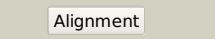
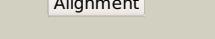
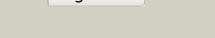
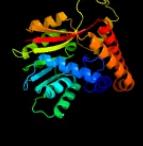
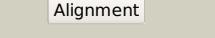
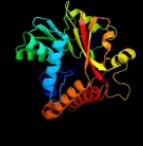
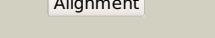


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD0643c_(mmaA3)_737271_738152
Date	Fri Jul 26 01:50:21 BST 2019
Unique Job ID	94b4ceaad3b1fe33

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5z9oA_			100.0	33	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
2	d1kpga_			100.0	65	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
3	d1kpia_			100.0	53	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
4	d1tpya_			100.0	67	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
5	c6bqcA_			100.0	32	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
6	c2fk8A_			100.0	62	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
7	d1l1ea_			100.0	64	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
8	d2fk8a1			100.0	63	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
9	c6gkvB_			100.0	22	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
10	d2o57a1			100.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
11	c5kn4B_			100.0	21	PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0

12	c5gm2E	Alignment		100.0	20	PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tied complexed with sah and teleocidin a1
13	c4pneA	Alignment		100.0	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
14	c5wp5A	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpm2) in complex with sah
15	c4krhB	Alignment		100.0	18	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
16	c4iv0B	Alignment		100.0	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
17	c4ineB	Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: protein pmt-2; PDBTitle: crystal structure of n-methyl transferase (pmt-2) from caenorhabditis elegans complexed with s-adenosyl homocysteine and phosphoethanolamine
18	c3ujcA	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium falciparum in complex with phosphocholine
19	c3busB	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
20	c3vc2J	Alignment		100.0	18	PDB header: transferase Chain: J: PDB Molecule: geranyl diphosphate 2-c-methyltransferase; PDBTitle: crystal structure of geranyl diphosphate c-methyltransferase from streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine
21	d1nkva	Alignment	not modelled	100.0	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein YjhP PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
22	c3f4kA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
23	c6ectA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257
24	c3e7pA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase from bacteroides vulgaris atcc 8482
25	c6ecvB	Alignment	not modelled	99.9	19	PDB header: transferase Chain: B: PDB Molecule: std protein; PDBTitle: std o-mt residues 976-1266
26	c3bkxB	Alignment	not modelled	99.9	13	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
27	c4kdcA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubiq
28	c3ocjA	Alignment	not modelled	99.9	14	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
29	c2yr0A_	Alignment	not modelled	99.9	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
30	c5eqpB_	Alignment	not modelled	99.9	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
31	d1xtpa_	Alignment	not modelled	99.9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
32	c5fcda_	Alignment	not modelled	99.9	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
33	c4gnuH_	Alignment	not modelled	99.9	PDB header: transferase Chain: H: PDB Molecule: tRNA (mo5u34)-methyltransferase; PDBTitle: crystal structure of crmob bound with cx-sam in p21212
34	d2ex4a1	Alignment	not modelled	99.9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
35	d1vl5a_	Alignment	not modelled	99.9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbIE/COQ5-like
36	c4p7cB_	Alignment	not modelled	99.9	PDB header: transferase Chain: B: PDB Molecule: tRNA (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
37	c1vl5B_	Alignment	not modelled	99.9	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
38	c5w7kA_	Alignment	not modelled	99.9	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag
39	c3bgvC_	Alignment	not modelled	99.9	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
40	d1xxla_	Alignment	not modelled	99.9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbIE/COQ5-like
41	c3mggB_	Alignment	not modelled	99.9	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanoscincus2 mazei
42	c5ubbA_	Alignment	not modelled	99.9	PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
43	c5bp9A_	Alignment	not modelled	99.9	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
44	c6f5zB_	Alignment	not modelled	99.9	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
45	c5je0B_	Alignment	not modelled	99.9	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of burkholderia glumiae tox with bound S-adenosylhomocysteine (sah) and 1,6-didemethylxanthine
46	c3ou7A_	Alignment	not modelled	99.9	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
47	d1wzna1	Alignment	not modelled	99.9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
48	c4qttB_	Alignment	not modelled	99.9	PDB header: transferase Chain: B: PDB Molecule: putative methyltransferase bud23; PDBTitle: structure of S. cerevisiae bud23-trm112 complex involved in formation2 of m7g1575 on 18s rRNA (apo-form)
49	d1ri5a_	Alignment	not modelled	99.9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
50	c3lccA_	Alignment	not modelled	99.9	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
51	c1z3cA_	Alignment	not modelled	99.9	PDB header: transferase Chain: A: PDB Molecule: mRNA capping enzyme; PDBTitle: encephalitozoan cuniculi mRNA cap (guanine-n7)2 methyltransferase in complex with azoadomet
52	c4qdkB_	Alignment	not modelled	99.9	PDB header: transferase Chain: B: PDB Molecule: magnesium-protoporphyrin o-methyltransferase; PDBTitle: crystal structure of magnesium protoporphyrin IX methyltransferase2 (chlm) from synechocystis pcc 6803 with bound sah
53	c3ccrfB	Alignment	not modelled	99.9	PDB header: transferase Chain: B: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase;

53	c3cc1p	Alignment	not modelled	99.9	12	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 <i>pseudomonas putida</i> kt2440 at 2.103 Å resolution
54	c3e8sA	Alignment	not modelled	99.9	13	PDB header: transferase Chain: C: PDB Molecule: putative sam-dependent methyltransferase; PDBTitle: conversion of a disulfide bond into a thioacetal group during 2 echinomycin biosynthesis
55	c4necC	Alignment	not modelled	99.9	20	PDB header: transferase/antibiotic Chain: D: PDB Molecule: 2-methoxy-6-polypropenyl-1,4-benzoquinol methylase, PDBTitle: crystal structure of yeast coq5 in the apo form
56	c4obxD	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: arsenic (iii) s-adenosylmethionine methyltransferase with as (iii)
57	c3qnhA	Alignment	not modelled	99.9	21	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 2 <i>rhodopseudomonas palustris</i> , northeast structural genomics consortium target rpr299
58	c3e23A	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosyl-l-methionine-dependent PDBTitle: crystal structure of a putative s-adenosyl-l-methionine-dependent methyltransferase (mmp1179) from <i>methanococcus maripaludis</i> at 1.15 Å resolution
59	c3dlcA	Alignment	not modelled	99.9	16	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
60	c6g4wq	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of the sam-dependent methyltransferase cg3271 from 2 <i>corynebacterium glutamicum</i> in complex with s-adenosyl-l-homocysteine3 and pyrophosphate. northeast structural genomics consortium target 4 cgr113a
61	c3h2bB	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine-dependent methyltransferase; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 from <i>Escherichia coli</i> in complex with s-adenosylmethionine.
62	c4htfA	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
63	d1im8a	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from <i>thermus thermophilus hb8</i>
64	c2gs9A	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
65	d1jqeA	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
66	d2gh1a1	Alignment	not modelled	99.9	9	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
67	c4rvgA	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: 16s rrna methyltransferase; PDBTitle: crystal structure of 16s rrna methyltransferase kamb
68	c3mq2A	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
69	d1r74a	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a putative methyltransferase (bce_1332) from 2 <i>Bacillus cereus</i> atcc 10987 at 1.64 Å resolution
70	c3cc8A	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: streptomyces sphaeroides novo (8-demethylnovobioc acid c(8)-methyltransferase; PDBTitle: streptomyces sphaeroides novo (8-demethylnovobioc acid2 methyltransferase) with sah
71	c5mgzA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from 2 <i>archaeoglobus fulgidus</i>
72	c3dliB	Alignment	not modelled	99.9	14	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 Acidiphilicia</i>
73	c3g2qA	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
74	c4x1oA	Alignment	not modelled	99.8	11	PDB header: transferase Chain: A: PDB Molecule: 16s rrna (adenine(1408)-n(1))-2 methyltransferase from <i>Catenulisporales Acidiphilicia</i>
75	c5evjA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: arsenite methyltransferase; PDBTitle: x-ray crystal structure of crarsm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from <i>chlamydomonas reinhardtii</i>

76	c3dtnA	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methyltransferase mm_2633; PDBTitle: crystal structure of putative methyltransferase-mm_2633 from methanoscincus maezi .
77	d1ve3a1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
78	c4krkB	Alignment	not modelled	99.8	15	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
79	d2a14a1	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase PDB header: transferase
80	c3ndjA	Alignment	not modelled	99.8	16	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
81	c3g5IA	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
82	c3I8dA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
83	c5t39A	Alignment	not modelled	99.8	10	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
84	d1zx0a1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
85	c6mroA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: methyl transferase from methanoscincina acetivorans; PDBTitle: crystal structure of methyl transferase from methanoscincina acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nsg) target mvr53.
86	c5ufmB	Alignment	not modelled	99.8	15	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
87	c3m70A	Alignment	not modelled	99.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: telurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
88	c3hnxA	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase bt9727_4108; PDBTitle: crystal structure of a probable methyltransferase2 bt9727_4108 from bacillus thuringiensis subsp. northeast3 structural genomics consortium target id bur219
89	c3gwzB	Alignment	not modelled	99.8	11	PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr
90	c4hgyC	Alignment	not modelled	99.8	13	PDB header: transferase Chain: C: PDB Molecule: ccbj; PDBTitle: structure of the ccbj methyltransferase from streptomyces caelestis
91	d1y8ca	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
92	c6dcba	Alignment	not modelled	99.8	14	PDB header: transferase/rna Chain: A: PDB Molecule: 7sk srna methylphosphate capping enzyme; PDBTitle: structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna
93	c6ccaA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: dsra protein; PDBTitle: crystal structure of dsra carbon methyltransferase
94	c3pfhD	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 from streptomyces fradiae in complex with sah and dtdp-quip3n
95	c3ofkA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: nodulation protein s; PDBTitle: crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wnm9 in complex with s-adenosyl-l-homocysteine (sah)
96	d1xvaa	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
97	c3sm3A	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferases; PDBTitle: crystal structure of sam-dependent methyltransferases q8pk2_metta2 from methanoscincus maezi. northeast structural genomics consortium3 target mar262.
98	c2p35A	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from agrobacterium tumefaciens
99	d1vrla	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent

99	d1x1a_	Alignment	not modelled	99.8	14	methyltransferases Family: Guanidinoacetate methyltransferase Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
100	d1yzha1	Alignment	not modelled	99.8	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
101	d1pjza_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: glycine sarcosine n-methyltransferase; PDBTitle: crystal structure of glycine sarcosine n-methyltransferase from2 methanohalophilus portocalensis in complex with betaine
102	c5hijA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast
103	c3g5tA_	Alignment	not modelled	99.8	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
104	d1qzza2	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: n-dimethyltransferase; PDBTitle: crystal structure of streptomyces venezuelae desv
105	c3bxoA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: n,n-dimethyltransferase; PDBTitle: crystal structure of streptomyces venezuelae desv
106	c3d2lC_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: C: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exiguobacterium sp. 255-15 at 1.90 a resolution
107	c3lstB_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: B: PDB Molecule: calo1 methyltransferase; PDBTitle: crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
108	c5eovA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: 16s/23s rrna (cytidine-2'-o)-methyltransferase tlya; PDBTitle: c-terminal domain of the 16s/23s rrna (cytidine-2'-o)-2 methyltransferase tlya.
109	c4gekG_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: G: PDB Molecule: tRNA (cmo5u34)-methyltransferase; PDBTitle: crystal structure of wild-type cmoa from e.coli
110	c2xvmB_	Alignment	not modelled	99.8	14	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
111	c5bxyB_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: B: PDB Molecule: RNA methyltransferase; PDBTitle: crystal structure of RNA methyltransferase from salinibacter ruber in2 complex with S-adenosyl-l-homocysteine
112	c3ggdA_	Alignment	not modelled	99.8	15	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
113	c3opnA_	Alignment	not modelled	99.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hemolysin; PDBTitle: the crystal structure of a putative hemolysin from lactococcus lactis
114	c5bszA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: n-methyltransferase; PDBTitle: x-ray structure of the sugar n-methyltransferase keds8 from streptallocteichus sp atcc 53650
115	c2p8jA_	Alignment	not modelled	99.8	11	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 2.0 a resolution
116	c3egeA_	Alignment	not modelled	99.8	16	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	c3jwgA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: methyltransferase type 12; PDBTitle: crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c
118	c2iipD_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: D: PDB Molecule: nicotinamide n-methyltransferase; PDBTitle: human nicotinamide n-methyltransferase
119	c3lecA_	Alignment	not modelled	99.8	15	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
120	d1d2ha_	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase