isp restriction-modification enzyme llabibii bound2 to dna
14	<a href="#">c5e72A</a>	Alignment		99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n2, n2-dimethylguanosine trna methyltransferase; <b>PDBTitle:</b> crystal structure of the archaeal trna m2g/m22g10 methyltransferase2 (atrm11) in complex with s-adenosyl-l-methionine (sam) from3 thermococcus kodakarensis
15	<a href="#">c3lduA</a>	Alignment		99.8	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.
16	<a href="#">c3ldgA</a>	Alignment		99.8	13	<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
17	<a href="#">c6h2uA</a>	Alignment		99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein 5; <b>PDBTitle:</b> crystal structure of human mettl5-trmt112 complex, the 18s rrna2 m6a1832 methyltransferase at 1.6a resolution
18	<a href="#">c3k0bA</a>	Alignment		99.8	19	<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 methyltransferase2 from listeria monocytogenes str. 4b f2365
19	<a href="#">c3tmaA</a>	Alignment		99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of trmn from thermus thermophilus
20	<a href="#">d1wy7a1</a>	Alignment		99.7	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
21	<a href="#">c3tm4A</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine n2)-methyltransferase trm14; <b>PDBTitle:</b> crystal structure of trm14 from pyrococcus furiosus in complex with s-2 adenosylmethionine
22	<a href="#">d1nv8a</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> N5-glutamine methyltransferase, HemK
23	<a href="#">c3evzA</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
24	<a href="#">c3fuxB</a>	Alignment	not modelled	99.6	19	<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 (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
25	<a href="#">c6h1dA</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hemk methyltransferase family member 2; <b>PDBTitle:</b> crystal structure of c21orf127-trmt112 in complex with sah
26	<a href="#">d1zq9a1</a>	Alignment	not modelled	99.6	14	<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
27	<a href="#">c2ozvA</a>	Alignment	not modelled	99.5	19	<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 atu06362 from agrobacterium tumefaciens. <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases

28	d2as0a2	Alignment	not modelled	99.5	17	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase <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
29	d2b3ta1	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1493; <b>PDB Title:</b> thermus thermophilus m5c1942 methyltransferase rimo
30	c4dmga_	Alignment	not modelled	99.5	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase l; <b>PDB Title:</b> crystal structure of bifunctional methyltransferase ycbv (rlmk) from escherichia coli, sam binding
31	c3v8vB_	Alignment	not modelled	99.5	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDB Title:</b> methyltransferase domain of human trimethylguanosine synthase 1 (tgs1) 2 bound to m7gtp and adenosyl-homocysteine (active form)
32	c3gdhc_	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDB Title:</b> methyltransferase domain of human trimethylguanosine synthase tgs12 bound to m7gpppa (inactive form)
33	c3begiA_	Alignment	not modelled	99.5	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein smu.776; <b>PDB Title:</b> a putative sam-dependent methyltransferase from streptococcus mutans
34	c2b78A_	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> rRNA adenine dimethylase-like
35	d1qyra_	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase c; <b>PDB Title:</b> crystal structure of 16s rRNA methyltransferase rsmc
36	c2pjda_	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> Hypothetical protein MJ0882
37	d1dusa_	Alignment	not modelled	99.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0064 protein yccw; <b>PDB Title:</b> crystal structure of a ribosomal rna methyltransferase
38	c3c0kb_	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 RNA methyltransferase
39	d2b78a2	Alignment	not modelled	99.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyladenosine transferase; <b>PDB Title:</b> crystal structure of the complex between s-adenosyl homocysteine and 2 methanocaldococcus jannaschi dim1.
40	c3grmA_	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase g; <b>PDB Title:</b> crystal structure of methyltransferase rlmg modifying g1835 of 23s rRNA in escherichia coli
41	c4dcma_	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-3" methyltransferase; <b>PDB Title:</b> crystal structure of a methyltransferase involved in the biosynthesis of gentamicin in complex with the geneticin
42	c5u18A_	Alignment	not modelled	99.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dimethyladenosine transferase; <b>PDB Title:</b> crystal structure of dim1 from the thermophilic archeon, 2 methanocaldococcus jannaschi
43	c3fydA_	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> Ta1320-like
44	d1ne2a_	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 450aa long hypothetical fmu protein; <b>PDB Title:</b> crystal structure of ph0851
45	c2yxIA_	Alignment	not modelled	99.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1915; <b>PDB Title:</b> crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
46	c2as0A_	Alignment	not modelled	99.4	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a; <b>PDB Title:</b> ksga from bacillus subtilis 168
47	c6ifsb_	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> rRNA methyltransferase AviRa
48	d1o9ga_	Alignment	not modelled	99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDB Title:</b> crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
49	c3lpmA_	Alignment	not modelled	99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDB Title:</b> crystal structure of methyltransferase
50	c3vseA_	Alignment	not modelled	99.4	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
51	d1sqga2	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0793; <b>PDB Title:</b> crystal structure of p. horikoshii tyw2 in complex with mesado
52	c3a26A_	Alignment	not modelled	99.4	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent
53	d1wvvv2	Alignment	not modelled	99.4	16	

53	<a href="#">c2yvwtA</a>	Alignment	not modelled	99.4	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 sadenosyl-l-methionine <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
54	<a href="#">c3axtA</a>	Alignment	not modelled	99.4	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 sadenosyl-l-methionine <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
55	<a href="#">d2frna1</a>	Alignment	not modelled	99.3	13	<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 sadenosyl-l-methionine <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
56	<a href="#">d1yuba</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable rRNA adenine dimethylase-like <b>PDBTitle:</b> crystal structure of rRNA adenine dimethylase-like
57	<a href="#">d2fpoa1</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable rRNA adenine dimethylase-like <b>PDBTitle:</b> crystal structure of rRNA adenine dimethylase-like
58	<a href="#">c3uzuA</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a; <b>PDBTitle:</b> the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
59	<a href="#">c4jxjA</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a; <b>PDBTitle:</b> crystal structure of ribosomal rna small subunit methyltransferase a2 from rickettsia bellii determined by iodide sad phasing
60	<a href="#">c1wxwA</a>	Alignment	not modelled	99.3	14	<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-dependent methyltransferase from thermus thermophilus hb8
61	<a href="#">c3g87B</a>	Alignment	not modelled	99.3	13	<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 e. cuniculi mtq2-trm112 complex responsible for the2 methylation of erf1 translation termination factor
62	<a href="#">c5yacA</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tRNA (guanine(37)-n1)-methyltransferase trm5b; <b>PDBTitle:</b> crystal structure of wt trm5b from pyrococcus abyssi
63	<a href="#">c3dmga</a>	Alignment	not modelled	99.3	21	<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
64	<a href="#">c3lbyA</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1697c; <b>PDBTitle:</b> crystal structure of smu.1697c, a putative methyltransferase from2 streptococcus mutans in complex with sah
65	<a href="#">d2ifta1</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>PDBTitle:</b> crystal structure of S-adenosyl-L-methionine-dependent methyltransferases
66	<a href="#">d1uwva2</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uracil-5-(methyltransferase) <b>PDBTitle:</b> crystal structure of uracil-5-(methyltransferase)
67	<a href="#">c3e05B</a>	Alignment	not modelled	99.3	14	<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
68	<a href="#">c3eeyl</a>	Alignment	not modelled	99.3	16	<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
69	<a href="#">d1qama</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>PDBTitle:</b> crystal structure of S-adenosyl-L-methionine-dependent methyltransferases
70	<a href="#">c1sqgA</a>	Alignment	not modelled	99.3	16	<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
71	<a href="#">c3a4tA</a>	Alignment	not modelled	99.2	13	<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
72	<a href="#">c3tqsB</a>	Alignment	not modelled	99.2	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
73	<a href="#">c2h1rA</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyladenosine transferase, putative; <b>PDBTitle:</b> crystal structure of a dimethyladenosine transferase from plasmodium falciparum
74	<a href="#">d1m6ya2</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>PDBTitle:</b> crystal structure of S-adenosyl-L-methionine-dependent methyltransferases
75	<a href="#">c2esrB</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> conserved hypothetical protein- streptococcus pyogenes
76	<a href="#">c5hjmA</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tRNA (guanine(37)-n1)-methyltransferase trm5a; <b>PDBTitle:</b> crystal structure of pyrococcus abyssi trm5a complexed with mta

77	<a href="#">d1ws6a1</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> YhhF-like
78	<a href="#">c5zvdB_</a>		Alignment	not modelled	99.2	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> 389aa long hypothetical nucleolar protein; <b>PDBTitle:</b> the crystal structure of nsun6 from pyrococcus horikoshii
79	<a href="#">d2igta1</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> hypothetical RNA methyltransferase
80	<a href="#">d1o54a_</a>		Alignment	not modelled	99.2	24	<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
81	<a href="#">c3mb5A_</a>		Alignment	not modelled	99.2	22	<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
82	<a href="#">c4dzrA_</a>		Alignment	not modelled	99.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-(glutamine-n5) methyltransferase, release factor- <b>PDBTitle:</b> the crystal structure of protein-(glutamine-n5) methyltransferase2 (release factor-specific) from alicyclobacillus acidocaldarius subsp.3 acidocaldarius dsm 446
83	<a href="#">c2yvIB_</a>		Alignment	not modelled	99.2	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 trmi from aquifex2 aeolicus
84	<a href="#">c3a27A_</a>		Alignment	not modelled	99.2	10	<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="#">d2h00a1</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> Methyltransferase 10 domain
86	<a href="#">d1i9ga_</a>		Alignment	not modelled	99.2	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
87	<a href="#">c3p9nA_</a>		Alignment	not modelled	99.2	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
88	<a href="#">d1yzha1</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> TrmB-like
89	<a href="#">d2fhpa1</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> YhhF-like
90	<a href="#">c6b92A_</a>		Alignment	not modelled	99.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> u6 small nuclear rna (adenine-(43)-n(6))-methyltransferase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of human mett16 in complex2 with sah
91	<a href="#">d1ixka_</a>		Alignment	not modelled	99.1	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
92	<a href="#">c1uwvA_</a>		Alignment	not modelled	99.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 23s rRNA (uracil-5-)methyltransferase rumra; <b>PDBTitle:</b> crystal structure of rumra, the iron-sulfur cluster2 containing e. coli 23s ribosomal rRNA 5-methyluridine3 methyltransferase
93	<a href="#">c2yx1A_</a>		Alignment	not modelled	99.1	19	<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
94	<a href="#">c3g5tA_</a>		Alignment	not modelled	99.1	16	<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-methyltransferase from yeast
95	<a href="#">c3fteA_</a>		Alignment	not modelled	99.1	20	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of a. aeolicus ksga in complex with rRNA
96	<a href="#">c4gc5A_</a>		Alignment	not modelled	99.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyladenosine transferase 1, mitochondrial; <b>PDBTitle:</b> crystal structure of murine tfb1m
97	<a href="#">c3mtiA_</a>		Alignment	not modelled	99.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rRNA methyltransferase; <b>PDBTitle:</b> the crystal structure of a rRNA methyltransferase from streptococcus2 thermophilus to 1.95a
98	<a href="#">d2esra1</a>		Alignment	not modelled	99.1	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
99	<a href="#">c5bxyB_</a>		Alignment	not modelled	99.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> RNA methyltransferase; <b>PDBTitle:</b> crystal structure of RNA methyltransferase from salinibacter ruber in2 complex with s-adenosyl-l-homocysteine
100	<a href="#">c2pwYB_</a>		Alignment	not modelled	99.1	18	<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
101	<a href="#">c5ccbA_</a>		Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> tRNA (adenine(58)-n(1))-methyltransferase catalytic subunit

						<b>PDBTitle:</b> crystal structure of human m1a58 methyltransferase in a complex with tRNA <sub>3</sub> lys and sah <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
102	<a href="#">d2fcaa1</a>	Alignment	not modelled	99.1	15	<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 from <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>
103	<a href="#">c3grzA</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein pmt-2; <b>PDBTitle:</b> crystal structure of n-methyl transferase (pmt-2) from <i>Caenorhabditis elegans</i> complexed with S-adenosyl homocysteine and phosphoethanolamine
104	<a href="#">c4ineB</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n(4)-bis(aminopropyl)spermidine synthase; <b>PDBTitle:</b> crystal structure of the branched-chain polyamine synthase from <i>Thermus thermophilus</i> (ttb-bpsa) in complex with N4-3 aminopropylspermidine and 5'-methylthioadenosine
105	<a href="#">c6j27D</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> transferase <b>Chain:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Precorrin-6Y methyltransferase (CbiT)
106	<a href="#">d1l3ia</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> tRNA (uracil-5')-methyltransferase; <b>PDBTitle:</b> structure of <i>E. coli</i> 5-methyluridine methyltransferase trma in complex with 19 nucleotide t-arm analogue
107	<a href="#">c3bt7A</a>	Alignment	not modelled	99.0	14	<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)
108	<a href="#">c2yxdA</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60S ribosomal protein l18-a; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the 2 assembly pathway of nucleolar pre-60S ribosomes
109	<a href="#">c6em5q</a>	Alignment	not modelled	99.0	12	<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 <i>Rhodobacter capsulatus</i>
110	<a href="#">c3njrB</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized RNA methyltransferase sp_1029; <b>PDBTitle:</b> structure of sprlmc d with u747 rna
111	<a href="#">c5xj2C</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tRNA (guanine-n(7))-methyltransferase; <b>PDBTitle:</b> crystal structure of ectrmb in complex with SAM
112	<a href="#">d2nxca1</a>	Alignment	not modelled	99.0	26	<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
113	<a href="#">c3dxyA</a>	Alignment	not modelled	99.0	16	<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 <i>E. coli</i>
114	<a href="#">d2b9ea1</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of <i>Streptococcus pneumoniae</i> sp1610, a putative tRNA2 (m1a22) methyltransferase, in complex with S-adenosyl-L-methionine
115	<a href="#">c2frxD</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine N-methyltransferase 2; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine N-methyltransferase 22 in complex with S-adenosyl-L-methionine
116	<a href="#">c3ku1E</a>	Alignment	not modelled	98.9	16	<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 from <i>Escherichia coli</i>
117	<a href="#">c4krhB</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative RNA methylase; <b>PDBTitle:</b> the crystal structure of a putative SAM-dependent methyltransferase, Ytqb, from <i>Bacillus subtilis</i>
118	<a href="#">c3lbfC</a>	Alignment	not modelled	98.9	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> fibrillarin homologue
119	<a href="#">c4ponB</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
120	<a href="#">d1prya</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> Fibrillarin homologue