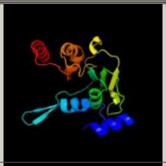
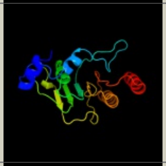
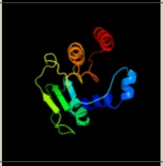
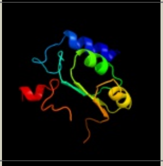
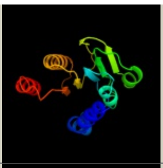
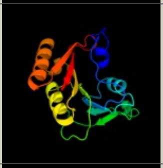
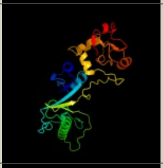
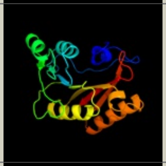
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0ADR6
Date	Thu Jan 5 11:21:40 GMT 2012
Unique Job ID	a2f54fd99549edbe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2p41a1	Alignment		99.9	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap methylase
2	c3gczA_	Alignment		99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** yokose virus methyltransferase in complex with adomet
3	c3lkzB_	Alignment		99.9	26	**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
4	c2p3qA_	Alignment		99.8	26	**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
5	c3evaA_	Alignment		99.8	25	**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
6	c2px2B_	Alignment		99.8	27	**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	c3hp7A_	Alignment		99.7	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
8	c2wa1A_	Alignment		99.6	19	**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)
9	c3douA_	Alignment		99.5	28	**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
10	c2plwA_	Alignment		99.5	17	**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).
11	c2nyuA_	Alignment		99.5	21	**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

12	d1ej0a_	Alignment		99.4	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**RNA methyltransferase FtsJ
13	c3opnA_	Alignment		99.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hemolysin; **PDBTitle:** the crystal structure of a putative hemolysin from lactococcus lactis
14	d1g8aa_	Alignment		98.7	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
15	d1nt2a_	Alignment		98.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
16	d1prya_	Alignment		98.6	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
17	d1g8sa_	Alignment		98.6	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
18	c3lduA_	Alignment		98.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methylase; **PDBTitle:** the crystal structure of a possible methylase from2 clostridium difficile 630.
19	c2ipxA_	Alignment		98.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna 2'-o-methyltransferase fibrillarin; **PDBTitle:** human fibrillarin
20	c3id5F_	Alignment		98.5	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
21	c3mtiA_	Alignment	not modelled	98.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
22	c3elyA_	Alignment	not modelled	98.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** wesselsbron virus methyltransferase in complex with adohcy
23	c3eeyJ_	Alignment	not modelled	98.3	15	**PDB header:**transferase **Chain:** J: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of putative rrna-methylase from clostridium2 thermocellum
24	c2oxtC_	Alignment	not modelled	98.2	27	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**nucleoside-2'-o-methyltransferase; **PDBTitle:** crystal structure of meaban virus nucleoside-2'-o-2 methyltransferase
25	d1qama_	Alignment	not modelled	98.2	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
26	d1l3ia_	Alignment	not modelled	98.1	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
27	d2i6ga1	Alignment	not modelled	98.0	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TehB-like
28	d1vl5a_	Alignment	not modelled	98.0	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like

29	c1vl5B_	Alignment	not modelled	98.0	13	**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
30	d1ixka_	Alignment	not modelled	98.0	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
31	c2yxdA_	Alignment	not modelled	98.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable cobalt-precorrin-6y c(15)-methyltransferase **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbit)
32	d1wg8a2	Alignment	not modelled	97.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
33	d1vbfa_	Alignment	not modelled	97.9	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
34	c3bkxB_	Alignment	not modelled	97.9	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
35	c3grrA_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
36	c3fydA_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable dimethyladenosine transferase; **PDBTitle:** crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
37	c3gdhC_	Alignment	not modelled	97.9	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**trimethylguanosine synthase homolog; **PDBTitle:** methyltransferase domain of human trimethylguanosine2 synthase 1 (tgs1) bound to m7gtp and adenosyl-homocysteine3 (active form)
38	c3cggB_	Alignment	not modelled	97.9	14	**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
39	d2ex4a1	Alignment	not modelled	97.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
40	c3tqsB_	Alignment	not modelled	97.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
41	d1ve3a1	Alignment	not modelled	97.9	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
42	c2fk8A_	Alignment	not modelled	97.9	17	**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
43	c3e05B_	Alignment	not modelled	97.8	9	**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
44	c3lecA_	Alignment	not modelled	97.8	9	**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
45	c3ujcA_	Alignment	not modelled	97.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase; **PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
46	c3egeA_	Alignment	not modelled	97.8	19	**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
47	d2fk8a1	Alignment	not modelled	97.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
48	c2yr0A_	Alignment	not modelled	97.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha0223; **PDBTitle:** crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
49	d1xxla_	Alignment	not modelled	97.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
50	d1dusa_	Alignment	not modelled	97.8	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
51	c2yxlA_	Alignment	not modelled	97.8	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
52	d1dl5a1	Alignment	not modelled	97.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent

52	d1dr5a1	Alignment	not modelled	97.8	18	methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
53	d2igta1	Alignment	not modelled	97.8	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
54	c3m33B_	Alignment	not modelled	97.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein from2 deinococcus radiodurans r1
55	d2nxca1	Alignment	not modelled	97.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
56	d1g6q1_	Alignment	not modelled	97.7	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
57	c3njrB_	Alignment	not modelled	97.7	9	**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
58	d1i9ga_	Alignment	not modelled	97.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
59	d2b78a2	Alignment	not modelled	97.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
60	d1fp2a2	Alignment	not modelled	97.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
61	d2fyta1	Alignment	not modelled	97.7	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
62	c3mggB_	Alignment	not modelled	97.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyl transferase from methanosarcina2 mazei
63	c3e7pA_	Alignment	not modelled	97.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
64	c3mb5A_	Alignment	not modelled	97.7	18	**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
65	d2b9ea1	Alignment	not modelled	97.7	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
66	d2o57a1	Alignment	not modelled	97.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
67	c3fuxB_	Alignment	not modelled	97.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
68	c3ofkA_	Alignment	not modelled	97.7	15	**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)
69	c3ku1E_	Alignment	not modelled	97.6	14	**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
70	c3e23A_	Alignment	not modelled	97.6	13	**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
71	c3grzA_	Alignment	not modelled	97.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
72	c3cc8A_	Alignment	not modelled	97.6	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
73	d1yuba_	Alignment	not modelled	97.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
74	d1nkva_	Alignment	not modelled	97.6	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical Protein YjhP
75	d1wxxa2	Alignment	not modelled	97.6	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
76	d1oria_	Alignment	not modelled	97.6	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
						PDB header:transferase

77	c1wxwA_	Alignment	not modelled	97.6	19	**Chain:** A: **PDB Molecule:**hypothetical protein ttha1280; **PDBTitle:** crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophillus hb8
78	d2avna1	Alignment	not modelled	97.6	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
79	c3ccfB_	Alignment	not modelled	97.6	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
80	c3lbfC_	Alignment	not modelled	97.6	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
81	d1m6ya2	Alignment	not modelled	97.6	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
82	c3a27A_	Alignment	not modelled	97.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mj1557; **PDBTitle:** crystal structure of m. jannaschii tyw2 in complex with2 adomet
83	c3gnlB_	Alignment	not modelled	97.6	11	**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
84	d2fpoa1	Alignment	not modelled	97.5	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
85	c1orhA_	Alignment	not modelled	97.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 1; **PDBTitle:** structure of the predominant protein arginine methyltransferase prmt1
86	d1f3la_	Alignment	not modelled	97.5	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
87	d1zq9a1	Alignment	not modelled	97.5	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
88	d1uwva2	Alignment	not modelled	97.5	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**(Uracil-5-)-methyltransferase
89	c3m70A_	Alignment	not modelled	97.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
90	c3f4kA_	Alignment	not modelled	97.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
91	d2p7ia1	Alignment	not modelled	97.5	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
92	d2esra1	Alignment	not modelled	97.5	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
93	d1pjza_	Alignment	not modelled	97.5	6	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
94	d1xdza_	Alignment	not modelled	97.5	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
95	d1l1ea_	Alignment	not modelled	97.5	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
96	c3g5tA_	Alignment	not modelled	97.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast
97	c2pwyB_	Alignment	not modelled	97.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
98	c3egiA_	Alignment	not modelled	97.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trimethylguanosine synthase homolog; **PDBTitle:** methyltransferase domain of human trimethylguanosine2 synthase tgs1 bound to m7gpppa (inactive form)
99	c1sqgA_	Alignment	not modelled	97.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sun protein; **PDBTitle:** the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
100	c3dliB_	Alignment	not modelled	97.4	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
101	c2ozvA_	Alignment	not modelled	97.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein atu0636; **PDBTitle:** crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.

102	c3l8dA_	Alignment	not modelled	97.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyltransferase from bacillus2 thuringiensis
103	c2yxeB_	Alignment	not modelled	97.4	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of l-isoaspartyl protein carboxyl methyltranferase
104	c1wg8B_	Alignment	not modelled	97.4	16	**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.
105	d1i1na_	Alignment	not modelled	97.4	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
106	d1o54a_	Alignment	not modelled	97.4	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
107	c2yvlB_	Alignment	not modelled	97.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
108	c3a26A_	Alignment	not modelled	97.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein ph0793; **PDBTitle:** crystal structure of p. horikoshii tyw2 in complex with2 mesado
109	c3b3jA_	Alignment	not modelled	97.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
110	d1wy7a1	Alignment	not modelled	97.4	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
111	d1xtpa_	Alignment	not modelled	97.4	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
112	c1dl5A_	Alignment	not modelled	97.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase
113	c3busB_	Alignment	not modelled	97.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of rebm
114	c1yb2A_	Alignment	not modelled	97.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
115	d1yb2a1	Alignment	not modelled	97.4	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
116	c3mq2A_	Alignment	not modelled	97.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methyltransferase; **PDBTitle:** crystal structure of 16s rrna methyltranferase kamb
117	d1kpia_	Alignment	not modelled	97.4	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
118	d2frna1	Alignment	not modelled	97.4	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Met-10+ protein-like
119	c3ggdA_	Alignment	not modelled	97.3	14	**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
120	d2b3ta1	Alignment	not modelled	97.3	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK