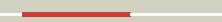
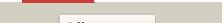
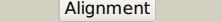
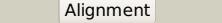
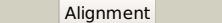


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD3037c_(-)_3397225_3398301
Date	Thu Aug 8 16:20:21 BST 2019
Unique Job ID	8de3b8ecf5d3c95a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3lI7A</a>			100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase pg_1098 from <i>2 porphyromonas gingivalis</i> w83
2	<a href="#">c3egiA</a>			99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine synthase tgs12 bound to m7gpppa (inactive form)
3	<a href="#">c3gdhC</a>			99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine synthase 1 (tgs1)2 bound to m7gtp and adenosyl-homocysteine (active form)
4	<a href="#">c2vs1A</a>			99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rna methyltransferase pyrab10780; <b>PDBTitle:</b> the crystal structure of <i>pyrococcus abyssi</i> trna (uracil-54, c5)-2 methyltransferase in complex with s-adenosyl-l-homocysteine
5	<a href="#">d2igta1</a>			99.7	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
6	<a href="#">c1uwvA</a>			99.6	18	<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 <i>e. coli</i> 23s ribosomal rna 5-methyluridine3 methyltransferase
7	<a href="#">d1uwva2</a>			99.6	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> (Uracil-5-)methyltransferase
8	<a href="#">d2oyra1</a>			99.6	28	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhiQ-like
9	<a href="#">d1wy7a1</a>			99.6	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
10	<a href="#">c5xj2C</a>			99.6	14	<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 with u747 rna
11	<a href="#">c3vseA</a>			99.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of methyltransferase

12	<a href="#">c3bt7A</a>			99.5	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 trm4 in complex2 with 19 nucleotide t-arm analogue
13	<a href="#">d2as0a2</a>			99.5	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
14	<a href="#">c1wxwA</a>			99.5	22	<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
15	<a href="#">c4dmgA</a>			99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein ttha1493; <b>PDBTitle:</b> thermus thermophilus m5c1942 methyltransferase rimo
16	<a href="#">d2pkwa1</a>			99.5	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhiQ-like
17	<a href="#">c2r6zA</a>			99.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> upf0341 protein in rsp 3' region; <b>PDBTitle:</b> crystal structure of the sam-dependent methyltransferase ngo1261 from2 neisseria gonorrhoeae, northeast structural genomics consortium3 target ngr48
18	<a href="#">c3c0kB</a>			99.5	14	<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 methyltranferase
19	<a href="#">d1wxxa2</a>			99.5	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
20	<a href="#">c2b78A</a>			99.5	14	<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 from streptococcus mutans
21	<a href="#">c6h2uA</a>		not modelled	99.5	25	<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-trmt12 complex, the 18s rRNA2 m6A1832 methyltransferase at 1.6a resolution
22	<a href="#">d2fpoa1</a>		not modelled	99.5	17	<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 <b>Chain:</b> A; <b>PDB Molecule:</b> probable ribosomal rna small subunit methyltransferase;
23	<a href="#">c3dmgA</a>		not modelled	99.5	20	<b>PDB Title:</b> t. thermophilus 16s rRNA n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
24	<a href="#">c5yacA</a>		not modelled	99.5	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
25	<a href="#">c3v8vB</a>		not modelled	99.4	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase I; <b>PDBTitle:</b> crystal structure of bifunctional methyltransferase ycbY (rlmk) from2 escherichia coli, sam binding
26	<a href="#">c2as0A</a>		not modelled	99.4	14	<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
27	<a href="#">c5u18A</a>		not modelled	99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> n-3" methyltransferase; <b>PDBTitle:</b> crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin
28	<a href="#">d2b78a2</a>		not modelled	99.4	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent

28	<a href="#">u2070a2</a>	Alignment	not modelled	99.4	10	methyltransferases <b>Family:</b> hypothetical RNA methyltransferase <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)
29	<a href="#">c2yxdaA</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> N5-glutamine methyltransferase, HemK
30	<a href="#">d1nv8a</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
31	<a href="#">d2fhpa1</a>	Alignment	not modelled	99.4	12	<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 from2 thermus thermophilus (ttb-psa) in complex with n4-3 aminopropylspermidine and 5'-methylthioadenosine
32	<a href="#">c6j27D</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> conserved hypothetical protein- streptococcus pyogenes
33	<a href="#">c2esrB</a>	Alignment	not modelled	99.4	15	<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
34	<a href="#">c3p9nA</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> evdm01; <b>PDBTitle:</b> crystal structure of the n-terminal domain of evdm01 in the presence2 of sah and d-fucose
35	<a href="#">c5t39A</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wbdd; <b>PDBTitle:</b> crystal structure of monomeric wbdd.
36	<a href="#">c4azwA</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> Met-10+ protein-like
37	<a href="#">d2frna1</a>	Alignment	not modelled	99.3	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
38	<a href="#">d2esra1</a>	Alignment	not modelled	99.3	15	<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
39	<a href="#">c6h1dA</a>	Alignment	not modelled	99.3	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
40	<a href="#">c3grzA</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ribosomal protein L11 methyltransferase PrmA
41	<a href="#">d2nxca1</a>	Alignment	not modelled	99.3	20	<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
42	<a href="#">c3lbfC</a>	Alignment	not modelled	99.3	13	<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
43	<a href="#">c3lbyA</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> C: <b>PDB Molecule:</b> putative sam-dependent methyltransferase; <b>PDBTitle:</b> conversion of a disulfide bond into a thioacetal group during2 echinomycin biosynthesis
44	<a href="#">c4necC</a>	Alignment	not modelled	99.3	30	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
45	<a href="#">d2ifta1</a>	Alignment	not modelled	99.3	14	<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
46	<a href="#">c5hjmA</a>	Alignment	not modelled	99.3	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
47	<a href="#">c3e05B</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mj0883; <b>PDBTitle:</b> crystal structure of m.jannaschii tRNA m1g37 methyltransferase
48	<a href="#">c2yx1A</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> tRNA (adenine(22)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of the b. subtilis m1a22 tRNA methyltransferase trmk
49	<a href="#">c6g56C</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> Precorrin-6Y methyltransferase (CbtT)
50	<a href="#">d1l3ia</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal RNA small subunit methyltransferase c; <b>PDBTitle:</b> crystal structure of 16S rRNA methyltransferase rsmc
51	<a href="#">c2pjda</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases

52	<a href="#">d1dusa_</a>	Alignment	not modelled	99.3	16	<b>Supertamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882 <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
53	<a href="#">c3a26A_</a>	Alignment	not modelled	99.3	14	<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-rossmann superfamily2 from streptococcus agalactiae to 1.8a
54	<a href="#">c3lecA_</a>	Alignment	not modelled	99.3	14	<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, a putative tRNA2 (m1a22) methyltransferase, in complex with s-adenosyl-L-methionine
55	<a href="#">c3ku1E_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
56	<a href="#">c3evzA_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
57	<a href="#">d1ws6a1</a>	Alignment	not modelled	99.3	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
58	<a href="#">c3m70A_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmof2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (lmof2365_1472) from listeria2 monocytogenes serotype 4b
59	<a href="#">c3gnlB_</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmof2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (lmof2365_1472) from listeria2 monocytogenes serotype 4b
60	<a href="#">d1ne2a_</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> Ta1320-like
61	<a href="#">c4azsA_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase wbdd; <b>PDBTitle:</b> high resolution (2.2 a) crystal structure of wbdd.
62	<a href="#">c3lpmA_</a>	Alignment	not modelled	99.2	14	<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
63	<a href="#">d2b3ta1</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> N5-glutamine methyltransferase, HemK
64	<a href="#">c2yxeB_</a>	Alignment	not modelled	99.2	15	<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
65	<a href="#">d1jg1a_</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
66	<a href="#">c3mtiA_</a>	Alignment	not modelled	99.2	21	<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
67	<a href="#">c4krhB_</a>	Alignment	not modelled	99.2	16	<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
68	<a href="#">c2yxIA_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 450aa long hypothetical fmw protein; <b>PDBTitle:</b> crystal structure of ph0851
69	<a href="#">c3a27A_</a>	Alignment	not modelled	99.2	13	<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
70	<a href="#">d1vbfa_</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
71	<a href="#">c6b92A_</a>	Alignment	not modelled	99.2	10	<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 mettl16 in complex2 with sah
72	<a href="#">c6qe6A_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tRNA (adenine(22)-n(1))-methyltransferase; <b>PDBTitle:</b> structure of m. capricolum trmk in complex with the natural cofactor2 product s-adenosyl-homocysteine (sah)
73	<a href="#">c6em5q_</a>	Alignment	not modelled	99.2	14	<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 assembly pathway of nucleolar pre-60s ribosomes
74	<a href="#">c4dcma_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal RNA large subunit methyltransferase g; <b>PDBTitle:</b> crystal structure of methyltransferase rlmG modifying g1835 of 23S2 rRNA in escherichia coli
75	<a href="#">c3mb5A_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of p. abyssi tRNA m1a58 methyltransferase in complex2 with s-adenosyl-L-methionine
76	<a href="#">c2ozvA_</a>	Alignment	not modelled	99.2	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.
77	<a href="#">c4l7vA</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> crystal structure of protein l-isoaspartyl-o-methyltransferase of <i>vibrio cholerae</i>
78	<a href="#">c1yb2A</a>	Alignment	not modelled	99.2	15	<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> .
79	<a href="#">d1yb2a1</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
80	<a href="#">d2h00a1</a>	Alignment	not modelled	99.2	8	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Methyltransferase 10 domain
81	<a href="#">c1dl5A</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> protein-l-isoaspartate o-methyltransferase
82	<a href="#">c3lcvB</a>	Alignment	not modelled	99.2	16	<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
83	<a href="#">d1o54a</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> tRNA(1-methyladenosine) methyltransferase-like
84	<a href="#">c2fk8A</a>	Alignment	not modelled	99.2	18	<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
85	<a href="#">d1dl5a1</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> Protein-L-isoaspartyl O-methyltransferase
86	<a href="#">c6ec3C</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein; <b>PDBTitle:</b> crystal structure of evdm01
87	<a href="#">c3njrB</a>	Alignment	not modelled	99.2	13	<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
88	<a href="#">c5e72A</a>	Alignment	not modelled	99.2	25	<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) from <i>thermococcus kodakarensis</i>
89	<a href="#">d1ixka</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> NOL1/NOP2/sun
90	<a href="#">c6gkvB</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> coclaurine n-methyltransferase; <b>PDBTitle:</b> crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah
91	<a href="#">c5ergB</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tRNA (adenine(58)-n(1))-methyltransferase catalytic subunit <b>PDBTitle:</b> crystal structure of the two-subunit tRNA m1a58 methyltransferase2 trm6-trm61 in complex with sam
92	<a href="#">d1sqga2</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> NOL1/NOP2/sun
93	<a href="#">c5dpIB</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein lysine methyltransferase 2; <b>PDBTitle:</b> the structure of pkmt2 from rickettsia typhi in complex with adohcy
94	<a href="#">c5kn4B</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pavine n-methyltransferase; <b>PDBTitle:</b> pavine n-methyltransferase apoenzyme ph 6.0
95	<a href="#">c1sqgA</a>	Alignment	not modelled	99.1	25	<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
96	<a href="#">c3fzgA</a>	Alignment	not modelled	99.1	13	<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
97	<a href="#">d2b9ea1</a>	Alignment	not modelled	99.1	25	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
98	<a href="#">d1yzha1</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
99	<a href="#">c5zvdB</a>	Alignment	not modelled	99.1	17	<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
100	<a href="#">c6bqcA</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> cyclopropane fatty acid synthase from e. coli
101	<a href="#">d1zq9a1</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> rRNA adenine dimethylase-like
102	<a href="#">c5ccbA_</a>	Alignment	not modelled	99.1	15	<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 tRNA3lys and sah
103	<a href="#">d1jsxa_</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glucose-inhibited division protein B (GidB)
104	<a href="#">d1kpia_</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
105	<a href="#">d2fk8a1</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> Mycolic acid cyclopropane synthase
106	<a href="#">c3b89A_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16S rRNA methylase; <b>PDBTitle:</b> crystal structure of rRNA methylase from escherichia coli
107	<a href="#">c6pi9A_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16S rRNA (guanine(1405)-n(7))-methyltransferase; <b>PDBTitle:</b> crystal structure of 16S rRNA methylase RMTf in complex with s-2 adenosyl-L-homocysteine
108	<a href="#">c4ineB_</a>	Alignment	not modelled	99.1	20	<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 caenorhabditis elegans complexed with S-adenosyl homocysteine and phosphoethanolamine
109	<a href="#">c2yvLB_</a>	Alignment	not modelled	99.1	17	<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 aquifex aeolicus
110	<a href="#">c3axtA_</a>	Alignment	not modelled	99.1	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 S-adenosyl-L-methionine
111	<a href="#">c3tm4A_</a>	Alignment	not modelled	99.1	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
112	<a href="#">c5wp5A_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomethyl ethanolamine N-methyltransferase 2; <b>PDBTitle:</b> arabidopsis thaliana phosphoethanolamine N-methyltransferase 22 (AtPMT2) in complex with sah
113	<a href="#">d1i1na_</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
114	<a href="#">c3vc2j_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> geranyl diphosphate 2-c-methyltransferase; <b>PDBTitle:</b> crystal structure of geranyl diphosphate C-methyltransferase from Streptomyces coelicolor A3(2) in complex with Mg <sup>2+</sup> , geranyl diphosphate, and S-adenosyl-L-homocysteine
115	<a href="#">d1l1ea_</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> Mycolic acid cyclopropane synthase
116	<a href="#">c3eeyl_</a>	Alignment	not modelled	99.1	21	<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 Clostridium 2 thermocellum
117	<a href="#">c5do0A_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein lysine methyltransferase 1; <b>PDBTitle:</b> the structure of Pkm1 from rickettsia prowazekii
118	<a href="#">c5z9oA_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus
119	<a href="#">c3m33B_</a>	Alignment	not modelled	99.1	19	<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 Deinococcus radiodurans R1
120	<a href="#">d1plca_</a>	Alignment	not modelled	99.1	7	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase