

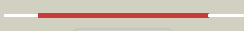




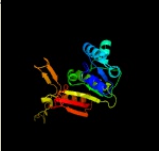



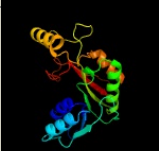












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1498c_(-)_1689309_1689926
Date	Fri Aug 2 13:30:08 BST 2019
Unique Job ID	8ad8dcc6be7a5d04

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r74a_	 Alignment		99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
2	c4hgyC_	 Alignment		99.9	16	PDB header: transferase Chain: C: PDB Molecule: ccbaj; PDBTitle: structure of the ccbj methyltransferase from streptomyces caelestis
3	c5hijA_	 Alignment		99.9	17	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
4	c3g2qA_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
5	c4krhB_	 Alignment		99.9	22	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
6	c3ocjA_	 Alignment		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
7	d1y8ca_	 Alignment		99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
8	d1xvaa_	 Alignment		99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
9	c5wp5A_	 Alignment		99.9	23	PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
10	c3qnhA_	 Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: arsenic methyltransferase; PDBTitle: arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
11	d1d2ha_	 Alignment		99.9	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase

12	c4ineB_	Alignment		99.9	24	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
13	c3h2bB_	Alignment		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
14	c6dcbA_	Alignment		99.9	18	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
15	c4p7cB_	Alignment		99.9	19	PDB header: transferase Chain: B; PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
16	d1wzna1	Alignment		99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
17	c3e23A_	Alignment		99.9	23	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
18	c4qnuH_	Alignment		99.9	19	PDB header: transferase Chain: H; PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
19	c3vc2J_	Alignment		99.9	16	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
20	c3d2lC_	Alignment		99.9	19	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
21	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
22	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
23	c5w7kA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A; PDB Molecule: oxag; PDBTitle: crystal structure of oxag
24	d2ex4a1	Alignment	not modelled	99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
25	c2iipD_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: D; PDB Molecule: nicotinamide n-methyltransferase; PDBTitle: human nicotinamide n-methyltransferase
26	c5evjA_	Alignment	not modelled	99.9	24	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	c3sm3A_	Alignment	not modelled	99.9	20	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.
28	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

					didemethylthioflavin and s-adenosylhomocysteine
29	c3bgvC_	Alignment	not modelled	99.9	15 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
30	c5bszA_	Alignment	not modelled	99.9	16 PDB header: transferase Chain: A: PDB Molecule: n-methyltransferase; PDBTitle: x-ray structure of the sugar n-methyltransferase keds8 from2 streptoalloteichus sp atcc 53650
31	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
32	d1im8a_	Alignment	not modelled	99.9	19 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
33	c4necC_	Alignment	not modelled	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
34	c3g2qB_	Alignment	not modelled	99.9	16 PDB header: transferase Chain: B: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
35	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.
36	c5egpB_	Alignment	not modelled	99.9	18 PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
37	c5t39A_	Alignment	not modelled	99.9	13 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
38	c5bp9A_	Alignment	not modelled	99.9	15 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
39	c3lccA_	Alignment	not modelled	99.9	21 PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
40	c3g5lA_	Alignment	not modelled	99.9	15 PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
41	c3e7pA_	Alignment	not modelled	99.9	15 PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
42	c3bxoA_	Alignment	not modelled	99.9	21 PDB header: transferase Chain: A: PDB Molecule: n,n-dimethyltransferase; PDBTitle: crystal structure of streptomyces venezuelae desvi
43	c3pfdD_	Alignment	not modelled	99.9	20 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
44	c6ccaA_	Alignment	not modelled	99.9	20 PDB header: transferase Chain: A: PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
45	c1vl5B_	Alignment	not modelled	99.9	19 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
46	c3dlcA_	Alignment	not modelled	99.9	21 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
47	d1vl5a_	Alignment	not modelled	99.9	19 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
48	d2o57a1	Alignment	not modelled	99.9	25 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
49	c3dliB_	Alignment	not modelled	99.9	17 PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
50	c3ujcA_	Alignment	not modelled	99.9	17 PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
51	c3bkxB_	Alignment	not modelled	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
					PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein

52	c5ubbA_	Alignment	not modelled	99.9	19	methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
53	d1ve3a1	Alignment	not modelled	99.9	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
54	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
55	d1kpga_	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
56	c4kdcA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
57	c2fk8A_	Alignment	not modelled	99.9	16	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
58	c5z9oA_	Alignment	not modelled	99.9	19	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
59	d1jqea_	Alignment	not modelled	99.9	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
60	c3ou7A_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
61	c6mroA_	Alignment	not modelled	99.9	23	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.
62	c4gekG_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: G: PDB Molecule: trna (cmo5u34)-methyltransferase; PDBTitle: crystal structure of wild-type cmoa from e.coli
63	c3dtnA_	Alignment	not modelled	99.9	16	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 .
64	c3e8sA_	Alignment	not modelled	99.9	14	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
65	c3f4kA_	Alignment	not modelled	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.
66	d2fk8a1	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
67	d1l1ea_	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
68	c3cc8A_	Alignment	not modelled	99.9	18	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
69	c2yr0A_	Alignment	not modelled	99.9	25	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
70	d1ri5a_	Alignment	not modelled	99.9	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
71	c1z3cA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozoan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
72	c3g07C_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: 7sk snrna methylphosphate capping enzyme; PDBTitle: methyltransferase domain of human bicoid-interacting protein 3 homolog2 (drosophila)
73	c4x1oA_	Alignment	not modelled	99.9	16	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
74	d1tpya_	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
75	c3hnrA_	Alignment	not modelled	99.9	17	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
76	c5mptA	Alignment	not modelled	99.9	19 PDB header: transferase Chain: A: PDB Molecule: citrinin polyketide synthase; PDBTitle: structure of the citrinin polyketide synthase cmet domain
77	c4obxD	Alignment	not modelled	99.9	19 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
78	c3m70A	Alignment	not modelled	99.9	19 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
79	c4iv0B	Alignment	not modelled	99.8	19 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
80	c4pneA	Alignment	not modelled	99.8	28 PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
81	c3jwgA	Alignment	not modelled	99.8	16 PDB header: transferase Chain: A: PDB Molecule: methyltransferase type 12; PDBTitle: crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c
82	d1xxla	Alignment	not modelled	99.8	23 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
83	c3g5tA	Alignment	not modelled	99.8	23 PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast
84	d1kpia	Alignment	not modelled	99.8	15 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
85	c5fcdA	Alignment	not modelled	99.8	15 PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
86	c5cm2Z	Alignment	not modelled	99.8	21 PDB header: transferase Chain: Z: PDB Molecule: trna methyltransferase; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
87	d2gh1a1	Alignment	not modelled	99.8	18 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
88	c4krkB	Alignment	not modelled	99.8	19 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
89	c6g4wq	Alignment	not modelled	99.8	20 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
90	d2p7ia1	Alignment	not modelled	99.8	18 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
91	d1yzha1	Alignment	not modelled	99.8	14 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
92	c2p7iB	Alignment	not modelled	99.8	18 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
93	c5je0B	Alignment	not modelled	99.8	13 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
94	c6ecvB	Alignment	not modelled	99.8	20 PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
95	c3l8dA	Alignment	not modelled	99.8	20 PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
96	c6ectA	Alignment	not modelled	99.8	23 PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257
97	c3cggB	Alignment	not modelled	99.8	21 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
98	c3bgdB	Alignment	not modelled	99.8	16 PDB header: transferase Chain: B: PDB Molecule: thiopurine s-methyltransferase; PDBTitle: thiopurine s-methyltransferase
99	c2p8jA	Alignment	not modelled	99.8	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

100	d2bzga1	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
101	c6f5zB_	Alignment	not modelled	99.8	26	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
102	c5mgzA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobiocic acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah
103	d1pjza_	Alignment	not modelled	99.8	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
104	c4qdkB_	Alignment	not modelled	99.8	18	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
105	d1nkva_	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein Yjhp
106	c4rvga_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
107	c3mq2A_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: 16s rrna methyltransferase; PDBTitle: crystal structure of 16s rrna methyltransferase kamb
108	c5gm2E_	Alignment	not modelled	99.8	24	PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
109	c5do0A_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
110	c5dplB_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy
111	c4xcxA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: small rna 2'-o-methyltransferase; PDBTitle: methyltransferase domain of small rna 2'-o-methyltransferase
112	c6ec3C_	Alignment	not modelled	99.8	18	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdm1
113	c6bqaA_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
114	c4rwzA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: putative rrna methyltransferase; PDBTitle: crystal structure of the antibiotic-resistance methyltransferase kmr
115	c3mgaB_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazi
116	c2gs9A_	Alignment	not modelled	99.8	25	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from thermus thermophilis hb8
117	d2fcaa1	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
118	c4xrpF_	Alignment	not modelled	99.8	17	PDB header: protein binding Chain: F: PDB Molecule: hen1; PDBTitle: structure of the pnkp1/rnl/hen1 rna repair complex
119	c3mcaB_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase; PDBTitle: the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
120	c3opnA_	Alignment	not modelled	99.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hemolysin; PDBTitle: the crystal structure of a putative hemolysin from lactococcus lactis