Phyre^2

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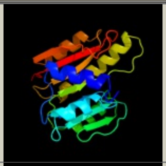
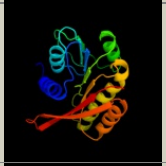
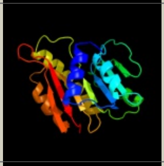
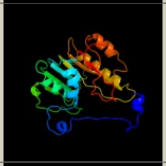
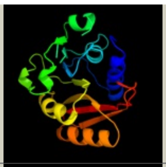
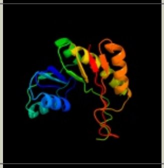
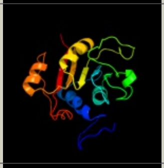
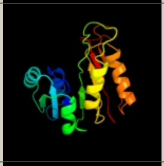
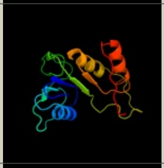
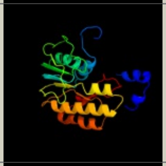
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ej0a_	Alignment		100.0	100	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**RNA methyltransferase FtsJ
2	c2nyuA_	Alignment		100.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative ribosomal rna methyltransferase 2; **PDBTitle:** crystal structure of human ftsj homolog 2 (e.coli) protein2 in complex with s-adenosylmethionine
3	c2plwA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna methyltransferase, putative; **PDBTitle:** crystal structure of a ribosomal rna methyltransferase, putative, from2 plasmodium falciparum (pf13_0052).
4	c3douA_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase j; **PDBTitle:** crystal structure of methyltransferase involved in cell2 division from thermoplasma volcanicum gss1
5	c2wa1A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**non-structural protein 5; **PDBTitle:** structure of the methyltransferase domain from modoc virus,2 a flavivirus with no known vector (nkv)
6	c2px2B_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**genome polyprotein [contains: capsid protein c **PDBTitle:** crystal structure of the murray valley encephalitis virus2 ns5 2'-o methyltransferase domain in complex with sah3 (monoclinic form 1)
7	c2p3qA_	Alignment		100.0	19	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**type ii methyltransferase; **PDBTitle:** crystal structure of dengue methyltransferase in complex with gpppg2 and s-adenosyl-l-homocysteine
8	c3lkzB_	Alignment		100.0	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**non-structural protein 5; **PDBTitle:** structural and functional analyses of a conserved hydrophobic pocket2 of flavivirus methyltransferase
9	c3gczA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** yokose virus methyltransferase in complex with adomet
10	d2p41a1	Alignment		100.0	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap methylase
11	c3evaA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase ns5; **PDBTitle:** crystal structure of yellow fever virus methyltransferase complexed2 with s-adenosyl-l-homocysteine

12	c3opnA_	Alignment		99.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hemolysin; **PDBTitle:** the crystal structure of a putative hemolysin from lactococcus lactis
13	c2frxD_	Alignment		99.9	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
14	c3m6wA_	Alignment		99.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
15	c3hp7A_	Alignment		99.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
16	c3m4xA_	Alignment		99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
17	c2yxlA_	Alignment		99.8	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
18	d1ixka_	Alignment		99.8	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
19	c3elyA_	Alignment		99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** wesselsbron virus methyltransferase in complex with adohcy
20	c1sqgA_	Alignment		99.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sun protein; **PDBTitle:** the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
21	c2oxtC_	Alignment	not modelled	99.7	21	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**nucleoside-2'-o-methyltransferase; **PDBTitle:** crystal structure of meaban virus nucleoside-2'-o-2 methyltransferase
22	c3a4tA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase mj0026; **PDBTitle:** crystal structure of atrm4 from m.jannaschii with sinefungin
23	d1wg8a2	Alignment	not modelled	99.6	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
24	d1sqga2	Alignment	not modelled	99.6	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
25	c3eeyJ_	Alignment	not modelled	99.6	21	**PDB header:**transferase **Chain:** J: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of putative rrna-methylase from clostridium2 thermocellum
26	d1m6ya2	Alignment	not modelled	99.6	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
27	d2b9ea1	Alignment	not modelled	99.5	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
28	d1g8aa_	Alignment	not modelled	99.5	25	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue

29	c2ipxA_	Alignment	not modelled	99.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna 2'-o-methyltransferase fibrillarin; **PDBTitle:** human fibrillarin
30	c3id5F_	Alignment	not modelled	99.5	20	**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
31	d1prya_	Alignment	not modelled	99.4	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
32	c3bkxB_	Alignment	not modelled	99.4	15	**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
33	d2as0a2	Alignment	not modelled	99.4	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
34	d1yb2a1	Alignment	not modelled	99.4	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
35	c1yb2A_	Alignment	not modelled	99.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
36	c3mtiA_	Alignment	not modelled	99.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
37	d1o54a_	Alignment	not modelled	99.4	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
38	d1i9ga_	Alignment	not modelled	99.4	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
39	c3mb5A_	Alignment	not modelled	99.4	23	**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
40	d1g8sa_	Alignment	not modelled	99.4	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
41	d2b78a2	Alignment	not modelled	99.3	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
42	c2as0A_	Alignment	not modelled	99.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph1915; **PDBTitle:** crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
43	c2ozvA_	Alignment	not modelled	99.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein atu0636; **PDBTitle:** crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
44	d1nt2a_	Alignment	not modelled	99.3	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
45	c3g5tA_	Alignment	not modelled	99.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast
46	c2yvlB_	Alignment	not modelled	99.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
47	c2b78A_	Alignment	not modelled	99.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein smu.776; **PDBTitle:** a putative sam-dependent methyltransferase from2 streptococcus mutans
48	c2fk8A_	Alignment	not modelled	99.3	22	**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
49	d1wxxa2	Alignment	not modelled	99.3	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
50	d1yzha1	Alignment	not modelled	99.3	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
51	d2fk8a1	Alignment	not modelled	99.3	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
52	d1l1ea_	Alignment	not modelled	99.3	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
53	c3e05B_	Alignment	not modelled	99.3	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

54	d1kpia_	Alignment	not modelled	99.3	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
55	c2pwyB_	Alignment	not modelled	99.3	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
56	d2b3ta1	Alignment	not modelled	99.3	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
57	d1kpga_	Alignment	not modelled	99.3	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
58	c1wxwA_	Alignment	not modelled	99.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha1280; **PDBTitle:** crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophillus hb8
59	c3ujcA_	Alignment	not modelled	99.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase; **PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
60	d1tpya_	Alignment	not modelled	99.2	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
61	c3bgvC_	Alignment	not modelled	99.2	18	**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
62	c3c0kB_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0064 protein yccw; **PDBTitle:** crystal structure of a ribosomal rna methyltranferase
63	c3lpmA_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
64	d1l3ia_	Alignment	not modelled	99.2	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
65	c3ofkA_	Alignment	not modelled	99.2	14	**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)
66	c3ku1E_	Alignment	not modelled	99.2	15	**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
67	d1i1na_	Alignment	not modelled	99.2	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
68	d2b25a1	Alignment	not modelled	99.2	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
69	c3grzA_	Alignment	not modelled	99.2	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
70	c1wg8B_	Alignment	not modelled	99.2	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted s-adenosylmethionine-dependent **PDBTitle:** crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
71	d1dusa_	Alignment	not modelled	99.2	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
72	c3lecA_	Alignment	not modelled	99.1	15	**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
73	d1dl5a1	Alignment	not modelled	99.1	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
74	d2nxca1	Alignment	not modelled	99.1	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
75	d1jqea_	Alignment	not modelled	99.1	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Histamine methyltransferase
76	c3e23A_	Alignment	not modelled	99.1	14	**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
77	d1xcla_	Alignment	not modelled	99.1	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
						PDB header:transferase

78	c3a26A_	Alignment	not modelled	99.1	19	**Chain:** A: **PDB Molecule:**uncharacterized protein ph0793; **PDBTitle:** crystal structure of p. horikoshii tyw2 in complex with2 mesado
79	c3ggdA_	Alignment	not modelled	99.1	12	**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
80	d1ve3a1	Alignment	not modelled	99.1	25	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
81	c1m6yA_	Alignment	not modelled	99.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
82	c3hm2G_	Alignment	not modelled	99.1	13	**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
83	d2o57a1	Alignment	not modelled	99.1	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
84	d2igta1	Alignment	not modelled	99.1	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
85	c3e7pA_	Alignment	not modelled	99.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
86	d1nkva_	Alignment	not modelled	99.1	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical Protein YjhP
87	c3evzA_	Alignment	not modelled	99.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal strucure of methyltransferase from pyrococcus furiosus
88	d1nv8a_	Alignment	not modelled	99.1	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
89	c3gnlB_	Alignment	not modelled	99.1	14	**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
90	d2gh1a1	Alignment	not modelled	99.1	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**BC2162-like
91	c3dliB_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
92	c3ccfB_	Alignment	not modelled	99.1	17	**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
93	d2frna1	Alignment	not modelled	99.1	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Met-10+ protein-like
94	d2fcaa1	Alignment	not modelled	99.1	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
95	c1z3cA_	Alignment	not modelled	99.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
96	d1ri5a_	Alignment	not modelled	99.0	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap (Guanine N-7) methyltransferase
97	c3ocjA_	Alignment	not modelled	99.0	12	**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
98	c3dmgA_	Alignment	not modelled	99.0	17	**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
99	c3f4kA_	Alignment	not modelled	99.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
100	c1dl5A_	Alignment	not modelled	99.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase
101	d1zx0a1	Alignment	not modelled	99.0	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
						PDB header:transferase

102	c3njrB_	Alignment	not modelled	99.0	16	**Chain:** B: **PDB Molecule:**precorrin-6y methylase; **PDBTitle:** crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
103	d2ex4a1	Alignment	not modelled	99.0	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
104	c2yxeB_	Alignment	not modelled	99.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of l-isoaspartyl protein carboxyl methyltranferase
105	c3dxyA_	Alignment	not modelled	99.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of ectrmb in complex with sam
106	c3h2bB_	Alignment	not modelled	99.0	20	**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
107	d1r18a_	Alignment	not modelled	99.0	25	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
108	c2pbfA_	Alignment	not modelled	99.0	14	**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
109	c3a27A_	Alignment	not modelled	99.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mj1557; **PDBTitle:** crystal structure of m. jannaschii tyw2 in complex with2 adomet
110	d1p1ca_	Alignment	not modelled	99.0	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
111	d1xxla_	Alignment	not modelled	99.0	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
112	c2yx1A_	Alignment	not modelled	99.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein mj0883; **PDBTitle:** crystal structure of m.jannaschii trna m1g37 methyltransferase
113	c2yxdA_	Alignment	not modelled	99.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable cobalt-precorrin-6y c(15)-methyltransferase **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbit)
114	c3duwB_	Alignment	not modelled	99.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase, putative; **PDBTitle:** crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah
115	c2yr0A_	Alignment	not modelled	99.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha0223; **PDBTitle:** crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
116	c3cc8A_	Alignment	not modelled	99.0	13	**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
117	d1r74a_	Alignment	not modelled	99.0	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
118	c1vl5B_	Alignment	not modelled	99.0	19	**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
119	d1y8ca_	Alignment	not modelled	99.0	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
120	c2pjdA_	Alignment	not modelled	99.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase c; **PDBTitle:** crystal structure of 16s rrna methyltransferase rsmc