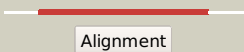

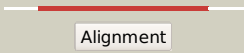

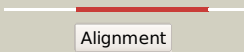

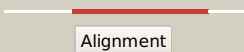

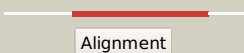

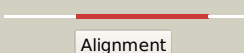

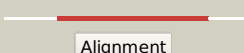





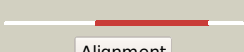

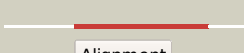












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0447c_(ufaA1)_535227_536510
Date	Tue Jul 23 14:50:52 BST 2019
Unique Job ID	169cdf5e63b20dc7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5z9oA_	 Alignment		100.0	32	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	c6bqcA_	 Alignment		100.0	31	PDB header: transferase Chain: A; PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
3	d1kpia_	 Alignment		100.0	27	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
4	d1kpga_	 Alignment		100.0	32	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
5	d1tpya_	 Alignment		100.0	32	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
6	c2fk8A_	 Alignment		100.0	33	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	c6gkvB_	 Alignment		100.0	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
8	d2fk8a1	 Alignment		100.0	33	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
9	d1llea_	 Alignment		100.0	31	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
10	c5kn4B_	 Alignment		100.0	19	PDB header: transferase Chain: B; PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0
11	d2o57a1	 Alignment		100.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase

12	c5gm2E_	Alignment		100.0	19	PDB header: transferase Chain: E; PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
13	c4pneA_	Alignment		100.0	16	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 (atpmt2) in complex with sah
15	c4krhB_	Alignment		100.0	21	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	c4ineB_	Alignment		100.0	17	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
17	c3vc2J_	Alignment		100.0	19	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
18	c3busB_	Alignment		100.0	20	PDB header: transferase Chain: B; PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
19	c6ectA_	Alignment		100.0	20	PDB header: transferase Chain: A; PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257
20	c4iv0B_	Alignment		100.0	14	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
21	c6ecvB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B; PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
22	c3ujcA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A; PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
23	c3f4kA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A; PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
24	d1nkva_	Alignment	not modelled	100.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein Yjhp
25	c3e7pA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A; PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
26	c3bkbB_	Alignment	not modelled	99.9	16	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	c2yr0A_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A; PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
						PDB header: transferase

28	c4qnuH_	Alignment	not modelled	99.9	16	Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
29	c4kdcA_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
30	c5fcdA_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
31	c4p7cB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
32	c4necC_	Alignment	not modelled	99.9	22	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
33	d1vl5a_	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
34	c5egpB_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
35	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
36	c1vl5B_	Alignment	not modelled	99.9	12	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
37	c3mggB_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei
38	d1xxla_	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
39	c3lccA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
40	c6c5bB_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure analysis of laphzm
41	c3mq2A_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 16s rna methyltransferase; PDBTitle: crystal structure of 16s rna methyltransferase kamb
42	c6f5zB_	Alignment	not modelled	99.9	17	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
43	c4htfA_	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 escherichia coli in complex with s-adenosylmethionine.
44	c5u18A_	Alignment	not modelled	99.9	19	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
45	c4x1oA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: 16s rna (adenine(1408)-n(1))-methyltransferase; PDBTitle: crystal structure of the 16s rna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
46	c3bgvC_	Alignment	not modelled	99.9	14	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
47	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)
48	c1z3cA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozooan cuculici mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
49	d1ri5a_	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
50	c5w7kA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag
51	c3gwzB_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr
52	c6g4wq_	Alignment	not modelled	99.9	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
						PDB header: transferase

53	c3ccfB	Alignment	not modelled	99.9	15	Chain: B; PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: crystal structure of putative methyltransferase (yp_321342.1) from2 anabaena variabilis atcc 29413 at 1.90 a resolution
54	c4rvgA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A; PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
55	c4gdkB	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 synechocystis pcc 6803 with bound sah
56	c3m70A	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
57	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
58	d2gh1a1	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
59	c3dlcA	Alignment	not modelled	99.9	17	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
60	d1pjza	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
61	c5bp9A	Alignment	not modelled	99.9	14	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
62	d1xtpa	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
63	c6ccaA	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A; PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
64	c5evjA	Alignment	not modelled	99.9	17	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
65	c5dplB	Alignment	not modelled	99.9	24	PDB header: transferase Chain: B; PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy
66	d1jqea	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
67	c4krkB	Alignment	not modelled	99.9	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
68	c6mroA	Alignment	not modelled	99.9	14	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.
69	c6clwA	Alignment	not modelled	99.9	16	PDB header: biosynthetic protein Chain: A; PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of tmh
70	c5do0A	Alignment	not modelled	99.9	24	PDB header: transferase Chain: A; PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
71	c3lstB	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B; PDB Molecule: calo1 methyltransferase; PDBTitle: crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
72	c2xvmB	Alignment	not modelled	99.9	16	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
73	c3ou7A	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A; PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
74	c2r3sA	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative o-methyltransferase (npun_r0239) from2 nostoc punctiforme pcc 73102 at 2.15 a resolution
75	c2p35A	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A; PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
76	d1qz3a	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent

76	c1qzaz	Alignment	not modelled	99.9	18	methyltransferases Family: Plant O-methyltransferase, C-terminal domain PDB header: transferase
77	c5mgzA	Alignment	not modelled	99.9	29	Chain: A: PDB Molecule: 8-demethylnovobiocic acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah PDB header: transferase
78	c4qttB	Alignment	not modelled	99.9	19	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) Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
79	d1r74a	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase PDB header: transferase
80	c3g2qA	Alignment	not modelled	99.9	17	Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtf2 complexed with sinefungin Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
81	d1ve3a1	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase PDB header: transferase
82	d1xvaa	Alignment	not modelled	99.9	19	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 PDB header: transferase
83	c3h2bB	Alignment	not modelled	99.9	16	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) PDB header: transferase
84	c3ofkA	Alignment	not modelled	99.9	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 PDB header: structural genomics, unknown function
85	c3ndjA	Alignment	not modelled	99.9	14	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 PDB header: transferase
86	c3e23A	Alignment	not modelled	99.9	17	Chain: B: PDB Molecule: o-methyltransferase family 2; PDBTitle: crystal structure of o-methyltransferase family 2 protein plim_11472 from planctomyces limnophilus dsm 3776 complex with apigenin PDB header: transferase
87	c5i2hB	Alignment	not modelled	99.9	13	Chain: A: PDB Molecule: carminomycin 4-o-methyltransferase; PDBTitle: crystal structure of carminomycin-4-o-methyltransferase (dnrk) in2 complex with s-adenosyl-l-homocystein (sah) and 4-methoxy-e-3 rhodomycin t (m-et) PDB header: transferase
88	c1tw3A	Alignment	not modelled	99.9	18	Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482 PDB header: transferase
89	c3dp7B	Alignment	not modelled	99.9	14	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 PDB header: transferase
90	c5ufmB	Alignment	not modelled	99.9	15	Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of burkholderia glumae toxa with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethyltoxoflavin PDB header: transferase
91	c5je0B	Alignment	not modelled	99.9	18	Chain: C: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli PDB header: transferase
92	c3lbfC	Alignment	not modelled	99.9	22	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 PDB header: transferase
93	c3cc8A	Alignment	not modelled	99.9	15	Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
94	c3g5tA	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO) PDB header: transferase,lyase
95	d1tw3a2	Alignment	not modelled	99.9	19	Chain: B: PDB Molecule: curj; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase
96	d1im8a	Alignment	not modelled	99.9	16	PDB header: transferase
97	c5thyB	Alignment	not modelled	99.9	15	Chain: A: PDB Molecule: methyltransferase type 12; PDBTitle: crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c PDB header: transferase
98	d1dl5a1	Alignment	not modelled	99.9	19	
99	c3jwgA	Alignment	not modelled	99.9	17	

100	d1wzn1	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
101	c5ubbA	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
102	c6dcbA	Alignment	not modelled	99.9	21	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
103	c3ggdA	Alignment	not modelled	99.9	11	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
104	d2bzga1	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
105	c3egeA	Alignment	not modelled	99.9	19	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
106	c2gs9A	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from thermus thermophilis hb8
107	c5bxyB	Alignment	not modelled	99.9	20	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
108	c4iscA	Alignment	not modelled	99.9	23	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a putative methyltransferase from pseudomonas2 syringae
109	c5mptA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: citrinin polyketide synthase; PDBTitle: structure of the citrinin polyketide synthase cmet domain
110	c2ip2B	Alignment	not modelled	99.8	12	PDB header: transferase Chain: B: PDB Molecule: probable phenazine-specific methyltransferase; PDBTitle: structure of the pyocyanin biosynthetic protein phzm
111	c6ec3C	Alignment	not modelled	99.8	16	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdm01
112	c3i53A	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
113	c3l8dA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
114	c3mczB	Alignment	not modelled	99.8	18	PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase; PDBTitle: the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
115	d1dusa	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein MJ0882
116	c3bgdB	Alignment	not modelled	99.8	19	PDB header: transferase Chain: B: PDB Molecule: thiopurine s-methyltransferase; PDBTitle: thiopurine s-methyltransferase
117	c3dliB	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
118	d1jg1a	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase
119	c5t39A	Alignment	not modelled	99.8	12	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
120	c4l7vA	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of protein l-isoaspartyl-o-methyltransferase of2 vibrio cholerae