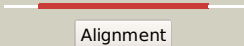

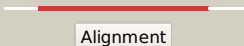

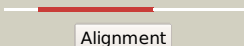

















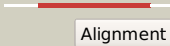

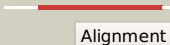

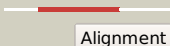






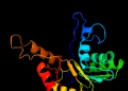
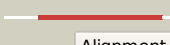






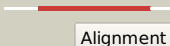
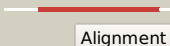

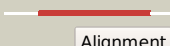

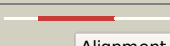
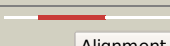


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2067c (-) _2324655_2325878
Date	Mon Aug 5 13:25:18 BST 2019
Unique Job ID	51b6285a473edc18

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5do0A_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
2	c5dplB_	 Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy
3	c4krhB_	 Alignment		100.0	19	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	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
5	c5wp5A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
6	c3vc2J_	 Alignment		100.0	11	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
7	c4p7cB_	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
8	d2o57a1	 Alignment		100.0	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
9	c5kn4B_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0
10	c5egpB_	 Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
11	c6gkvB_	 Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: coclaurine n-methyltransferase; PDBTitle: crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylhelamine and sah

12	c5w7kA	 Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag
13	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
14	c6ecvB	 Alignment		99.9	15	PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
15	c1vl5B	 Alignment		99.9	18	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
16	d1vl5a	 Alignment		99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
17	d1kpga	 Alignment		99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
18	c5z9oA	 Alignment		99.9	20	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
19	d1kpia	 Alignment		99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
20	c3f4kA	 Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
21	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
22	c3bkxB	 Alignment	not modelled	99.9	18	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
23	d1tpya	 Alignment	not modelled	99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
24	c4necC	 Alignment	not modelled	99.9	18	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
25	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
26	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
27	c3e7pA	 Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
28	c6ectA	 Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: stie protein;

						PDBTitle: stie o-mt residues 961-1257
29	c2yr0A_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
30	d2gh1a1	Alignment	not modelled	99.9	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
31	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
32	c4qnuH_	Alignment	not modelled	99.9	26	PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
33	c6ec3C_	Alignment	not modelled	99.9	20	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdmo1
34	d1xxla_	Alignment	not modelled	99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
35	c3qnhA_	Alignment	not modelled	99.9	25	PDB header: transferase Chain: A: PDB Molecule: arsenic methyltransferase; PDBTitle: arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
36	c3ocjA_	Alignment	not modelled	99.9	18	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
37	c5fcdA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
38	d1nkva_	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein Yjhp
39	c4kdcA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
40	c5evjA_	Alignment	not modelled	99.9	23	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
41	c6bqcA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
42	d1jqea_	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
43	c4krqB_	Alignment	not modelled	99.9	14	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
44	c5mgzA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovbiocic acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovbiocic acid2 methyltransferase) with sah
45	c4kwcA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: bpuml; PDBTitle: structure of the plantazolicin methyltransferase bpuml in complex with2 sah
46	c4pneA_	Alignment	not modelled	99.9	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
47	c3mggB_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei
48	c4kvzA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: baml; PDBTitle: crystal structure of the plantazolicin methyltransferase baml in2 complex with sah
49	c4htfA_	Alignment	not modelled	99.9	20	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.
50	c3dlcA_	Alignment	not modelled	99.9	16	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
51	c3ujcA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
						PDB header: transferase

52	c4x1oA_	Alignment	not modelled	99.9	16	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
53	d1yzha1	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
54	c5u18A_	Alignment	not modelled	99.9	18	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
55	c6d6yA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: apra methyltransferase 2; PDBTitle: apra methyltransferase 2 - gnat didomain in complex with sah
56	c3bgvC_	Alignment	not modelled	99.9	16	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
57	d1r74a_	Alignment	not modelled	99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
58	c5gm2E_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
59	c4iscA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a putative methyltransferase from pseudomonas2 syringae
60	c5mptA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: citrinin polyketide synthase; PDBTitle: structure of the citrinin polyketide synthase cmet domain
61	d2ex4a1	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
62	d1xvaa_	Alignment	not modelled	99.9	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
63	c2qs9A_	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
64	c4iv0B_	Alignment	not modelled	99.9	17	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
65	c4azwA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: crystal structure of monomeric wbdd.
66	d2fcaa1	Alignment	not modelled	99.9	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
67	c3mtiA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: rrna methylase; PDBTitle: the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
68	c3m70A_	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
69	c3lccA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
70	c4dcmA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase g; PDBTitle: crystal structure of methyltransferase rlmg modifying g1835 of 23s2 rrna in escherichia coli
71	c6dcbA_	Alignment	not modelled	99.9	13	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
72	c4obxD_	Alignment	not modelled	99.9	12	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
73	d1xcla_	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
74	c3busB_	Alignment	not modelled	99.9	25	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
75	c5je0B_	Alignment	not modelled	99.9	18	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
76	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

77	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
78	d1ri5a_	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
79	c3l8dA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
80	c1z3cA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
81	d1ve3a1	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
82	d1zx0a1	Alignment	not modelled	99.9	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
83	c3lecA_	Alignment	not modelled	99.9	12	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
84	d2p7ia1	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
85	c6ccaA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
86	c4azsA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: methyltransferase wbdd; PDBTitle: high resolution (2.2 a) crystal structure of wbdd.
87	c3ofkA_	Alignment	not modelled	99.9	15	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)
88	c3dxyA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(7)-)-methyltransferase; PDBTitle: crystal structure of ectrmb in complex with sam
89	c3egeA_	Alignment	not modelled	99.9	18	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
90	c4qttB_	Alignment	not modelled	99.9	20	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)
91	d1im8a_	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
92	d1xtpa_	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
93	d1jg1a_	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase
94	c3ku1E_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: E: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of streptococcus pneumoniae sp1610, a putative trna2 (m1a22) methyltransferase, in complex with s-adenosyl-l-methionine
95	d2bzga1	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
96	c3g07C_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: C: PDB Molecule: 7sk snrna methylphosphate capping enzyme; PDBTitle: methyltransferase domain of human bicoid-interacting protein 3 homolog2 (drosophila)
97	c2xvmB_	Alignment	not modelled	99.9	21	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
98	c1yb2A_	Alignment	not modelled	99.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0852; PDBTitle: structure of a putative methyltransferase from thermoplasma2 acidophilum.
99	d1yb2a1	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like
100	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
						PDB header: transferase

101	c4rvgA_	Alignment	not modelled	99.9	17	Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
102	c3bgdB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: thiopurine s-methyltransferase; PDBTitle: thiopurine s-methyltransferase
103	c3gnlB_	Alignment	not modelled	99.9	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein, duf633, lmf2365_1472; PDBTitle: structure of uncharacterized protein (lmf2365_1472) from listeria2 monocytogenes serotype 4b
104	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
105	d1dusa_	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein MJ0882
106	c3h2bB_	Alignment	not modelled	99.9	17	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
107	c3g5lA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
108	c3eeyl_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: J: PDB Molecule: putative rna methylase; PDBTitle: crystal structure of putative rna-methylase from clostridium2 thermocellum
109	c3dmgA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: probable ribosomal rna small subunit methyltransferase; PDBTitle: t. thermophilus 16s rna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
110	d1dl5a1	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase
111	c3lbfC_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: C: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
112	c4xcxA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: small rna 2'-o-methyltransferase; PDBTitle: methyltransferase domain of small rna 2'-o-methyltransferase
113	c2p8jA_	Alignment	not modelled	99.9	20	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
114	c3lpmA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
115	d1pjza_	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
116	c5thyB_	Alignment	not modelled	99.9	13	PDB header: transferase,lyase Chain: B: PDB Molecule: curj; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase
117	c4uw0A_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: low resolution structure of wbdd with c-terminal bundle ordered to2 residue 505
118	c3e05B_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: precocorrin-6y c5,15-methyltransferase (decarboxylating); PDBTitle: crystal structure of precocorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
119	c3fzgA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: 16s rna methylase; PDBTitle: structure of the 16s rna methylase arma
120	c2yxeB_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of l-isoaspartyl protein carboxyl methyltransferase