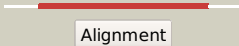



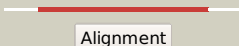

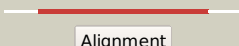

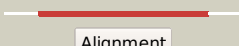

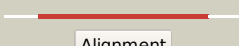

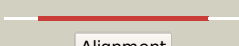











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0642c_(mmaA4)_736301_737206
 Date Fri Jul 26 01:50:20 BST 2019
 Unique Job ID 2980145096883c0a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5z9oA_	 Alignment		100.0	31	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
2	c2fk8A_	 Alignment		100.0	100	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
3	d1kpga_	 Alignment		100.0	57	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
4	c6bqcA_	 Alignment		100.0	29	PDB header: transferase Chain: A; PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
5	d2fk8a1	 Alignment		100.0	100	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
6	d1kpia_	 Alignment		100.0	51	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
7	d1tpya_	 Alignment		100.0	56	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
8	d1llea_	 Alignment		100.0	56	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
9	c6gkvB_	 Alignment		100.0	22	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
10	c5gm2E_	 Alignment		100.0	18	PDB header: transferase Chain: E; PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1
11	c4pneA_	 Alignment		100.0	15	PDB header: biosynthetic protein Chain: A; PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf

12	c5kn4B_	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0
13	d2o57a1	Alignment		100.0	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
14	c5wp5A_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
15	c4krhB_	Alignment		100.0	18	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
16	c4ineB_	Alignment		100.0	19	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
17	c3busB_	Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of rebm
18	c4iv0B_	Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase, putative; PDBTitle: crystal structure of n-methyl transferase from plasmodium vivax2 complexed with s-adenosyl methionine and phosphate
19	c3ujcA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
20	c3vc2J_	Alignment		100.0	19	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
21	c6ectA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257
22	d1nkva_	Alignment	not modelled	100.0	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein YjhP
23	c3e7pA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
24	c3f4kA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
25	c6ecvB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266
26	c3bkxB_	Alignment	not modelled	99.9	12	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
27	c5egpB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta
28	c5fcdA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein

29	c3ocjA_	Alignment	not modelled	99.9	12	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
30	c4kdcA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig
31	c3mggB_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei
32	c4qnuH_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212
33	c1vl5B_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: unknown conserved protein bh2331; PDBTitle: crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution
34	d1vl5a_	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
35	c2yr0A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
36	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
37	c5w7kA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag
38	c4p7cB_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
39	c1z3cA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
40	d1ri5a_	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase
41	c3bgvC_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: C: PDB Molecule: mrna cap guanine-n7 methyltransferase; PDBTitle: crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
42	d1xtpa_	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
43	c3ccfB_	Alignment	not modelled	99.9	15	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
44	d1xxla_	Alignment	not modelled	99.9	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like
45	c6f5zB_	Alignment	not modelled	99.9	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
46	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.
47	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
48	c3mq2A_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: 16s rrna methyltransferase; PDBTitle: crystal structure of 16s rrna methyltransferase kamb
49	c5bp9A_	Alignment	not modelled	99.9	16	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
50	c3lccA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
51	c5subbA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
52	c5je0B_	Alignment	not modelled	99.9	17	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
						PDB header: transferase

53	c3ou7A_	Alignment	not modelled	99.9	11	Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex
54	c3qnhA_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: arsenic methyltransferase; PDBTitle: arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
55	c3e23A_	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rpa2492; PDBTitle: crystal structure of the rpa2492 protein in complex with sam from2 rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr299
56	d1im8a_	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
57	c3dlcA_	Alignment	not modelled	99.9	15	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
58	d2gh1a1	Alignment	not modelled	99.9	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
59	c5evjA_	Alignment	not modelled	99.9	15	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
60	d1wzna1	Alignment	not modelled	99.9	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
61	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
62	c4qttB_	Alignment	not modelled	99.9	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 rna (apo-form)
63	c3lecA_	Alignment	not modelled	99.9	10	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
64	c4qdkB_	Alignment	not modelled	99.9	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
65	c3h2bB_	Alignment	not modelled	99.9	12	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
66	c3e8sA_	Alignment	not modelled	99.9	13	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
67	d1jqea_	Alignment	not modelled	99.9	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase
68	d1r74a_	Alignment	not modelled	99.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
69	c4x1oA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: 16s rna (adenine(1408)-n(1))-methyltransferase; PDBTitle: crystal structure of the 16s rna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
70	c3gwzB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr
71	c5ufmB_	Alignment	not modelled	99.9	16	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
72	c5mgzA_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobioc acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobioc acid2 methyltransferase) with sah
73	d1xvaa_	Alignment	not modelled	99.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
74	c6g4wq_	Alignment	not modelled	99.9	24	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
75	c3cc8A_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a putative methyltransferase

						(bce_1332) from <i>Bacillus cereus</i> ATCC 10987 at 1.64 Å resolution
76	c2gs9A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from <i>Thermus thermophilus</i> hb8
77	c4krqB_	Alignment	not modelled	99.9	15	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
78	c3g2qA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
79	c4rvqA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
80	c3ofkA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: nodulation protein s; PDBTitle: crystal structure of n-methyltransferase nods from <i>Bradyrhizobium japonicum</i> wm9 in complex with s-adenosyl-L-homocysteine (sah)
81	c3lstB_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: calo1 methyltransferase; PDBTitle: crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
82	c3dtnA_	Alignment	not modelled	99.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methyltransferase mm_2633; PDBTitle: crystal structure of putative methyltransferase-mm_2633 from <i>Methanosarcina mazei</i>
83	c4hgyC_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: C: PDB Molecule: ccbaj; PDBTitle: structure of the ccbj methyltransferase from <i>Streptomyces caelestis</i>
84	c3dliB_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from <i>Archaeoglobus fulgidus</i>
85	c5t39A_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: evdm01; PDBTitle: crystal structure of the n-terminal domain of evdm01 in the presence of sah and d-fucose
86	d2a14a1	Alignment	not modelled	99.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase
87	d1ve3a1	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
88	c4gekG_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: G: PDB Molecule: trna (cmo5u34)-methyltransferase; PDBTitle: crystal structure of wild-type cmoa from <i>E. coli</i>
89	c3hnrA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase bt9727_4108; PDBTitle: crystal structure of a probable methyltransferase2 bt9727_4108 from <i>Bacillus thuringiensis</i> subsp. northeast3 structural genomics consortium target id bur219
90	d1qzza2	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
91	d1pjza_	Alignment	not modelled	99.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
92	c3g5tA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast
93	c3l8dA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from <i>Bacillus thuringiensis</i>
94	c2p35A_	Alignment	not modelled	99.8	10	PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from <i>Agrobacterium tumefaciens</i>
95	c5hijA_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: A: PDB Molecule: glycine sarcosine n-methyltransferase; PDBTitle: crystal structure of glycine sarcosine n-methyltransferase from <i>Methanohalophilus portucalensis</i> in complex with betaine
96	c6ccaA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
97	c6mroA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: methyl transferase from <i>Methanosarcina acetivorans</i> ; PDBTitle: crystal structure of methyl transferase from <i>Methanosarcina acetivorans</i> at 1.6 Å resolution, northeast structural genomics consortium (nesg) target mvr53.
98	c5bxyB_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: B: PDB Molecule: rna methyltransferase; PDBTitle: crystal structure of rna methyltransferase from <i>Salinibacter ruber</i> in2 complex with s-adenosyl-L-homocysteine
99	d1y8ca_	Alignment	not modelled	99.8	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like
						PDB header: transferase

100	c3g5IA_	Alignment	not modelled	99.8	16	Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
101	c5u18A_	Alignment	not modelled	99.8	20	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
102	c3jwgA_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: methyltransferase type 12; PDBTitle: crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c
103	c6clwA_	Alignment	not modelled	99.8	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of tmh
104	c4qvgC_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: C: PDB Molecule: sibl; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 sibl in its apo form
105	d1l3ia_	Alignment	not modelled	99.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Precorrin-6Y methyltransferase (CbiT)
106	c3m70A_	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae
107	c3ku1E_	Alignment	not modelled	99.8	16	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
108	c3dh0B_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: sam dependent methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
109	c3ndjA_	Alignment	not modelled	99.8	16	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
110	d1zx0a1	Alignment	not modelled	99.8	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
111	c5do0A_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
112	d1tw3a2	Alignment	not modelled	99.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
113	d1xcla_	Alignment	not modelled	99.8	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase
114	c3pfhD_	Alignment	not modelled	99.8	16	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
115	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
116	c2xvmB_	Alignment	not modelled	99.8	12	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
117	c6c5bB_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure analysis of laphzm
118	c3opnA_	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hemolysin; PDBTitle: the crystal structure of a putative hemolysin from lactococcus lactis
119	c3d2lC_	Alignment	not modelled	99.8	18	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
120	c5mptA_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: citrinin polyketide synthase; PDBTitle: structure of the citrinin polyketide synthase cmet domain