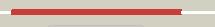
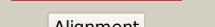
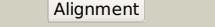
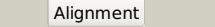
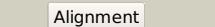
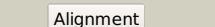


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD2956_(-)_3308678_3309409
Date	Thu Aug 8 16:20:11 BST 2019
Unique Job ID	44dc2aa308e31ed5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2py6a1</a>			100.0	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> FkbM-like
2	<a href="#">c4df3B</a>			98.5	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fibrillarin-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of aeropyrum pernix fibrillarin in complex with2 natively bound s-adenosyl-l-methionine at 1.7a
3	<a href="#">c3hm2G</a>			98.5	13	<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
4	<a href="#">c3a27A</a>			98.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj1557; <b>PDBTitle:</b> crystal structure of m. jannaschii tyw2 in complex with2 adomet
5	<a href="#">c3e05B</a>			98.4	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
6	<a href="#">c3id5F</a>			98.2	15	<b>PDB header:</b> transferase/ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> fibrillarin-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarin, l7ae and a split half c/d rna
7	<a href="#">d1dl5a1</a>			98.2	21	<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
8	<a href="#">c3a26A</a>			98.1	14	<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
9	<a href="#">c3gnlB</a>			98.1	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
10	<a href="#">c1dl5A</a>			98.1	20	<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
11	<a href="#">c6qe6A</a>			98.1	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)

12	<a href="#">c2gpyB_</a>			98.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of putative o-methyltransferase from bacillus2 halodurans
13	<a href="#">c4o29A_</a>			98.1	20	<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 from pyrobaculum aerophilum2 in complex with s-adenosyl-l-homocysteine
14	<a href="#">c3njrB_</a>			98.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y methylase; <b>PDBTitle:</b> crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
15	<a href="#">c2yxEB_</a>			98.1	16	<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
16	<a href="#">d2frna1</a>			98.0	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
17	<a href="#">d1g8sa_</a>			98.0	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
18	<a href="#">c3lecA_</a>			98.0	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-rossmann superfamily2 from streptococcus agalactiae to 1.8a
19	<a href="#">d1qama_</a>			98.0	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA adenine dimethylase-like
20	<a href="#">c2yxDA_</a>			98.0	17	<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)
21	<a href="#">c1m6yA_</a>		not modelled	98.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-methyltransferase mraw; <b>PDBTitle:</b> crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah
22	<a href="#">c5ccbA_</a>		not modelled	97.9	16	<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 with2 tRNA3lys and sah
23	<a href="#">c5xj2C_</a>		not modelled	97.9	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 sprlmcld with u747 RNA
24	<a href="#">c6q56C_</a>		not modelled	97.9	16	<b>PDB header:</b> RNA binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> tRNA (adenine(22)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the b. subtilis m1a22 tRNA methyltransferase trmk
25	<a href="#">c6pdmA_</a>		not modelled	97.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine N-methyltransferase 9; <b>PDBTitle:</b> crystal structure of human protein arginine methyltransferase 92 (prmt9)
26	<a href="#">c3g5tA_</a>		not modelled	97.9	14	<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
27	<a href="#">c3fydA_</a>		not modelled	97.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of dim1 from the thermophilic archaeon,2 methanocaldococcus jannaschi
28	<a href="#">d1vbfa_</a>		not modelled	97.9	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases

29	<a href="#">c3grrA</a>	Alignment	not modelled	97.9	15	<b>Family:</b> Protein-L-isoaspartyl O-methyltransferase <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
30	<a href="#">c3eeyL</a>	Alignment	not modelled	97.9	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
31	<a href="#">c4jxjA</a>	Alignment	not modelled	97.9	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
32	<a href="#">c3ku1E</a>	Alignment	not modelled	97.9	17	<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
33	<a href="#">d1i1na</a>	Alignment	not modelled	97.9	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
34	<a href="#">c5zy5B</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable catechol o-methyltransferase 1; <b>PDBTitle:</b> spcomt apo structure
35	<a href="#">c6h1dA</a>	Alignment	not modelled	97.9	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
36	<a href="#">c6if5B</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal RNA small subunit methyltransferase a; <b>PDBTitle:</b> ksga from bacillus subtilis 168
37	<a href="#">d2cl5a1</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
38	<a href="#">c2ipxA</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rRNA 2'-o-methyltransferase fibrillarin; <b>PDBTitle:</b> human fibrillarin
39	<a href="#">c2pwvB</a>	Alignment	not modelled	97.8	20	<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
40	<a href="#">c4c4aA</a>	Alignment	not modelled	97.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 7; <b>PDBTitle:</b> crystal structure of mouse protein arginine methyltransferase 7 in2 complex with sah
41	<a href="#">c4gc5A</a>	Alignment	not modelled	97.8	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
42	<a href="#">d1m6ya2</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> MraW-like putative methyltransferases
43	<a href="#">c3mb5A</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of p. abyssi tRNA m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine
44	<a href="#">c3lbfC</a>	Alignment	not modelled	97.8	17	<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
45	<a href="#">c2pbFA</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase beta-aspartate <b>PDBTitle:</b> crystal structure of a putative protein-l-isoaspartate o-2 methyltransferase beta-aspartate methyltransferase (pcmt) from3 plasmodium falciparum in complex with s-adenosyl-l-homocysteine
46	<a href="#">d1o54a</a>	Alignment	not modelled	97.7	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
47	<a href="#">c3tqsB</a>	Alignment	not modelled	97.7	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
48	<a href="#">c4l7vA</a>	Alignment	not modelled	97.7	13	<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 of2 vibrio cholerae
49	<a href="#">c3evzA</a>	Alignment	not modelled	97.7	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
50	<a href="#">c5lkjA</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-arginine methyltransferase carm1; <b>PDBTitle:</b> crystal structure of mouse carm1 in complex with ligand sa684
51	<a href="#">c5fubA</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine methyltransferase 2; <b>PDBTitle:</b> crystal structure of zebrafish protein arginine methyltransferase 22 catalytic domain with sah
52	<a href="#">d2fhns1</a>	Alignment	not modelled	97.7	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent

52	<a href="#">d2impa1</a>	Alignment	not modelled	97.7	10	<b>methyltransferases</b> <b>Family:</b> YhhF-like <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
53	<a href="#">d1prya_</a>	Alignment	not modelled	97.7	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
54	<a href="#">d1nt2a_</a>	Alignment	not modelled	97.7	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
55	<a href="#">d1g8aa_</a>	Alignment	not modelled	97.7	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
56	<a href="#">d1qyra_</a>	Alignment	not modelled	97.7	9	<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 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0852; <b>PDBTitle:</b> structure of a putative methyltransferase from thermoplasma2 acidophilum.
57	<a href="#">c1yb2A_</a>	Alignment	not modelled	97.7	16	<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
58	<a href="#">d1yb2a1</a>	Alignment	not modelled	97.7	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
59	<a href="#">d2b3ta1</a>	Alignment	not modelled	97.7	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
60	<a href="#">c5zw3B_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-methyltransferase yrrm; <b>PDBTitle:</b> crystal structure of trmr from b. subtilis
61	<a href="#">c5kn4B_</a>	Alignment	not modelled	97.7	5	<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
62	<a href="#">c5mgzA_</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-demethylnovobioc acid c(8)-methyltransferase; <b>PDBTitle:</b> streptomyces sphaeroides novo (8-demethylnovobioc acid2 methyltransferase) with sah
63	<a href="#">c6gkvB_</a>	Alignment	not modelled	97.7	12	<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
64	<a href="#">d2b25a1</a>	Alignment	not modelled	97.7	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like <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
65	<a href="#">c3mggB_</a>	Alignment	not modelled	97.7	9	<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 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum
66	<a href="#">d1j9ga_</a>	Alignment	not modelled	97.6	21	<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 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of pyrococcus abyssi trm5a complexed with mta
67	<a href="#">d1zq9a1</a>	Alignment	not modelled	97.6	23	<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 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of pyrococcus abyssi trm5a complexed with mta
68	<a href="#">c3c3yB_</a>	Alignment	not modelled	97.6	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glucose-inhibited division protein B (GidB) <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (guanine(37)-n1)-methyltransferase trm5a; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution
69	<a href="#">d1f3la_</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of pyrococcus abyssi trm5a complexed with mta
70	<a href="#">d1jsxa_</a>	Alignment	not modelled	97.6	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glucose-inhibited division protein B (GidB) <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
71	<a href="#">c5hjmA_</a>	Alignment	not modelled	97.6	9	<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
72	<a href="#">c1vl5B_</a>	Alignment	not modelled	97.6	10	<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
73	<a href="#">c3tr6A_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> structure of a o-methyltransferase from coxiella burnetii
74	<a href="#">c4m38A_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> transferase/transferase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 7; <b>PDBTitle:</b> crystal structure of trypanosoma brucei protein arginine2 methyltransferase 7 complex with adhcy and histone h4 peptide
75	<a href="#">c2esrB_</a>	Alignment	not modelled	97.6	13	<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="#">d1vl5a_</a>	Alignment	not modelled	97.6	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ubile/COQ5-like
77	<a href="#">d2fcfaa1</a>	Alignment	not modelled	97.6	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like

						<b>PDB header:</b> transferase
78	<a href="#">c5n5dA</a>	Alignment	not modelled	97.6	16	<b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of the o-methyltransferase tomg from streptomyces2 achromogenes involved in tomaymycin synthesis in complex with sam
79	<a href="#">c2h1rA</a>	Alignment	not modelled	97.6	11	<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 from2 plasmodium falciparum
80	<a href="#">d1nv8a</a>	Alignment	not modelled	97.6	15	<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
81	<a href="#">c2yx1A</a>	Alignment	not modelled	97.6	18	<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
82	<a href="#">c5ergB</a>	Alignment	not modelled	97.6	16	<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
83	<a href="#">c5fwaA</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 2; <b>PDBTitle:</b> crystal structure of mus musculus protein arginine methyltransferase 22 with cp1
84	<a href="#">d2esra1</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Yhhf-like
85	<a href="#">d1g6q1</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
86	<a href="#">d1jg1a</a>	Alignment	not modelled	97.6	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
87	<a href="#">c4dzrA</a>	Alignment	not modelled	97.6	17	<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
88	<a href="#">c4lwoG</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> arginine n-methyltransferase, putative; <b>PDBTitle:</b> crystal structure of prmt6
89	<a href="#">c6dnzB</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> arginine n-methyltransferase, putative; <b>PDBTitle:</b> trypanosoma brucei prmt1 enzyme-prozyme heterotetrameric complex with2 adochy
90	<a href="#">d1xxla</a>	Alignment	not modelled	97.5	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
91	<a href="#">c3ntvB</a>	Alignment	not modelled	97.5	9	<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
92	<a href="#">c6ectA</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
93	<a href="#">d1sqga2</a>	Alignment	not modelled	97.5	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
94	<a href="#">d1wy7a1</a>	Alignment	not modelled	97.5	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
95	<a href="#">d2fpoa1</a>	Alignment	not modelled	97.5	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Yhhf-like
96	<a href="#">c5bxyB</a>	Alignment	not modelled	97.5	17	<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
97	<a href="#">c2hnkC</a>	Alignment	not modelled	97.5	12	<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 from pathogenic2 bacterium leptospira interrogans
98	<a href="#">c3lbyA</a>	Alignment	not modelled	97.5	11	<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
99	<a href="#">c3cbgA</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> functional and structural characterization of a cation-dependent o-2 methyltransferase from the cyanobacterium synechocystis sp. strain3 pcc 6803
100	<a href="#">d1oria</a>	Alignment	not modelled	97.5	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
101	<a href="#">c4hc4A</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 6; <b>PDBTitle:</b> human hmt1 hnrrp methyltransferase-like protein 6 (s. cerevisiae)
						<b>PDB header:</b> transferase

102	<a href="#">c3mq2A</a>	Alignment	not modelled	97.5	25	<b>Chain: A: PDB Molecule:</b> 16s rRNA methyltransferase; <b>PDBTitle:</b> crystal structure of 16s rRNA methyltransferase kamb
103	<a href="#">c5yacA</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> rna binding protein <b>Chain: A: PDB Molecule:</b> tRNA (guanine(37)-n1)-methyltransferase trm5b; <b>PDBTitle:</b> crystal structure of wt trm5b from pyrococcus abyssi
104	<a href="#">c1uwvA</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> transferase <b>Chain: A: 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
105	<a href="#">d2avda1</a>	Alignment	not modelled	97.5	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
106	<a href="#">c3r0qA</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> probable protein arginine n-methyltransferase 4.2; <b>PDBTitle:</b> a uniquely open conformation revealed in the crystal structure of 2 arabidopsis thaliana protein arginine methyltransferase 10
107	<a href="#">c3wssA</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> protein arginine n-methyltransferase 7; <b>PDBTitle:</b> crystal structure of c.elegans prmt7 in complex with sah (p43212)
108	<a href="#">c4dcmA</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> transferase <b>Chain: A: 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
109	<a href="#">d1uwva2</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> (Uracil-5-)methyltransferase
110	<a href="#">c2yvIB</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of tRNA (m1a58) methyltransferase trmi from aquifex2 aeolicus
111	<a href="#">c4y30B</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> protein arginine n-methyltransferase 6; <b>PDBTitle:</b> crystal structure of human protein arginine methyltransferase prmt62 bound to sah and epz020411
112	<a href="#">d1yzha1</a>	Alignment	not modelled	97.4	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
113	<a href="#">c3b3jA</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> histone-arginine methyltransferase carm1; <b>PDBTitle:</b> the 2.55 Å crystal structure of the apo catalytic domain of 2 coactivator-associated arginine methyl transferase i (carm1:28-507,3 residues 28-146 and 479-507 not ordered)
114	<a href="#">d2b9ea1</a>	Alignment	not modelled	97.4	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
115	<a href="#">c2v7eB</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> histone-arginine methyltransferase carm1; <b>PDBTitle:</b> crystal structure of coactivator-associated arginine2 methyltransferase 1 (carm1), unliganded
116	<a href="#">d1dusa</a>	Alignment	not modelled	97.4	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
117	<a href="#">c2ozvA</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> hypothetical protein atu0636; <b>PDBTitle:</b> crystal structure of a predicted o-methyltransferase, protein atu06362 from agrobacterium tumefaciens.
118	<a href="#">c3gdhC</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> transferase <b>Chain: C: 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)
119	<a href="#">c4oa8A</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> o-methyltransferase family protein; <b>PDBTitle:</b> x-ray crystal structure of o-methyltransferase from anaplasma2 phagocytophilum in apo form
120	<a href="#">c3p2kA</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> 16s rRNA methylase; <b>PDBTitle:</b> structure of an antibiotic related methyltransferase