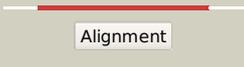
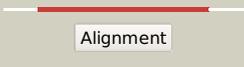
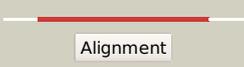
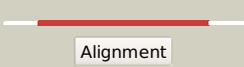


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3832c_(-)_4306414_4306989
Date	Fri Aug 9 18:20:54 BST 2019
Unique Job ID	7459ff6052ff32c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ocjA_			99.9	22	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
2	c3e23A_			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
3	c5ufmB_			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
4	c5wp5A_			99.9	19	PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
5	c4krhB_			99.9	21	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 2; PDBTitle: semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine
6	c3h2bB_			99.9	15	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
7	c4ineB_			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
8	c3ou7A_			99.9	19	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
9	d1im8a_			99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
10	c3l8dA_			99.9	18	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
11	c5bszA_			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

12	c3ujcA	Alignment		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
13	c3g2qA	Alignment		99.9	19	PDB header: transferase Chain: A; PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
14	d1y8ca	Alignment		99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
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	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
17	c5cm2Z	Alignment		99.9	11	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
18	c3dlcA	Alignment		99.9	18	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
19	d2a14a1	Alignment		99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase
20	d2fk8a1	Alignment		99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
21	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)
22	d1kpga	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
23	c4iv0B	Alignment	not modelled	99.9	18	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
24	c4gekG	Alignment	not modelled	99.9	16	PDB header: transferase Chain: G; PDB Molecule: trna (cmo5u34)-methyltransferase; PDBTitle: crystal structure of wild-type cmoa from e.coli
25	c3vc2J	Alignment	not modelled	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
26	c3lccA	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A; PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
27	c4qnuH	Alignment	not modelled	99.9	18	PDB header: transferase Chain: H; PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
						PDB header: transferase

28	c3pfhD_	Alignment	not modelled	99.9	20	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
29	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
30	d2o57a1	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
31	d2ex4a1	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
32	c5z9oA_	Alignment	not modelled	99.9	15	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
33	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
34	c3d2lC_	Alignment	not modelled	99.9	22	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
35	c1vl5B_	Alignment	not modelled	99.9	20	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
36	c3sm3A_	Alignment	not modelled	99.9	18	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.
37	d1vl5a_	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
38	c3hnrA_	Alignment	not modelled	99.9	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
39	c3dliB_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
40	d1kpia_	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
41	c4obxD_	Alignment	not modelled	99.9	17	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
42	c5egpB_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
43	c3bxoA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: n,n-dimethyltransferase; PDBTitle: crystal structure of streptomyces venezuelae desvi
44	d1tpya_	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
45	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
46	d1l1ea_	Alignment	not modelled	99.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
47	c3cc8A_	Alignment	not modelled	99.9	17	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
48	c3bkxB_	Alignment	not modelled	99.9	21	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
49	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 .
50	c4kdcA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
51	c5hijA_	Alignment	not modelled	99.9	18	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
52	c6f5zB_	Alignment	not modelled	99.8	18	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
53	d1nkva_	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein YjhP
54	c3f4kA_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
55	c4pneA_	Alignment	not modelled	99.8	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
56	d1xxla_	Alignment	not modelled	99.8	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
57	c3g2qB_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: B: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
58	c4hgyC_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: C: PDB Molecule: ccbj; PDBTitle: structure of the ccbj methyltransferase from streptomyces caelestis
59	c2gs9A_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from thermus thermophilus hb8
60	c5w7kA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag
61	c2iipD_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: D: PDB Molecule: nicotinamide n-methyltransferase; PDBTitle: human nicotinamide n-methyltransferase
62	c4htfA_	Alignment	not modelled	99.8	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.
63	c2yr0A_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
64	d2gh1a1	Alignment	not modelled	99.8	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
65	c3ccfB_	Alignment	not modelled	99.8	20	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
66	d1xtpa_	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
67	c5ubbA_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
68	c5gm2E_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
69	c3qnhA_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: arsenic methyltransferase; PDBTitle: arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
70	c3merA_	Alignment	not modelled	99.8	17	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
71	c6g4wq_	Alignment	not modelled	99.8	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
72	c5mptA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: citritrin polyketide synthase; PDBTitle: structure of the citritrin polyketide synthase cmet domain
73	c4qttB_	Alignment	not modelled	99.8	16	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)
74	d1r74a_	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
75	c3mggB_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazi
76	c3g8eA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: putative sam dependent methyltransferase;

76	c66sA	Alignment	not modelled	99.8	10	PDBTitle: crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
77	d1jqea	Alignment	not modelled	99.8	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
78	c4a6dA	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: hydroxyindole o-methyltransferase; PDBTitle: crystal structure of human n-acetylserotonin2 methyltransferase (asmt) in complex with sam
79	c3g5lA	Alignment	not modelled	99.8	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
80	c4necC	Alignment	not modelled	99.8	16	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
81	c4rvqA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
82	c6bqcA	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
83	c6d6yA	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: apra methyltransferase 2; PDBTitle: apra methyltransferase 2 - gnat didomain in complex with sah
84	c3ndjA	Alignment	not modelled	99.8	15	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
85	d1wzna1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
86	c5t39A	Alignment	not modelled	99.8	22	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
87	c4qdkB	Alignment	not modelled	99.8	13	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
88	c6mroA	Alignment	not modelled	99.8	13	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 (nesh) target mvr53.
89	c2p7lB	Alignment	not modelled	99.8	14	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
90	c3busB	Alignment	not modelled	99.8	18	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
91	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
92	c3bgvC	Alignment	not modelled	99.8	19	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
93	c5fcdA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
94	c5evjA	Alignment	not modelled	99.8	22	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
95	d2nxca1	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ribosomal protein L11 methyltransferase PrmA
96	c3mczB	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase; PDBTitle: the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
97	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
98	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
99	c6ectA	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257

100	d2p7ia1	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
101	d1zx0a1	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
102	c3egeA	Alignment	not modelled	99.8	17	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
103	d1vlma	Alignment	not modelled	99.8	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
104	c1x1aA	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: crtf-related protein; PDBTitle: crystal structure of bchu complexed with s-adenosyl-L-methionine
105	d1ve3a1	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
106	c3mq2A	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: 16s rrna methyltransferase; PDBTitle: crystal structure of 16s rrna methyltransferase kamb
107	c6c5bB	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure analysis of laphzm
108	c5thyB	Alignment	not modelled	99.8	19	PDB header: transferase,lyase Chain: B: PDB Molecule: curj; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase
109	d1xvaa	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
110	d1xcla	Alignment	not modelled	99.8	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
111	c1z3cA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozoon cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
112	c2p35A	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
113	d2g72a1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase
114	c3cggB	Alignment	not modelled	99.8	16	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
115	d1ri5a	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
116	c6ecvB	Alignment	not modelled	99.8	19	PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
117	c4x1oA	Alignment	not modelled	99.8	13	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
118	c4e70A	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: coniferyl alcohol 9-o-methyltransferase; PDBTitle: crystal structure analysis of coniferyl alcohol 9-o-methyltransferase2 from linum nodiflorum in complex with coniferyl alcohol
119	c3m70A	Alignment	not modelled	99.8	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
120	c3bkwB	Alignment	not modelled	99.8	21	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