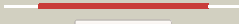



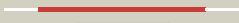




























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0893c (- )_995321_996298
Date	Fri Jul 26 01:50:48 BST 2019
Unique Job ID	c4b90a14124933cf

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2uyoa1</a>	 Alignment		100.0	41	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> ML2640-like
2	<a href="#">d1rjda_</a>	 Alignment		100.0	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Leucine carboxy methyltransferase Ppm1
3	<a href="#">c3ieiD_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 1; <b>PDBTitle:</b> crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
4	<a href="#">c3mntA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 1; <b>PDBTitle:</b> crystal structure of human leucine carboxyl methyltransferase 1
5	<a href="#">c2zwaA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 2; <b>PDBTitle:</b> crystal structure of trna wybutosine synthesizing enzyme2 tyw4
6	<a href="#">c2qe6B_</a>	 Alignment		99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein tfu_2867; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (tfu_2867) from2 thermobifida fusca yx at 1.95 a resolution
7	<a href="#">c3giwA_</a>	 Alignment		99.5	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function duf574; <b>PDBTitle:</b> crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
8	<a href="#">c3gwb_</a>	 Alignment		98.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mmcr; <b>PDBTitle:</b> structure of the mitomycin 7-o-methyltransferase mmcr
9	<a href="#">c4qvqC_</a>	 Alignment		98.2	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sibl; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 sibl in its apo form
10	<a href="#">c3mcb_</a>	 Alignment		98.1	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
11	<a href="#">c6clwA_</a>	 Alignment		98.0	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of tmnh

12	<a href="#">c2ip2B</a>	Alignment		97.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable phenazine-specific methyltransferase; <b>PDBTitle:</b> structure of the pyocyanin biosynthetic protein phzm
13	<a href="#">d1tw3a2</a>	Alignment		97.9	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
14	<a href="#">c3p9kD</a>	Alignment		97.8	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> caffeic acid o-methyltransferase; <b>PDBTitle:</b> crystal structure of perennial ryegrass lpomt1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
15	<a href="#">c3dp7B</a>	Alignment		97.8	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
16	<a href="#">c6c5bB</a>	Alignment		97.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure analysis of laphzm
17	<a href="#">c4d7kB</a>	Alignment		97.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferases; <b>PDBTitle:</b> crystal structure of n,n-8-amino-8-demethyl-d-riboflavin2 dimethyltransferase (rosa) from streptomyces davawensis
18	<a href="#">c1tw3A</a>	Alignment		97.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carminomycin 4-o-methyltransferase; <b>PDBTitle:</b> crystal structure of carminomycin-4-o-methyltransferase (dnrk) in2 complex with s-adenosyl-l-homocystein (sah) and 4-methoxy-e-3 rhodomycin t (m-et)
19	<a href="#">d1qzza2</a>	Alignment		97.7	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
20	<a href="#">c1x1aA</a>	Alignment		97.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> crtf-related protein; <b>PDBTitle:</b> crystal structure of bchu complexed with s-adenosyl-l-methionine
21	<a href="#">c3i53A</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
22	<a href="#">c5i2hB</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase family 2; <b>PDBTitle:</b> crystal structure of o-methyltransferase family 2 protein plim_11472 from planctomyces limnophilus dsm 3776 complex with apigenin
23	<a href="#">c1xduA</a>	Alignment	not modelled	97.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein rdmb; <b>PDBTitle:</b> crystal structure of aclacinomycin-10-hydroxylase (rdmb) in complex2 with sinefungin (sfg)
24	<a href="#">c3ociA</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> the crystal structure of a possilbe exported protein from bordetella2 parapertussis
25	<a href="#">c6i5zA</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase 1; <b>PDBTitle:</b> papaver somniferum o-methyltransferase
26	<a href="#">c4uy5A</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine-specific methyltransferase egtg; <b>PDBTitle:</b> crystal structure of histidine-specific methyltransferase egtg from2 mycobacterium smegmatis
27	<a href="#">d1kyza2</a>	Alignment	not modelled	97.4	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> coniferyl alcohol 9-o-methyltransferase;

28	<a href="#">c4e70A_</a>	Alignment	not modelled	97.3	10	<b>PDBTitle:</b> crystal structure analysis of coniferyl alcohol 9-o-methyltransferase2 from linum nodiflorum in complex with coniferyl alcohol
29	<a href="#">c4a6dA_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyindole o-methyltransferase; <b>PDBTitle:</b> crystal structure of human n-acetylserotonin2 methyltransferase (asmt) in complex with sam
30	<a href="#">c5dplB_</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein lysine methyltransferase 2; <b>PDBTitle:</b> the structure of pkmt2 from rickettsia typhi in complex with adohcy
31	<a href="#">c3g2qA_</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.24; <b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mtf2 complexed with sinefungin
32	<a href="#">c5do0A_</a>	Alignment	not modelled	97.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein lysine methyltransferase 1; <b>PDBTitle:</b> the structure of pkmt1 from rickettsia prowazekii
33	<a href="#">c3lccA_</a>	Alignment	not modelled	97.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyl chloride transferase; <b>PDBTitle:</b> structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
34	<a href="#">c3lstB_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calo1 methyltransferase; <b>PDBTitle:</b> crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
35	<a href="#">c5cvvB_</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> (iso)eugenol o-methyltransferase; <b>PDBTitle:</b> coniferyl alcohol bound monolignol 4-o-methyltransferase 9
36	<a href="#">c4p7cB_</a>	Alignment	not modelled	97.1	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
37	<a href="#">c4necC_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> C: <b>PDB Molecule:</b> putative sam-dependent methyltransferase; <b>PDBTitle:</b> conversion of a disulfide bond into a thioacetal group during2 echinomycin biosynthesis
38	<a href="#">c1fpqA_</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoliquiritigenin 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase
39	<a href="#">c2r3sA_</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase (npun_r0239) from2 nostoc punctiforme pcc 73102 at 2.15 a resolution
40	<a href="#">d1fp2a2</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
41	<a href="#">c5xohA_</a>	Alignment	not modelled	96.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bergaptol o-methyltransferase; <b>PDBTitle:</b> crystal structure of bergaptol o-methyltransferase complex
42	<a href="#">d1fp1d2</a>	Alignment	not modelled	96.7	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
43	<a href="#">c6mroA_</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyl transferase from methanosarcina acetivorans; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
44	<a href="#">c5wp5A_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomethylethanolamine n-methyltransferase 2; <b>PDBTitle:</b> arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
45	<a href="#">d1tpya_</a>	Alignment	not modelled	96.6	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
46	<a href="#">c6iv7B_</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase lepi; <b>PDBTitle:</b> the crystal structure of a sam-dependent enzyme from aspergillus2 flavus
47	<a href="#">d2fk8a1</a>	Alignment	not modelled	96.5	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
48	<a href="#">c1kyzC_</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> caffeic acid 3-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of caffeic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex
49	<a href="#">c5thyB_</a>	Alignment	not modelled	96.4	14	<b>PDB header:</b> transferase,lyase <b>Chain:</b> B: <b>PDB Molecule:</b> curj; <b>PDBTitle:</b> crystal structure of semet-substituted curj carbon methyltransferase
50	<a href="#">d1wzna1</a>	Alignment	not modelled	96.4	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
51	<a href="#">d1im8a_</a>	Alignment	not modelled	96.3	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein HI0319 (YecO)
52	<a href="#">d2o57a1</a>	Alignment	not modelled	96.3	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases

						<b>Family:</b> Mycolic acid cyclopropane synthase <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
53	<a href="#">d1r74a_</a>	Alignment	not modelled	96.3	12	<b>Family:</b> Glycine N-methyltransferase
54	<a href="#">d1oria_</a>	Alignment	not modelled	96.3	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
55	<a href="#">c3g2qB_</a>	Alignment	not modelled	96.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pcza361.24; <b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mtf2 complexed with sinefungin
56	<a href="#">d1f3la_</a>	Alignment	not modelled	96.2	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
57	<a href="#">c6pi9A_</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna (guanine(1405)-n(7))-methyltransferase; <b>PDBTitle:</b> crystal structure of 16s rrna methylase rmtf in complex with s-2 adenosyl-l-homocysteine
58	<a href="#">c4krhB_</a>	Alignment	not modelled	96.2	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 2; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine
59	<a href="#">c1zgaA_</a>	Alignment	not modelled	96.1	12	<b>PDB header:</b> plant protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoflavanone 4'-o-methyltransferase'; <b>PDBTitle:</b> crystal structure of isoflavanone 4'-o-methyltransferase complexed2 with (+)-6a-hydroxyrnaackian
60	<a href="#">c4z2yA_</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calo6; <b>PDBTitle:</b> crystal structure of methyltransferase calo6
61	<a href="#">c1orhA_</a>	Alignment	not modelled	96.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 1; <b>PDBTitle:</b> structure of the predominant protein arginine methyltransferase prmt1
62	<a href="#">d1l1ea_</a>	Alignment	not modelled	96.1	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
63	<a href="#">c5xlxD_</a>	Alignment	not modelled	96.1	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> chemotaxis protein methyltransferase 1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of cher1 containing sah
64	<a href="#">c4htfA_</a>	Alignment	not modelled	96.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 from escherichia coli in complex with s-adenosylmethionine.
65	<a href="#">c2fk8A_</a>	Alignment	not modelled	96.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methoxy mycolic acid synthase 4; <b>PDBTitle:</b> crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
66	<a href="#">c5iceA_</a>	Alignment	not modelled	96.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-norcoclaurine 6-o-methyltransferase; <b>PDBTitle:</b> crystal structure of (s)-norcoclaurine 6-o-methyltransferase with s-2 adenosyl-l-homocysteine and norlaudanosoline
67	<a href="#">d1kpga_</a>	Alignment	not modelled	95.9	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
68	<a href="#">c3cggB_</a>	Alignment	not modelled	95.8	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
69	<a href="#">c5lkjA_</a>	Alignment	not modelled	95.8	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-arginine methyltransferase carm1; <b>PDBTitle:</b> crystal structure of mouse carm1 in complex with ligand sa684
70	<a href="#">c4ineB_</a>	Alignment	not modelled	95.7	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein pmt-2; <b>PDBTitle:</b> crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
71	<a href="#">d1xvaa_</a>	Alignment	not modelled	95.7	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
72	<a href="#">c5z9oA_</a>	Alignment	not modelled	95.7	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus
73	<a href="#">c3h2bB_</a>	Alignment	not modelled	95.7	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> 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
74	<a href="#">c2p8jA_</a>	Alignment	not modelled	95.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 (np_349143.1) from clostridium acetobutylicum at 2.00 a resolution
75	<a href="#">c5fwaA_</a>	Alignment	not modelled	95.6	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 2;

75	<a href="#">c1waA</a>	Alignment	not modelled	95.0	0	<b>PDBTitle:</b> crystal structure of mus musculus protein arginine methyltransferase 22 with cp1
76	<a href="#">d1g6q1</a>	Alignment	not modelled	95.6	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
77	<a href="#">c4kifB</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase mppj; <b>PDBTitle:</b> crystal structure of methyltransferase from streptomyces hygroscopicus2 complexed with phenylpyruvic acid
78	<a href="#">c3bgvC</a>	Alignment	not modelled	95.5	9	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> mrna cap guanine-n7 methyltransferase; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
79	<a href="#">c3vc2J</a>	Alignment	not modelled	95.5	12	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> geranyl diphosphate 2-c-methyltransferase; <b>PDBTitle:</b> crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine
80	<a href="#">c3ggdA</a>	Alignment	not modelled	95.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anabaena variabilis atcc 29413 at 2.11 a resolution
81	<a href="#">c3ou7A</a>	Alignment	not modelled	95.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
82	<a href="#">d1kpia</a>	Alignment	not modelled	95.3	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
83	<a href="#">c3f4kA</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
84	<a href="#">c4x1oA</a>	Alignment	not modelled	95.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna (adenine(1408)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
85	<a href="#">c2v7eB</a>	Alignment	not modelled	95.2	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histone-arginine methyltransferase carm1; <b>PDBTitle:</b> crystal structure of coactivator-associated arginine2 methyltransferase 1 (carm1), unliganded
86	<a href="#">c4gdkB</a>	Alignment	not modelled	95.2	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> magnesium-protoporphyrin o-methyltransferase; <b>PDBTitle:</b> crystal structure of magnesium protoporphyrin ix methyltransferase2 (chlm) from synechocystis pcc 6803 with bound sah
87	<a href="#">c3m70A</a>	Alignment	not modelled	95.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein tehb homolog; <b>PDBTitle:</b> crystal structure of tehb from haemophilus influenzae
88	<a href="#">c5fubA</a>	Alignment	not modelled	95.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine methyltransferase 2; <b>PDBTitle:</b> crystal structure of zebrafish protein arginine methyltransferase 22 catalytic domain with sah
89	<a href="#">c3b89A</a>	Alignment	not modelled	95.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methylase; <b>PDBTitle:</b> crystal structure of rrna methylase from escherichia coli
90	<a href="#">d2fyta1</a>	Alignment	not modelled	95.1	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
91	<a href="#">d1d2ha</a>	Alignment	not modelled	95.1	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
92	<a href="#">c1fp2A</a>	Alignment	not modelled	95.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoflavone o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of isoflavone o-methyltransferase
93	<a href="#">c6dnzA</a>	Alignment	not modelled	95.1	14	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> arginine n-methyltransferase, putative; <b>PDBTitle:</b> trypanosoma brucei prmt1 enzyme-prozyme heterotetrameric complex with2 adohcy
94	<a href="#">c4y30B</a>	Alignment	not modelled	95.1	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein arginine n-methyltransferase 6; <b>PDBTitle:</b> crystal structure of human protein arginine methyltransferase prmt62 bound to sah and epz020411
95	<a href="#">d1pjza</a>	Alignment	not modelled	95.0	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
96	<a href="#">c5w7sA</a>	Alignment	not modelled	95.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxac; <b>PDBTitle:</b> crystal structure of oxac in complex with sinefungin and meleagrln
97	<a href="#">c5ubbA</a>	Alignment	not modelled	94.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha n-terminal protein methyltransferase 1b; <b>PDBTitle:</b> crystal structure of human alpha n-terminal protein methyltransferase2 1b
98	<a href="#">c3jwgA</a>	Alignment	not modelled	94.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c
99	<a href="#">d2nvc1</a>	Alignment	not modelled	94.8	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent



99	<a href="#">c21kcg1</a>	Alignment	not modelled	94.8	27	methyltransferases <b>Family:</b> Ribosomal protein L11 methyltransferase PrmA
100	<a href="#">c6ccaA</a>	Alignment	not modelled	94.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> disa protein; <b>PDBTitle:</b> crystal structure of dsza carbon methyltransferase
101	<a href="#">c4krkB</a>	Alignment	not modelled	94.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 1; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine
102	<a href="#">c3cc8A</a>	Alignment	not modelled	94.6	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bce_1332) from <i>Bacillus cereus</i> atcc 10987 at 1.64 a resolution
103	<a href="#">c4qnuH</a>	Alignment	not modelled	94.5	8	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of cmob bound with cx-sam in p21212
104	<a href="#">c4kdcA</a>	Alignment	not modelled	94.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-demethylubiquinone-9 3-methyltransferase; <b>PDBTitle:</b> crystal structure of ubig
105	<a href="#">c3b3jA</a>	Alignment	not modelled	94.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-arginine methyltransferase carm1; <b>PDBTitle:</b> the 2.55 a crystal structure of the apo catalytic domain of 2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
106	<a href="#">c3ofkA</a>	Alignment	not modelled	94.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nodulation protein s; <b>PDBTitle:</b> crystal structure of n-methyltransferase nods from <i>bradyrhizobium2 japonicum</i> wm9 in complex with s-adenosyl-homocysteine (sah)
107	<a href="#">d1ve3a1</a>	Alignment	not modelled	94.3	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
108	<a href="#">c5gm2E</a>	Alignment	not modelled	94.3	13	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase tled complexed with sah and 2 teleocidin a1
109	<a href="#">c3r0qA</a>	Alignment	not modelled	94.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable protein arginine n-methyltransferase 4.2; <b>PDBTitle:</b> a uniquely open conformation revealed in the crystal structure of 2 arabidopsis thaliana protein arginine methyltransferase 10
110	<a href="#">c5ufmB</a>	Alignment	not modelled	94.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase domain protein; <b>PDBTitle:</b> crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine
111	<a href="#">c3jwhA</a>	Alignment	not modelled	94.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hen1; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of 2 bacterial-avhen1-c
112	<a href="#">c5hijA</a>	Alignment	not modelled	93.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine sarcosine n-methyltransferase; <b>PDBTitle:</b> crystal structure of glycine sarcosine n-methyltransferase from 2 methanohalophilus portucalensis in complex with betaine
113	<a href="#">c4xcxA</a>	Alignment	not modelled	93.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> small rna 2'-o-methyltransferase; <b>PDBTitle:</b> methyltransferase domain of small rna 2'-o-methyltransferase
114	<a href="#">c2vdwA</a>	Alignment	not modelled	93.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vaccinia virus capping enzyme d1 subunit; <b>PDBTitle:</b> guanosine n7 methyl-transferase sub-complex (d1-d12) of the 2 vaccinia virus mrna capping enzyme
115	<a href="#">c3lcvB</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sisomicin-gentamicin resistance methylase sgm; <b>PDBTitle:</b> crystal structure of antibiotic related methyltransferase
116	<a href="#">d1l3ia</a>	Alignment	not modelled	93.8	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Precorin-6Y methyltransferase (CbiT)
117	<a href="#">c3qnhA</a>	Alignment	not modelled	93.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenic methyltransferase; <b>PDBTitle:</b> arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)
118	<a href="#">d1nkva</a>	Alignment	not modelled	93.5	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein Yjhp
119	<a href="#">c5bszA</a>	Alignment	not modelled	93.3	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray structure of the sugar n-methyltransferase keds8 from 2 streptoalloteichus sp atcc 53650
120	<a href="#">c6ectA</a>	Alignment	not modelled	93.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257