Phyre^2

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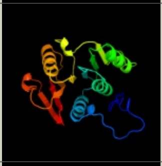
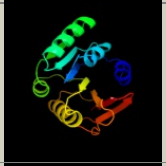
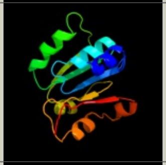
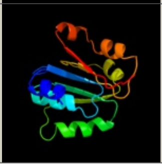
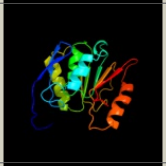
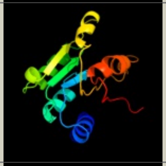
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fpoa1	Alignment		100.0	98	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
2	d2fhpa1	Alignment		100.0	30	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
3	c3p9nA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible methyltransferase (methylase); **PDBTitle:** rv2966c of m. tuberculosis is a rsmd-like methyltransferase
4	d2ifta1	Alignment		100.0	56	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
5	d1ws6a1	Alignment		100.0	32	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
6	c2esrB_	Alignment		100.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** conserved hypothetical protein- streptococcus pyogenes
7	d2esra1	Alignment		100.0	28	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
8	d1nv8a_	Alignment		99.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
9	c2b78A_	Alignment		99.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein smu.776; **PDBTitle:** a putative sam-dependent methyltransferase from2 streptococcus mutans
10	c3grzA_	Alignment		99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
11	d2b78a2	Alignment		99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase

12	d2as0a2	Alignment		99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
13	d1dusa_	Alignment		99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
14	c3c0kB_	Alignment		99.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0064 protein yccw; **PDBTitle:** crystal structure of a ribosomal rna methyltranferase
15	d2b3ta1	Alignment		99.8	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
16	d2igta1	Alignment		99.8	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
17	c2as0A_	Alignment		99.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph1915; **PDBTitle:** crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
18	d1wy7a1	Alignment		99.8	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
19	c1wxwA_	Alignment		99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha1280; **PDBTitle:** crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophillus hb8
20	c3evzA_	Alignment		99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal strucure of methyltransferase from pyrococcus furiosus
21	d2nxca1	Alignment	not modelled	99.8	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
22	c3dmgA_	Alignment	not modelled	99.8	23	**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
23	c3lpmA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
24	d1wxxa2	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
25	c1uwvA_	Alignment	not modelled	99.8	20	**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
26	c2vs1A_	Alignment	not modelled	99.8	17	**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
27	d1uwva2	Alignment	not modelled	99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases

						Family:(Uracil-5-)-methyltransferase
28	d2frna1	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Met-10+ protein-like
29	c3egiA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trimethylguanosine synthase homolog; **PDBTitle:** methyltransferase domain of human trimethylguanosine2 synthase tgs1 bound to m7gpppa (inactive form)
30	c2yxdA_	Alignment	not modelled	99.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable cobalt-precorrin-6y c(15)-methyltransferase **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbit)
31	d1ne2a_	Alignment	not modelled	99.7	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
32	c2pjdA_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase c; **PDBTitle:** crystal structure of 16s rrna methyltransferase rsmc
33	c3gdhC_	Alignment	not modelled	99.7	15	**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)
34	c3a26A_	Alignment	not modelled	99.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein ph0793; **PDBTitle:** crystal structure of p. horikoshii tyw2 in complex with2 mesado
35	c3ku1E_	Alignment	not modelled	99.7	17	**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
36	d1l3ia_	Alignment	not modelled	99.7	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
37	c3lduA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methylase; **PDBTitle:** the crystal structure of a possible methylase from2 clostridium difficile 630.
38	c3bt7A_	Alignment	not modelled	99.7	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
39	c3mtiA_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
40	c3e05B_	Alignment	not modelled	99.7	25	**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
41	c2ozvA_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein atu0636; **PDBTitle:** crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
42	d2dula1	Alignment	not modelled	99.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TRM1-like
43	d1yzha1	Alignment	not modelled	99.7	8	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
44	c3ldgA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.472; **PDBTitle:** crystal structure of smu.472, a putative methyltransferase complexed2 with sah
45	c3gnlB_	Alignment	not modelled	99.7	13	**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
46	c3e7pA_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
47	c3lecA_	Alignment	not modelled	99.7	17	**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
48	d1g6q1_	Alignment	not modelled	99.7	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
49	d1jsxa_	Alignment	not modelled	99.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
50	c2yx1A_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein mj0883; **PDBTitle:** crystal structure of m.jannaschii trna m1g37 methyltransferase
51	d1f3la_	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase

52	c3f4kA_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
53	c3axtA_	Alignment	not modelled	99.6	15	**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
54	d2h00a1	Alignment	not modelled	99.6	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Methyltransferase 10 domain
55	c3b3jA_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
56	d2fyta1	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
57	c3mb5A_	Alignment	not modelled	99.6	13	**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
58	c3a27A_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mj1557; **PDBTitle:** crystal structure of m. jannaschii tyw2 in complex with2 adomet
59	c3njrB_	Alignment	not modelled	99.6	24	**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
60	d1xvaa_	Alignment	not modelled	99.6	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
61	d2fcaa1	Alignment	not modelled	99.6	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
62	c3q87B_	Alignment	not modelled	99.6	15	**PDB header:**transferase activator/transferase **Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase; **PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
63	c3m70A_	Alignment	not modelled	99.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
64	d1oria_	Alignment	not modelled	99.6	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
65	c3eeyJ_	Alignment	not modelled	99.6	10	**PDB header:**transferase **Chain:** J: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of putative rrna-methylase from clostridium2 thermocellum
66	c1orhA_	Alignment	not modelled	99.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 1; **PDBTitle:** structure of the predominant protein arginine methyltransferase prmt1
67	c3k0bA_	Alignment	not modelled	99.6	19	**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
68	d1r74a_	Alignment	not modelled	99.6	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
69	c3opnA_	Alignment	not modelled	99.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hemolysin; **PDBTitle:** the crystal structure of a putative hemolysin from lactococcus lactis
70	c2v7eB_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** crystal structure of coactivator-associated arginine2 methyltransferase 1 (carm1), unliganded
71	d1o54a_	Alignment	not modelled	99.6	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
72	c1yb2A_	Alignment	not modelled	99.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
73	d1yb2a1	Alignment	not modelled	99.6	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
74	c3g5tA_	Alignment	not modelled	99.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast
75	d2ex4a1	Alignment	not modelled	99.6	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
						Fold:S-adenosyl-L-methionine-dependent methyltransferases

76	d1ri5a_	Alignment	not modelled	99.6	9	**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap (Guanine N-7) methyltransferase
77	c3c6kC_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**spermine synthase; **PDBTitle:** crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
78	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
79	c2gpyB_	Alignment	not modelled	99.6	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** crystal structure of putative o-methyltransferase from bacillus2 halodurans
80	c1z3cA_	Alignment	not modelled	99.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
81	c2pwyB_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
82	c2yr0A_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha0223; **PDBTitle:** crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
83	c3dxyA_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of ectrmb in complex with sam
84	d1i9ga_	Alignment	not modelled	99.5	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
85	d1jg1a_	Alignment	not modelled	99.5	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
86	d1zq9a1	Alignment	not modelled	99.5	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
87	c3dlcA_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative s-adenosyl-l-methionine-dependent **PDBTitle:** crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
88	d1nkva_	Alignment	not modelled	99.5	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical Protein YjhP
89	c3fydA_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable dimethyladenosine transferase; **PDBTitle:** crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
90	c2fk8A_	Alignment	not modelled	99.5	13	**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
91	c3lbfC_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
92	c3grrA_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
93	c3bgvC_	Alignment	not modelled	99.5	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mrna cap guanine-n7 methyltransferase; **PDBTitle:** crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
94	c2yvlB_	Alignment	not modelled	99.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
95	d1m6ya2	Alignment	not modelled	99.5	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
96	d1sqga2	Alignment	not modelled	99.5	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
97	d2o57a1	Alignment	not modelled	99.5	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
98	d1dl5a1	Alignment	not modelled	99.5	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
99	d2cl5a1	Alignment	not modelled	99.5	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**COMT-like
100	c1vl5B_	Alignment	not modelled	99.5	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**unknown conserved protein bh2331; **PDBTitle:** crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution

101	d1vl5a_	Alignment	not modelled	99.5	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
102	c2yxeB_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of l-isoaspartyl protein carboxyl methyltranferase
103	d1zx0a1	Alignment	not modelled	99.5	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
104	d1xdza_	Alignment	not modelled	99.5	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
105	d1nt2a_	Alignment	not modelled	99.5	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
106	d1kpia_	Alignment	not modelled	99.5	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
107	c3ll7A_	Alignment	not modelled	99.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase pg_1098 from2 porphyromonas gingivalis w83
108	d1p1ca_	Alignment	not modelled	99.5	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
109	d1ve3a1	Alignment	not modelled	99.5	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
110	d2i6ga1	Alignment	not modelled	99.5	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TehB-like
111	d1l1ea_	Alignment	not modelled	99.5	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
112	d2fk8a1	Alignment	not modelled	99.5	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
113	c3ocjA_	Alignment	not modelled	99.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** the crystal structure of a possilbe exported protein from bordetella2 parapertussis
114	c3g07C_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**7sk snrna methylphosphate capping enzyme; **PDBTitle:** methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
115	d1pjza_	Alignment	not modelled	99.5	8	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
116	d1xcla_	Alignment	not modelled	99.5	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
117	d2bzga1	Alignment	not modelled	99.5	7	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
118	c3lcvB_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sisomicin-gentamicin resistance methylase sgm; **PDBTitle:** crystal structure of antibiotic related methyltransferase
119	d1qama_	Alignment	not modelled	99.5	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
120	d1tpya_	Alignment	not modelled	99.5	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase