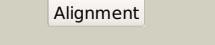
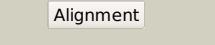
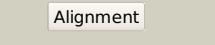
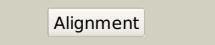
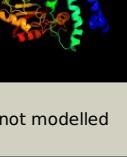


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD2258c_(-)_2530846_2531907
Date	Mon Aug 5 13:25:39 BST 2019
Unique Job ID	5d3b8caf47fe07f2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gwzB_</a>			100.0	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
2	<a href="#">c2ip2B_</a>			100.0	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
3	<a href="#">c5cvvB_</a>			100.0	15	<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
4	<a href="#">c3dp7B_</a>			100.0	10	<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
5	<a href="#">c4a6dA_</a>			100.0	15	<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
6	<a href="#">c4e70A_</a>			100.0	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
7	<a href="#">c4qvgC_</a>			100.0	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
8	<a href="#">c4d7kB_</a>			100.0	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 davaensis
9	<a href="#">c5xohA_</a>			100.0	13	<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
10	<a href="#">c2r3sA_</a>			100.0	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) from nostoc punctiforme pcc 73102 at 2.15 a resolution
11	<a href="#">c3p9kD_</a>			100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> caffeoic acid o-methyltransferase; <b>PDBTitle:</b> crystal structure of perennial ryegrass lpmot1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde

12	<a href="#">c6c5bB</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure analysis of laphzm
13	<a href="#">c5iceA</a>	Alignment		100.0	15	<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
14	<a href="#">c3lstB</a>	Alignment		100.0	13	<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
15	<a href="#">c1fp2A</a>	Alignment		100.0	11	<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
16	<a href="#">c6iv7B</a>	Alignment		100.0	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
17	<a href="#">c3mczB</a>	Alignment		100.0	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.
18	<a href="#">c4kifB</a>	Alignment		100.0	19	<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
19	<a href="#">c1kyzC</a>	Alignment		100.0	14	<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
20	<a href="#">c5w7sA</a>	Alignment		100.0	15	<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
21	<a href="#">c6clwA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of tnrmh
22	<a href="#">c1tw3A</a>	Alignment	not modelled	100.0	14	<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="#">c6i5zA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase 1; <b>PDBTitle:</b> papaver somniferum o-methyltransferase
24	<a href="#">c1x1aA</a>	Alignment	not modelled	100.0	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
25	<a href="#">c1zgaA</a>	Alignment	not modelled	100.0	17	<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
26	<a href="#">c5i2hB</a>	Alignment	not modelled	100.0	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
27	<a href="#">c1xdwA</a>	Alignment	not modelled	100.0	17	<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)
28	<a href="#">c3i53A</a>	Alignment	not modelled	100.0	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)
29	<a href="#">c4z2yA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calo6; <b>PDBTitle:</b> crystal structure of methyltransferase calo6
30	<a href="#">c1fpqA</a>	Alignment	not modelled	100.0	12	<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="#">c5thyB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase,lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cjur; <b>PDBTitle:</b> crystal structure of semet-substituted curj carbon methyltransferase
32	<a href="#">c6ccaA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dsia protein; <b>PDBTitle:</b> crystal structure of dsza carbon methyltransferase
33	<a href="#">c6d6yA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aprA methyltransferase 2; <b>PDBTitle:</b> aprA methyltransferase 2 - gnat didomain in complex with sah
34	<a href="#">c5mptA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citrinin polyketide synthase; <b>PDBTitle:</b> structure of the citrinin polyketide synthase cmet domain
35	<a href="#">d1fp1d2</a>	Alignment	not modelled	99.9	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
36	<a href="#">d1kyza2</a>	Alignment	not modelled	99.9	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
37	<a href="#">d1fp2a2</a>	Alignment	not modelled	99.9	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
38	<a href="#">d1gzza2</a>	Alignment	not modelled	99.9	20	<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
39	<a href="#">d1tw3a2</a>	Alignment	not modelled	99.9	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
40	<a href="#">c3ocjA</a>	Alignment	not modelled	99.8	22	<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
41	<a href="#">c4qnuH</a>	Alignment	not modelled	99.8	22	<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
42	<a href="#">d1im8a</a>	Alignment	not modelled	99.8	14	<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)
43	<a href="#">c4ineB</a>	Alignment	not modelled	99.8	20	<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 2 elegans complexed with s-adenosyl homocysteine and3 phosphoethanolamine
44	<a href="#">c4krhB</a>	Alignment	not modelled	99.8	22	<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
45	<a href="#">c5wp5A</a>	Alignment	not modelled	99.8	29	<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 (atpm2t) in complex with sah
46	<a href="#">c4obxD</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-methoxy-6-polypropenyl-1,4-benzoquinol methylase, <b>PDBTitle:</b> crystal structure of yeast coq5 in the apo form
47	<a href="#">c3dlcA</a>	Alignment	not modelled	99.8	14	<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
48	<a href="#">c6ectA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
49	<a href="#">c3dtmA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase mm_2633; <b>PDBTitle:</b> crystal structure of putative methyltransferase-mm_2633 from2 methanoscirina maezi .
50	<a href="#">c3mggB</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanoscirina2 maezi
51	<a href="#">c5ufmB</a>	Alignment	not modelled	99.7	20	<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
52	<a href="#">d2ex4a1</a>	Alignment	not modelled	99.7	19	<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

53	<a href="#">c4p7cB</a>		Alignment	not modelled	99.7	20	<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 pseudomonas syringae pv. tomato
54	<a href="#">d2gh1a1</a>		Alignment	not modelled	99.7	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
55	<a href="#">c3vc2j</a>		Alignment	not modelled	99.7	13	<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 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine
56	<a href="#">c5t39A</a>		Alignment	not modelled	99.7	13	<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
57	<a href="#">c4gekG</a>		Alignment	not modelled	99.7	13	<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
58	<a href="#">c2fk8A</a>		Alignment	not modelled	99.7	14	<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 (mma4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
59	<a href="#">c3qnhA</a>		Alignment	not modelled	99.7	26	<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)
60	<a href="#">d2o57a1</a>		Alignment	not modelled	99.7	22	<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
61	<a href="#">c6ecvB</a>		Alignment	not modelled	99.7	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
62	<a href="#">c5egpB</a>		Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ubie/coq5 family methyltransferase, putative; <b>PDBTitle:</b> crystal structure of the s-methyltransferase tmta
63	<a href="#">c5w7kA</a>		Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
64	<a href="#">d2fk8a1</a>		Alignment	not modelled	99.7	14	<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
65	<a href="#">c3bkxB</a>		Alignment	not modelled	99.7	13	<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 lactobacillus casei atcc 334 at 1.853 a resolution
66	<a href="#">c5gm2E</a>		Alignment	not modelled	99.7	21	<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 and teleocidin a1
67	<a href="#">c6f5zB</a>		Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 24-sterol c-methyltransferase; <b>PDBTitle:</b> complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
68	<a href="#">c5evjA</a>		Alignment	not modelled	99.7	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenite methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of crarsm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii
69	<a href="#">c2yr0A</a>		Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha0223; <b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from thermus thermophilus hb8
70	<a href="#">d1kpga</a>		Alignment	not modelled	99.7	17	<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
71	<a href="#">d1xtpa</a>		Alignment	not modelled	99.7	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
72	<a href="#">d1l1ea</a>		Alignment	not modelled	99.7	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
73	<a href="#">c4pneA</a>		Alignment	not modelled	99.7	25	<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 snpf
74	<a href="#">c3e23A</a>		Alignment	not modelled	99.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rpa2492; <b>PDBTitle:</b> crystal structure of the rpa2492 protein in complex with sam from rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr299
75	<a href="#">c6dcba</a>		Alignment	not modelled	99.7	22	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> 7sk srna methylphosphate capping enzyme; <b>PDBTitle:</b> structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna
76	<a href="#">c4kdcA</a>		Alignment	not modelled	99.7	17	<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
							<b>PDB header:</b> transferase

77	<a href="#">c3g2qA</a>	Alignment	not modelled	99.7	12	<b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.24; <b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin <b>PDB header:</b> transferase
78	<a href="#">c1vl5B</a>	Alignment	not modelled	99.7	21	<b>Chain:</b> B: <b>PDB Molecule:</b> unknown conserved protein bh2331; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
79	<a href="#">d1vl5a</a>	Alignment	not modelled	99.7	21	<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
80	<a href="#">c5ubbA</a>	Alignment	not modelled	99.6	14	<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	99.6	18	<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
82	<a href="#">d1tpya</a>	Alignment	not modelled	99.6	17	<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
83	<a href="#">c3h2bB</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical Protein YjhP
84	<a href="#">d1nkva</a>	Alignment	not modelled	99.6	23	<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
85	<a href="#">d1kpia</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of a sam-dependent methyltransferase from2 aquifex aeolicus
86	<a href="#">c3dh0B</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of a sam-dependent methyltransferase from2 methanohalophilus portucalensis in complex with betaine
87	<a href="#">c5hijA</a>	Alignment	not modelled	99.6	15	<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 from2 methanohalophilus portucalensis in complex with betaine
88	<a href="#">c3e8sA</a>	Alignment	not modelled	99.6	17	<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 methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
89	<a href="#">d1y8ca</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
90	<a href="#">c3f4ka</a>	Alignment	not modelled	99.6	17	<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.
91	<a href="#">c4iv0B</a>	Alignment	not modelled	99.6	16	<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 plasmodium vivax2 complexed with s-adenosyl methionine and phosphate
92	<a href="#">d1xxla</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
93	<a href="#">c3ujcA</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase; <b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from plasmid2 falciparum in complex with phosphocholine
94	<a href="#">c4htfA</a>	Alignment	not modelled	99.6	16	<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.
95	<a href="#">c3d2lC</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exiguobacterium sp. 255-15 at 1.90 a resolution
96	<a href="#">c3busB</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
97	<a href="#">c4hgyC</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ccbj; <b>PDBTitle:</b> structure of the ccbj methyltransferase from streptomyces caelestis
98	<a href="#">c5z9oA</a>	Alignment	not modelled	99.6	20	<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
99	<a href="#">c3merA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> slr1183 protein; <b>PDBTitle:</b> crystal structure of the methyltransferase slr1183 from synechocystis2 sp. pcc 6803, northeast structural genomics

						consortium target sgr145
100	<a href="#">c3g5IA</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosylmethionine dependent methyltransferase; <b>PDBTitle:</b> crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes
101	<a href="#">c3e7pA</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
102	<a href="#">c3l8dA</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus thuringiensis
103	<a href="#">c5bszA</a>		Alignment	not modelled	99.6	<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 from2 streptoalloteichus sp atcc 53650
104	<a href="#">c3lccA</a>		Alignment	not modelled	99.6	<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
105	<a href="#">c5bp9A</a>		Alignment	not modelled	99.6	<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
106	<a href="#">d2a14a1</a>		Alignment	not modelled	99.6	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
107	<a href="#">c6gkvB</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> coclaurine n-methyltransferase; <b>PDBTitle:</b> crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah
108	<a href="#">c5je0B</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase; <b>PDBTitle:</b> crystal structure of burkholderia glumiae tox a with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethylxoflavin
109	<a href="#">c3sm3A</a>		Alignment	not modelled	99.6	<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 consortium target mar262.
110	<a href="#">c3hnrA</a>		Alignment	not modelled	99.6	<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
111	<a href="#">c2gs9A</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tt1324; <b>PDBTitle:</b> crystal structure of tt1324 from thermus thermophilis hb8
112	<a href="#">c5kn4B</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pavine n-methyltransferase; <b>PDBTitle:</b> pavine n-methyltransferase apoenzyme ph 6.0
113	<a href="#">d1jqa</a>		Alignment	not modelled	99.6	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
114	<a href="#">c3bkW</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine dependent methyltransferase2 (np_104914.1) from mesorhizobium loti at 1.60 a resolution
115	<a href="#">c5mgzA</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-demethylnovobiocic acid c(8)-methyltransferase; <b>PDBTitle:</b> streptomyces sphaeroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah
116	<a href="#">c6ec3C</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein; <b>PDBTitle:</b> crystal structure of evdm01
117	<a href="#">c2iipD</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
118	<a href="#">c3ccfB</a>		Alignment	not modelled	99.6	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> crystal structure of putative methyltransferase (yp_321342.1) from2 anabaena variabilis atcc 29413 at 1.90 a resolution
119	<a href="#">c4x1oA</a>		Alignment	not modelled	99.6	<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
120	<a href="#">c4rwzA</a>		Alignment	not modelled	99.5	<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