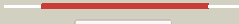



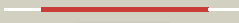






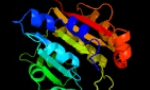





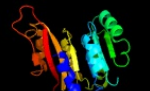






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2165c_(mraW)_2428243_2429433
Date	Mon Aug 5 13:25:28 BST 2019
Unique Job ID	2eea4478e36cd1f2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1m6yA</a>	 Alignment		100.0	45	<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
2	<a href="#">c1wg8B</a>	 Alignment		100.0	47	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted s-adenosylmethionine-dependent <b>PDBTitle:</b> crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
3	<a href="#">c3tkaA</a>	 Alignment		100.0	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase h; <b>PDBTitle:</b> crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
4	<a href="#">d1wg8a1</a>	 Alignment		100.0	49	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Putative methyltransferase TM0872, insert domain <b>Family:</b> Putative methyltransferase TM0872, insert domain
5	<a href="#">d1m6ya1</a>	 Alignment		100.0	46	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Putative methyltransferase TM0872, insert domain <b>Family:</b> Putative methyltransferase TM0872, insert domain
6	<a href="#">d1wg8a2</a>	 Alignment		100.0	54	<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
7	<a href="#">d1m6ya2</a>	 Alignment		100.0	44	<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
8	<a href="#">c3mtiA</a>	 Alignment		99.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> the crystal structure of a rna methylase from streptococcus2 thermophilus to 1.95a
9	<a href="#">c4ponB</a>	 Alignment		99.1	35	<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,2 ytqb, from bacillus subtilis
10	<a href="#">c1sqgA</a>	 Alignment		99.0	23	<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
11	<a href="#">c2yxIA</a>	 Alignment		98.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 450aa long hypothetical fmu protein; <b>PDBTitle:</b> crystal structure of ph0851

12	<a href="#">c3eeyl_</a>	Alignment		98.9	24	<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
13	<a href="#">c3a4tA_</a>	Alignment		98.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase mj0026; <b>PDBTitle:</b> crystal structure of atrm4 from m.jannaschii with sinefungin
14	<a href="#">d1ixka_</a>	Alignment		98.8	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
15	<a href="#">d1sqa2</a>	Alignment		98.8	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
16	<a href="#">d2as0a2</a>	Alignment		98.8	28	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
17	<a href="#">c1wxwA_</a>	Alignment		98.7	29	<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
18	<a href="#">c5e72A_</a>	Alignment		98.6	30	<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
19	<a href="#">c5zvdB_</a>	Alignment		98.6	24	<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
20	<a href="#">c3e05B_</a>	Alignment		98.6	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-6y c5,15-methyltransferase (decarboxylating); <b>PDBTitle:</b> crystal structure of precocorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
21	<a href="#">c2ozvA_</a>	Alignment	not modelled	98.6	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 atu6362 from agrobacterium tumefaciens.
22	<a href="#">c3lbyA_</a>	Alignment	not modelled	98.5	26	<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
23	<a href="#">d1i9ga_</a>	Alignment	not modelled	98.5	29	<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
24	<a href="#">c4dmgA_</a>	Alignment	not modelled	98.4	30	<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
25	<a href="#">c2frxD_</a>	Alignment	not modelled	98.4	19	<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 e.coli
26	<a href="#">c6h1dA_</a>	Alignment	not modelled	98.4	17	<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
27	<a href="#">c3cbgA_</a>	Alignment	not modelled	98.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> functional and structural characterization of a cationdependent o-2 methyltransferase from the cyanobacterium synechocystis sp. strain3 pcc 6803
						<b>PDB header:</b> transferase

28	<a href="#">c3vseA_</a>	Alignment	not modelled	98.3	14	<b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of methyltransferase
29	<a href="#">d2b3ta1</a>	Alignment	not modelled	98.3	24	<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="#">c5ccbA_</a>	Alignment	not modelled	98.3	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 with2 trna3lys and sah
31	<a href="#">d1wxax2</a>	Alignment	not modelled	98.3	31	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
32	<a href="#">d2b78a2</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
33	<a href="#">c2yvlB_</a>	Alignment	not modelled	98.3	29	<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
34	<a href="#">d2nxca1</a>	Alignment	not modelled	98.3	29	<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
35	<a href="#">c3mb5A_</a>	Alignment	not modelled	98.3	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
36	<a href="#">d2b9ea1</a>	Alignment	not modelled	98.3	34	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
37	<a href="#">d1yzha1</a>	Alignment	not modelled	98.2	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
38	<a href="#">c2yx1A_</a>	Alignment	not modelled	98.2	31	<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
39	<a href="#">d1l3ia_</a>	Alignment	not modelled	98.2	31	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Precorrin-6Y methyltransferase (CbiT)
40	<a href="#">d1dl5a1</a>	Alignment	not modelled	98.2	18	<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
41	<a href="#">c1dl5A_</a>	Alignment	not modelled	98.2	18	<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
42	<a href="#">c3tm4A_</a>	Alignment	not modelled	98.2	23	<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
43	<a href="#">c2pjdA_</a>	Alignment	not modelled	98.1	23	<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
44	<a href="#">d1o54a_</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
45	<a href="#">c3gdhC_</a>	Alignment	not modelled	98.1	25	<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)
46	<a href="#">d1zx0a1</a>	Alignment	not modelled	98.1	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
47	<a href="#">c3lpmA_</a>	Alignment	not modelled	98.0	20	<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
48	<a href="#">c1yb2A_</a>	Alignment	not modelled	98.0	20	<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.
49	<a href="#">d1yb2a1</a>	Alignment	not modelled	98.0	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
50	<a href="#">c4dzaA_</a>	Alignment	not modelled	98.0	25	<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
51	<a href="#">c6em5q_</a>	Alignment	not modelled	98.0	17	<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 the2 assembly pathway of nucleolar pre-60s ribosomes
52	<a href="#">c4fp9F_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> methyltransferase nsun4; <b>PDBTitle:</b> human mterf4-nsun4 protein complex

53	<a href="#">c3m6wA</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> multi-site-specific 16s rna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
54	<a href="#">c5yacA</a>	Alignment	not modelled	98.0	34	<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
55	<a href="#">c3m4xA</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nol1/nop2/sun family protein; <b>PDBTitle:</b> structure of a ribosomal methyltransferase
56	<a href="#">c2gpyB</a>	Alignment	not modelled	97.9	20	<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
57	<a href="#">c2yxeB</a>	Alignment	not modelled	97.9	22	<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
58	<a href="#">c3c0kB</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0064 protein yccw; <b>PDBTitle:</b> crystal structure of a ribosomal rna methyltransferase
59	<a href="#">d2b2ca1</a>	Alignment	not modelled	97.9	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
60	<a href="#">d1i1na</a>	Alignment	not modelled	97.9	25	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
61	<a href="#">c3dmgA</a>	Alignment	not modelled	97.9	23	<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
62	<a href="#">c4df3B</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fibrillar-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of aeropyrum pernix fibrillar in complex with2 natively bound s-adenosyl-l-methionine at 1.7a
63	<a href="#">d2fhpa1</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
64	<a href="#">c3grrA</a>	Alignment	not modelled	97.8	12	<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.
65	<a href="#">c3fydA</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dimethyladenosine transferase; <b>PDBTitle:</b> crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
66	<a href="#">d1dusa</a>	Alignment	not modelled	97.8	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
67	<a href="#">d1ej0a</a>	Alignment	not modelled	97.8	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> RNA methyltransferase FtsJ
68	<a href="#">c3c3yB</a>	Alignment	not modelled	97.8	13	<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
69	<a href="#">c2r6zA</a>	Alignment	not modelled	97.8	23	<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
70	<a href="#">c3ll7A</a>	Alignment	not modelled	97.8	15	<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 from2 porphyromonas gingivalis w83
71	<a href="#">d1susa1</a>	Alignment	not modelled	97.8	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
72	<a href="#">c2pwyB</a>	Alignment	not modelled	97.8	23	<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
73	<a href="#">c1uwvA</a>	Alignment	not modelled	97.8	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 e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
74	<a href="#">c5hjmA</a>	Alignment	not modelled	97.8	10	<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
75	<a href="#">c3grzA</a>	Alignment	not modelled	97.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein l11 methyltransferase; <b>PDBTitle:</b> crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
76	<a href="#">d1uwv2</a>	Alignment	not modelled	97.8	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> (Uracil-5-)-methyltransferase

77	<a href="#">c3egiA_</a>	Alignment	not modelled	97.7	25	<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)
78	<a href="#">d2avda1</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
79	<a href="#">d2cl5a1</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> COMT-like
80	<a href="#">d1qama_</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
81	<a href="#">d1zq9a1</a>	Alignment	not modelled	97.7	17	<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
82	<a href="#">c3evzA_</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
83	<a href="#">c5wwrA_</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase nsun6; <b>PDBTitle:</b> crystal structure of human nsun6/trna/sfg
84	<a href="#">d2b25a1</a>	Alignment	not modelled	97.7	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
85	<a href="#">c4jxjA_</a>	Alignment	not modelled	97.7	16	<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
86	<a href="#">d2fpoa1</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
87	<a href="#">d1jg1a_</a>	Alignment	not modelled	97.7	19	<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
88	<a href="#">c6q56C_</a>	Alignment	not modelled	97.7	13	<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
89	<a href="#">c3duwB_</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase, putative; <b>PDBTitle:</b> crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah
90	<a href="#">d1nv8a_</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
91	<a href="#">c3a26A_</a>	Alignment	not modelled	97.7	15	<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
92	<a href="#">d1g8aa_</a>	Alignment	not modelled	97.6	36	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarlin homologue
93	<a href="#">c5ergB_</a>	Alignment	not modelled	97.6	14	<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
94	<a href="#">c5n5dA_</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> transferase <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
95	<a href="#">c4o29A_</a>	Alignment	not modelled	97.6	22	<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
96	<a href="#">c3tr6A_</a>	Alignment	not modelled	97.6	22	<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
97	<a href="#">c2as0A_</a>	Alignment	not modelled	97.6	20	<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
98	<a href="#">c3id5F_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> transferase/ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> fibrillarlin-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarlin, l7ae and a split half c/d rna
99	<a href="#">c2pssC_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> the structure of plasmodium falciparum spermidine synthase in its apo-2 form
100	<a href="#">c2yxdA_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cobalt-precorrin-6y c(15)-methyltransferase <b>PDBTitle:</b> crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbt)

101	<a href="#">c2pbfA_</a>	Alignment	not modelled	97.6	18	<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
102	<a href="#">c3njrB_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-6y methylase; <b>PDBTitle:</b> crystal structure of c-terminal domain of precocorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
103	<a href="#">c2hncC_</a>	Alignment	not modelled	97.6	17	<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
104	<a href="#">c3tfwB_</a>	Alignment	not modelled	97.6	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
105	<a href="#">c3lbfC_</a>	Alignment	not modelled	97.6	24	<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
106	<a href="#">d1wy7a1</a>	Alignment	not modelled	97.6	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
107	<a href="#">c5xj2C_</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized rna methyltransferase sp_1029; <b>PDBTitle:</b> structure of sprlmcD with u747 rna
108	<a href="#">d1vbfA_</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> Protein-L-isoaspartyl O-methyltransferase
109	<a href="#">c3ntvB_</a>	Alignment	not modelled	97.6	12	<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
110	<a href="#">d1r18a_</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> Protein-L-isoaspartyl O-methyltransferase
111	<a href="#">c5dplB_</a>	Alignment	not modelled	97.6	22	<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
112	<a href="#">d2fcaa1</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> TrmB-like
113	<a href="#">c6ifsB_</a>	Alignment	not modelled	97.5	13	<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
114	<a href="#">c5wp5A_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomethylethanolamine n-methyltransferase 2; <b>PDBTitle:</b> arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
115	<a href="#">d1prya_</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> Fibrillarlin homologue
116	<a href="#">c5u18A_</a>	Alignment	not modelled	97.5	25	<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
117	<a href="#">d2igta1</a>	Alignment	not modelled	97.5	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
118	<a href="#">c3lecA_</a>	Alignment	not modelled	97.5	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
119	<a href="#">c2ipxA_</a>	Alignment	not modelled	97.5	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna 2'-o-methyltransferase fibrillarlin; <b>PDBTitle:</b> human fibrillarlin
120	<a href="#">c4gc5A_</a>	Alignment	not modelled	97.4	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