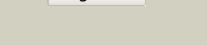
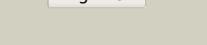
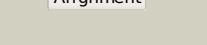


# Phyre<sup>2</sup>

Email	i.a.kelley@imperial.ac.uk
Description	P76145
Date	Thu Jan 5 12:19:38 GMT 2012
Unique Job ID	c1aba0699df13f54

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2p35A_</a>			100.0	44	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> trans-aconitate 2-methyltransferase; <b>PDBTitle:</b> crystal structure of trans-aconitate methyltransferase from agrobacterium tumefaciens
2	<a href="#">c3ccfB_</a>			100.0	21	<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) from anabaena variabilis atcc 29413 at 1.90 a resolution
3	<a href="#">c3g5tA_</a>			99.9	19	<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-methyltransferase2 from yeast
4	<a href="#">c2yr0A_</a>			99.9	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 thermus thermophilus hb8
5	<a href="#">c1vl5B_</a>			99.9	12	<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) from bacillus halodurans c-125 at 1.95 a resolution
6	<a href="#">c3mggB_</a>			99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyl transferase from methanosaarcina2 mazei
7	<a href="#">d1vl5a_</a>			99.9	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
8	<a href="#">c3bkxB_</a>			99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution
9	<a href="#">d2o57a1</a>			99.9	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
10	<a href="#">d1jgea_</a>			99.9	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Histamine methyltransferase
11	<a href="#">c3busB_</a>			99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm

12	<a href="#">d1xxla</a>	Alignment		99.9	11	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> UbiE/COQ5-like
13	<a href="#">c2fk8A</a>	Alignment		99.9	12	<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-adenosyl methionine
14	<a href="#">d1nkva</a>	Alignment		99.9	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
15	<a href="#">d2fk8a1</a>	Alignment		99.9	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
16	<a href="#">c3ujcA</a>	Alignment		99.8	17	<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
17	<a href="#">c3cc8A</a>	Alignment		99.8	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
18	<a href="#">d1kpga</a>	Alignment		99.8	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
19	<a href="#">c3e7pA</a>	Alignment		99.8	18	<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 vulgaris atcc 8482
20	<a href="#">d1kpia</a>	Alignment		99.8	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
21	<a href="#">c3gegA</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase from antibiotic biosynthesis <b>PDBTitle:</b> crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution
22	<a href="#">d1l1ea</a>	Alignment	not modelled	99.8	11	<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
23	<a href="#">c3f4kA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
24	<a href="#">d1tpya</a>	Alignment	not modelled	99.8	11	<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
25	<a href="#">c3dtmA</a>	Alignment	not modelled	99.8	21	<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_26332 from methanoscincus mazei .
26	<a href="#">c3e23A</a>	Alignment	not modelled	99.8	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 with2 sam from rhodopseudomonas palustris, northeast structural3 genomics consortium target rpr299
27	<a href="#">c3dlcA</a>	Alignment	not modelled	99.8	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
28	<a href="#">d2gh1a1</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> BC2162-like
29	<a href="#">c2gs9A</a>	Alignment	not modelled	99.8	18	<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
30	<a href="#">c3l8dA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from bacillus2 thuringiensis
31	<a href="#">d2p7ia1</a>	Alignment	not modelled	99.8	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
32	<a href="#">d1vlma</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> UbiE/COQ5-like
33	<a href="#">c3e8sA</a>	Alignment	not modelled	99.7	21	<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
34	<a href="#">c3dlIB</a>	Alignment	not modelled	99.7	18	<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
35	<a href="#">c3ou7A</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> dphi-sam-hep complex
36	<a href="#">c2p7iB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a sam dependent methyl-transferase type 12 family2 protein (eca1738) from pectobacterium atrosepticum scri1043 at 1.74 a3 resolution
37	<a href="#">d1p91a</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> rRNA methyltransferase R1mA
38	<a href="#">d1lim8a</a>	Alignment	not modelled	99.7	21	<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)
39	<a href="#">c3mq2A</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methyltransferase; <b>PDBTitle:</b> crystal structure of 16s rrna methyltranferase kamb
40	<a href="#">d2avna1</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> UbiE/COQ5-like
41	<a href="#">c3pfhD</a>	Alignment	not modelled	99.7	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
42	<a href="#">c3ocjA</a>	Alignment	not modelled	99.7	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
43	<a href="#">c3dh0B</a>	Alignment	not modelled	99.7	15	<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
44	<a href="#">c3ofkA</a>	Alignment	not modelled	99.7	23	<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 wmm9 in complex with s-adenosyl-l-homocysteine (sah)
45	<a href="#">d1xtpa</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> AD-003 protein-like
46	<a href="#">c3hnrA</a>	Alignment	not modelled	99.7	19	<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
47	<a href="#">c3h2bb</a>	Alignment	not modelled	99.7	19	<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 methyltransferase2 cg3271 from corynebacterium glutamicum in complex with s-3 adenosyl-l-homocysteine and pyrophosphate. northeast4 structural genomics consortium target cgr113a
48	<a href="#">d1kyza2</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> Plant O-methyltransferase, C-terminal domain
49	<a href="#">d1wzna1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> CAC2371-like
50	<a href="#">c3ndjA</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
51	<a href="#">c3bowC</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> mrna cap guanine-n7 methyltransferase;

51	<a href="#">c3oyvc</a>	Alignment	not modelled	99.7	17	<b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosylmethionine dependent <b>PDBTitle:</b> crystal structure of putative s-adenosylmethionine2 dependent methyltransferase from listeria monocytogenes
52	<a href="#">c3g5IA</a>	Alignment	not modelled	99.7	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 mesorhizobium loti at 1.60 a resolution
53	<a href="#">c3bkwB</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calo1 methyltransferase; <b>PDBTitle:</b> crystal structure of calo1, methyltransferase in calicheamicin biosynthesis, sah bound form
54	<a href="#">c3lstB</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> Plant O-methyltransferase, C-terminal domain
55	<a href="#">d1fp1d2</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyl chloride transferase; <b>PDBTitle:</b> structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
56	<a href="#">c3lccA</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethyltransferase; <b>PDBTitle:</b> crystal structure of streptomyces venezuelae desvi
57	<a href="#">c3bxoA</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> AD-003 protein-like
58	<a href="#">d2ex4a1</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> TrmB-like
59	<a href="#">d1yzha1</a>	Alignment	not modelled	99.6	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.
60	<a href="#">d1y8ca</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase (npun_r0239) from2 nostoc punctiforme pcc 73102 at 2.15 a resolution
61	<a href="#">c3mczB</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> CAC2371-like
62	<a href="#">c2r3sA</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> crystal structure of a sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
63	<a href="#">d1ri5a</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hemolysin; <b>PDBTitle:</b> the crystal structure of a putative hemolysin from lactococcus lactis
64	<a href="#">c1z3cA</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mrna cap (guanine N-7) methyltransferase in complexed with azadomet
65	<a href="#">c3opnA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hemolysin; <b>PDBTitle:</b> the crystal structure of a putative hemolysin from lactococcus lactis
66	<a href="#">d1qzza2</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> Plant O-methyltransferase, C-terminal domain
67	<a href="#">c3dp7B</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative hemolysin; <b>PDBTitle:</b> the crystal structure of a putative hemolysin from bacteroides2 vulgatus atcc 8482
68	<a href="#">c3g2qA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.24; <b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
69	<a href="#">d1ve3a1</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> CAC2371-like
70	<a href="#">d1tw3a2</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> Plant O-methyltransferase, C-terminal domain
71	<a href="#">c3sm3A</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hemolysin; <b>PDBTitle:</b> the crystal structure of a putative hemolysin from bacteroides2 vulgatus atcc 8482
72	<a href="#">d2a14a1</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> Arylamine N-methyltransferase
73	<a href="#">d1xcla</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> Guanidinoacetate methyltransferase
74	<a href="#">c3gwzB</a>	Alignment	not modelled	99.6	14	<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
75	<a href="#">d1m6ya2</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> MraW-like putative methyltransferases

76	<a href="#">c3merA</a>		Alignment	not modelled	99.6	12	<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 from2 synechocystis sp. pcc 6803, northeast structural genomics3 consortium target sgr145
77	<a href="#">c3p9kD</a>		Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> caffeic acid o-methyltransferase; <b>PDBTitle:</b> crystal structure of perennial ryegrass lpm0t1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
78	<a href="#">d1zx0a1</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> Guanidinoacetate methyltransferase
79	<a href="#">c1kyzC</a>		Alignment	not modelled	99.6	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-hydroxyferulic acid 3/5-o-methyltransferase ferulic acid complex
80	<a href="#">c3i53A</a>		Alignment	not modelled	99.6	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)
81	<a href="#">c3ggdA</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 sam-dependent methyltransferase (yp_325210.1)2 from anabaena variabilis atcc 29413 at 2.11 a resolution
82	<a href="#">d1xvaa</a>		Alignment	not modelled	99.6	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
83	<a href="#">c2iipD</a>		Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinamide n-methyltransferase; <b>PDBTitle:</b> human nicotinamide n-methyltransferase
84	<a href="#">c1x1aA</a>		Alignment	not modelled	99.6	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
85	<a href="#">d1d2ha</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> Glycine N-methyltransferase
86	<a href="#">d2fcfa1</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> Trrm-like
87	<a href="#">c2zfuA</a>		Alignment	not modelled	99.5	15	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> cerebral protein 1; <b>PDBTitle:</b> structure of the methyltransferase-like domain of nucleomethylin
88	<a href="#">c2ip2B</a>		Alignment	not modelled	99.5	13	<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
89	<a href="#">c3g07C</a>		Alignment	not modelled	99.5	27	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 7sk srna methylphosphate capping enzyme; <b>PDBTitle:</b> methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
90	<a href="#">c3cgkB</a>		Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
91	<a href="#">c3jwgA</a>		Alignment	not modelled	99.5	19	<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 domain2 of bacterial-cthen1-c
92	<a href="#">d2i6ga1</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> TehB-like
93	<a href="#">c3lecA</a>		Alignment	not modelled	99.5	11	<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-rossmann2 superfamily from streptococcus agalactiae to 1.8a
94	<a href="#">c3i9fB</a>		Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative type 11 methyltransferase; <b>PDBTitle:</b> crystal structure of a putative type 11 methyltransferase2 from sulfolobus solfataricus
95	<a href="#">d1g8sa</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> Fibrillarin homologue
96	<a href="#">c3dxyA</a>		Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tRNA (guanine-n(7)-)methyltransferase; <b>PDBTitle:</b> crystal structure of ectrbm in complex with sam
97	<a href="#">c3d2IC</a>		Alignment	not modelled	99.5	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
98	<a href="#">d1pjza</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> Thiopurine S-methyltransferase
99	<a href="#">d1dusa</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> Hypothetical protein MJ0882 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases

100	<a href="#">d1fp2a2</a>	Alignment	not modelled	99.5	12	<b>Supertamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0852; <b>PDBTitle:</b> structure of a putative methyltransferase from thermoplasma2 acidophilum.
101	<a href="#">d1yb2a1</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0852; <b>PDBTitle:</b> structure of a putative methyltransferase from thermoplasma2 acidophilum.
102	<a href="#">c1yb2A_</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
103	<a href="#">d1r74a_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rRNA methylase; <b>PDBTitle:</b> structure of an antibiotic related methyltransferase
104	<a href="#">c3p2kA_</a>	Alignment	not modelled	99.5	16	<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
105	<a href="#">c3mtiA_</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> Guanidinoacetate methyltransferase
106	<a href="#">d1p1ca_</a>	Alignment	not modelled	99.5	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-methyltransferase2 (dnrk) in complex with s-adenosyl-l-homocysteine (sah) and 3 4-methoxy-e-rhodomycin t (m-et)
107	<a href="#">c1tw3A_</a>	Alignment	not modelled	99.5	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
108	<a href="#">c1zgaA_</a>	Alignment	not modelled	99.5	16	<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
109	<a href="#">c3m70A_</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> tRNA(1-methyladenosine) methyltransferase-like
110	<a href="#">d1o54a_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of p. abyssi trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine
111	<a href="#">c3mb5A_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, Imof2365_1472; <b>PDBTitle:</b> structure of uncharacterized protein (Imof2365_1472) from2 listeria monocytogenes serotype 4b
112	<a href="#">c3gnlB_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein rdmb; <b>PDBTitle:</b> crystal structure of aclacinomycin-10-hydroxylase (rdmb) in complex2 with sinefungin (sfg)
113	<a href="#">c1xdUa_</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> MraW-like putative methyltransferases
114	<a href="#">d1wg8a2</a>	Alignment	not modelled	99.5	17	<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
115	<a href="#">c3eeyl_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hen1; <b>PDBTitle:</b> crystal structure analysis of the methyltransferase domain2 of bacterial-avhen1-c
116	<a href="#">c3jwhA_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus
117	<a href="#">c2yvLB_</a>	Alignment	not modelled	99.4	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ribosomal protein L11 methyltransferase PrmA
118	<a href="#">d2nxca1</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoliquiritinigen 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase
119	<a href="#">c1fpqA_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase (decarboxylating); <b>PDBTitle:</b> crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
120	<a href="#">c3e05B_</a>	Alignment	not modelled	99.4	16	