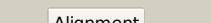
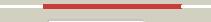
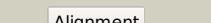
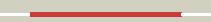


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1896c_(-)_2143542_2144453
Date	Fri Aug 2 13:30:51 BST 2019
Unique Job ID	3a48c0e86b381192

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2uyoA1</a>			100.0	39	<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>			100.0	17	<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>			100.0	16	<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>			100.0	20	<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>			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="#">c2qgeB</a>			99.8	19	<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>			99.6	19	<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="#">c4gvgC</a>			98.7	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sbl; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 sbl in its apo form
9	<a href="#">c6clwA</a>			98.6	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of tnmh
10	<a href="#">c3mczb</a>			98.6	14	<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="#">c3gwzB</a>			98.6	19	<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

12	<a href="#">c3dp7B_</a>			98.5	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
13	<a href="#">c3p9kD_</a>			98.4	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 lpmot1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
14	<a href="#">c6c5bB_</a>			98.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure analysis of laphzm
15	<a href="#">c5i2hB_</a>			98.3	14	<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
16	<a href="#">c3ocjA_</a>			98.3	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
17	<a href="#">d1tw3a2</a>			98.3	16	<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
18	<a href="#">c6i5zA_</a>			98.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase 1; <b>PDBTitle:</b> papaver somniferum o-methyltransferase
19	<a href="#">c1x1aA_</a>			98.3	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
20	<a href="#">d1fp1d2</a>			98.3	12	<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
21	<a href="#">c5xohA_</a>		not modelled	98.3	12	<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
22	<a href="#">c1tw3A_</a>		not modelled	98.3	16	<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)
23	<a href="#">c1xdwA_</a>		not modelled	98.2	14	<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="#">c2ip2B_</a>		not modelled	98.2	18	<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
25	<a href="#">d1qzza2</a>		not modelled	98.2	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
26	<a href="#">c4uy5A_</a>		not modelled	98.2	16	<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
27	<a href="#">c4a6dA_</a>		not modelled	98.2	13	<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
28	<a href="#">c2r3sA_</a>		not modelled	98.2	11	<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
29	<a href="#">c5cvvB</a>	Alignment	not modelled	98.2	12 <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="#">c1fpqA</a>	Alignment	not modelled	98.2	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
31	<a href="#">c4d7kB</a>	Alignment	not modelled	98.2	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
32	<a href="#">c4e70A</a>	Alignment	not modelled	98.1	11 <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
33	<a href="#">d1fp2a2</a>	Alignment	not modelled	98.1	16 <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>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
34	<a href="#">d1kyza2</a>	Alignment	not modelled	98.1	10 <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)
35	<a href="#">c3i53A</a>	Alignment	not modelled	98.1	18 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> caffeoic acid 3-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of caffeoic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex
36	<a href="#">c1kyzC</a>	Alignment	not modelled	98.1	13 <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-hydroxymackiain <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)
37	<a href="#">c1zgaA</a>	Alignment	not modelled	98.0	12 <b>PDB header:</b> 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-hydroxymackiain <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases
38	<a href="#">d1im8a</a>	Alignment	not modelled	98.0	13 <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
39	<a href="#">c3lstB</a>	Alignment	not modelled	98.0	11 <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
40	<a href="#">c5thyB</a>	Alignment	not modelled	97.9	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
41	<a href="#">c3lccA</a>	Alignment	not modelled	97.9	15 <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 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine-dependent methyltransferase;
42	<a href="#">c4htfA</a>	Alignment	not modelled	97.9	13 <b>PDB header:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 from escherichia coli in complex with s-adenosylmethionine. <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases
43	<a href="#">d1tpya</a>	Alignment	not modelled	97.9	11 <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase <b>PDB header:</b> transferase
44	<a href="#">c3g2qA</a>	Alignment	not modelled	97.9	24 <b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.24; <b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
45	<a href="#">c5iceA</a>	Alignment	not modelled	97.8	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-norcooclaurine 6-o-methyltransferase; <b>PDBTitle:</b> crystal structure of (s)-norcooclaurine 6-o-methyltransferase with s-2 adenosyl-l-homocysteine and norlaudanosoline
46	<a href="#">c2fk8A</a>	Alignment	not modelled	97.8	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
47	<a href="#">c6iv7B</a>	Alignment	not modelled	97.8	15 <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
48	<a href="#">c5z9oA</a>	Alignment	not modelled	97.8	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
49	<a href="#">c4p7cB</a>	Alignment	not modelled	97.7	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
50	<a href="#">c4krhB</a>	Alignment	not modelled	97.7	14 <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 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases
51	<a href="#">d1l1ea</a>	Alignment	not modelled	97.7	8 <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase <b>PDB header:</b> transferase
52	<a href="#">c4lifR</a>	Alignment	not modelled	97.7	10 <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase mppj;

52	<a href="#">c4nid</a>	Alignment	not modelled	97.7	10	<b>PDBTitle:</b> crystal structure of methyltransferase from streptomyces hygroscopicus2 complexed with phenylpyruvic acid <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
53	<a href="#">d2fk8a1</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> disa protein; <b>PDBTitle:</b> crystal structure of dsza carbon methyltransferase
54	<a href="#">c6ccaA</a>	Alignment	not modelled	97.7	15	<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
55	<a href="#">c3h2bB</a>	Alignment	not modelled	97.6	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
56	<a href="#">d1kpga</a>	Alignment	not modelled	97.6	10	<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
57	<a href="#">c1fp2A</a>	Alignment	not modelled	97.6	15	<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
58	<a href="#">d2o57a1</a>	Alignment	not modelled	97.5	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
59	<a href="#">d1r74a</a>	Alignment	not modelled	97.5	15	<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
60	<a href="#">c5do0A</a>	Alignment	not modelled	97.5	5	<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
61	<a href="#">c3bgvC</a>	Alignment	not modelled	97.5	10	<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
62	<a href="#">c5dpIB</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyl transferase from methanoscincus acetivorans; <b>PDBTitle:</b> crystal structure of methyl transferase from methanoscincus acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nsg) target mvr53.
63	<a href="#">c3vc2J</a>	Alignment	not modelled	97.4	11	<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 plasmidum vivax2 complexed with s-adenosyl methionine and phosphate
64	<a href="#">c6mroA</a>	Alignment	not modelled	97.4	9	<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
65	<a href="#">c4iv0B</a>	Alignment	not modelled	97.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calo6; <b>PDBTitle:</b> crystal structure of methyltransferase calo6
66	<a href="#">c5wp5A</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
67	<a href="#">c4z2yA</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> transferase <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
68	<a href="#">c3g2qB</a>	Alignment	not modelled	97.3	22	<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 mtfa2 complexed with sinefungin
69	<a href="#">c4necC</a>	Alignment	not modelled	97.3	18	<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-quin3n
70	<a href="#">c3pfhD</a>	Alignment	not modelled	97.3	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
71	<a href="#">c3ggdA</a>	Alignment	not modelled	97.3	13	<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 dimethyltoxoflavin-n1-methyltransferase with bound 1,6-3 dimethyltoxoflavin and s-adenosylhomocysteine
72	<a href="#">c5ufmB</a>	Alignment	not modelled	97.3	16	<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)
73	<a href="#">c3qnHA</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase tld complexed with sah and2 teleocidin a1
74	<a href="#">c5gm2E</a>	Alignment	not modelled	97.2	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase;
75	<a href="#">c5ig0R</a>	Alignment	not modelled	97.2	10	

75	<a href="#">c3je0p</a>	Alignment	not modelled	97.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable methyltransferase bt9727_4108; <b>PDBTitle:</b> crystal structure of a probable methyltransferase2 bt9727_4108 from bacillus thuringiensis subsp. northeast3 structural genomics consortium target id bur219
76	<a href="#">c3hnra</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of the [4+2]-cyclase spnf
77	<a href="#">c4pneA</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> tRNA (cmo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of wild-type cmoa from e.coli
78	<a href="#">c4gekG</a>	Alignment	not modelled	97.2	13	<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 caenorhabditis elegans complexed with s-adenosyl homocysteine and 3 phosphoethanolamine
79	<a href="#">c4ineB</a>	Alignment	not modelled	97.2	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
80	<a href="#">d2a14a1</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhp1-sam-hep complex
81	<a href="#">c3ou7A</a>	Alignment	not modelled	97.2	15	<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
82	<a href="#">c4qnuH</a>	Alignment	not modelled	97.2	14	<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
83	<a href="#">c4qdkB</a>	Alignment	not modelled	97.1	8	<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 catenulispores acidiphila
84	<a href="#">c4x1oA</a>	Alignment	not modelled	97.1	19	<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 meleagrin
85	<a href="#">c5w7sA</a>	Alignment	not modelled	97.1	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
86	<a href="#">d1xvaa</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferases; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferases q8pu2_k_metma2 from methanoscincus mazaei. northeast structural genomics consortium3 target mar262.
87	<a href="#">c3sm3A</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> CAC2371-like
88	<a href="#">d1wzna1</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase; <b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
89	<a href="#">c3ujcA</a>	Alignment	not modelled	97.1	10	<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
90	<a href="#">c3m70A</a>	Alignment	not modelled	97.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosyl-l-methionine-dependent <b>PDBTitle:</b> crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
91	<a href="#">c3dlcA</a>	Alignment	not modelled	97.0	9	<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 bacterium cereus at 1.64 a resolution
92	<a href="#">c3cc8A</a>	Alignment	not modelled	97.0	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
93	<a href="#">c5ubbA</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-demethylubiquinone-9 3-methyltransferase; <b>PDBTitle:</b> crystal structure of ubiq
94	<a href="#">c4kdcA</a>	Alignment	not modelled	97.0	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
95	<a href="#">d1kpia</a>	Alignment	not modelled	96.9	9	<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 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
96	<a href="#">c3f4ka</a>	Alignment	not modelled	96.9	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sam dependent methyltransferase; <b>PDBTitle:</b> crystal structure of putative sam dependent methyltransferase2 in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
97	<a href="#">c3e8sa</a>	Alignment	not modelled	96.9	11	<b>PDB header:</b> transferase

98	<a href="#">c6ectA_</a>	Alignment	not modelled	96.8	13	<b>Chain: A: PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
99	<a href="#">c6pi9A_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> transferase <b>Chain: A: 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
100	<a href="#">d1xtpa_</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> AD-003 protein-like
101	<a href="#">c5hijA_</a>	Alignment	not modelled	96.8	10	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> glycine sarcosine n-methyltransferase; <b>PDBTitle:</b> crystal structure of glycine sarcosine n-methyltransferase from <i>2 methanohalophilus portocalensis</i> in complex with betaine
102	<a href="#">c6f5zB_</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> 24-sterol c-methyltransferase; <b>PDBTitle:</b> complex between the haloferax volcanii trm12 methyltransferase2 activator and the hvo_0019 putative methyltransferase
103	<a href="#">c4rvgA_</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> d-mycarose 3-c-methyltransferase; <b>PDBTitle:</b> crystal structure of mtmc in complex with sam and tdp
104	<a href="#">d2ex4a1</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> AD-003 protein-like
105	<a href="#">c4krgB_</a>	Alignment	not modelled	96.7	10	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> phosphoethanolamine n-methyltransferase 1; <b>PDBTitle:</b> <i>semet haemonchus contortus</i> phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine
106	<a href="#">c5t39A_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> evdm01; <b>PDBTitle:</b> crystal structure of the n-terminal domain of evdm01 in the presence of sah and d-fucose
107	<a href="#">d1nkva_</a>	Alignment	not modelled	96.6	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
108	<a href="#">c2iipD_</a>	Alignment	not modelled	96.6	10	<b>PDB header:</b> transferase <b>Chain: D: PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
109	<a href="#">c5bszA_</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray structure of the sugar n-methyltransferase keds8 from <i>streptomyces sp atcc 53650</i>
110	<a href="#">c3lcvB_</a>	Alignment	not modelled	96.6	19	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> sisomicin-gentamicin resistance methylase sgm; <b>PDBTitle:</b> crystal structure of antibiotic related methyltransferase
111	<a href="#">c4rwzA_</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> putative rrna methyltransferase; <b>PDBTitle:</b> crystal structure of the antibiotic-resistance methyltransferase kmr
112	<a href="#">c2yr0A_</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> hypothetical protein ttha0223; <b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from <i>thermus thermophilus hb8</i>
113	<a href="#">c3jwgA_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of bacterial-cthen1-c
114	<a href="#">c5bp9A_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> putative methyltransferase protein; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from <i>bacteroides2 fragilis</i> in complex with s-adenosyl-L-homocysteine
115	<a href="#">c3b89A_</a>	Alignment	not modelled	96.5	18	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> 16s rRNA methylase; <b>PDBTitle:</b> crystal structure of rrna methylase from <i>escherichia coli</i>
116	<a href="#">c3cggb_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from <i>corynebacterium glutamicum atcc 13032</i> kitasato at 3.2.00 a resolution
117	<a href="#">c3l8dA_</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from <i>bacillus thuringiensis</i>
118	<a href="#">d1ve3a1</a>	Alignment	not modelled	96.5	8	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
119	<a href="#">c5evjA_</a>	Alignment	not modelled	96.4	14	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> arsenite methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of crarsm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from <i>chlamydomonas reinhardtii</i>
120	<a href="#">c3bkxB_</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> transferase <b>Chain: 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 atcc 334</i> at 1.853 a resolution