



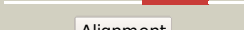











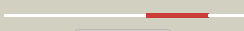

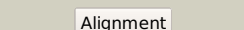

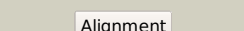



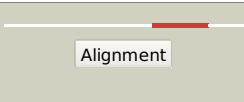
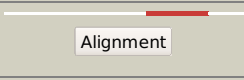
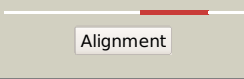
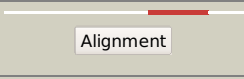
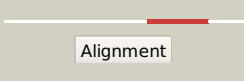
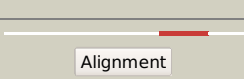
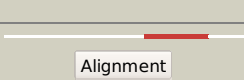
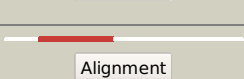
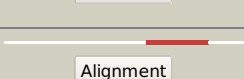
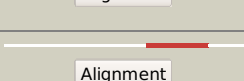
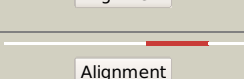
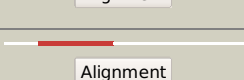
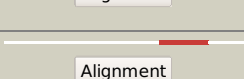
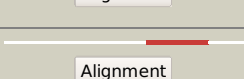
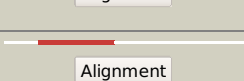
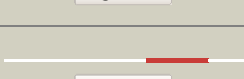
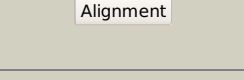
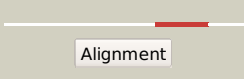
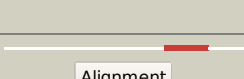
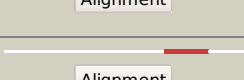
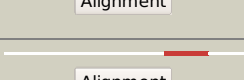
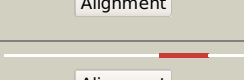
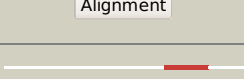
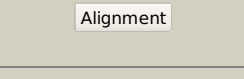
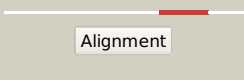
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3729_(-)_4178463_4180793
Date	Fri Aug 9 18:20:42 BST 2019
Unique Job ID	fc99b653ed12ae6c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c4krhB_	 Alignment		100.0	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
3	c4ineB_	 Alignment		100.0	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
4	c2fk8A_	 Alignment		100.0	15	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
5	d2o57a1	 Alignment		100.0	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
6	c5z9oA_	 Alignment		100.0	17	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
7	d2fk8a1	 Alignment		100.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
8	d1kpga_	 Alignment		100.0	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
9	c3vc2J_	 Alignment		100.0	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
10	d1l1ea_	 Alignment		100.0	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
11	c3e7pA_	 Alignment		100.0	18	PDB header: transferase Chain: A; PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482

12	d1kpia_	Alignment		100.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
13	d1tpya_	Alignment		100.0	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
14	c4pneA_	Alignment		100.0	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
15	c5gm2E_	Alignment		100.0	24	PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
16	c4iv0B_	Alignment		100.0	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
17	c3f4kA_	Alignment		100.0	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.
18	c6bqcA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
19	d1nkva_	Alignment		100.0	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein Yjhp
20	c3busB_	Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
21	c6efnA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
22	c3ujcA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
23	c5fcdA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein
24	d1tv8a_	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
25	c5v1tA_	Alignment	not modelled	100.0	16	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suis bound to precursor2 peptide sua
26	c5egpB_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
27	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)
28	c5w7kA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag

29	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
30	c6ecvB	 Alignment	not modelled	99.9	19	PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
31	c6gkvB	 Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: coclaurine n-methyltransferase; PDBTitle: crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah
32	c5kn4B	 Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0
33	c3bkbB	 Alignment	not modelled	99.9	20	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
34	c4p7cB	 Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
35	c2yr0A	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
36	c4k39A	 Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmece with bound adomet and cp18cys peptide
37	c1vl5B	 Alignment	not modelled	99.9	22	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
38	d1vl5a	 Alignment	not modelled	99.9	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
39	c6ectA	 Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257
40	c5wggA	 Alignment	not modelled	99.9	17	PDB header: peptide binding protein Chain: A: PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the biosynthesis2 of sactipeptides
41	c4qnuH	 Alignment	not modelled	99.9	13	PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
42	c3mggB	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei
43	c6b4cH	 Alignment	not modelled	99.9	19	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
44	c4htfA	 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 from escherichia coli in complex with s-adenosylmethionine.
45	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
46	c3ocjA	 Alignment	not modelled	99.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: the crystal structure of a possibe exported protein from bordetella2 parapertussis
47	c6ec3C	 Alignment	not modelled	99.9	22	PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdm01
48	c5t39A	 Alignment	not modelled	99.9	21	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
49	c4kdcA	 Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
50	c4x1oA	 Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 16s rrna (adenine(1408)-n(1))-methyltransferase; PDBTitle: crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
51	c6f5zB	 Alignment	not modelled	99.9	24	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
52	c2yx0A	 Alignment	not modelled	99.9	18	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
		 Alignment				Fold: S-adenosyl-L-methionine-dependent methyltransferases

53	d1xxla_	Alignment	not modelled	99.9	23	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
54	d2gh1a1	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
55	c6c8vA_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
56	c2p35A_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
57	c3lccA_	Alignment	not modelled	99.9	23	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
58	c3ccfB_	Alignment	not modelled	99.9	17	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
59	d2ex4a1	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
60	c5vslB_	Alignment	not modelled	99.9	15	PDB header: antiviral protein Chain: B: PDB Molecule: radical s-adenosyl methionine domain-containing protein 2; PDBTitle: crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)
61	d1jqea_	Alignment	not modelled	99.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
62	c4necC_	Alignment	not modelled	99.9	24	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
63	c3g5tA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast
64	d1xtpa_	Alignment	not modelled	99.9	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
65	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
66	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
67	c6g4wq_	Alignment	not modelled	99.9	23	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
68	c5mgzA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobiocic acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah
69	c6d6yA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: apra methyltransferase 2; PDBTitle: apra methyltransferase 2 - gnat didomain in complex with sah
70	c6ccaA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
71	c3h2bB_	Alignment	not modelled	99.8	18	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
72	c5je0B_	Alignment	not modelled	99.8	20	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
73	d1xcla_	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
74	d1im8a_	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
75	c1z3cA_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozoan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
76	c4qttB_	Alignment	not modelled	99.8	21	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)
						PDB header: transferase

77	c3mq2A_	Alignment	not modelled	99.8	14	Chain: A: PDB Molecule: 16s rrna methyltransferase; PDBTitle: crystal structure of 16s rrna methyltransferase kamb
78	c3l8dA_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis
79	c4kwCA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: bpum1; PDBTitle: structure of the plantazolicin methyltransferase bpum1 in complex with2 sah
80	c5ubbA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
81	d1r74a_	Alignment	not modelled	99.8	24	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
82	c3g2qA_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
83	c5do0A_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
84	d1zx0a1	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
85	c5dplB_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: B: PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy
86	d1ri5a_	Alignment	not modelled	99.8	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
87	c4kvzA_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: baml; PDBTitle: crystal structure of the plantazolicin methyltransferase baml in2 complex with sah
88	c3egeA_	Alignment	not modelled	99.8	20	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
89	c4obxD_	Alignment	not modelled	99.8	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
90	c3cc8A_	Alignment	not modelled	99.8	15	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
91	c2gs9A_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from thermus thermophilis hb8
92	c4krGB_	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
93	d1xvaa_	Alignment	not modelled	99.8	28	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
94	c3lecA_	Alignment	not modelled	99.8	13	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
95	c6dcbA_	Alignment	not modelled	99.8	17	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
96	c5thyB_	Alignment	not modelled	99.8	14	PDB header: transferase,lyase Chain: B: PDB Molecule: curj; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase
97	c3g5lA_	Alignment	not modelled	99.8	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
98	c3e23A_	Alignment	not modelled	99.8	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 rhodospseudomonas palustris, northeast structural genomics consortium3 target rpr299
99	c5bp9A_	Alignment	not modelled	99.8	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
100	c4hgyC_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: C: PDB Molecule: ccbj; PDBTitle: structure of the ccbj methyltransferase from streptomyces caelestis
						Fold: S-adenosyl-L-methionine-dependent methyltransferases

101	d2p7ia1	Alignment	not modelled	99.8	14	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
102	d1yzha1	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
103	c5u18A	Alignment	not modelled	99.8	23	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
104	c4njka	Alignment	not modelled	99.8	18	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
105	c3ou7A	Alignment	not modelled	99.8	25	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
106	c6mroA	Alignment	not modelled	99.8	18	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.
107	c5bxyB	Alignment	not modelled	99.8	17	PDB header: transferase Chain: B: PDB Molecule: rna methyltransferase; PDBTitle: crystal structure of rna methyltransferase from salinibacter ruber in2 complex with s-adenosyl-l-homocysteine
108	c3m70A	Alignment	not modelled	99.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
109	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
110	c3gwb	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr
111	c3p2ka	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: 16s rna methylase; PDBTitle: structure of an antibiotic related methyltransferase
112	d2bzga1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
113	c4rwzA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: putative rna methyltransferase; PDBTitle: crystal structure of the antibiotic-resistance methyltransferase kmr
114	c5ufmB	Alignment	not modelled	99.8	21	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
115	c3ofkA	Alignment	not modelled	99.8	16	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)
116	d1p1ca	Alignment	not modelled	99.8	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
117	c3ku1E	Alignment	not modelled	99.8	11	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
118	c3g07C	Alignment	not modelled	99.8	17	PDB header: transferase Chain: C: PDB Molecule: 7sk srna methylphosphate capping enzyme; PDBTitle: methyltransferase domain of human bicoid-interacting protein 3 homolog2 (drosophila)
119	c3dliB	Alignment	not modelled	99.8	19	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
120	c4qdkB	Alignment	not modelled	99.8	17	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