



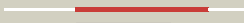
















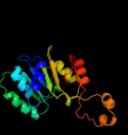











#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2o57a1	 Alignment		100.0	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
2	d1vl5a_	 Alignment		100.0	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
3	c1vl5B_	 Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: unknown conserved protein bh2331; PDBTitle: crystal structure of a putative methyltransferase (bh2331) from <i>Bacillus halodurans</i> c-125 at 1.95 Å resolution
4	c3busB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
5	d1nkva_	 Alignment		100.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein YjHP
6	c3g5lA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent PDBTitle: crystal structure of putative s-adenosylmethionine2 dependent methyltransferase from <i>Listeria monocytogenes</i>
7	d1kpiA_	 Alignment		100.0	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
8	c2fk8A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: methoxy mycolic acid synthase 4; PDBTitle: crystal structure of hma (mmaa4) from <i>Mycobacterium tuberculosis</i> 2 complexed with s-adenosylmethionine
9	d1l1ea_	 Alignment		100.0	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
10	c3e7pA_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from <i>Bacteroides2 vulgatus</i> atcc 8482
11	d2fk8a1	 Alignment		99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase

12	d1kpga_	Alignment		99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
13	d1tpya_	Alignment		99.9	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
14	c3bkxB_	Alignment		99.9	14	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
15	c3bkWB_	Alignment		99.9	20	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of s-adenosylmethionine dependent methyltransferase2 (np_104914.1) from mesorhizobium loti at 1.60 a resolution
16	d1jqea_	Alignment		99.9	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
17	c3cc8A_	Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a putative methyltransferase (bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution
18	d2gh1a1	Alignment		99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
19	c3e23A_	Alignment		99.9	21	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 rhodospseudomonas palustris, northeast structural3 genomics consortium target rpr299
20	c3f4kA_	Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
21	c3ocjA_	Alignment	not modelled	99.9	19	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
22	c3ccfB_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: crystal structure of putative methyltransferase (yp_321342.1) from2 anabaena variabilis atcc 29413 at 1.90 a resolution
23	d1xxla_	Alignment	not modelled	99.9	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
24	d2p7ia1	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
25	c2yr0A_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
26	c3lccA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
27	c2p7iB_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sam dependent methyl-transferase type 12 family2 protein (eca1738) from pectobacterium atrosepticum scri1043 at 1.74 a3 resolution
						PDB header: transferase

28	c3ujcA	Alignment	not modelled	99.9	15	Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
29	c3dliB	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
30	d2ex4a1	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
31	c3mggB	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei
32	c3dlcA	Alignment	not modelled	99.9	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
33	c3l8dA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus2 thuringiensis
34	c3e8sA	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: putative sam dependent methyltransferase; PDBTitle: crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
35	c3bgvC	Alignment	not modelled	99.9	16	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
36	d1r74a	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
37	c1z3cA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozoan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
38	d1ri5a	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
39	c3g2qA	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
40	d1im8a	Alignment	not modelled	99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
41	c3h2bB	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of the sam-dependent methyltransferase2 cg3271 from corynebacterium glutamicum in complex with s-3 adenosyl-l-homocysteine and pyrophosphate. northeast4 structural genomics consortium target cgr113a
42	d1xtpa	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
43	c3ou7A	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
44	d2a14a1	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase
45	d1xvaa	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
46	c2p35A	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
47	c2qs9A	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from thermus thermophilis hb8
48	d1y8ca	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
49	c3g5tA	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase2 from yeast
50	c3ndjA	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
51	d1vlma	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
						PDB header: structural genomics, unknown function

52	c3m70A_	Alignment	not modelled	99.9	15	Chain: A: PDB Molecule: tellurite resistance protein tehh homolog; PDBTitle: crystal structure of tehh from haemophilus influenzae
53	c3ofkA_	Alignment	not modelled	99.9	17	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)
54	d1xcla_	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
55	c3dh0B_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: sam dependent methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
56	c3egeA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase from antibiotic biosynthesis PDBTitle: crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution
57	d1wzna1	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
58	c3opnA_	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hemolysin; PDBTitle: the crystal structure of a putative hemolysin from lactococcus lactis
59	c3dtnA_	Alignment	not modelled	99.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methyltransferase mm_2633; PDBTitle: crystal structure of putative methyltransferase-mm_26332 from methanosarcina mazel .
60	c3hnrA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase bt9727_4108; PDBTitle: crystal structure of a probable methyltransferase2 bt9727_4108 from bacillus thuringiensis subsp. northeast3 structural genomics consortium target id bur219
61	c3sm3A_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferases; PDBTitle: crystal structure of sam-dependent methyltransferases q8puk2_metma2 from methanosarcina mazel. northeast structural genomics consortium3 target mar262.
62	d1ve3a1	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
63	c1yb2A_	Alignment	not modelled	99.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0852; PDBTitle: structure of a putative methyltransferase from thermoplasma2 acidophilum.
64	d1yb2a1	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like
65	c3mq2A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 16s rrna methyltransferase; PDBTitle: crystal structure of 16s rrna methyltransferase kamb
66	d1zx0a1	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
67	c3jwgA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: methyltransferase type 12; PDBTitle: crystal structure analysis of the methyltransferase domain2 of bacterial-cthen1-c
68	c3g07C_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: C: PDB Molecule: 7sk snrna methylphosphate capping enzyme; PDBTitle: methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
69	c3merA_	Alignment	not modelled	99.9	12	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
70	c2iipD_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: D: PDB Molecule: nicotinamide n-methyltransferase; PDBTitle: human nicotinamide n-methyltransferase
71	d1d2ha_	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
72	c3gwzB_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr
73	c3d21C_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: C: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exiguobacterium sp. 255-15 at 1.90 a resolution
74	c1x1aA_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: crtf-related protein; PDBTitle: crystal structure of bchu complexed with s-adenosyl-l-methionine
75	c3bxoA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: n,n-dimethyltransferase; PDBTitle: crystal structure of streptomyces venezuelae desvi
						PDB header: transferase

76	c2r3sA_	Alignment	not modelled	99.9	15	Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative o-methyltransferase (npun_r0239) from2 nostoc punctiforme pcc 73102 at 2.15 a resolution
77	c3lecA_	Alignment	not modelled	99.9	18	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
78	c3pfhD_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: D: PDB Molecule: n-methyltransferase; PDBTitle: x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n
79	d1o54a_	Alignment	not modelled	99.9	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like
80	d1yzha1	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
81	d2avna1	Alignment	not modelled	99.8	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
82	d2fcaa1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
83	c3gnlB_	Alignment	not modelled	99.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein, duf633, lmf2365_1472; PDBTitle: structure of uncharacterized protein (lmf2365_1472) from2 listeria monocytogenes serotype 4b
84	c3ku1E_	Alignment	not modelled	99.8	16	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
85	d1pjza_	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
86	d1p1ca_	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
87	d1dusa_	Alignment	not modelled	99.8	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein MJ0882
88	c3dp7B_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
89	c3dxyA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(7)-)-methyltransferase; PDBTitle: crystal structure of ectmb in complex with sam
90	d2bzga1	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
91	c2pwyB_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: trna (adenine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a m1a58 trna methyltransferase
92	d1qzza2	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
93	d2nxca1	Alignment	not modelled	99.8	27	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ribosomal protein L11 methyltransferase PrmA
94	d2g72a1	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase
95	c3mczB_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase; PDBTitle: the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
96	c3i53A_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
97	c2p8jA_	Alignment	not modelled	99.8	20	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
98	c3jwhA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: hen1; PDBTitle: crystal structure analysis of the methyltransferase domain2 of bacterial-avhen1-c
99	c3mtiA_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: rrna methylase; PDBTitle: the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
100	c3grzA_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: ribosomal protein l11 methyltransferase; PDBTitle: crystal structure of ribosomal protein l11 methylase

						from2 lactobacillus delbrueckii subsp. bulgaricus
101	d2i6ga1	Alignment	not modelled	99.8	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TehB-like
102	c3ggdA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anabaena variabilis atcc 29413 at 2.11 a resolution
103	c2vdwA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: vaccinia virus capping enzyme d1 subunit; PDBTitle: guanosine n7 methyl-transferase sub-complex (d1-d12) of the2 vaccinia virus mrna capping enzyme
104	c2ip2B	Alignment	not modelled	99.8	19	PDB header: transferase Chain: B: PDB Molecule: probable phenazine-specific methyltransferase; PDBTitle: structure of the pyocyanin biosynthetic protein phzm
105	c3p2kA	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: 16s rrna methylase; PDBTitle: structure of an antibiotic related methyltransferase
106	c3lstB	Alignment	not modelled	99.8	10	PDB header: transferase Chain: B: PDB Molecule: calo1 methyltransferase; PDBTitle: crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
107	d1l3ia	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Precorin-6Y methyltransferase (CbiT)
108	c2g8nB	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: phenylethanolamine n-methyltransferase; PDBTitle: structure of hpnmt with inhibitor 3-hydroxymethyl-7-(n-4-2 chlorophenylaminosulfonyl)-thiq and adohcy
109	c3cggB	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
110	c2pxxA	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein mgc2408; PDBTitle: human putative methyltransferase mgc2408
111	c3bgdB	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: thiopurine s-methyltransferase; PDBTitle: thiopurine s-methyltransferase
112	c3giwA	Alignment	not modelled	99.8	14	PDB header: unknown function Chain: A: PDB Molecule: protein of unknown function duf574; PDBTitle: crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
113	d1tw3a2	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
114	d1m6ya2	Alignment	not modelled	99.8	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: MraW-like putative methyltransferases
115	c3njrB	Alignment	not modelled	99.8	21	PDB header: transferase Chain: B: PDB Molecule: precorin-6y methylase; PDBTitle: crystal structure of c-terminal domain of precorin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
116	d1vbfa	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase
117	d1af7a2	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Chemotaxis receptor methyltransferase CheR, C-terminal domain
118	c3eeyl	Alignment	not modelled	99.8	17	PDB header: transferase Chain: J: PDB Molecule: putative rrna methylase; PDBTitle: crystal structure of putative rrna-methylase from clostridium2 thermocellum
119	c3e05B	Alignment	not modelled	99.8	19	PDB header: transferase Chain: B: PDB Molecule: precorin-6y c5,15-methyltransferase (decarboxylating); PDBTitle: crystal structure of precorin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
120	c3lpmA	Alignment	not modelled	99.8	10	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes