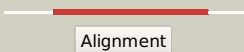

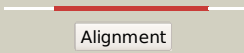



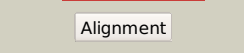



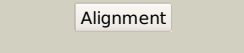

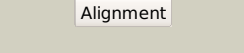
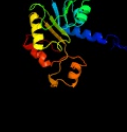


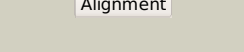

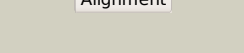
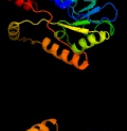
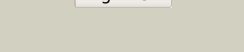























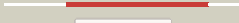





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2003c (-)_2248571_2249428
Date	Mon Aug 5 13:25:11 BST 2019
Unique Job ID	95079cac9bfde32c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vlma_	 Alignment		100.0	32	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
2	c2qs9A_	 Alignment		100.0	34	PDB header: transferase Chain: A; PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from thermus thermophilis hb8
3	c4p7cB_	 Alignment		100.0	17	PDB header: transferase Chain: B; PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
4	c5wp5A_	 Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
5	c4krhB_	 Alignment		99.9	23	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
6	c4ineB_	 Alignment		99.9	18	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
7	c3vc2J_	 Alignment		99.9	20	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
8	c4rvqA_	 Alignment		99.9	17	PDB header: transferase Chain: A; PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
9	c4kdcA_	 Alignment		99.9	20	PDB header: transferase Chain: A; PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
10	c2yr0A_	 Alignment		99.9	26	PDB header: transferase Chain: A; PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
11	c6f5zB_	 Alignment		99.9	21	PDB header: transferase Chain: B; PDB Molecule: 24-sterol c-methyltransferase; PDBTitle: complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase

12	c4qnuH_	 Alignment		99.9	19	PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
13	d1jqea_	 Alignment		99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
14	c5je0B_	 Alignment		99.9	20	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
15	c5w7kA_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag
16	c3h2bB_	 Alignment		99.9	23	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
17	c4htfA_	 Alignment		99.9	16	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.
18	c1vl5B_	 Alignment		99.9	21	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
19	d1vl5a_	 Alignment		99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
20	c3ou7A_	 Alignment		99.9	24	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
21	c3bkxB_	 Alignment	not modelled	99.9	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
22	d2o57a1	 Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
23	c4kwcA_	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: bpuml; PDBTitle: structure of the plantazolicin methyltransferase bpuml in complex with2 sah
24	c3ndjA_	 Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
25	c3g5lA_	 Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
26	c3cc8A_	 Alignment	not modelled	99.9	17	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
27	c5egpB_	 Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
28	c3gnhA_	 Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: arsenic methyltransferase;

28	c3qma	Alignment	not modelled	99.9	20	PDBTitle: arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii) Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
29	d2p7ia1	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosyl-L-methionine-dependent
30	c3dlcA	Alignment	not modelled	99.9	17	PDBTitle: crystal structure of a putative s-adenosyl-L-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution 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
31	c4necC	Alignment	not modelled	99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase RImA
32	d1p91a	Alignment	not modelled	99.9	21	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
33	c5bp9A	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase from bacteroides2 vulgatus atcc 8482
34	c3e7pA	Alignment	not modelled	99.9	13	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdm01
35	c6ec3C	Alignment	not modelled	99.9	24	PDB header: transferase Chain: A: PDB Molecule: bam1; PDBTitle: crystal structure of the plantazolicin methyltransferase bam1 in2 complex with sah
36	c4kvzA	Alignment	not modelled	99.9	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
37	d2avna1	Alignment	not modelled	99.9	28	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
38	c3l8dA	Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sam dependent methyl-transferase type 12 family2 protein (eca1738) from pectobacterium atrosepticum scri1043 at 1.74 a3 resolution
39	c2p7iB	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: citrinin polyketide synthase; PDBTitle: structure of the citrinin polyketide synthase cmet domain
40	c5mptA	Alignment	not modelled	99.9	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
41	d1r74a	Alignment	not modelled	99.9	20	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
42	c5evjA	Alignment	not modelled	99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
43	d1kpga	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
44	c3f4kA	Alignment	not modelled	99.9	14	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
45	c3pfdD	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of s-adenosylmethionine dependent methyltransferase2 (np_104914.1) from mesorhizobium loti at 1.60 a resolution
46	c3bkWB	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
47	c3dliB	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: putative sam dependent methyltransferase; PDBTitle: crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
48	c3e8sA	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: putative sam dependent methyltransferase; PDBTitle: crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
49	c4pneA	Alignment	not modelled	99.9	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
50	c6g4wq	Alignment	not modelled	99.9	22	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
51	d2gh1a1	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like

52	c5t39A	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: evdmo1; PDBTitle: crystal structure of the n-terminal domain of evdmo1 in the presence of sah and d-fucose
53	c5bszA	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: n-methyltransferase; PDBTitle: x-ray structure of the sugar n-methyltransferase keds8 from <i>Streptococcus pneumoniae</i> sp atcc 53650
54	c4qdkB	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: magnesium-protoporphyrin o-methyltransferase; PDBTitle: crystal structure of magnesium protoporphyrin ix methyltransferase2 (chlm) from <i>Synechocystis</i> pcc 6803 with bound sah
55	d1nkva	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein YjhP
56	d1wzna1	Alignment	not modelled	99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
57	d1xxla	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
58	c3ujcA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from <i>Plasmodium falciparum</i> in complex with phosphocholine
59	d1y8ca	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
60	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 <i>Mycobacterium tuberculosis</i> complexed with s-adenosylmethionine
61	c4x1oA	Alignment	not modelled	99.9	16	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 <i>Catenulisporales acidiphilia</i>
62	c3e23A	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rpa2492; PDBTitle: crystal structure of the rpa2492 protein in complex with sam from <i>Rhodospseudomonas palustris</i> , northeast structural genomics consortium3 target rpr299
63	c6d6yA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: apra methyltransferase 2; PDBTitle: apra methyltransferase 2 - gnat didomain in complex with sah
64	d1xtpa	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
65	c3d2IC	Alignment	not modelled	99.9	27	PDB header: transferase Chain: C: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from <i>Exiguobacterium</i> sp. 255-15 at 1.90 Å resolution
66	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
67	c3g5tA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast
68	c4iv0B	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase, putative; PDBTitle: crystal structure of n-methyl transferase from <i>Plasmodium vivax</i> 2 complexed with s-adenosyl methionine and phosphate
69	d1ve3a1	Alignment	not modelled	99.9	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
70	d1l1ea	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
71	d2a14a1	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase
72	c3bxoA	Alignment	not modelled	99.9	23	PDB header: transferase Chain: A: PDB Molecule: n,n-dimethyltransferase; PDBTitle: crystal structure of streptomyces venezuelae desvi
73	d1im8a	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
74	c3ocjA	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: the crystal structure of a possible exported protein from <i>Bordetella parapertussis</i>
75	c5z9oA	Alignment	not modelled	99.9	12	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
76	c5mgzA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobiocic acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah
77	d2fk8a1	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
78	c2p35A_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
79	c6ccaA_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
80	c3dtnA_	Alignment	not modelled	99.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methyltransferase mm_2633; PDBTitle: crystal structure of putative methyltransferase-mm_2633 from2 methanosarcina mazei .
81	c3ofkA_	Alignment	not modelled	99.9	23	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)
82	c3g2qA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtf2a2 complexed with sinefungin
83	d1kpia_	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
84	c3mggB_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei
85	d1tpya_	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
86	c5fcdA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
87	c5ufmB_	Alignment	not modelled	99.9	18	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
88	d1xvaa_	Alignment	not modelled	99.9	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
89	c5gm2E_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
90	c2zfuA_	Alignment	not modelled	99.9	20	PDB header: nuclear protein Chain: A: PDB Molecule: cerebral protein 1; PDBTitle: structure of the methyltransferase-like domain of nucleomethylin
91	c3bgvC_	Alignment	not modelled	99.9	15	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
92	c3egeA_	Alignment	not modelled	99.9	20	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
93	c5hijA_	Alignment	not modelled	99.9	17	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
94	c6ecvB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
95	d1zx0a1	Alignment	not modelled	99.9	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
96	c3busB_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
97	c5cm2Z_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: Z: PDB Molecule: trna methyltransferase; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
98	c5ubba_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
99	c4obxD_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: D: PDB Molecule: 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, PDBTitle: crystal structure of yeast coq5 in the apo form

100	c3ccfB_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: crystal structure of putative methyltransferase (yp_321342.1) from <i>anabaena variabilis</i> atcc 29413 at 1.90 a resolution
101	d1xcla_	Alignment	not modelled	99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
102	c3lccA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from <i>arabidopsis2 thaliana</i>
103	c6ectA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257
104	c3mq2A_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: 16s rRNA methyltransferase; PDBTitle: crystal structure of 16s rRNA methyltransferase kamb
105	c4iscA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a putative methyltransferase from <i>pseudomonas2 syringae</i>
106	c3hnrA_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase bt9727_4108; PDBTitle: crystal structure of a probable methyltransferase2 bt9727_4108 from <i>Bacillus thuringiensis</i> subsp. <i>northeast3</i> structural genomics consortium target id bur219
107	c2iipD_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: D: PDB Molecule: nicotinamide n-methyltransferase; PDBTitle: human nicotinamide n-methyltransferase
108	c4rwzA_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: putative rRNA methyltransferase; PDBTitle: crystal structure of the antibiotic-resistance methyltransferase kmr
109	c5thyB_	Alignment	not modelled	99.8	20	PDB header: transferase,lyase Chain: B: PDB Molecule: curj; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase
110	c4qttB_	Alignment	not modelled	99.8	29	PDB header: transferase Chain: B: PDB Molecule: putative methyltransferase bud23; PDBTitle: structure of <i>S. cerevisiae</i> bud23-trm112 complex involved in formation2 of m7g1575 on 18s rRNA (apo-form)
111	c6dcbA_	Alignment	not modelled	99.8	20	PDB header: transferase/rna Chain: A: PDB Molecule: 7sk srRNA methylphosphate capping enzyme; PDBTitle: structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna
112	c4hgyC_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: C: PDB Molecule: ccbj; PDBTitle: structure of the ccbj methyltransferase from <i>Streptomyces caelestis</i>
113	c6bqcA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from <i>E. coli</i>
114	c3cggB_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from <i>Corynebacterium glutamicum</i> atcc 13032 kitasato at3 2.00 a resolution
115	c3g2qB_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: B: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
116	c6mroA_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: methyl transferase from <i>Methanosarcina acetivorans</i> ; PDBTitle: crystal structure of methyl transferase from <i>Methanosarcina2 acetivorans</i> at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
117	c3opnA_	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hemolysin; PDBTitle: the crystal structure of a putative hemolysin from <i>Lactococcus lactis</i>
118	c3ggdA_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from <i>anabaena variabilis</i> atcc 29413 at 2.11 a resolution
119	c5kn4B_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0
120	c4krqB_	Alignment	not modelled	99.8	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