Phyre^2

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Description	RVBD2675c_(-)_2991194_2991946
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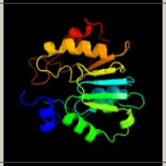
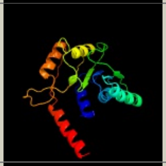
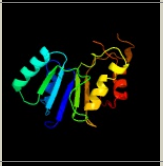
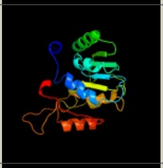
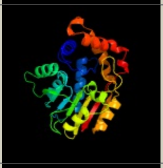
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4necC_	Alignment		100.0	41	**PDB header:**transferase/antibiotic **Chain:** C: **PDB Molecule:**putative sam-dependent methyltransferase; **PDBTitle:** conversion of a disulfide bond into a thioacetal group during2 echinomycin biosynthesis
2	c3lccA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyl chloride transferase; **PDBTitle:** structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
3	c6mroA_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyl transferase from methanosarcina acetivorans; **PDBTitle:** crystal structure of methyl transferase from methanosarcina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
4	c5wp5A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphomethylethanolamine n-methyltransferase 2; **PDBTitle:** arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
5	d2bzga1	Alignment		100.0	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
6	c3bgdB_	Alignment		100.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiopurine s-methyltransferase; **PDBTitle:** thiopurine s-methyltransferase
7	c4krhB_	Alignment		99.9	20	**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
8	c4ineB_	Alignment		99.9	20	**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
9	c3vc2J_	Alignment		99.9	15	**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
10	c2yr0A_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha0223; **PDBTitle:** crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
11	c4p7cB_	Alignment		99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (mo5u34)-methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato

12	d2o57a1	Alignment		99.9	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
13	c6ec3C_	Alignment		99.9	18	**PDB header:**transferase, oxidoreductase **Chain:** C: **PDB Molecule:**methyltransferase domain-containing protein; **PDBTitle:** crystal structure of evdmo1
14	c3m70A_	Alignment		99.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
15	c3e7pA_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
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	d1pjza_	Alignment		99.9	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
18	c4pneA_	Alignment		99.9	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**methyltransferase-like protein; **PDBTitle:** crystal structure of the [4+2]-cyclase spnf
19	c3g2qA_	Alignment		99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pcza361.24; **PDBTitle:** crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
20	c2fk8A_	Alignment		99.9	13	**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
21	c5w7kA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oxag; **PDBTitle:** crystal structure of oxag
22	c5t39A_	Alignment	not modelled	99.9	18	**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
23	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
24	c5egpB_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ubie/coq5 family methyltransferase, putative; **PDBTitle:** crystal structure of the s-methyltransferase tmta
25	c5evjA_	Alignment	not modelled	99.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arsenite methyltransferase; **PDBTitle:** x-ray crystal structure of crarsm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii
26	c4krgB_	Alignment	not modelled	99.9	18	**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
27	d1ve3a1	Alignment	not modelled	99.9	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
28	c4kdcA	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-demethylubiquinone-9 3-

28	c4kdcA_	Alignment	not modelled	99.9	22	methyltransferase; **PDBTitle:** crystal structure of ubig
29	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
30	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
31	c3f4kA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
32	c6g4wq_	Alignment	not modelled	99.9	21	**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
33	c1vl5B_	Alignment	not modelled	99.9	27	**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
34	d1vl5a_	Alignment	not modelled	99.9	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
35	c3e23A_	Alignment	not modelled	99.9	17	**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 rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr299
36	d1kpga_	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
37	c5bp9A_	Alignment	not modelled	99.9	18	**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
38	d2fk8a1	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
39	c3l8dA_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyltransferase from bacillus thuringiensis
40	c3ggdA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anabaena variabilis atcc 29413 at 2.11 a resolution
41	c5ufmB_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase domain protein; **PDBTitle:** crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine
42	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
43	c3qnhA_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arsenic methyltransferase; **PDBTitle:** arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
44	c4qdkB_	Alignment	not modelled	99.9	24	**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
45	c2pxxA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mgc2408; **PDBTitle:** human putative methyltransferase mgc2408
46	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
47	d2a14a1	Alignment	not modelled	99.9	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arylamine N-methyltransferase
48	c6ecvB_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**stid protein; **PDBTitle:** stid o-mt residues 976-1266
49	d1r74a_	Alignment	not modelled	99.9	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
50	c3g5tA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase from yeast
51	c2xvmB_	Alignment	not modelled	99.9	17	**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
						Fold:S-adenosyl-L-methionine-dependent methyltransferases

52	d2ex4a1	Alignment	not modelled	99.9	11	**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
53	c3ofkA_	Alignment	not modelled	99.9	13	**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)
54	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
55	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
56	c4htfA_	Alignment	not modelled	99.9	23	**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.
57	c6ectA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**stie protein; **PDBTitle:** stie o-mt residues 961-1257
58	c5mgzA_	Alignment	not modelled	99.9	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**8-demethylnovobiocic acid c(8)-methyltransferase; **PDBTitle:** streptomyces spheroides novo (8-demethylnovbiocic acid2 methyltransferase) with sah
59	d1xxla_	Alignment	not modelled	99.9	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
60	c5kn4B_	Alignment	not modelled	99.9	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pavine n-methyltransferase; **PDBTitle:** pavine n-methyltransferase apoenzyme ph 6.0
61	c5fcdA_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mccd; **PDBTitle:** crystal structure of mccd protein
62	d1jqea_	Alignment	not modelled	99.9	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Histamine methyltransferase
63	c4azwA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wbdd; **PDBTitle:** crystal structure of monomeric wbdd.
64	c3merA_	Alignment	not modelled	99.9	20	**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
65	d1xvaa_	Alignment	not modelled	99.9	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
66	c4x1oA_	Alignment	not modelled	99.9	18	**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
67	c3dlcA_	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-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
68	d1xtpa_	Alignment	not modelled	99.9	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
69	c6gkvB_	Alignment	not modelled	99.9	19	**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
70	d1zx0a1	Alignment	not modelled	99.9	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
71	c4iv0B_	Alignment	not modelled	99.9	13	**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
72	c3ujcA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase; **PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
73	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
74	c1z3cA_	Alignment	not modelled	99.9	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
75	c3cc8A_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a putative methyltransferase

						(bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution
76	c6bqcA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclopropane-fatty-acyl-phospholipid synthase; **PDBTitle:** cyclopropane fatty acid synthase from e. coli
77	c4kwcA_	Alignment	not modelled	99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bpuml; **PDBTitle:** structure of the plantazolicin methyltransferase bpuml in complex with2 sah
78	c4qttB_	Alignment	not modelled	99.9	15	**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)
79	d1ri5a_	Alignment	not modelled	99.9	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap (Guanine N-7) methyltransferase
80	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
81	c5je0B_	Alignment	not modelled	99.9	24	**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
82	c5do0A_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein lysine methyltransferase 1; **PDBTitle:** the structure of pkmt1 from rickettsia prowazekii
83	c2iipD_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinamide n-methyltransferase; **PDBTitle:** human nicotinamide n-methyltransferase
84	c4kvzA_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**baml; **PDBTitle:** crystal structure of the plantazolicin methyltransferase baml in2 complex with sah
85	d2gh1a1	Alignment	not modelled	99.9	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**BC2162-like
86	c5dplB_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein lysine methyltransferase 2; **PDBTitle:** the structure of pkmt2 from rickettsia typhi in complex with adohcy
87	c3cggB_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
88	d1yzha1	Alignment	not modelled	99.9	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
89	c4iscA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of a putative methyltransferase from pseudomonas2 syringae
90	c5ubbA_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha n-terminal protein methyltransferase 1b; **PDBTitle:** crystal structure of human alpha n-terminal protein methyltransferase2 1b
91	c2gs9A_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein tt1324; **PDBTitle:** crystal structure of tt1324 from thermus thermophilis hb8
92	d1xcla_	Alignment	not modelled	99.9	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
93	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
94	c5u18A_	Alignment	not modelled	99.9	22	**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
95	c3e8sA_	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
96	c5mptA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrinin polyketide synthase; **PDBTitle:** structure of the citrinin polyketide synthase cmet domain
97	c3dmgA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable ribosomal rna small subunit methyltransferase; **PDBTitle:** t. thermophilus 16s rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
98	c3ou7A_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** dhpi-sam-hep complex
99	c4hg2B_	Alignment	not modelled	99.9	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase type 11; **PDBTitle:** the structure of a putative type ii methyltransferase from2 anaeromyxobacter dehalogenans.

100	d1y8ca_	Alignment	not modelled	99.9	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
101	c5gm2E_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** E: **PDB Molecule:**o-methylransferase; **PDBTitle:** crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
102	c6dcbA_	Alignment	not modelled	99.9	25	**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	c2p8jA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine-dependent methyltransferase; **PDBTitle:** crystal structure of s-adenosylmethionine-dependent methyltransferase2 (np_349143.1) from clostridium acetobutylicum at 2.00 a resolution
104	c6f5zB_	Alignment	not modelled	99.9	19	**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
105	d2avna1	Alignment	not modelled	99.9	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
106	d1d2ha_	Alignment	not modelled	99.9	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
107	c4hgyC_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ccbj; **PDBTitle:** structure of the ccbj methyltransferase from streptomyces caelestis
108	c3g2qB_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pcza361.24; **PDBTitle:** crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
109	d2p7ia1	Alignment	not modelled	99.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
110	c3mq2A_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methyltransferase; **PDBTitle:** crystal structure of 16s rrna methyltranferase kamb
111	c3pfhD_	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
112	c3dliB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
113	c3lecA_	Alignment	not modelled	99.9	14	**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
114	c5hijA_	Alignment	not modelled	99.9	21	**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
115	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
116	c3busB_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of rebm
117	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)
118	c6d6yA_	Alignment	not modelled	99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**apra methyltransferase 2; **PDBTitle:** apra methyltransferase 2 - gnat didomain in complex with sah
119	d1vbfa_	Alignment	not modelled	99.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
120	d1wzna1	Alignment	not modelled	99.8	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like