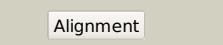
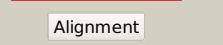
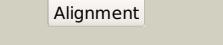
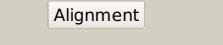
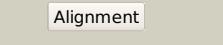


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD0567_(-)_658324_659343
Date	Fri Jul 26 01:50:12 BST 2019
Unique Job ID	876801b9fbdaf06c

Detailed template information

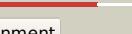
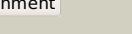
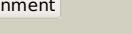
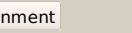
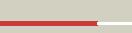
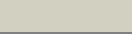
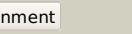
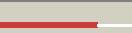
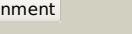
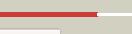
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gwzB_</a>			100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> mmcr; <b>PDBTitle:</b> structure of the mitomycin 7-o-methyltransferase mmcr
2	<a href="#">c4a6dA_</a>			100.0	28	<b>PDB 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
3	<a href="#">c4d7kB_</a>			100.0	21	<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 dawawensis
4	<a href="#">c6c5bB_</a>			100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure analysis of laphzm
5	<a href="#">c2ip2B_</a>			100.0	21	<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
6	<a href="#">c5cvvB_</a>			100.0	20	<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
7	<a href="#">c4e70A_</a>			100.0	21	<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
8	<a href="#">c4gvgC_</a>			100.0	26	<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="#">c1tw3A_</a>			100.0	23	<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-homocysteine (sah) and 4-methoxy-e-3 rhodomycin t (m-et)
10	<a href="#">c3lstB_</a>			100.0	21	<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
11	<a href="#">c1kyzC_</a>			100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> caffein acid 3-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of caffein acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex

12	<a href="#">c2r3sA</a>	Alignment		100.0	23	<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 (pnun_r0239) from <i>nostoc punctiforme</i> pcc 73102 at 2.15 a resolution
13	<a href="#">c3p9kD</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> caffeinic acid o-methyltransferase; <b>PDBTitle:</b> crystal structure of perennial ryegrass lpmot1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
14	<a href="#">c6clwA</a>	Alignment		100.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of tmnh
15	<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 <i>aspergillus2</i> flavus
16	<a href="#">c5iceA</a>	Alignment		100.0	22	<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
17	<a href="#">c3i53A</a>	Alignment		100.0	22	<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) from <i>neocarzinostatin</i> biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
18	<a href="#">c3mczB</a>	Alignment		100.0	24	<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 from <i>burkholderia thailandensis</i> .
19	<a href="#">c6i5zA</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o-methyltransferase 1; <b>PDBTitle:</b> papaver somniferum o-methyltransferase
20	<a href="#">c1xdvA</a>	Alignment		100.0	22	<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 (sgf)
21	<a href="#">c1fp2A</a>	Alignment	not modelled	100.0	19	<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 <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="#">c5xohA</a>	Alignment	not modelled	100.0	21	<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 <i>bacteroides2 vulgatus</i> atcc 8482
23	<a href="#">c3dp7B</a>	Alignment	not modelled	100.0	19	<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 <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
24	<a href="#">c1zgaA</a>	Alignment	not modelled	100.0	25	<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 <i>planctomyces limnophilus</i> dsm 3776 complex with apigenin <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
25	<a href="#">c5w7sA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> crft-related protein; <b>PDBTitle:</b> crystal structure of bchu complexed with s-adenosyl-l-methionine
26	<a href="#">c5i2hB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> isoliquiritigenin 2'-o-methyltransferase;
27	<a href="#">c1x1aA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> crft-related protein; <b>PDBTitle:</b> crystal structure of bchu complexed with s-adenosyl-l-methionine
28	<a href="#">c1fpqA</a>	Alignment	not modelled	100.0	17	<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

29	<a href="#">c4z2yA</a>	Alignment	not modelled	100.0	26	<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="#">c4kifB</a>	Alignment	not modelled	100.0	17	<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
31	<a href="#">d1qzza2</a>	Alignment	not modelled	100.0	23	<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
32	<a href="#">d1fp2a2</a>	Alignment	not modelled	100.0	22	<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
33	<a href="#">d1tw3a2</a>	Alignment	not modelled	100.0	23	<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	100.0	24	<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="#">c5thyB</a>	Alignment	not modelled	100.0	13	<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
36	<a href="#">c6ccaA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> disa protein; <b>PDBTitle:</b> crystal structure of dsza carbon methyltransferase
37	<a href="#">d1fp1d2</a>	Alignment	not modelled	100.0	19	<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="#">c6d6yA</a>	Alignment	not modelled	99.9	13	<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
39	<a href="#">c5mpmA</a>	Alignment	not modelled	99.9	13	<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
40	<a href="#">d1im8a</a>	Alignment	not modelled	99.8	17	<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)
41	<a href="#">c3ocjA</a>	Alignment	not modelled	99.8	18	<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
42	<a href="#">c5z9oA</a>	Alignment	not modelled	99.8	15	<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
43	<a href="#">c5wp5A</a>	Alignment	not modelled	99.8	12	<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
44	<a href="#">c6ecvB</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> std protein; <b>PDBTitle:</b> std o-mt residues 976-1266
45	<a href="#">c3dtmA</a>	Alignment	not modelled	99.8	17	<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 methanoscarsina mazel .
46	<a href="#">d1kpga</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> Mycolic acid cyclopropane synthase
47	<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 (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
48	<a href="#">c6ectA</a>	Alignment	not modelled	99.7	16	<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="#">d1l1ea</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
50	<a href="#">d2fk8a1</a>	Alignment	not modelled	99.7	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
51	<a href="#">c4gekG</a>	Alignment	not modelled	99.7	23	<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
52	<a href="#">d1kpia</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
53	<a href="#">d1tpya</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
54	<a href="#">d2o57a1</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
55	<a href="#">c5gm2E</a>	Alignment	not modelled	99.7	19	<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
56	<a href="#">c4ineB</a>	Alignment	not modelled	99.7	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 caenorhabditis elegans elegans complexed with s-adenosyl homocysteine and3 phosphoethanolamine
57	<a href="#">c4krhB</a>	Alignment	not modelled	99.7	18	<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
58	<a href="#">c3vc2J</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> geranyl diphosphate 2-c-methyltransferase; <b>PDBTitle:</b> crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg <sup>2+</sup> , geranyl3 diphosphate, and s-adenosyl-l-homocysteine
59	<a href="#">c3mggB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosaerica2 mazei
60	<a href="#">c4pneA</a>	Alignment	not modelled	99.7	20	<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
61	<a href="#">c3dlcA</a>	Alignment	not modelled	99.7	16	<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
62	<a href="#">c4iv0B</a>	Alignment	not modelled	99.7	10	<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
63	<a href="#">d2ex4a1</a>	Alignment	not modelled	99.7	11	<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
64	<a href="#">c3busB</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
65	<a href="#">c6f5zB</a>	Alignment	not modelled	99.7	16	<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
66	<a href="#">c5ubbA</a>	Alignment	not modelled	99.7	11	<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
67	<a href="#">c4obxD</a>	Alignment	not modelled	99.7	14	<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
68	<a href="#">c3ujcA</a>	Alignment	not modelled	99.7	10	<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
69	<a href="#">c5ufmB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase domain protein; <b>PDBTitle:</b> crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine
70	<a href="#">d1xtpa</a>	Alignment	not modelled	99.7	11	<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
71	<a href="#">c3bkxB</a>	Alignment	not modelled	99.7	14	<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
72	<a href="#">d1nkva</a>	Alignment	not modelled	99.6	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
73	<a href="#">c3e7pA</a>	Alignment	not modelled	99.6	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 bacteroides2 vulgaris atcc 8482
74	<a href="#">c1vl5B</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <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
75	<a href="#">c4gnuH</a>	Alignment	not modelled	99.6	16	<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
76	<a href="#">d1vl5a</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;

77	<a href="#">c3f4kA</a>	Alignment	not modelled	99.6	13	<b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309. <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
78	<a href="#">d1xxla</a>	Alignment	not modelled	99.6	13	<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
79	<a href="#">c3hnrA</a>	Alignment	not modelled	99.6	13	<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
80	<a href="#">c4qdkB</a>	Alignment	not modelled	99.6	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
81	<a href="#">c3lccA</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> cyclopropane fatty acid synthase from e. coli
82	<a href="#">c6bqcA</a>	Alignment	not modelled	99.6	15	<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
83	<a href="#">c5egpB</a>	Alignment	not modelled	99.6	11	<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
84	<a href="#">c3dh0B</a>	Alignment	not modelled	99.6	13	<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 aquifex aeolicus
85	<a href="#">c4p7cB</a>	Alignment	not modelled	99.6	13	<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
86	<a href="#">c4kdcA</a>	Alignment	not modelled	99.6	14	<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
87	<a href="#">c5evjA</a>	Alignment	not modelled	99.6	19	<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
88	<a href="#">c5w7kA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
89	<a href="#">c5fcda</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
90	<a href="#">c3qnhA</a>	Alignment	not modelled	99.6	20	<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)
91	<a href="#">c3ou7A</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
92	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
93	<a href="#">c3h2bb</a>	Alignment	not modelled	99.6	12	<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
94	<a href="#">c4rwzA</a>	Alignment	not modelled	99.5	17	<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
95	<a href="#">c3mq2A</a>	Alignment	not modelled	99.5	17	<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
96	<a href="#">c3e23A</a>	Alignment	not modelled	99.5	20	<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 from2 rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr299
97	<a href="#">c6gkvB</a>	Alignment	not modelled	99.5	15	<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
98	<a href="#">c5kn4B</a>	Alignment	not modelled	99.5	12	<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
99	<a href="#">c5hijA</a>	Alignment	not modelled	99.5	12	<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 portcalensis in complex with betaine
100	<a href="#">c4htfA</a>	Alignment	not modelled	99.5	9	<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.

101	<a href="#">c2yr0A_</a>		Alignment	not modelled	99.5	13	<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 <i>thermus thermophilus</i> hb8
102	<a href="#">c3sm3A_</a>		Alignment	not modelled	99.5	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 <i>methanoscincina mazei</i> . northeast structural genomics consortium3 target mar262.
103	<a href="#">c6dcba_</a>		Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> 7sk snrna methylphosphate capping enzyme; <b>PDBTitle:</b> structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna
104	<a href="#">c5je0B_</a>		Alignment	not modelled	99.5	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase; <b>PDBTitle:</b> crystal structure of <i>burkholderia glumae</i> tox a with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethylxanthin
105	<a href="#">c5t39A_</a>		Alignment	not modelled	99.5	12	<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
106	<a href="#">c4necC_</a>		Alignment	not modelled	99.5	17	<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
107	<a href="#">d1jqa_</a>		Alignment	not modelled	99.5	6	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
108	<a href="#">c6mroA_</a>		Alignment	not modelled	99.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyl transferase from <i>methanoscincina acetivorans</i> ; <b>PDBTitle:</b> crystal structure of methyl transferase from <i>methanoscincina2 acetivorans</i> at 1.6 angstroms resolution, northeast structural3 genomics consortium (nsg) target mvr53.
109	<a href="#">c3e8sA_</a>		Alignment	not modelled	99.5	15	<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 <i>pseudomonas putida</i> kt2440 at 2.103 a resolution
110	<a href="#">c4uy5A_</a>		Alignment	not modelled	99.5	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 from <i>mycobacterium smegmatis</i>
111	<a href="#">d1vlma_</a>		Alignment	not modelled	99.5	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
112	<a href="#">c4x1oA_</a>		Alignment	not modelled	99.5	11	<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 <i>catenulisporales acidiphilia</i>
113	<a href="#">c3bkwb_</a>		Alignment	not modelled	99.5	17	<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 <i>mesorhizobium loti</i> at 1.60 a resolution
114	<a href="#">d1g8sa_</a>		Alignment	not modelled	99.4	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarin homologue
115	<a href="#">c5mgzA_</a>		Alignment	not modelled	99.4	14	<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="#">c3dlib_</a>		Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a sam dependent methyltransferase from <i>archaeoglobus fulgidus</i>
117	<a href="#">c4rvga_</a>		Alignment	not modelled	99.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-mycarose 3-c-methyltransferase; <b>PDBTitle:</b> crystal structure of mtmc in complex with sam and tdp
118	<a href="#">c3g5IA_</a>		Alignment	not modelled	99.4	16	<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 <i>listeria monocytogenes</i>
119	<a href="#">c2xvmB_</a>		Alignment	not modelled	99.4	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tellurite resistance protein tehb; <b>PDBTitle:</b> crystal structure of the tellurite detoxification protein tehb from <i>e. coli</i> in complex with sah
120	<a href="#">d1wzna1</a>		Alignment	not modelled	99.4	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like