

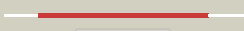








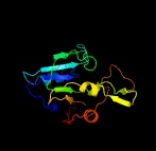
















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1506c_(-) _1695949_1696449
Date	Fri Aug 2 13:30:09 BST 2019
Unique Job ID	52b9e8b72bb63863

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5wp5A_</a>	 Alignment		99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomethylethanolamine n-methyltransferase 2; <b>PDBTitle:</b> arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
2	<a href="#">c4ineB_</a>	 Alignment		99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein pmt-2; <b>PDBTitle:</b> crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
3	<a href="#">c4krhB_</a>	 Alignment		99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 2; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine
4	<a href="#">c3h2bB_</a>	 Alignment		99.8	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of the sam-dependent methyltransferase cg3271 from2 corynebacterium glutamicum in complex with s-adenosyl-l-homocysteine3 and pyrophosphate. northeast structural genomics consortium target4 cgr113a
5	<a href="#">c3e23A_</a>	 Alignment		99.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rpa2492; <b>PDBTitle:</b> crystal structure of the rpa2492 protein in complex with sam from2 rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr299
6	<a href="#">c3bkxB_</a>	 Alignment		99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution
7	<a href="#">c4xcxA_</a>	 Alignment		99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> small rna 2'-o-methyltransferase; <b>PDBTitle:</b> methyltransferase domain of small rna 2'-o-methyltransferase
8	<a href="#">c6ec3C_</a>	 Alignment		99.8	21	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein; <b>PDBTitle:</b> crystal structure of evdmo1
9	<a href="#">c5t39A_</a>	 Alignment		99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> evdmo1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of evdmo1 in the presence2 of sah and d-fucose
10	<a href="#">c3ocjA_</a>	 Alignment		99.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> the crystal structure of a possilbe exported protein from bordetella2 parapertussis
11	<a href="#">c4p7cB_</a>	 Alignment		99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato

12	<a href="#">d1jqea_</a>	Alignment		99.7	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
13	<a href="#">c6ectA_</a>	Alignment		99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
14	<a href="#">c4kwcA_</a>	Alignment		99.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bpuml; <b>PDBTitle:</b> structure of the plantazolicin methyltransferase bpuml in complex with2 sah
15	<a href="#">c5ufmB_</a>	Alignment		99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase domain protein; <b>PDBTitle:</b> crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine
16	<a href="#">c4kvzA_</a>	Alignment		99.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> baml; <b>PDBTitle:</b> crystal structure of the plantazolicin methyltransferase baml in2 complex with sah
17	<a href="#">c6f5zB_</a>	Alignment		99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 24-sterol c-methyltransferase; <b>PDBTitle:</b> complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
18	<a href="#">c4rvqA_</a>	Alignment		99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-mycarose 3-c-methyltransferase; <b>PDBTitle:</b> crystal structure of mtmc in complex with sam and tdp
19	<a href="#">c5kn4B_</a>	Alignment		99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pavine n-methyltransferase; <b>PDBTitle:</b> pavine n-methyltransferase apoenzyme ph 6.0
20	<a href="#">c3ujcA_</a>	Alignment		99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase; <b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
21	<a href="#">c4qnuH_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of cmob bound with cx-sam in p21212
22	<a href="#">c4xrpF_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> hen1; <b>PDBTitle:</b> structure of the pnpk1/rnl/hen1 rna repair complex
23	<a href="#">c6gkvB_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> coclaurine n-methyltransferase; <b>PDBTitle:</b> crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah
24	<a href="#">c6g4wq_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 40s ribosomal protein s16; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state a
25	<a href="#">c3bgvC_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> mrna cap guanine-n7 methyltransferase; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
26	<a href="#">c3qnha_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenic methyltransferase; <b>PDBTitle:</b> arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
27	<a href="#">c4qttB_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative methyltransferase bud23; <b>PDBTitle:</b> structure of s. cerevisiae bud23-trm112 complex involved in formation2 of m7g1575 on 18s rrna (apo-form)
28	<a href="#">c5bp9A_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase protein; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from bacteroides2 fragilis in complex with s-adenosyl-l-homocysteine <b>PDB header:</b> transferase

29	<a href="#">c3ofkA</a>	Alignment	not modelled	99.7	14	<b>Chain:</b> A: <b>PDB Molecule:</b> nodulation protein s; <b>PDBTitle:</b> crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah)
30	<a href="#">d1r74a</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase <b>PDB header:</b> transferase
31	<a href="#">c3vc2j</a>	Alignment	not modelled	99.7	11	<b>Chain:</b> J: <b>PDB Molecule:</b> geranyl diphosphate 2-c-methyltransferase; <b>PDBTitle:</b> crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine <b>PDB header:</b> transferase/rna
32	<a href="#">c6dcbA</a>	Alignment	not modelled	99.7	13	<b>Chain:</b> A: <b>PDB Molecule:</b> 7sk snrna methylphosphate capping enzyme; <b>PDBTitle:</b> structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna
33	<a href="#">d2ex4a1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> AD-003 protein-like <b>PDB header:</b> transferase
34	<a href="#">c6ecvB</a>	Alignment	not modelled	99.7	20	<b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
35	<a href="#">c3jwgA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c
36	<a href="#">d1kpia</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase <b>PDB header:</b> transferase
37	<a href="#">c4krqB</a>	Alignment	not modelled	99.7	15	<b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 1; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine <b>PDB header:</b> transferase
38	<a href="#">c3jwhA</a>	Alignment	not modelled	99.7	18	<b>Chain:</b> A: <b>PDB Molecule:</b> hen1; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of2 bacterial-avhen1-c <b>PDB header:</b> transferase
39	<a href="#">c6d6yA</a>	Alignment	not modelled	99.7	19	<b>Chain:</b> A: <b>PDB Molecule:</b> apra methyltransferase 2; <b>PDBTitle:</b> apra methyltransferase 2 - gnat didomain in complex with sah <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
40	<a href="#">d2a14a1</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
41	<a href="#">c3bgdB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosyl-l-methionine-dependent <b>PDBTitle:</b> crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
42	<a href="#">c3dlcA</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase <b>PDB header:</b> transferase
43	<a href="#">d1pjza</a>	Alignment	not modelled	99.7	15	<b>Chain:</b> B: <b>PDB Molecule:</b> unknown conserved protein bh2331; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution <b>PDB header:</b> transferase
44	<a href="#">c1vl5B</a>	Alignment	not modelled	99.7	12	<b>Chain:</b> C: <b>PDB Molecule:</b> 7sk snrna methylphosphate capping enzyme; <b>PDBTitle:</b> methyltransferase domain of human bicoid-interacting protein 3 homolog2 (drosophila) <b>PDB header:</b> transferase
45	<a href="#">c3g07C</a>	Alignment	not modelled	99.7	13	<b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
46	<a href="#">c3e7pA</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N5-glutamine methyltransferase, HemK <b>PDB header:</b> transferase
47	<a href="#">d1vl5a</a>	Alignment	not modelled	99.7	11	<b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product <b>PDB header:</b> transferase
48	<a href="#">d2b3ta1</a>	Alignment	not modelled	99.7	19	<b>Chain:</b> A: <b>PDB Molecule:</b> glycine sarcosine n-methyltransferase; <b>PDBTitle:</b> crystal structure of glycine sarcosine n-methyltransferase from2 methanohalophilus portucalensis in complex with betaine <b>PDB header:</b> transferase
49	<a href="#">c3ndjA</a>	Alignment	not modelled	99.7	15	<b>Chain:</b> A: <b>PDB Molecule:</b> putative methyl chloride transferase; <b>PDBTitle:</b> structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana <b>PDB header:</b> transferase
50	<a href="#">c5hijA</a>	Alignment	not modelled	99.7	18	<b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase, putative; <b>PDBTitle:</b> crystal structure of n-methyl transferase from
51	<a href="#">c3lccA</a>	Alignment	not modelled	99.7	13	
52	<a href="#">c4iv0B</a>	Alignment	not modelled	99.7	15	

						plasmodium vivax2 complexed with s-adenosyl methionine and phosphate
53	<a href="#">d1xvaa_</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
54	<a href="#">c5mgzA_</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-demethylnovobioc acid c(8)-methyltransferase; <b>PDBTitle:</b> streptomyces spheroides novo (8-demethylnovobioc acid2 methyltransferase) with sah
55	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
56	<a href="#">c3dliB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
57	<a href="#">c5w7kA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
58	<a href="#">d2o57a1</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
59	<a href="#">d2bzga1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
60	<a href="#">c3dtnA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase mm_2633; <b>PDBTitle:</b> crystal structure of putative methyltransferase-mm_2633 from2 methanosarcina mazei .
61	<a href="#">c5egpB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ubie/coq5 family methyltransferase, putative; <b>PDBTitle:</b> crystal structure of the s-methyltransferase tmta
62	<a href="#">c3opnA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hemolysin; <b>PDBTitle:</b> the crystal structure of a putative hemolysin from lactococcus lactis
63	<a href="#">c3g5tA_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-aconitate 3-methyltransferase; <b>PDBTitle:</b> crystal structure of trans-aconitate 3-methyltransferase from yeast
64	<a href="#">d1xtpa_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> AD-003 protein-like
65	<a href="#">c3cc8A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution
66	<a href="#">c4pneA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of the [4+2]-cyclase spnf
67	<a href="#">c3i9fB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative type 11 methyltransferase; <b>PDBTitle:</b> crystal structure of a putative type 11 methyltransferase from2 sulfolobus solfataricus
68	<a href="#">c5z9oA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus
69	<a href="#">c4kdcA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-demethylubiquinone-9 3-methyltransferase; <b>PDBTitle:</b> crystal structure of ubig
70	<a href="#">c2iipD_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
71	<a href="#">d1ri5a_</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> mRNA cap (Guanine N-7) methyltransferase
72	<a href="#">c6bqcA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> cyclopropane fatty acid synthase from e. coli
73	<a href="#">d1xxla_</a>	Alignment	not modelled	99.7	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
74	<a href="#">c1z3cA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> encephalitozooan cuculici mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
75	<a href="#">c3m70A_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein tehb homolog; <b>PDBTitle:</b> crystal structure of tehb from haemophilus influenzae
76	<a href="#">c3egeA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase from antibiotic biosynthesis <b>PDBTitle:</b> crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution
77	<a href="#">d1nkye_</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent

77	<a href="#">u1tkva_</a>	Alignment	not modelled	99.7	18	methyltransferases <b>Family:</b> Hypothetical Protein YjHP
78	<a href="#">c5mptA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citrinin polyketide synthase; <b>PDBTitle:</b> structure of the citrinin polyketide synthase cmet domain
79	<a href="#">c6mroA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyl transferase from methanosarcina acetivorans; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nseg) target mvr53.
80	<a href="#">c5dplB_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein lysine methyltransferase 2; <b>PDBTitle:</b> the structure of pkmt2 from rickettsia typhi in complex with adohcY
81	<a href="#">c5cm2Z_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> Z: <b>PDB Molecule:</b> trna methyltransferase; <b>PDBTitle:</b> insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
82	<a href="#">d2fcaa1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
83	<a href="#">c5evjA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenite methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of crasm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii
84	<a href="#">d1yzha1</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
85	<a href="#">d1llea_</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
86	<a href="#">c4necC_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> C: <b>PDB Molecule:</b> putative sam-dependent methyltransferase; <b>PDBTitle:</b> conversion of a disulfide bond into a thioacetal group during2 echinomycin biosynthesis
87	<a href="#">c4x1oA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna (adenine(1408)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
88	<a href="#">c3mggB_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 mazei
89	<a href="#">c2fk8A_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methoxy mycolic acid synthase 4; <b>PDBTitle:</b> crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
90	<a href="#">c4qdkB_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> magnesium-protoporphyrin o-methyltransferase; <b>PDBTitle:</b> crystal structure of magnesium protoporphyrin ix methyltransferase2 (chlm) from synechocystis pcc 6803 with bound sah
91	<a href="#">d1kpga_</a>	Alignment	not modelled	99.6	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
92	<a href="#">c5subbA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha n-terminal protein methyltransferase 1b; <b>PDBTitle:</b> crystal structure of human alpha n-terminal protein methyltransferase2 1b
93	<a href="#">d2i6ga1</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TehB-like
94	<a href="#">c2yr0A_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha0223; <b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
95	<a href="#">c5fcdA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
96	<a href="#">c3eeyL_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> putative rrna methylase; <b>PDBTitle:</b> crystal structure of putative rrna-methylase from clostridium2 thermocellum
97	<a href="#">c3f4kA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
98	<a href="#">c5do0A_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein lysine methyltransferase 1; <b>PDBTitle:</b> the structure of pkmt1 from rickettsia prowazekii
99	<a href="#">c3l8dA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus thuringiensis
100	<a href="#">d2fk8a1</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases



101	<a href="#">d1m6ya2</a>	Alignment	not modelled	99.6	16	<b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> MraW-like putative methyltransferases
102	<a href="#">d1im8a</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein HI0319 (YecO)
103	<a href="#">c4azwA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wbdd; <b>PDBTitle:</b> crystal structure of monomeric wbdd.
104	<a href="#">c2pxxA</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mgc2408; <b>PDBTitle:</b> human putative methyltransferase mgc2408
105	<a href="#">c4obxD</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, <b>PDBTitle:</b> crystal structure of yeast coq5 in the apo form
106	<a href="#">c3cggB</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
107	<a href="#">c5thyB</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase,lyase <b>Chain:</b> B: <b>PDB Molecule:</b> curj; <b>PDBTitle:</b> crystal structure of semet-substituted curj carbon methyltransferase
108	<a href="#">c4iscA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase from pseudomonas2 syringae
109	<a href="#">d1ve3a1</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
110	<a href="#">d1d2ha</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
111	<a href="#">c3merA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> slr1183 protein; <b>PDBTitle:</b> crystal structure of the methyltransferase sir1183 from synechocystis2 sp. pcc 6803, northeast structural genomics consortium target sgr145
112	<a href="#">d2p7ia1</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
113	<a href="#">c5eovA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s/23s rrna (cytidine-2'-o)-methyltransferase tlya; <b>PDBTitle:</b> c-terminal domain of the 16s/23s rrna (cytidine-2'-o)-2 methyltransferase tlya.
114	<a href="#">c2xvmB</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tellurite resistance protein tehb; <b>PDBTitle:</b> crystal structure of the tellurite detoxification protein2 tehb from e. coli in complex with sah
115	<a href="#">c5je0B</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase; <b>PDBTitle:</b> crystal structure of burkholderia glumae toxa with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethyltoxoflavin
116	<a href="#">c4azsA</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase wbdd; <b>PDBTitle:</b> high resolution (2.2 a) crystal structure of wbdd.
117	<a href="#">d1zx0a1</a>	Alignment	not modelled	99.6	8	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
118	<a href="#">c3e8sA</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sam dependent methyltransferase; <b>PDBTitle:</b> crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
119	<a href="#">c3hnrA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable methyltransferase bt9727_4108; <b>PDBTitle:</b> crystal structure of a probable methyltransferase2 bt9727_4108 from bacillus thuringiensis subsp. northeast3 structural genomics consortium target id bur219
120	<a href="#">d1tpya</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase