Phyre^2

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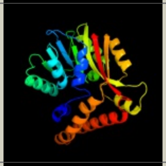
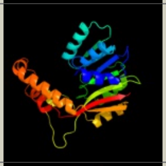
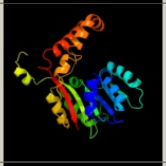
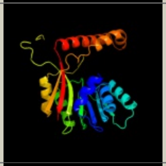
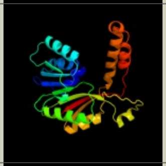
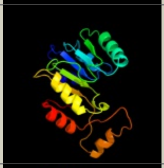
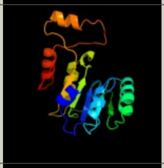
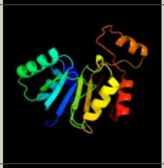
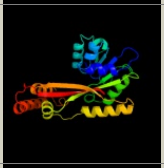
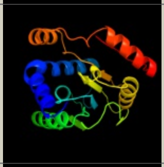
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nkva_	Alignment		100.0	98	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical Protein YjhP
2	c3e7pA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
3	c3f4kA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
4	d2o57a1	Alignment		100.0	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
5	c3ujcA_	Alignment		99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase; **PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
6	d1kpga_	Alignment		99.9	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
7	c2fk8A_	Alignment		99.9	11	**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
8	d1l1ea_	Alignment		99.9	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
9	d1kpia_	Alignment		99.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
10	d1tpya_	Alignment		99.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
11	c3bkxB_	Alignment		99.9	17	**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

12	d2fk8a1	Alignment		99.9	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
13	c3busB_	Alignment		99.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of rebm
14	c1vl5B_	Alignment		99.9	16	**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
15	d1vl5a_	Alignment		99.9	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
16	c3mggB_	Alignment		99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyl transferase from methanosarcina2 mazei
17	d1xxla_	Alignment		99.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
18	c2yr0A_	Alignment		99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha0223; **PDBTitle:** crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
19	c3dlcA_	Alignment		99.9	16	**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
20	d1jqea_	Alignment		99.9	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Histamine methyltransferase
21	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
22	c3ccfB_	Alignment	not modelled	99.9	16	**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	d2gh1a1	Alignment	not modelled	99.9	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**BC2162-like
24	c3ocjA_	Alignment	not modelled	99.9	16	**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
25	d2ex4a1	Alignment	not modelled	99.9	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
26	c3lccA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyl chloride transferase; **PDBTitle:** structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
27	c3l8dA_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyltransferase from bacillus2 thuringiensis
28	c3bgvC	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mrna cap guanine-n7 methyltransferase;

28	c3bgvC_	Alignment	not modelled	99.8	14	**PDBTitle:** crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
29	c3g5tA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast
30	c3egeA_	Alignment	not modelled	99.8	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
31	d1xtpa_	Alignment	not modelled	99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
32	c3ndjA_	Alignment	not modelled	99.8	17	**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
33	c3mq2A_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methyltransferase; **PDBTitle:** crystal structure of 16s rrna methyltranferase kamb
34	c3cc8A_	Alignment	not modelled	99.8	17	**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
35	c3dh0B_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam dependent methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
36	c3dliB_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
37	c3ou7A_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** dhpi-sam-hep complex
38	d1xcla_	Alignment	not modelled	99.8	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
39	c3h2bB_	Alignment	not modelled	99.8	18	**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
40	c3e23A_	Alignment	not modelled	99.8	17	**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
41	c2gs9A_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein tt1324; **PDBTitle:** crystal structure of tt1324 from thermus thermophilis hb8
42	d1im8a_	Alignment	not modelled	99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein HI0319 (YecO)
43	d1zx0a1	Alignment	not modelled	99.8	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
44	c3g5lA_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative s-adenosylmethionine dependent **PDBTitle:** crystal structure of putative s-adenosylmethionine2 dependent methyltransferase from listeria monocytogenes
45	c3g2qA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pcza361.24; **PDBTitle:** crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
46	c3e8sA_	Alignment	not modelled	99.8	19	**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
47	c3bkwB_	Alignment	not modelled	99.8	19	**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
48	c2r3sA_	Alignment	not modelled	99.8	13	**PDB header:**transferase **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
49	c3dtnA_	Alignment	not modelled	99.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative methyltransferase mm_2633; **PDBTitle:** crystal structure of putative methyltransferase-mm_26332 from methanosarcina mazei .
50	d1qzza2	Alignment	not modelled	99.8	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
51	c3opnA_	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hemolysin; **PDBTitle:** the crystal structure of a putative hemolysin from

						lactococcus lactis
52	c3lstB_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calo1 methyltransferase; **PDBTitle:** crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
53	d1vlma_	Alignment	not modelled	99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
54	c3ofkA_	Alignment	not modelled	99.8	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)
55	d2avna1	Alignment	not modelled	99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
56	d1ri5a_	Alignment	not modelled	99.8	25	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap (Guanine N-7) methyltransferase
57	c1z3cA_	Alignment	not modelled	99.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
58	d1tw3a2	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
59	c3gwzB_	Alignment	not modelled	99.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mmcr; **PDBTitle:** structure of the mitomycin 7-o-methyltransferase mmcr
60	c3hnrA_	Alignment	not modelled	99.8	18	**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	d1ve3a1	Alignment	not modelled	99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
62	d2a14a1	Alignment	not modelled	99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arylamine N-methyltransferase
63	c3dp7B_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
64	d1yzha1	Alignment	not modelled	99.7	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
65	d2p7ia1	Alignment	not modelled	99.7	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
66	c1tw3A_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carminomycin 4-o-methyltransferase; **PDBTitle:** crystal structure of carminomycin-4-o-methyltransferase2 (dnrk) in complex with s-adenosyl-l-homocystein (sah) and3 4-methoxy-e-rhodomycin t (m-et)
67	c2p7iB_	Alignment	not modelled	99.7	14	**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
68	c1yb2A_	Alignment	not modelled	99.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
69	d1yb2a1	Alignment	not modelled	99.7	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
70	c3i53A_	Alignment	not modelled	99.7	15	**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)
71	d1o54a_	Alignment	not modelled	99.7	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
72	c3mczB_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
73	c3merA_	Alignment	not modelled	99.7	23	**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
74	d1p1ca_	Alignment	not modelled	99.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
75	c3mb5A_	Alignment	not modelled	99.7	22	**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
76	d1xvaa_	Alignment	not modelled	99.7	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
77	c3lecA_	Alignment	not modelled	99.7	13	**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	c3g07C_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**7sk snrna methylphosphate capping enzyme; **PDBTitle:** methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
79	d1pjza_	Alignment	not modelled	99.7	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
80	d1kyza2	Alignment	not modelled	99.7	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
81	d2nxca1	Alignment	not modelled	99.7	25	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
82	d1dusa_	Alignment	not modelled	99.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
83	c2iipD_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinamide n-methyltransferase; **PDBTitle:** human nicotinamide n-methyltransferase
84	c3m70A_	Alignment	not modelled	99.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
85	c3bxoA_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n,n-dimethyltransferase; **PDBTitle:** crystal structure of streptomyces venezuelae desvi
86	c1x1aA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**crtf-related protein; **PDBTitle:** crystal structure of bchu complexed with s-adenosyl-l-methionine
87	d1m6ya2	Alignment	not modelled	99.7	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
88	c3ggdA_	Alignment	not modelled	99.7	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
89	c2pwyB_	Alignment	not modelled	99.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
90	d1wzna1	Alignment	not modelled	99.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
91	c3gnlB_	Alignment	not modelled	99.7	12	**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
92	c2ip2B_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable phenazine-specific methyltransferase; **PDBTitle:** structure of the pyocyanin biosynthetic protein phzm
93	c3sm3A_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferases; **PDBTitle:** crystal structure of sam-dependent methyltransferases q8puk2_metma2 from methanosarcina mazei. northeast structural genomics consortium3 target mar262.
94	d1r74a_	Alignment	not modelled	99.7	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
95	c1xduA_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein rdmb; **PDBTitle:** crystal structure of aclacinomycin-10-hydroxylase (rdmb) in complex2 with sinefungin (sfg)
96	d1jg1a_	Alignment	not modelled	99.7	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
97	d2fcaa1	Alignment	not modelled	99.7	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
98	c3ku1E_	Alignment	not modelled	99.7	13	**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
99	c3pfhD_	Alignment	not modelled	99.7	18	**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
100	c3iwgA_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase type 12;

100	c3jwgA_	Alignment	not modelled	99.7	18	**PDBTitle:** crystal structure analysis of the methyltransferase domain2 of bacterial-cthen1-c
101	c3njrB_	Alignment	not modelled	99.7	21	**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
102	c2pxxA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mgc2408; **PDBTitle:** human putative methyltransferase mgc2408
103	d1d2ha_	Alignment	not modelled	99.7	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
104	c3e05B_	Alignment	not modelled	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
105	d1wg8a2	Alignment	not modelled	99.7	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
106	c3p2kA_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of an antibiotic related methyltransferase
107	d1fp1d2	Alignment	not modelled	99.7	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
108	d1g8sa_	Alignment	not modelled	99.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
109	d2bzga1	Alignment	not modelled	99.7	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
110	c2p8jA_	Alignment	not modelled	99.7	15	**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
111	d2i6ga1	Alignment	not modelled	99.7	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TehB-like
112	d1l3ia_	Alignment	not modelled	99.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
113	d1y8ca_	Alignment	not modelled	99.7	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
114	c3grzA_	Alignment	not modelled	99.7	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
115	c2yvlB_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
116	c3dxyA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of ectrmb in complex with sam
117	c1kyzC_	Alignment	not modelled	99.7	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**caffeic acid 3-o-methyltransferase; **PDBTitle:** crystal structure analysis of caffeic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex
118	d1vbfa_	Alignment	not modelled	99.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
119	c3id5F_	Alignment	not modelled	99.7	19	**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
120	c3d2lC_	Alignment	not modelled	99.7	16	**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