

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wp5A_	Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
2	c3e8sA_	Alignment		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
3	c4krhB_	Alignment		99.9	14	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
4	c1vI5B_	Alignment		99.9	16	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
5	d1vI5a_	Alignment		99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
6	c4ineB_	Alignment		99.9	12	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	c2yr0A_	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
8	c4kdcA_	Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
9	d2gh1a1	Alignment		99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
10	d1xxla_	Alignment		99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
11	c3vc2J_	Alignment		99.9	14	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

12	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
13	c4necC_	Alignment		99.9	19	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
14	c5egpB_	Alignment		99.9	12	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
15	d1jqea_	Alignment		99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
16	c3qnhA_	Alignment		99.9	19	PDB header: transferase Chain: A: PDB Molecule: arsenic methyltransferase; PDBTitle: arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
17	c3bkxB_	Alignment		99.9	14	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
18	c3e7pA_	Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
19	c6f5zB_	Alignment		99.9	15	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
20	d1kpga_	Alignment		99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
21	c3lccA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
22	c3ou7A_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
23	d2o57a1	Alignment	not modelled	99.9	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
24	d1kpia_	Alignment	not modelled	99.9	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
25	c4htfA_	Alignment	not modelled	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.
26	c5evjA_	Alignment	not modelled	99.9	19	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
27	c3dlcA_	Alignment	not modelled	99.9	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

28	c2gs9A	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from thermus thermophilis hb8
29	c3f4kA	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
30	c5ufmB	Alignment	not modelled	99.9	19	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
31	c5w7kA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag
32	c4qnuH	Alignment	not modelled	99.9	19	PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
33	d1xtpa	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
34	c6ectA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257
35	c3busB	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
36	d2ex4a1	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
37	d1tpya	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
38	c3ujcA	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
39	c3l8dA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
40	c5z9oA	Alignment	not modelled	99.9	13	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
41	c5mptA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: citritin polyketide synthase; PDBTitle: structure of the citritin polyketide synthase cmet domain
42	c3g2qA	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
43	c5je0B	Alignment	not modelled	99.9	15	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
44	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
45	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
46	c4p7cB	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
47	c3e23A	Alignment	not modelled	99.9	18	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
48	c3cc8A	Alignment	not modelled	99.9	19	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
49	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 possilbe exported protein from bordetella2 parapertussis
50	c2fk8A	Alignment	not modelled	99.9	11	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
51	c4pneA	Alignment	not modelled	99.9	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
52	d1nkva	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein Yjhp

53	c3mvggB_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei
54	d2a14a1	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase
55	c5ubbA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
56	c2p35A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
57	c5bp9A_	Alignment	not modelled	99.9	17	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
58	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
59	d1y8ca_	Alignment	not modelled	99.9	9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
60	c5gm2E_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
61	c3g5tA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast
62	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
63	c6ecvB_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
64	c6mroA_	Alignment	not modelled	99.9	16	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.
65	c5mgzA_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobioc acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobioc acid2 methyltransferase) with sah
66	c5fcdA_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
67	c4iv0B_	Alignment	not modelled	99.9	12	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
68	d1im8a_	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
69	d1vlma_	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
70	c5t39A_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: evdmo1; PDBTitle: crystal structure of the n-terminal domain of evdmo1 in the presence2 of sah and d-fucose
71	c3g5lA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
72	c2p7iB_	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
73	d2p7ia1	Alignment	not modelled	99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
74	d1zx0a1	Alignment	not modelled	99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
75	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
76	c6bqcA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli

77	c2iipD_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: D: PDB Molecule: nicotinamide n-methyltransferase; PDBTitle: human nicotinamide n-methyltransferase
78	c3ccfB_	Alignment	not modelled	99.9	16	PDB header: transferase 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
79	d1xvaa_	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
80	c5hijA_	Alignment	not modelled	99.9	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
81	c3dliB_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
82	c3ndjA_	Alignment	not modelled	99.9	17	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
83	c6ccaA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
84	d1r74a_	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
85	c3ofkA_	Alignment	not modelled	99.9	17	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)
86	d1wzna1	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
87	c6g4wq_	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
88	c3sm3A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferases; PDBTitle: crystal structure of sam-dependent methyltransferases q8puk2_metma2 from methanosarcina mazei. northeast structural genomics consortium3 target mar262.
89	c3m70A_	Alignment	not modelled	99.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
90	c5thyB_	Alignment	not modelled	99.9	16	PDB header: transferase,lyase Chain: B: PDB Molecule: curj; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase
91	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 .
92	d1xcla_	Alignment	not modelled	99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
93	c4x1oA_	Alignment	not modelled	99.9	15	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
94	c6gkvB_	Alignment	not modelled	99.8	12	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
95	d1ve3a1	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
96	c5kn4B_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0
97	c3hnrA_	Alignment	not modelled	99.8	18	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
98	c3pfdD_	Alignment	not modelled	99.8	15	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
99	c4kvzA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: baml; PDBTitle: crystal structure of the plantazolin methyltransferase baml in2 complex with sah
100	c3d2lC_	Alignment	not modelled	99.8	18	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
						Fold: S-adenosyl-L-methionine-dependent methyltransferases

101	d2avna1	Alignment	not modelled	99.8	20	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
102	c4iscA	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a putative methyltransferase from pseudomonas2 syringae
103	c4kwcA	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: bpuml; PDBTitle: structure of the plantazolicin methyltransferase bpuml in complex with2 sah
104	c4krqB	Alignment	not modelled	99.8	17	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
105	c3bkwB	Alignment	not modelled	99.8	16	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
106	c3merA	Alignment	not modelled	99.8	14	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
107	c3bxoA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: n,n-dimethyltransferase; PDBTitle: crystal structure of streptomyces venezuelae desvi
108	c3egeA	Alignment	not modelled	99.8	13	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
109	c3mq2A	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: 16s rna methyltransferase; PDBTitle: crystal structure of 16s rna methyltransferase kamb
110	c5bszA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: n-methyltransferase; PDBTitle: x-ray structure of the sugar n-methyltransferase keds8 from2 streptoaloteichus sp atcc 53650
111	c3opnA	Alignment	not modelled	99.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hemolysin; PDBTitle: the crystal structure of a putative hemolysin from lactococcus lactis
112	c6dcbA	Alignment	not modelled	99.8	16	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
113	c3ggdA	Alignment	not modelled	99.8	13	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
114	c4rwzA	Alignment	not modelled	99.8	26	PDB header: transferase Chain: A: PDB Molecule: putative rna methyltransferase; PDBTitle: crystal structure of the antibiotic-resistance methyltransferase kmr
115	c4gdkB	Alignment	not modelled	99.8	16	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
116	c3gwzB	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr
117	c6ec3C	Alignment	not modelled	99.8	22	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdmo1
118	c4hgyC	Alignment	not modelled	99.8	16	PDB header: transferase Chain: C: PDB Molecule: ccbj; PDBTitle: structure of the ccj methyltransferase from streptomyces caelestis
119	c3lstB	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: calo1 methyltransferase; PDBTitle: crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
120	c6clwA	Alignment	not modelled	99.8	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of tmh