Phyre^2

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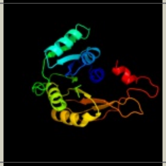
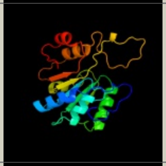
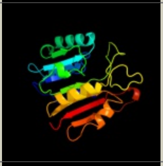
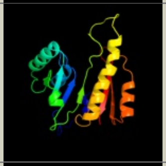
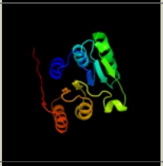
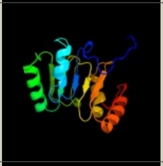
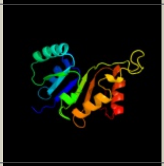
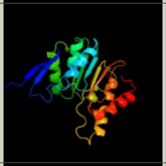
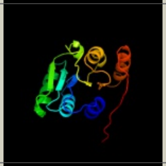
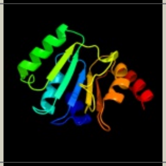
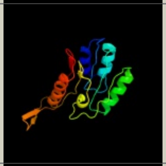
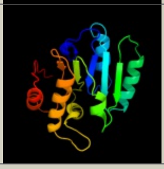
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lpmA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
2	c2ozvA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein atu0636; **PDBTitle:** crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
3	d1nv8a_	Alignment		99.9	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
4	c3evzA_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal strucure of methyltransferase from pyrococcus furiosus
5	c3eeyJ_	Alignment		99.9	16	**PDB header:**transferase **Chain:** J: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of putative rrna-methylase from clostridium2 thermocellum
6	d2b3ta1	Alignment		99.9	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
7	d2h00a1	Alignment		99.9	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Methyltransferase 10 domain
8	d1o54a_	Alignment		99.9	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
9	c1yb2A_	Alignment		99.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
10	d1yb2a1	Alignment		99.9	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
11	d2as0a2	Alignment		99.9	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase

12	c3q87B_	Alignment		99.9	15	**PDB header:**transferase activator/transferase **Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase; **PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
13	d1yzha1	Alignment		99.9	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
14	c3lecA_	Alignment		99.9	16	**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
15	d1xdza_	Alignment		99.9	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
16	c2as0A_	Alignment		99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph1915; **PDBTitle:** crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
17	c2pwyB_	Alignment		99.9	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
18	c3mb5A_	Alignment		99.9	28	**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
19	c2pjdA_	Alignment		99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase c; **PDBTitle:** crystal structure of 16s rrna methyltransferase rsmc
20	d1kpia_	Alignment		99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
21	c2fk8A_	Alignment	not modelled	99.8	16	**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
22	d1dusa_	Alignment	not modelled	99.8	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
23	c3e05B_	Alignment	not modelled	99.8	13	**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
24	d1kpga_	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
25	c3mtiA_	Alignment	not modelled	99.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
26	d1tpya_	Alignment	not modelled	99.8	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
27	d2nxca1	Alignment	not modelled	99.8	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
28	c2b78A_	Alignment	not modelled	99.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein smu.776; **PDBTitle:** a putative sam-dependent methyltransferase from2

						streptococcus mutans
29	d2fcaa1	Alignment	not modelled	99.8	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
30	d1l1ea_	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
31	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
32	c3grzA_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
33	c1wxwA_	Alignment	not modelled	99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha1280; **PDBTitle:** crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophillus hb8
34	d2igta1	Alignment	not modelled	99.8	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
35	d1l3ia_	Alignment	not modelled	99.8	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
36	d2fk8a1	Alignment	not modelled	99.8	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
37	c3bkxB_	Alignment	not modelled	99.8	20	**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
38	d1wxxa2	Alignment	not modelled	99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
39	c3c0kB_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0064 protein yccw; **PDBTitle:** crystal structure of a ribosomal rna methyltranferase
40	d2b78a2	Alignment	not modelled	99.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
41	c3gnlB_	Alignment	not modelled	99.8	16	**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
42	c3njrB_	Alignment	not modelled	99.8	14	**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
43	c3g8aF_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**ribosomal rna small subunit methyltransferase g; **PDBTitle:** t. thermophilus 16s rrna g527 methyltransferase in complex with adohcy2 in space group p61
44	c2esrB_	Alignment	not modelled	99.8	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** conserved hypothetical protein- streptococcus pyogenes
45	c1z3cA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** encephalitozoan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
46	d1ri5a_	Alignment	not modelled	99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap (Guanine N-7) methyltransferase
47	d2o57a1	Alignment	not modelled	99.8	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
48	d2fhpa1	Alignment	not modelled	99.8	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
49	c3e7pA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
50	d2b25a1	Alignment	not modelled	99.8	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
51	d2esra1	Alignment	not modelled	99.8	30	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
52	c3ocjA_	Alignment	not modelled	99.8	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
53	c2yxlA_	Alignment	not modelled	99.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein;

						PDBTitle: crystal structure of ph0851
54	c3g5tA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast
55	d2frna1	Alignment	not modelled	99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Met-10+ protein-like
56	c3dmgA_	Alignment	not modelled	99.8	26	**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
57	c2yx1A_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein mj0883; **PDBTitle:** crystal structure of m.jannaschii trna m1g37 methyltransferase
58	c3p9nA_	Alignment	not modelled	99.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible methyltransferase (methylase); **PDBTitle:** rv2966c of m. tuberculosis is a rsmd-like methyltransferase
59	d1i9ga_	Alignment	not modelled	99.8	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
60	c3f4kA_	Alignment	not modelled	99.8	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.
61	d1sqga2	Alignment	not modelled	99.8	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
62	c2yvlB_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
63	c3p2kA_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of an antibiotic related methyltransferase
64	d2fpoa1	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
65	d1ixka_	Alignment	not modelled	99.8	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
66	c2yxdA_	Alignment	not modelled	99.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable cobalt-precorrin-6y c(15)-methyltransferase **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbit)
67	d1p1ca_	Alignment	not modelled	99.8	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
68	d1jsxa_	Alignment	not modelled	99.8	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
69	c3a26A_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein ph0793; **PDBTitle:** crystal structure of p. horikoshii tyw2 in complex with2 mesado
70	d1wy7a1	Alignment	not modelled	99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
71	c1sqgA_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sun protein; **PDBTitle:** the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
72	c1vl5B_	Alignment	not modelled	99.8	20	**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
73	d1vl5a_	Alignment	not modelled	99.8	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
74	d1zx0a1	Alignment	not modelled	99.8	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
75	d1m6ya2	Alignment	not modelled	99.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**MraW-like putative methyltransferases
76	d1xcla_	Alignment	not modelled	99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
77	d2gh1a1	Alignment	not modelled	99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**BC2162-like
78	c3opnA_	Alignment	not modelled	99.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hemolysin; **PDBTitle:** the crystal structure of a putative hemolysin from

						lactococcus lactis
79	c3g2qA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pcza361.24; **PDBTitle:** crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
80	d1nkva_	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical Protein YjhP
81	c3id5F_	Alignment	not modelled	99.8	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
82	d2ex4a1	Alignment	not modelled	99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
83	c3bgvC_	Alignment	not modelled	99.8	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
84	d1g8sa_	Alignment	not modelled	99.8	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
85	c3hm2G_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** G: **PDB Molecule:**precorrin-6y c5,15-methyltransferase; **PDBTitle:** crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
86	d1xxla_	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
87	d1nt2a_	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
88	d1dl5a1	Alignment	not modelled	99.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
89	c3dlcA_	Alignment	not modelled	99.8	23	**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
90	c3dxyA_	Alignment	not modelled	99.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of ectrmb in complex with sam
91	c2yxeB_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of l-isoaspartyl protein carboxyl methyltranferase
92	c2ipxA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna 2'-o-methyltransferase fibrillarin; **PDBTitle:** human fibrillarin
93	d1r74a_	Alignment	not modelled	99.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
94	d1i1na_	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
95	d1prya_	Alignment	not modelled	99.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
96	c3e23A_	Alignment	not modelled	99.7	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
97	c3lccA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyl chloride transferase; **PDBTitle:** structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
98	c2pbfA_	Alignment	not modelled	99.7	17	**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
99	c3m70A_	Alignment	not modelled	99.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
100	c3ujcA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase; **PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
101	c3busB_	Alignment	not modelled	99.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of rebm
102	c3mggB	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase;

102	c3mggB_	Alignment	not modelled	99.7	17	**PDBTitle:** crystal structure of methyl transferase from methanosarcina2 mazei
103	d1xvaa_	Alignment	not modelled	99.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
104	c1dl5A_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase
105	d1g8aa_	Alignment	not modelled	99.7	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
106	c3egiA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trimethylguanosine synthase homolog; **PDBTitle:** methyltransferase domain of human trimethylguanosine2 synthase tgs1 bound to m7gpppa (inactive form)
107	c2yr0A_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha0223; **PDBTitle:** crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
108	c3m6wA_	Alignment	not modelled	99.7	14	**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
109	d1pjza_	Alignment	not modelled	99.7	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
110	c3tfwB_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative o-methyltransferase; **PDBTitle:** crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
111	d2ifta1	Alignment	not modelled	99.7	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
112	c3a4tA_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase mj0026; **PDBTitle:** crystal structure of atrm4 from m.jannaschii with sinefungin
113	c3c3yB_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum
114	d1uwva2	Alignment	not modelled	99.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**(Uracil-5-)-methyltransferase
115	c3g07C_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**7sk snrna methylphosphate capping enzyme; **PDBTitle:** methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
116	d1jqea_	Alignment	not modelled	99.7	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Histamine methyltransferase
117	c3m4xA_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
118	d1susa1	Alignment	not modelled	99.7	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**COMT-like
119	d1xtpa_	Alignment	not modelled	99.7	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
120	c3duwB_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase, putative; **PDBTitle:** crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah