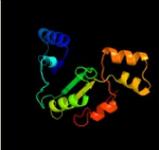
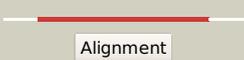
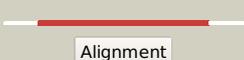
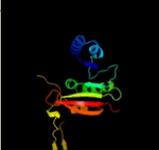


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0326 (-) _392273_392728
Date	Tue Jul 23 14:50:39 BST 2019
Unique Job ID	18cc7a8059255816

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ocjA_</a>			99.8	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 possible exported protein from bordetella2 parapertussis
2	<a href="#">c4krhB_</a>			99.8	23	<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
3	<a href="#">c5wp5A_</a>			99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomethylethanolamine n-methyltransferase 2; <b>PDBTitle:</b> arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah
4	<a href="#">c3m70A_</a>			99.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein tehb homolog; <b>PDBTitle:</b> crystal structure of tehb from haemophilus influenzae
5	<a href="#">c4ineB_</a>			99.7	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein pmt-2; <b>PDBTitle:</b> crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
6	<a href="#">d2a14a1</a>			99.7	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
7	<a href="#">c3vc2J_</a>			99.7	19	<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
8	<a href="#">c4necC_</a>			99.7	18	<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
9	<a href="#">c4qnuH_</a>			99.7	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
10	<a href="#">d2bzga1</a>			99.7	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
11	<a href="#">c3g2qA_</a>			99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.24; <b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin

12	<a href="#">c6mroA</a>	Alignment		99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyl transferase from methanosarcina acetivorans; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
13	<a href="#">c3lccA</a>	Alignment		99.7	17	<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
14	<a href="#">c3giwA</a>	Alignment		99.7	14	<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
15	<a href="#">d2ex4a1</a>	Alignment		99.7	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
16	<a href="#">c5ufmB</a>	Alignment		99.7	16	<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
17	<a href="#">c3bgdB</a>	Alignment		99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiopurine s-methyltransferase; <b>PDBTitle:</b> thiopurine s-methyltransferase
18	<a href="#">c3h2bB</a>	Alignment		99.7	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
19	<a href="#">c5z9oA</a>	Alignment		99.7	10	<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
20	<a href="#">c4p7cB</a>	Alignment		99.7	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
21	<a href="#">c5t39A</a>	Alignment	not modelled	99.7	14	<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
22	<a href="#">c3e23A</a>	Alignment	not modelled	99.6	25	<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
23	<a href="#">d2o57a1</a>	Alignment	not modelled	99.6	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
24	<a href="#">c4kdcA</a>	Alignment	not modelled	99.6	12	<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
25	<a href="#">c5cm2Z</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> Z: <b>PDB Molecule:</b> trna methyltransferase; <b>PDBTitle:</b> insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
26	<a href="#">d1l1ea</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
27	<a href="#">d1kpga</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> Mycolic acid cyclopropane synthase
28	<a href="#">d1kpia</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases

						Family:Mycolic acid cyclopropane synthase
29	<a href="#">c6ecvB</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
30	<a href="#">c3g2qB</a>	Alignment	not modelled	99.6	16	<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
31	<a href="#">c5w7kA</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oxag; <b>PDBTitle:</b> crystal structure of oxag
32	<a href="#">c3dlcA</a>	Alignment	not modelled	99.6	17	<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
33	<a href="#">c3qnhA</a>	Alignment	not modelled	99.6	23	<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)
34	<a href="#">d1tpya</a>	Alignment	not modelled	99.6	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
35	<a href="#">c2p8jA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 (np_349143.1) from clostridium acetobutylicum at 2.00 a resolution
36	<a href="#">c1z3cA</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> encephalitozoon cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
37	<a href="#">d1ri5a</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> mRNA cap (Guanine N-7) methyltransferase
38	<a href="#">c2xvmB</a>	Alignment	not modelled	99.6	20	<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 protein2 tehb from e. coli in complex with sah
39	<a href="#">c5kn4B</a>	Alignment	not modelled	99.6	15	<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
40	<a href="#">c6g4wq</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 40s ribosomal protein s16; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state a
41	<a href="#">d1r74a</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
42	<a href="#">c5egpB</a>	Alignment	not modelled	99.6	14	<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
43	<a href="#">c2fk8A</a>	Alignment	not modelled	99.6	8	<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
44	<a href="#">c6ectA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> stie protein; <b>PDBTitle:</b> stie o-mt residues 961-1257
45	<a href="#">c3ofkA</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nodulation protein s; <b>PDBTitle:</b> crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah)
46	<a href="#">c5gm2E</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase tied complexed with sah and2 teleocidin a1
47	<a href="#">c3bkxB</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 cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution
48	<a href="#">c3sm3A</a>	Alignment	not modelled	99.6	19	<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 q8puk2_metma2 from methanosarcina mazei. northeast structural genomics consortium3 target mar262.
49	<a href="#">c6bqcA</a>	Alignment	not modelled	99.6	18	<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
50	<a href="#">c5do0A</a>	Alignment	not modelled	99.6	14	<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
51	<a href="#">c4krqB</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 1; <b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine
52	<a href="#">c3p7nA</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;

52	<a href="#">c6e7pA</a>	Alignment	not modelled	99.6	20	<b>PDBTitle:</b> crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482 <b>PDB header:</b> transferase
53	<a href="#">c6gkvB</a>	Alignment	not modelled	99.6	11	<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
54	<a href="#">c4hgyC</a>	Alignment	not modelled	99.6	19	<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
55	<a href="#">c3ggdA</a>	Alignment	not modelled	99.6	12	<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
56	<a href="#">d1xvaa</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
57	<a href="#">c2iipD</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
58	<a href="#">c5hijA</a>	Alignment	not modelled	99.6	13	<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
59	<a href="#">c3bgvC</a>	Alignment	not modelled	99.6	21	<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="#">d2fk8a1</a>	Alignment	not modelled	99.6	8	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Mycolic acid cyclopropane synthase
61	<a href="#">c2g8nB</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylethanolamine n-methyltransferase; <b>PDBTitle:</b> structure of hpnmt with inhibitor 3-hydroxymethyl-7-(n-4-2 chlorophenylaminosulfonyl)-thiq and adohcy
62	<a href="#">d1jqea</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
63	<a href="#">c4pneA</a>	Alignment	not modelled	99.5	27	<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
64	<a href="#">c6dcbA</a>	Alignment	not modelled	99.5	11	<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
65	<a href="#">c5dplB</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein lysine methyltransferase 2; <b>PDBTitle:</b> the structure of pkmt2 from rickettsia typhi in complex with adohcy
66	<a href="#">d1xtpa</a>	Alignment	not modelled	99.5	10	<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
67	<a href="#">d2g72a1</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arylamine N-methyltransferase
68	<a href="#">d1pjza</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Thiopurine S-methyltransferase
69	<a href="#">c5mgzA</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-demethylnovobiocic acid c(8)-methyltransferase; <b>PDBTitle:</b> streptomyces spheroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah
70	<a href="#">c5eviA</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenite methyltransferase; <b>PDBTitle:</b> x-ray crystal structure of crasm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii
71	<a href="#">c3g5tA</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-aconitate 3-methyltransferase; <b>PDBTitle:</b> crystal structure of trans-aconitate 3-methyltransferase from yeast
72	<a href="#">c4htfA</a>	Alignment	not modelled	99.5	15	<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.
73	<a href="#">c3merA</a>	Alignment	not modelled	99.5	20	<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
74	<a href="#">d1y8ca</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
75	<a href="#">c2yr0A</a>	Alignment	not modelled	99.5	20	<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 from2 thermus thermophilus hb8
76	<a href="#">d1wzna1</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases

						<b>Family:</b> CAC2371-like
77	<a href="#">d1yzha1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
78	<a href="#">c5bp9A</a>	Alignment	not modelled	99.5	12	<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
79	<a href="#">c4kvzA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bam1; <b>PDBTitle:</b> crystal structure of the plantazolicin methyltransferase bam1 in2 complex with sah
80	<a href="#">c4x1oA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna (adenine(1408)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia
81	<a href="#">c5fcdA</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mccd; <b>PDBTitle:</b> crystal structure of mccd protein
82	<a href="#">c1vl5B</a>	Alignment	not modelled	99.5	18	<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
83	<a href="#">c6d6yA</a>	Alignment	not modelled	99.5	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
84	<a href="#">d1vl5a</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
85	<a href="#">c2qe6B</a>	Alignment	not modelled	99.5	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
86	<a href="#">c3e8sA</a>	Alignment	not modelled	99.5	16	<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
87	<a href="#">c5bszA</a>	Alignment	not modelled	99.5	19	<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
88	<a href="#">c5mptA</a>	Alignment	not modelled	99.5	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
89	<a href="#">d1xcla</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> Guanidinoacetate methyltransferase
90	<a href="#">c5ubbA</a>	Alignment	not modelled	99.5	14	<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
91	<a href="#">c5je0B</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase; <b>PDBTitle:</b> crystal structure of burkholderia glumae toxa with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethyltoxoflavin
92	<a href="#">d1af7a2</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> Chemotaxis receptor methyltransferase CheR, C-terminal domain
93	<a href="#">c6ec3C</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein; <b>PDBTitle:</b> crystal structure of evdmo1
94	<a href="#">d2fcaa1</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> TrmB-like
95	<a href="#">d1zx0a1</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
96	<a href="#">c3f4kA</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
97	<a href="#">c5u18A</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-3" methyltransferase; <b>PDBTitle:</b> crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin
98	<a href="#">c3eeyl</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> putative rrna methylase; <b>PDBTitle:</b> crystal structure of putative rrna-methylase from clostridium2 thermocellum
99	<a href="#">c2gs9A</a>	Alignment	not modelled	99.5	24	<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
100	<a href="#">c3ou7A</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dhpi-sam-hep complex
						<b>PDB header:</b> transferase

101	<a href="#">c4qttB</a>	Alignment	not modelled	99.5	21	<b>Chain:</b> B; <b>PDB Molecule:</b> putative methyltransferase bud23; <b>PDBTitle:</b> structure of s. cerevisiae bud23-trm112 complex involved in formation2 of m7g1575 on 18s rrna (apo-form)
102	<a href="#">d1d2ha</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> Glycine N-methyltransferase
103	<a href="#">d1xxla</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
104	<a href="#">d1nkva</a>	Alignment	not modelled	99.5	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
105	<a href="#">c3pfdD</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n
106	<a href="#">c3g5IA</a>	Alignment	not modelled	99.5	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 listeria monocytogenes
107	<a href="#">c3jwgA</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c
108	<a href="#">d1ve3a1</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
109	<a href="#">c4iscA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a putative methyltransferase from pseudomonas2 syringae
110	<a href="#">c3d2IC</a>	Alignment	not modelled	99.4	16	<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
111	<a href="#">c4obxD</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, <b>PDBTitle:</b> crystal structure of yeast coq5 in the apo form
112	<a href="#">c3dliB</a>	Alignment	not modelled	99.4	8	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
113	<a href="#">c2vdwA</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> vaccinia virus capping enzyme d1 subunit; <b>PDBTitle:</b> guanosine n7 methyl-transferase sub-complex (d1-d12) of the2 vaccinia virus mrna capping enzyme
114	<a href="#">c6ccaA</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> disa protein; <b>PDBTitle:</b> crystal structure of dsza carbon methyltransferase
115	<a href="#">c3lecA</a>	Alignment	not modelled	99.4	8	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> nadb-rossmann superfamily protein; <b>PDBTitle:</b> the crystal structure of a protein in the nadb-rossmann superfamily2 from streptococcus agalactiae to 1.8a
116	<a href="#">c3mtiA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
117	<a href="#">c3ujcA</a>	Alignment	not modelled	99.4	12	<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
118	<a href="#">c3mczB</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
119	<a href="#">c5xlxD</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> chemotaxis protein methyltransferase 1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of cher1 containing sah
120	<a href="#">c3cc8A</a>	Alignment	not modelled	99.4	15	<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) from2 bacillus cereus atcc 10987 at 1.64 a resolution