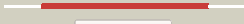



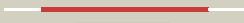








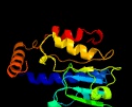








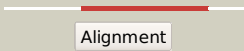

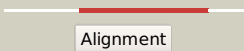

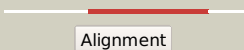



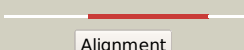

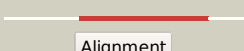

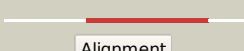

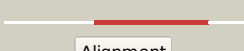



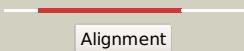
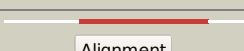

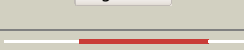
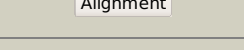

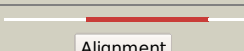



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3399_(-)_3816309_3817355
Date	Fri Aug 9 18:20:07 BST 2019
Unique Job ID	405d58eedf0c1d5



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2uyoa1</a>	 Alignment		100.0	40	<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="#">c3ieiD</a>	 Alignment		100.0	24	<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
3	<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
4	<a href="#">c3mntA</a>	 Alignment		100.0	28	<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	18	<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	24	<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		99.4	16	<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="#">c3gwzB</a>	 Alignment		98.2	17	<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		98.1	14	<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="#">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
11	<a href="#">c1xduA</a>	 Alignment		97.8	15	<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)

12	<a href="#">c3mczB_</a>			97.7	13	<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.
13	<a href="#">c3p9kD_</a>			97.7	14	<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
14	<a href="#">c1tw3A_</a>			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)
15	<a href="#">d1fp1d2</a>			97.7	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
16	<a href="#">d1tw3a2</a>			97.7	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
17	<a href="#">c1x1aA_</a>			97.6	12	<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
18	<a href="#">c2ip2B_</a>			97.6	16	<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
19	<a href="#">c5i2hB_</a>			97.5	15	<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
20	<a href="#">c4d7kB_</a>			97.5	17	<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
21	<a href="#">c4uy5A_</a>		not modelled	97.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine-specific methyltransferase egtd; <b>PDBTitle:</b> crystal structure of histidine-specific methyltransferase egtd from2 mycobacterium smegmatis
22	<a href="#">c6i5zA_</a>		not modelled	97.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase 1; <b>PDBTitle:</b> papaver somniferum o-methyltransferase
23	<a href="#">d1qzza2</a>		not modelled	97.4	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
24	<a href="#">c6c5bB_</a>		not modelled	97.4	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure analysis of laphzm
25	<a href="#">c3i53A_</a>		not modelled	97.4	16	<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)
26	<a href="#">c3ocjA_</a>		not modelled	97.4	14	<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
27	<a href="#">c2fk8A_</a>		not modelled	97.3	10	<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
28	<a href="#">c5do0A_</a>		not modelled	97.3	8	<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

29	<a href="#">c5cvvB</a>	Alignment	not modelled	97.3	13	<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
30	<a href="#">c4p7cB</a>	Alignment	not modelled	97.2	10	<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
31	<a href="#">c4krhB</a>	Alignment	not modelled	97.2	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
32	<a href="#">c5dpbB</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
33	<a href="#">d1l1ea</a>	Alignment	not modelled	97.1	10	<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
34	<a href="#">d1kyza2</a>	Alignment	not modelled	97.1	11	<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
35	<a href="#">d1tpya</a>	Alignment	not modelled	97.1	8	<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
36	<a href="#">d1r74a</a>	Alignment	not modelled	97.1	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
37	<a href="#">d2fk8a1</a>	Alignment	not modelled	97.1	10	<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
38	<a href="#">c3dp7B</a>	Alignment	not modelled	97.1	11	<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
39	<a href="#">c3g2qA</a>	Alignment	not modelled	97.1	18	<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 mfa2 complexed with sinefungin
40	<a href="#">c6iv7B</a>	Alignment	not modelled	97.0	20	<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
41	<a href="#">c4a6dA</a>	Alignment	not modelled	97.0	11	<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
42	<a href="#">c5xohA</a>	Alignment	not modelled	96.8	11	<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
43	<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
44	<a href="#">c1kyzC</a>	Alignment	not modelled	96.8	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
45	<a href="#">d1xvaa</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
46	<a href="#">c2r3sA</a>	Alignment	not modelled	96.8	9	<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
47	<a href="#">d1kpga</a>	Alignment	not modelled	96.8	10	<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="#">c4e70A</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> coniferyl alcohol 9-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of coniferyl alcohol 9-o-methyltransferase2 from linum nodiflorum in complex with coniferyl alcohol
49	<a href="#">c1fpqA</a>	Alignment	not modelled	96.7	15	<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
50	<a href="#">c5z9oA</a>	Alignment	not modelled	96.7	7	<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
51	<a href="#">c3lstB</a>	Alignment	not modelled	96.6	10	<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
52	<a href="#">c1zgaA</a>	Alignment	not modelled	96.5	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-hydroxymaackiain
53	<a href="#">c4ineB</a>	Alignment	not modelled	96.4	16	<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
54	<a href="#">c3bgvC</a>	Alignment	not modelled	96.3	10	<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
55	<a href="#">c3lccA</a>	Alignment	not modelled	96.3	12	<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
56	<a href="#">c6mroA</a>	Alignment	not modelled	96.3	11	<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.
57	<a href="#">c5wp5A</a>	Alignment	not modelled	96.3	13	<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
58	<a href="#">c4x1oA</a>	Alignment	not modelled	96.2	18	<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
59	<a href="#">c3lcvB</a>	Alignment	not modelled	96.2	20	<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
60	<a href="#">c3qnhA</a>	Alignment	not modelled	96.1	10	<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)
61	<a href="#">c4z2yA</a>	Alignment	not modelled	96.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calo6; <b>PDBTitle:</b> crystal structure of methyltransferase calo6
62	<a href="#">c6pi9A</a>	Alignment	not modelled	95.9	20	<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
63	<a href="#">c3cggB</a>	Alignment	not modelled	95.9	19	<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
64	<a href="#">d1oria</a>	Alignment	not modelled	95.9	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
65	<a href="#">c4necC</a>	Alignment	not modelled	95.8	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
66	<a href="#">c3g2qB</a>	Alignment	not modelled	95.8	18	<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 mfa2 complexed with sinefungin
67	<a href="#">d1im8a</a>	Alignment	not modelled	95.8	16	<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)
68	<a href="#">c5iceA</a>	Alignment	not modelled	95.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-norocclaurine 6-o-methyltransferase; <b>PDBTitle:</b> crystal structure of (s)-norocclaurine 6-o-methyltransferase with s-2 adenosyl-l-homocysteine and norlaudanosoline
69	<a href="#">c3b89A</a>	Alignment	not modelled	95.7	15	<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
70	<a href="#">d1f3la</a>	Alignment	not modelled	95.6	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
71	<a href="#">d1kpia</a>	Alignment	not modelled	95.6	8	<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
72	<a href="#">c5t39A</a>	Alignment	not modelled	95.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> evdmo1; <b>PDBTitle:</b> crystal structure of the n-terminal domain of evdmo1 in the presence2 of sah and d-fucose
73	<a href="#">c1orhA</a>	Alignment	not modelled	95.5	13	<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
74	<a href="#">c3h2bB</a>	Alignment	not modelled	95.5	14	<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
75	<a href="#">c5lkjA</a>	Alignment	not modelled	95.5	11	<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
76	<a href="#">c4krqB</a>	Alignment	not modelled	95.4	15	<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
77	<a href="#">c3cc8A_</a>	Alignment	not modelled	95.4	13	<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	
78	<a href="#">c4kifB_</a>	Alignment	not modelled	95.3	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase mppj; <b>PDBTitle:</b> crystal structure of methyltransferase from <i>Streptomyces hygroscopicus</i> 2 complexed with phenylpyruvic acid	
79	<a href="#">c3ou7A_</a>	Alignment	not modelled	95.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex	
80	<a href="#">c3f4kA_</a>	Alignment	not modelled	95.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from <i>Bacteroides thetaiotaomicron</i> . northeast structural3 genomics target btr309.	
81	<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	
82	<a href="#">c3bkbB_</a>	Alignment	not modelled	95.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from <i>Lactobacillus casei</i> atcc 334 at 1.853 a resolution	
83	<a href="#">c5fwaA_</a>	Alignment	not modelled	94.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 2; <b>PDBTitle:</b> crystal structure of mus musculus protein arginine methyltransferase 22 with cp1	
84	<a href="#">c3m70A_</a>	Alignment	not modelled	94.9	12	<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 <i>Haemophilus influenzae</i>	
85	<a href="#">c4qnuH_</a>	Alignment	not modelled	94.7	9	<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	
86	<a href="#">d1nkva_</a>	Alignment	not modelled	94.6	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein Yjhp	
87	<a href="#">c5ufmB_</a>	Alignment	not modelled	94.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase domain protein; <b>PDBTitle:</b> crystal structure of <i>Burkholderia thailandensis</i> 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine	
88	<a href="#">c6ccaA_</a>	Alignment	not modelled	94.6	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	
89	<a href="#">c2p8jA_</a>	Alignment	not modelled	94.5	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 (np_349143.1) from <i>Clostridium acetobutylicum</i> at 2.00 a resolution	
90	<a href="#">c4iv0B_</a>	Alignment	not modelled	94.5	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase, putative; <b>PDBTitle:</b> crystal structure of n-methyl transferase from <i>Plasmodium vivax</i> 2 complexed with s-adenosyl methionine and phosphate	
91	<a href="#">c3vc2J_</a>	Alignment	not modelled	94.5	14	<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 from <i>Streptomyces coelicolor</i> a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine	
92	<a href="#">d1g6q1_</a>	Alignment	not modelled	94.5	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase	
93	<a href="#">c5fubA_</a>	Alignment	not modelled	94.4	14	<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	
94	<a href="#">c3mq2A_</a>	Alignment	not modelled	94.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rRNA methyltransferase; <b>PDBTitle:</b> crystal structure of 16s rRNA methyltransferase kamb	
95	<a href="#">c5xlxD_</a>	Alignment	not modelled	94.4	15	<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	
96	<a href="#">c3jwhA_</a>	Alignment	not modelled	94.3	11	<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 <i>Bacterial-avhen1-c</i>	
97	<a href="#">d1pjza_</a>	Alignment	not modelled	94.3	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase	
98	<a href="#">c3e7pA_</a>	Alignment	not modelled	94.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from <i>Bacteroides vulgatus</i> atcc 8482	
99	<a href="#">d2a14a1</a>	Alignment	not modelled	94.2	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase	
						<b>PDB header:</b> transferase	

100	<a href="#">c2v7eB_</a>	Alignment	not modelled	94.0	10	<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
101	<a href="#">c6dnzA_</a>	Alignment	not modelled	94.0	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
102	<a href="#">c5w7sA_</a>	Alignment	not modelled	94.0	18	<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
103	<a href="#">c5thyB_</a>	Alignment	not modelled	94.0	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
104	<a href="#">c3pfdD_</a>	Alignment	not modelled	94.0	13	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n
105	<a href="#">d1wzna1</a>	Alignment	not modelled	93.9	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
106	<a href="#">c5bp9A_</a>	Alignment	not modelled	93.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative methyltransferase protein; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from bacteroides2 fragilis in complex with s-adenosyl-l-homocysteine
107	<a href="#">c5evjA_</a>	Alignment	not modelled	93.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> arsenite methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of crasm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii
108	<a href="#">c4htfA_</a>	Alignment	not modelled	93.6	12	<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.
109	<a href="#">c5gm2E_</a>	Alignment	not modelled	93.5	15	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase tied complexed with sah and2 teleocidin a1
110	<a href="#">c3g5tA_</a>	Alignment	not modelled	93.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> trans-aconitate 3-methyltransferase; <b>PDBTitle:</b> crystal structure of trans-aconitate 3-methyltransferase from yeast
111	<a href="#">c4y30B_</a>	Alignment	not modelled	93.5	16	<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
112	<a href="#">c4xcxA_</a>	Alignment	not modelled	93.3	12	<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
113	<a href="#">d2fytA1</a>	Alignment	not modelled	93.3	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
114	<a href="#">c4rwzA_</a>	Alignment	not modelled	93.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative rrna methyltransferase; <b>PDBTitle:</b> crystal structure of the antibiotic-resistance methyltransferase kmr
115	<a href="#">c5ubbA_</a>	Alignment	not modelled	93.2	13	<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
116	<a href="#">d1d2ha_</a>	Alignment	not modelled	93.1	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
117	<a href="#">c3ggdA_</a>	Alignment	not modelled	93.1	11	<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 anaabaena variabilis atcc 29413 at 2.11 a resolution
118	<a href="#">c6ectA_</a>	Alignment	not modelled	92.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
119	<a href="#">c3fzgA_</a>	Alignment	not modelled	92.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 16s rrna methylase; <b>PDBTitle:</b> structure of the 16s rrna methylase arma
120	<a href="#">d1l3ia_</a>	Alignment	not modelled	92.7	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Precorrin-6Y methyltransferase (Cbit)