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Description	P0A6U5
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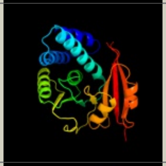
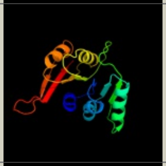
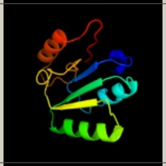
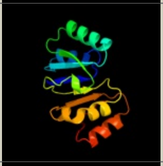
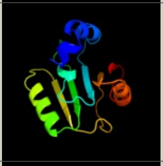
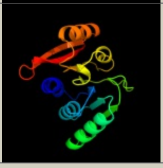
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xdza_	Alignment		100.0	34	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
2	d1jsxa_	Alignment		100.0	100	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
3	c3g8aF_	Alignment		100.0	31	**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
4	d2b3ta1	Alignment		99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
5	c3evzA_	Alignment		99.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal strucure of methyltransferase from pyrococcus furiosus
6	c2ozvA_	Alignment		99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein atu0636; **PDBTitle:** crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
7	c3mtiA_	Alignment		99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
8	c3lpmA_	Alignment		99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
9	d1yzha1	Alignment		99.7	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
10	c3e05B_	Alignment		99.7	16	**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
11	c3g5tA_	Alignment		99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast

12	d1nv8a_	Alignment		99.7	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
13	c3lecA_	Alignment		99.7	11	**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
14	c3gnlB_	Alignment		99.7	6	**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
15	c3ku1E_	Alignment		99.7	11	**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
16	c3m70A_	Alignment		99.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
17	c3hm2G_	Alignment		99.7	15	**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
18	d2gh1a1	Alignment		99.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**BC2162-like
19	d2fcaa1	Alignment		99.7	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
20	c3grzA_	Alignment		99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
21	c3fpjA_	Alignment	not modelled	99.7	9	**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
22	c1yb2A_	Alignment	not modelled	99.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
23	d1yb2a1	Alignment	not modelled	99.7	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
24	d1o54a_	Alignment	not modelled	99.7	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
25	d1dusa_	Alignment	not modelled	99.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
26	c3bkxB_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution
27	c3bgvC_	Alignment	not modelled	99.7	13	**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
28	d1dl5a1	Alignment	not modelled	99.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases

						Family: Protein-L-isoaspartyl O-methyltransferase
29	c2pjdA_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase c; **PDBTitle:** crystal structure of 16s rrna methyltransferase rsmc
30	c2yxdA_	Alignment	not modelled	99.7	14	**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	c3dxyA_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of ectrmb in complex with sam
32	d1ri5a_	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap (Guanine N-7) methyltransferase
33	c3eeyJ_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** J: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of putative rrna-methylase from clostridium2 thermocellum
34	c1z3cA_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
35	c2fk8A_	Alignment	not modelled	99.6	15	**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
36	d1xxla_	Alignment	not modelled	99.6	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
37	d1nt2a_	Alignment	not modelled	99.6	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
38	d1xcla_	Alignment	not modelled	99.6	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
39	c2yxeB_	Alignment	not modelled	99.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of l-isoaspartyl protein carboxyl methyltranferase
40	c3mb5A_	Alignment	not modelled	99.6	17	**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
41	c3e7pA_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
42	d1m6ya2	Alignment	not modelled	99.6	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
43	d1l1ea_	Alignment	not modelled	99.6	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
44	d2nxca1	Alignment	not modelled	99.6	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
45	c1vl5B_	Alignment	not modelled	99.6	18	**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
46	d1vl5a_	Alignment	not modelled	99.6	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
47	d1kpga_	Alignment	not modelled	99.6	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
48	d1nkva_	Alignment	not modelled	99.6	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical Protein YjhP
49	c1dl5A_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase
50	c3lccA_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyl chloride transferase; **PDBTitle:** structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
51	d1tpya_	Alignment	not modelled	99.6	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
52	d1kpia_	Alignment	not modelled	99.6	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
53	d2o57a1	Alignment	not modelled	99.6	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase

54	c3lbfC_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
55	c3mggB_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyl transferase from methanosarcina2 mazei
56	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
57	d2fk8a1	Alignment	not modelled	99.6	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
58	d1l3ia_	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
59	d1g8aa_	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
60	c3p2kA_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of an antibiotic related methyltransferase
61	d2h00a1	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Methyltransferase 10 domain
62	d1jg1a_	Alignment	not modelled	99.6	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
63	c3njrB_	Alignment	not modelled	99.6	12	**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
64	c3g07C_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**7sk snrna methylphosphate capping enzyme; **PDBTitle:** methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
65	c2gpyB_	Alignment	not modelled	99.6	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** crystal structure of putative o-methyltransferase from bacillus2 halodurans
66	d1ve3a1	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
67	d1prya_	Alignment	not modelled	99.6	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
68	d1zx0a1	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
69	c2yr0A_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha0223; **PDBTitle:** crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
70	d2frna1	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Met-10+ protein-like
71	d1r74a_	Alignment	not modelled	99.6	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
72	d1jqea_	Alignment	not modelled	99.6	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Histamine methyltransferase
73	c3ocjA_	Alignment	not modelled	99.6	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
74	d1xvaa_	Alignment	not modelled	99.6	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
75	c3opnA_	Alignment	not modelled	99.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hemolysin; **PDBTitle:** the crystal structure of a putative hemolysin from lactococcus lactis
76	d1y8ca_	Alignment	not modelled	99.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
77	c3id5F_	Alignment	not modelled	99.6	14	**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
78	d1p1ca_	Alignment	not modelled	99.6	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase

79	c2yvlB_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
80	c3mq2A_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methyltransferase; **PDBTitle:** crystal structure of 16s rrna methyltranferase kamb
81	c3merA_	Alignment	not modelled	99.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**slr1183 protein; **PDBTitle:** crystal structure of the methyltransferase slr1183 from2 synechocystis sp. pcc 6803, northeast structural genomics3 consortium target sgr145
82	c3tfwB_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative o-methyltransferase; **PDBTitle:** crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
83	c3ntvB_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mw1564 protein; **PDBTitle:** crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus
84	c3f4kA_	Alignment	not modelled	99.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
85	d2fpoa1	Alignment	not modelled	99.6	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
86	d1i1na_	Alignment	not modelled	99.6	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
87	c3p9nA_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible methyltransferase (methylase); **PDBTitle:** rv2966c of m. tuberculosis is a rsmd-like methyltransferase
88	c2vduE_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** E: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** structure of trm8-trm82, the yeast trna m7g methylation2 complex
89	c3dmgA_	Alignment	not modelled	99.6	18	**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
90	c2pwyB_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
91	d2ex4a1	Alignment	not modelled	99.6	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
92	d1vbfa_	Alignment	not modelled	99.6	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
93	c3ujcA_	Alignment	not modelled	99.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase; **PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
94	d1g8sa_	Alignment	not modelled	99.6	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
95	c3jwgA_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase type 12; **PDBTitle:** crystal structure analysis of the methyltransferase domain2 of bacterial-cthen1-c
96	c3b89A_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** crystal structure of rrna methylase from escherichia coli
97	c3dlcA_	Alignment	not modelled	99.5	20	**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
98	c3q87B_	Alignment	not modelled	99.5	16	**PDB header:**transferase activator/transferase **Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase; **PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
99	d2a14a1	Alignment	not modelled	99.5	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arylamine N-methyltransferase
100	d2avna1	Alignment	not modelled	99.5	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
101	c3g2qA_	Alignment	not modelled	99.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pcza361.24; **PDBTitle:** crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
102	c2p8jA_	Alignment	not modelled	99.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine-dependent methyltransferase; **PDBTitle:** crystal structure of s-adenosylmethionine-dependent methyltransferase2 (np_349143.1) from clostridium acetobutylicum at 2.00 a resolution

103	d1r18a_	Alignment	not modelled	99.5	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
104	c2pxxA_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mgc2408; **PDBTitle:** human putative methyltransferase mgc2408
105	c2esrB_	Alignment	not modelled	99.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** conserved hypothetical protein- streptococcus pyogenes
106	c2p35A_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 2-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
107	d1pjza_	Alignment	not modelled	99.5	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
108	c3a26A_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein ph0793; **PDBTitle:** crystal structure of p. horikoshii tyw2 in complex with2 mesado
109	c2pbfA_	Alignment	not modelled	99.5	27	**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
110	d1p91a_	Alignment	not modelled	99.5	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
111	c3ofkA_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nodulation protein s; **PDBTitle:** crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah)
112	c3busB_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of rebm
113	c3c3yB_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum
114	d2esra1	Alignment	not modelled	99.5	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
115	c3e23A_	Alignment	not modelled	99.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rpa2492; **PDBTitle:** crystal structure of the rpa2492 protein in complex with2 sam from rhodopseudomonas palustris, northeast structural3 genomics consortium target rpr299
116	d1wzna1	Alignment	not modelled	99.5	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
117	c3cbgA_	Alignment	not modelled	99.5	11	**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
118	d1susa1	Alignment	not modelled	99.5	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**COMT-like
119	c3lcvB_	Alignment	not modelled	99.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sisomicin-gentamicin resistance methylase sgm; **PDBTitle:** crystal structure of antibiotic related methyltransferase
120	d1d2ha_	Alignment	not modelled	99.5	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase