Phyre^2

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Description	P55135
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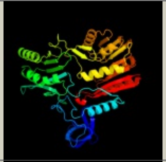
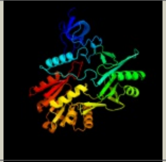
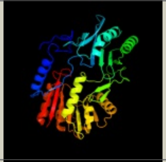
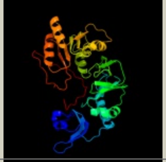
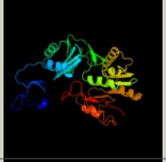
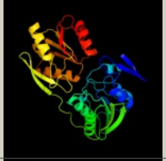
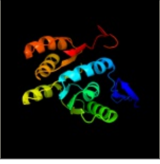
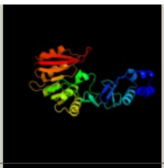
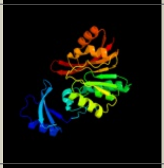
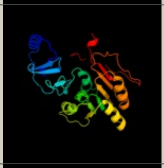
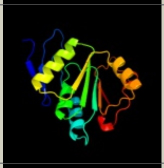
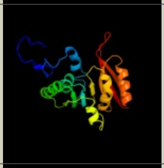
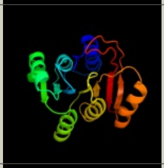
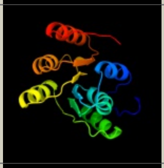
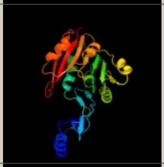
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1uwvA_	Alignment		100.0	97	**PDB header:**transferase **Chain:** A: **PDB Molecule:**23s rrna (uracil-5-)-methyltransferase ruma; **PDBTitle:** crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
2	c2vs1A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized rna methyltransferase pyrab10780; **PDBTitle:** the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine
3	d1uwva2	Alignment		100.0	97	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**(Uracil-5-)-methyltransferase
4	c3bt7A_	Alignment		100.0	23	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna (uracil-5-)-methyltransferase; **PDBTitle:** structure of e. coli 5-methyluridine methyltransferase trma2 in complex with 19 nucleotide t-arm analogue
5	c3c0kB_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0064 protein yccw; **PDBTitle:** crystal structure of a ribosomal rna methyltranferase
6	c1wxwA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha1280; **PDBTitle:** crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophillus hb8
7	c2b78A_	Alignment		100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein smu.776; **PDBTitle:** a putative sam-dependent methyltransferase from2 streptococcus mutans
8	c2as0A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph1915; **PDBTitle:** crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
9	c3dmgA_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable ribosomal rna small subunit methyltransferase; **PDBTitle:** t. thermophilus 16s rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
10	d2as0a2	Alignment		99.9	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
11	d1wxxa2	Alignment		99.9	28	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase

12	c3a26A_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein ph0793; **PDBTitle:** crystal structure of p. horikoshii tyw2 in complex with2 mesado
13	d2frna1	Alignment		99.9	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Met-10+ protein-like
14	d2b78a2	Alignment		99.9	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
15	d2igta1	Alignment		99.9	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
16	c3a27A_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mj1557; **PDBTitle:** crystal structure of m. jannaschii tyw2 in complex with2 adomet
17	d1wy7a1	Alignment		99.9	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
18	c2yxdA_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable cobalt-precorrin-6y c(15)-methyltransferase **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbit)
19	c2yx1A_	Alignment		99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein mj0883; **PDBTitle:** crystal structure of m.jannaschii trna m1g37 methyltransferase
20	d1prya_	Alignment		99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
21	d1l3ia_	Alignment	not modelled	99.8	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
22	d1nv8a_	Alignment	not modelled	99.8	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
23	d2b9ea1	Alignment	not modelled	99.7	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
24	c3e05B_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6y c5,15-methyltransferase (decarboxylating); **PDBTitle:** crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
25	c3egiA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trimethylguanosine synthase homolog; **PDBTitle:** methyltransferase domain of human trimethylguanosine2 synthase tgs1 bound to m7gpppa (inactive form)
26	c3mtiA_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
27	d2fpoa1	Alignment	not modelled	99.7	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
28	c3p9nA_	Alignment	not modelled	99.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible methyltransferase (methylase); **PDBTitle:** rv2966c of m. tuberculosis is a rsmd-like

						methyltransferase
29	c3njrB_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6y methylase; **PDBTitle:** crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
30	c3gdhC_	Alignment	not modelled	99.7	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**trimethylguanosine synthase homolog; **PDBTitle:** methyltransferase domain of human trimethylguanosine2 synthase 1 (tgs1) bound to m7gtp and adenosyl-homocysteine3 (active form)
31	d1uwva1	Alignment	not modelled	99.7	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
32	d2fhpa1	Alignment	not modelled	99.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
33	c3ll7A_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase pg_1098 from2 porphyromonas gingivalis w83
34	d2b3ta1	Alignment	not modelled	99.7	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
35	c3lpmA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
36	c2ozvA_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein atu0636; **PDBTitle:** crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
37	d2dula1	Alignment	not modelled	99.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TRM1-like
38	c2yxlA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
39	c3a4tA_	Alignment	not modelled	99.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase mj0026; **PDBTitle:** crystal structure of atrm4 from m.jannaschii with sinefungin
40	c3axtA_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable n(2),n(2)-dimethylguanosine trna methyltransferase **PDBTitle:** complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
41	d1sqga2	Alignment	not modelled	99.6	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
42	d1g8sa_	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
43	d2ifta1	Alignment	not modelled	99.6	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
44	d1ne2a_	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
45	d1dusa_	Alignment	not modelled	99.6	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
46	c2yvlB_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
47	c3hm2G_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** G: **PDB Molecule:**precorrin-6y c5,15-methyltransferase; **PDBTitle:** crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
48	c3lbfC_	Alignment	not modelled	99.6	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
49	d1o54a_	Alignment	not modelled	99.6	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
50	c3grzA_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
51	d1yeza1	Alignment		99.6	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
						PDB header:transferase **Chain:** A: **PDB Molecule:**upf0341 protein in rsp 3' region;

52	c2r6zA_	Alignment	not modelled	99.6	22	**PDBTitle:** crystal structure of the sam-dependent methyltransferase2 ngo1261 from neisseria gonorrhoeae, northeast structural3 genomics consortium target ngr48
53	c2esrB_	Alignment	not modelled	99.6	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** conserved hypothetical protein- streptococcus pyogenes
54	d1ixka_	Alignment	not modelled	99.6	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
55	c1sqgA_	Alignment	not modelled	99.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sun protein; **PDBTitle:** the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
56	c3evzA_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal strucure of methyltransferase from pyrococcus furiosus
57	d2esra1	Alignment	not modelled	99.5	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
58	c3mb5A_	Alignment	not modelled	99.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of p. abyssi trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine
59	d2nxca1	Alignment	not modelled	99.5	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
60	c3gnlB_	Alignment	not modelled	99.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein, duf633, lmof2365_1472; **PDBTitle:** structure of uncharacterized protein (lmof2365_1472) from2 listeria monocytogenes serotype 4b
61	d1yvca1	Alignment	not modelled	99.5	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
62	d1yb2a1	Alignment	not modelled	99.5	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
63	c1yb2A_	Alignment	not modelled	99.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
64	c3id5F_	Alignment	not modelled	99.5	15	**PDB header:**transferase/ribosomal protein/rna **Chain:** F: **PDB Molecule:**fibrillarin-like rrna/trna 2'-o-methyltransferase; **PDBTitle:** crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarin, l7ae and a split half c/d rna
65	d2h00a1	Alignment	not modelled	99.5	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Methyltransferase 10 domain
66	d1g8aa_	Alignment	not modelled	99.5	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
67	c2pwyB_	Alignment	not modelled	99.5	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
68	d1ws6a1	Alignment	not modelled	99.5	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
69	d1qama_	Alignment	not modelled	99.5	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
70	c2ipxA_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna 2'-o-methyltransferase fibrillarin; **PDBTitle:** human fibrillarin
71	c2pjdA_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase c; **PDBTitle:** crystal structure of 16s rrna methyltransferase rsmc
72	c3ku1E_	Alignment	not modelled	99.4	14	**PDB header:**transferase **Chain:** E: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of streptococcus pneumoniae sp1610, a2 putative trna (m1a22) methyltransferase, in complex with s-3 adenosyl-l-methionine
73	d1xdza_	Alignment	not modelled	99.4	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
74	c3lecA_	Alignment	not modelled	99.4	14	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**nadb-rossmann superfamily protein; **PDBTitle:** the crystal structure of a protein in the nadb-rossmann2 superfamily from streptococcus agalactiae to 1.8a
75	c2yxeB_	Alignment	not modelled	99.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of l-isoaspartyl protein carboxyl methyltranferase
76	c3eeyJ_	Alignment	not modelled	99.4	15	**PDB header:**transferase **Chain:** J: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of putative rrna-methylase from clostridium2 thermocellum
						PDB header:transferase activator/transferase

77	c3q87B_	Alignment	not modelled	99.4	15	**Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase; **PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
78	d1yzha1	Alignment	not modelled	99.4	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
79	d1jg1a_	Alignment	not modelled	99.4	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
80	c1dl5A_	Alignment	not modelled	99.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase
81	c3g8aF_	Alignment	not modelled	99.4	20	**PDB header:**transferase **Chain:** F: **PDB Molecule:**ribosomal rna small subunit methyltransferase g; **PDBTitle:** t. thermophilus 16s rrna g527 methyltransferase in complex with adohcy2 in space group p61
82	c3m6wA_	Alignment	not modelled	99.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
83	c3m4xA_	Alignment	not modelled	99.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
84	c3fydA_	Alignment	not modelled	99.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable dimethyladenosine transferase; **PDBTitle:** crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
85	c3grrA_	Alignment	not modelled	99.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
86	d1dl5a1	Alignment	not modelled	99.4	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
87	d1m6ya2	Alignment	not modelled	99.4	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
88	d2b25a1	Alignment	not modelled	99.3	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
89	d1i9ga_	Alignment	not modelled	99.3	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
90	c3k0bA_	Alignment	not modelled	99.3	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted n6-adenine-specific dna methylase; **PDBTitle:** crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365
91	c3jwgA_	Alignment	not modelled	99.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase type 12; **PDBTitle:** crystal structure analysis of the methyltransferase domain2 of bacterial-cthen1-c
92	d2fcaa1	Alignment	not modelled	99.3	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
93	c2frxD_	Alignment	not modelled	99.3	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
94	c3m70A_	Alignment	not modelled	99.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
95	d1zq9a1	Alignment	not modelled	99.3	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
96	d1vbfa_	Alignment	not modelled	99.3	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
97	d1qyra_	Alignment	not modelled	99.3	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
98	c2pbfA_	Alignment	not modelled	99.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase beta-aspartate **PDBTitle:** 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
99	d1kpia_	Alignment	not modelled	99.3	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
100	c3jwhA_	Alignment	not modelled	99.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure analysis of the methyltransferase domain2 of bacterial-avhen1-c
101	d1jsxa_	Alignment	not modelled	99.3	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)

102	d1l1ea_	Alignment	not modelled	99.3	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
103	c3lduA_	Alignment	not modelled	99.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methylase; **PDBTitle:** the crystal structure of a possible methylase from2 clostridium difficile 630.
104	d1kpga_	Alignment	not modelled	99.3	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
105	d1nt2a_	Alignment	not modelled	99.3	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
106	d2ex4a1	Alignment	not modelled	99.3	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
107	c3c3yB_	Alignment	not modelled	99.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum
108	d1wg8a2	Alignment	not modelled	99.2	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
109	c2fk8A_	Alignment	not modelled	99.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methoxy mycolic acid synthase 4; **PDBTitle:** crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
110	d1tpya_	Alignment	not modelled	99.2	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
111	c3cbgA_	Alignment	not modelled	99.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-methyltransferase; **PDBTitle:** functional and structural characterization of a2 cationdependent o-methyltransferase from the3 cyanobacterium synechocystis sp. strain pcc 6803
112	c3duwB_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase, putative; **PDBTitle:** crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah
113	c3ldgA_	Alignment	not modelled	99.2	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.472; **PDBTitle:** crystal structure of smu.472, a putative methyltransferase complexed2 with sah
114	d1xvaa_	Alignment	not modelled	99.2	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
115	c3fpjA_	Alignment	not modelled	99.2	17	**PDB header:**biosynthetic protein, transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of e81q mutant of mtnas in complex with s-2 adenosylmethionine
116	c3lccA_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyl chloride transferase; **PDBTitle:** structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
117	c3bgdB_	Alignment	not modelled	99.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiopurine s-methyltransferase; **PDBTitle:** thiopurine s-methyltransferase
118	c1m6yA_	Alignment	not modelled	99.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
119	c2h1rA_	Alignment	not modelled	99.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dimethyladenosine transferase, putative; **PDBTitle:** crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
120	d1i1na_	Alignment	not modelled	99.2	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase