


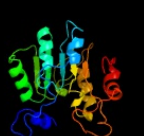













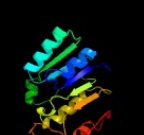









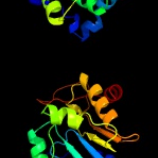
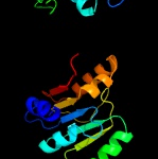
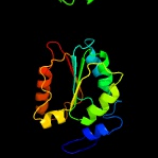
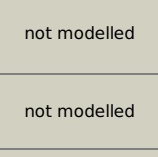


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3699_(-)_4142222_4142923
Date	Fri Aug 9 18:20:39 BST 2019
Unique Job ID	6d2b7f8f660c5fce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4necC_	 Alignment		100.0	39	PDB header: transferase/antibiotic Chain: C: PDB Molecule: putative sam-dependent methyltransferase; PDBTitle: conversion of a disulfide bond into a thioacetal group during2 echinomycin biosynthesis
2	d2bzga1	 Alignment		100.0	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
3	c6mroA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: methyl transferase from methanosarcina acetivorans; PDBTitle: crystal structure of methyl transferase from methanosarcina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
4	c3lccA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
5	c3bgdB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: thiopurine s-methyltransferase; PDBTitle: thiopurine s-methyltransferase
6	c3ggdA_	 Alignment		99.9	17	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
7	d1pjza_	 Alignment		99.9	23	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
8	c4krhB_	 Alignment		99.9	24	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 2; PDBTitle: semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine
9	c3m70A_	 Alignment		99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
10	c4ineB_	 Alignment		99.9	22	PDB header: transferase Chain: B: PDB Molecule: protein pmt-2; PDBTitle: crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
11	c5wp5A_	 Alignment		99.9	20	PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah

12	c3vc2l_	Alignment		99.9	13	PDB header: transferase Chain: J: PDB Molecule: geranyl diphosphate 2-c-methyltransferase; PDBTitle: crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine
13	c2xvmB_	Alignment		99.9	18	PDB header: transferase Chain: B: PDB Molecule: tellurite resistance protein tehb; PDBTitle: crystal structure of the tellurite detoxification protein2 tehb from e. coli in complex with sah
14	c4p7cB_	Alignment		99.9	15	PDB header: transferase Chain: B: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
15	d1xvaa_	Alignment		99.9	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
16	c3g5tA_	Alignment		99.9	19	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast
17	d1r74a_	Alignment		99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
18	c3e23A_	Alignment		99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rpa2492; PDBTitle: crystal structure of the rpa2492 protein in complex with sam from2 rhodospseudomonas palustris, northeast structural genomics consortium3 target rpr299
19	c3g2qA_	Alignment		99.9	19	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtfA2 complexed with sinefungin
20	c3ofkA_	Alignment		99.9	19	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)
21	d1ve3a1	Alignment	not modelled	99.9	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
22	c5do0A_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
23	c2fk8A_	Alignment	not modelled	99.9	14	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
24	c5dplB_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: B: PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy
25	c4krkB_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 1; PDBTitle: semet haemonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine
26	c5kn4B_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0
27	c2yr0A_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
28	c6gkvB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: coclaurine n-methyltransferase; PDBTitle: crystal structure of coclaurine n-methyltransferase (cnmt)

						bound to n-2 methylheliamine and sah
29	c3h2bB	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: 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
30	c3qnhA	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: arsenic methyltransferase; PDBTitle: arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
31	c5egpB	Alignment	not modelled	99.9	19	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
32	c5ufmB	Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: methyltransferase domain protein; PDBTitle: crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine
33	c5w7kA	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag
34	d1l1ea	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
35	c5z9oA	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus
36	c3e7pA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
37	d2ex4a1	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
38	c4qnuH	Alignment	not modelled	99.9	17	PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
39	c6bqcA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
40	d2fk8a1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
41	c6g4wq	Alignment	not modelled	99.8	18	PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s16; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a
42	c5u18A	Alignment	not modelled	99.8	24	PDB header: transferase Chain: A: PDB Molecule: n-3" methyltransferase; PDBTitle: crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin
43	c5mgzA	Alignment	not modelled	99.8	25	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobioc acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobioc acid2 methyltransferase) with sah
44	d1yzha1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
45	c4kdcA	Alignment	not modelled	99.8	24	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
46	c6ectA	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257
47	c4htfA	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine-dependent methyltransferase; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 from escherichia coli in complex with s-adenosylmethionine.
48	d1kpga	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
49	c5t39A	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: evdm01; PDBTitle: crystal structure of the n-terminal domain of evdm01 in the presence2 of sah and d-fucose
50	c5evjA	Alignment	not modelled	99.8	26	PDB header: transferase Chain: A: PDB Molecule: arsenite methyltransferase; PDBTitle: x-ray crystal structure of crasm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii
51	c1vl5B	Alignment	not modelled	99.8	24	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
52	d1vl5a	Alignment	not modelled	99.8	24	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases

						Family: UbiE/COQ5-like
53	d1tpya_	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
54	d2o57a1	Alignment	not modelled	99.8	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
55	c5fcdA_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
56	c3dlcA_	Alignment	not modelled	99.8	14	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
57	c3bgvC_	Alignment	not modelled	99.8	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
58	c3bkbB_	Alignment	not modelled	99.8	18	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
59	c3f4kA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
60	d1xtpa_	Alignment	not modelled	99.8	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
61	c4azwA_	Alignment	not modelled	99.8	27	PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: crystal structure of monomeric wbdd.
62	d1d2ha_	Alignment	not modelled	99.8	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
63	c3merA_	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: slr1183 protein; PDBTitle: crystal structure of the methyltransferase slr1183 from synechocystis2 sp. pcc 6803, northeast structural genomics consortium target sgr145
64	d2a14a1	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase
65	c6ecvB_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
66	c1z3cA_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozooan cuculici mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
67	d1xxla_	Alignment	not modelled	99.8	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
68	c4x1oA_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: 16s rrna (adenine(1408)-n(1))-methyltransferase; PDBTitle: crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
69	c6ec3C_	Alignment	not modelled	99.8	17	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdmo1
70	d1kpia_	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
71	d2fcaa1	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
72	d1ri5a_	Alignment	not modelled	99.8	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
73	c4hgyC_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: C: PDB Molecule: ccbj; PDBTitle: structure of the ccbj methyltransferase from streptomyces caelestis
74	c2pxxA_	Alignment	not modelled	99.8	24	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein mgc2408; PDBTitle: human putative methyltransferase mgc2408
75	d1jqea_	Alignment	not modelled	99.8	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
76	c6dcbA_	Alignment	not modelled	99.8	19	PDB header: transferase/rna Chain: A: PDB Molecule: 7sk snrna methylphosphate capping enzyme; PDBTitle: structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna

77	c3l8dA	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
78	c3cc8A	Alignment	not modelled	99.8	16	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
79	c3ou7A	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
80	d1zx0a1	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
81	c3g2qB	Alignment	not modelled	99.8	18	PDB header: transferase Chain: B: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtf2 complexed with sinefungin
82	c3ujcA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
83	c4kvzA	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: baml; PDBTitle: crystal structure of the plantazolin methyltransferase baml in2 complex with sah
84	c5bp9A	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase protein; PDBTitle: crystal structure of sam-dependent methyltransferase from bacteroides2 fragilis in complex with s-adenosyl-l-homocysteine
85	c4pneA	Alignment	not modelled	99.8	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
86	c3dliB	Alignment	not modelled	99.8	18	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
87	c4xcxA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: small rna 2'-o-methyltransferase; PDBTitle: methyltransferase domain of small rna 2'-o-methyltransferase
88	c4hg2B	Alignment	not modelled	99.8	23	PDB header: transferase Chain: B: PDB Molecule: methyltransferase type 11; PDBTitle: the structure of a putative type ii methyltransferase from2 anaeromyxobacter dehalogenans.
89	c3cggB	Alignment	not modelled	99.8	25	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
90	c2p8jA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine-dependent methyltransferase; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 (np_349143.1) from clostridium acetobutylicum at 2.00 a resolution
91	d1xcla	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
92	c3dxyA	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(7)-)-methyltransferase; PDBTitle: crystal structure of ectrmB in complex with sam
93	d1wzna1	Alignment	not modelled	99.8	29	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
94	c5hijA	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: glycine sarcosine n-methyltransferase; PDBTitle: crystal structure of glycine sarcosine n-methyltransferase from2 methanohalophilus portucalensis in complex with betaine
95	c5ubbA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
96	c4uw0A	Alignment	not modelled	99.8	27	PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: low resolution structure of wbdd with c-terminal bundle ordered to2 residue 505
97	c4iscA	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a putative methyltransferase from pseudomonas2 syringae
98	d2gh1a1	Alignment	not modelled	99.8	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
99	c4kwcA	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: bpuml; PDBTitle: structure of the plantazolin methyltransferase bpuml in complex with2 sah
100	c4iv0B	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase, putative; PDBTitle: crystal structure of n-methyl transferase from plasmodium vivax2 complexed with s-adenosyl methionine and phosphate Fold: S-adenosyl-L-methionine-dependent methyltransferases

101	d2avna1	Alignment	not modelled	99.8	24	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
102	c3mtiA	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A; PDB Molecule: rrna methylase; PDBTitle: the crystal structure of a rna methylase from streptococcus2 thermophilus to 1.95a
103	c2g8nB	Alignment	not modelled	99.8	18	PDB header: transferase Chain: B; PDB Molecule: phenylethanolamine n-methyltransferase; PDBTitle: structure of hpnmt with inhibitor 3-hydroxymethyl-7-(n-4-2 chlorophenylaminosulfonyl)-thiq and adohcy
104	c3ocjA	Alignment	not modelled	99.8	18	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
105	c3lecA	Alignment	not modelled	99.8	19	PDB header: structure genomics, unknown function Chain: A; PDB Molecule: nadb-rossmann superfamily protein; PDBTitle: the crystal structure of a protein in the nadb-rossmann superfamily2 from streptococcus agalactiae to 1.8a
106	d1nkva	Alignment	not modelled	99.8	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein Yjhp
107	c3mggB	Alignment	not modelled	99.8	23	PDB header: transferase Chain: B; PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazel
108	c4xrpF	Alignment	not modelled	99.8	12	PDB header: protein binding Chain: F; PDB Molecule: hen1; PDBTitle: structure of the pnpk1/rnl/hen1 rna repair complex
109	d1im8a	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
110	c5xlxD	Alignment	not modelled	99.8	23	PDB header: transferase Chain: D; PDB Molecule: chemotaxis protein methyltransferase 1; PDBTitle: crystal structure of the c-terminal domain of cher1 containing sah
111	c3pfdD	Alignment	not modelled	99.8	18	PDB header: transferase Chain: D; PDB Molecule: n-methyltransferase; PDBTitle: x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n
112	d1af7a2	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Chemotaxis receptor methyltransferase CheR, C-terminal domain
113	c4azsA	Alignment	not modelled	99.8	27	PDB header: transferase Chain: A; PDB Molecule: methyltransferase wbdd; PDBTitle: high resolution (2.2 a) crystal structure of wbdd.
114	d1dusa	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein MJ0882
115	d1y8ca	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
116	c3egeA	Alignment	not modelled	99.8	18	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
117	c3gnlB	Alignment	not modelled	99.8	11	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein, duf633, lmof2365_1472; PDBTitle: structure of uncharacterized protein (lmof2365_1472) from listeria2 monocytogenes serotype 4b
118	c5je0B	Alignment	not modelled	99.8	19	PDB header: transferase Chain: B; PDB Molecule: methyl transferase; PDBTitle: crystal structure of burkholderia glumae toxa with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethyltoxoflavin
119	d2i6ga1	Alignment	not modelled	99.8	23	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TehB-like
120	c3ku1E	Alignment	not modelled	99.8	18	PDB header: transferase Chain: E; PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of streptococcus pneumoniae sp1610, a putative trna2 (m1a22) methyltransferase, in complex with s-adenosyl-l-methionine