

# Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1uira_</a>	 Alignment		100.0	31	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
2	<a href="#">c2q41D_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> spermidine synthase 1; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of spermidine2 synthase from arabidopsis thaliana gene at1g23820
3	<a href="#">d1xj5a_</a>	 Alignment		100.0	32	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
4	<a href="#">d1inla_</a>	 Alignment		100.0	25	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
5	<a href="#">c3bwbA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> crystal structure of the apo form of spermidine synthase from2 trypanosoma cruzi at 2.5 a resolution
6	<a href="#">c6qmmA_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyamine aminopropyltransferase; <b>PDBTitle:</b> crystal structure of synecochoccus spermidine synthase in complex with2 putrescine, spermidine and mta
7	<a href="#">c6bq6B_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thermospermine synthase; <b>PDBTitle:</b> crystal structure of medicago truncatula thermospermine synthase2 (mttsp2) in complex with thermospermine
8	<a href="#">d1iy9a_</a>	 Alignment		100.0	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
9	<a href="#">d1mjfa_</a>	 Alignment		100.0	29	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
10	<a href="#">d2b2ca1</a>	 Alignment		100.0	28	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase
11	<a href="#">d2o07a1</a>	 Alignment		100.0	28	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Spermidine synthase

12	<a href="#">c2pssC_</a>	Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> the structure of plasmodium falciparum spermidine synthase in its apo-2 form
13	<a href="#">c2hteB_</a>	Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> the crystal structure of spermidine synthase from p. falciparum in2 complex with 5'-methylthioadenosine
14	<a href="#">c3adnB_</a>	Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> crystal structure of spermidine synthase from e. coli.
15	<a href="#">c2cmgA_</a>	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> crystal structure of spermidine synthase from helicobacter2 pylori
16	<a href="#">c3c6kC_</a>	Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> spermine synthase; <b>PDBTitle:</b> crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
17	<a href="#">c3gqvA_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> crystal structure of a probable spermidine synthase from2 corynebacterium glutamicum atcc 13032
18	<a href="#">c5wcjA_</a>	Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein 13; <b>PDBTitle:</b> crystal structure of human methyltransferase-like protein 13 in2 complex with sah
19	<a href="#">c2b78A_</a>	Alignment		99.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein smu.776; <b>PDBTitle:</b> a putative sam-dependent methyltransferase from streptococcus mutans
20	<a href="#">d2b78a2</a>	Alignment		99.3	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
21	<a href="#">c3vseA_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of methyltransferase
22	<a href="#">c3c0kB_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0064 protein yccw; <b>PDBTitle:</b> crystal structure of a ribosomal rna methyltransferase
23	<a href="#">c5n5dA_</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of the o-methyltransferase tomg from streptomyces2 achromogenes involved in tomaymycin synthesis in complex with sam
24	<a href="#">d2igta1</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
25	<a href="#">c3tr6A_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> structure of a o-methyltransferase from coxiella burnetii
26	<a href="#">c3tfwB_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
27	<a href="#">c3cbgA_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> functional and structural characterization of a cationdependent o-2 methyltransferase from the cyanobacterium synechocystis sp. strain3 pcc 6803
28	<a href="#">d2as0a2</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases

					<b>Family:</b> hypothetical RNA methyltransferase
29	<a href="#">c3duwB_</a>	Alignment	not modelled	99.1	24 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase, putative; <b>PDBTitle:</b> crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah
30	<a href="#">c4oa8A_</a>	Alignment	not modelled	99.1	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase family protein; <b>PDBTitle:</b> x-ray crystal structure of o-methyltransferase from anaplasma2 phagocytophilum in apo form
31	<a href="#">d1zx0a1</a>	Alignment	not modelled	99.1	21 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
32	<a href="#">d2avda1</a>	Alignment	not modelled	99.1	26 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
33	<a href="#">c1wxwA_</a>	Alignment	not modelled	99.1	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1280; <b>PDBTitle:</b> crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophilus hb8
34	<a href="#">c2as0A_</a>	Alignment	not modelled	99.1	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1915; <b>PDBTitle:</b> crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
35	<a href="#">c3c3yB_</a>	Alignment	not modelled	99.1	17 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum
36	<a href="#">c3dr5A_</a>	Alignment	not modelled	99.1	12 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of the q8nr3_corgl protein from corynebacterium2 glutamicum. northeast structural genomics consortium target cgr117.
37	<a href="#">c5x7fA_</a>	Alignment	not modelled	99.0	21 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase rv1220c; <b>PDBTitle:</b> structure of a o-methyltransferase from mycobacterium tuberculosis at2 2.0 resolution
38	<a href="#">d1wxxa2</a>	Alignment	not modelled	99.0	17 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
39	<a href="#">c5lhmA_</a>	Alignment	not modelled	99.0	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of safc from myxococcus xanthus apo-form
40	<a href="#">c2gpyB_</a>	Alignment	not modelled	99.0	22 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of putative o-methyltransferase from bacillus2 halodurans
41	<a href="#">c4dmgA_</a>	Alignment	not modelled	99.0	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1493; <b>PDBTitle:</b> thermus thermophilus m5c1942 methyltransferase rlmo
42	<a href="#">d1susa1</a>	Alignment	not modelled	99.0	15 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
43	<a href="#">c3ntvB_</a>	Alignment	not modelled	99.0	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mw1564 protein; <b>PDBTitle:</b> crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus
44	<a href="#">c2e58D_</a>	Alignment	not modelled	99.0	16 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> mnmc2; <b>PDBTitle:</b> crystal structure of mnmc2 from aquifex aeolicus
45	<a href="#">c5zw3B_</a>	Alignment	not modelled	99.0	20 <b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-methyltransferase yrrm; <b>PDBTitle:</b> crystal structure of trmr from b. subtilis
46	<a href="#">c3v8vB_</a>	Alignment	not modelled	98.9	17 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase I; <b>PDBTitle:</b> crystal structure of bifunctional methyltransferase ycbj (rlmlk) from2 escherichia coli, sam binding
47	<a href="#">c2ozvA_</a>	Alignment	not modelled	98.9	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0636; <b>PDBTitle:</b> crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
48	<a href="#">d1dusa_</a>	Alignment	not modelled	98.9	17 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
49	<a href="#">c4dcmA_</a>	Alignment	not modelled	98.9	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase g; <b>PDBTitle:</b> crystal structure of methyltransferase rlmg modifying g1835 of 23s2 rrna in escherichia coli
50	<a href="#">c2hncC_</a>	Alignment	not modelled	98.9	20 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent o-methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent o-methyltransferase from pathogenic2 bacterium leptospira interrogans
51	<a href="#">d1p1ca_</a>	Alignment	not modelled	98.9	22 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
52	<a href="#">c4ymhB_</a>	Alignment	not modelled	98.9	16 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sam-dependent o-methyltransferase; <b>PDBTitle:</b> crystal structure of sah-bound podospira anserina methyltransferase2 pamth1 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribosomal rna small subunit

53	<a href="#">c3dmgA_</a>	Alignment	not modelled	98.9	19	methyltransferase; <b>PDBTitle:</b> t. thermophilus 16s rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
54	<a href="#">d1xcla_</a>	Alignment	not modelled	98.9	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
55	<a href="#">c2pjdA_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase c; <b>PDBTitle:</b> crystal structure of 16s rrna methyltransferase rsmc
56	<a href="#">d1nv8a_</a>	Alignment	not modelled	98.9	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N5- glutamine methyltransferase, HemK
57	<a href="#">c3r3hA_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase, sam-dependent; <b>PDBTitle:</b> crystal structure of o-methyltransferase from legionella pneumophila
58	<a href="#">d2fcaa1</a>	Alignment	not modelled	98.8	19	<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	98.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
60	<a href="#">c5u18A_</a>	Alignment	not modelled	98.8	21	<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
61	<a href="#">c3mb5A_</a>	Alignment	not modelled	98.8	20	<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
62	<a href="#">c1yb2A_</a>	Alignment	not modelled	98.8	21	<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.
63	<a href="#">d1yb2a1</a>	Alignment	not modelled	98.8	21	<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
64	<a href="#">c3evzA_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
65	<a href="#">c3axtA_</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable n(2),n(2)-dimethylguanosine trna methyltransferase <b>PDBTitle:</b> complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
66	<a href="#">d1l3ia_</a>	Alignment	not modelled	98.8	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Precorrin-6Y methyltransferase (CbiT)
67	<a href="#">c3jwgA_</a>	Alignment	not modelled	98.7	22	<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
68	<a href="#">c3dxyA_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of ectrmb in complex with sam
69	<a href="#">c3lpmA_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
70	<a href="#">c2yvlB_</a>	Alignment	not modelled	98.7	22	<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
71	<a href="#">c5do0A_</a>	Alignment	not modelled	98.7	15	<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
72	<a href="#">c5dplB_</a>	Alignment	not modelled	98.7	20	<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
73	<a href="#">c4ineB_</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein pmt-2; <b>PDBTitle:</b> crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
74	<a href="#">c3e05B_</a>	Alignment	not modelled	98.7	22	<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
75	<a href="#">c5zy5B_</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable catechol o-methyltransferase 1; <b>PDBTitle:</b> spcomt apo structure
76	<a href="#">d2dula1</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TRM1-like
77	<a href="#">d1o54a_</a>	Alignment	not modelled	98.7	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> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(37)-n1)-methyltransferase

78	<a href="#">c5hjmA</a>	Alignment	not modelled	98.7	13	trm5a; <b>PDBTitle:</b> crystal structure of pyrococcus abyssi trm5a complexed with mta
79	<a href="#">c4iscA</a>	Alignment	not modelled	98.7	21	<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
80	<a href="#">d1dl5a1</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
81	<a href="#">d2nxca1</a>	Alignment	not modelled	98.7	21	<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
82	<a href="#">d2cl5a1</a>	Alignment	not modelled	98.6	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> COMT-like
83	<a href="#">c6gkvB</a>	Alignment	not modelled	98.6	19	<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
84	<a href="#">c6bqcA</a>	Alignment	not modelled	98.6	17	<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
85	<a href="#">d2ex4a1</a>	Alignment	not modelled	98.6	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
86	<a href="#">c3fpjA</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of e81q mutant of mtas in complex with s-2 adenosylmethionine
87	<a href="#">c1dl5A</a>	Alignment	not modelled	98.6	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> protein-l-isoaspartate o-methyltransferase
88	<a href="#">c3tm4A</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> trna (guanine n2-)-methyltransferase trm14; <b>PDBTitle:</b> crystal structure of trm14 from pyrococcus furiosus in complex with s-2 adenosylmethionine
89	<a href="#">c5z9oA</a>	Alignment	not modelled	98.6	17	<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
90	<a href="#">c4x1oA</a>	Alignment	not modelled	98.6	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
91	<a href="#">c3grzA</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal protein l11 methyltransferase; <b>PDBTitle:</b> crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
92	<a href="#">d1i9ga</a>	Alignment	not modelled	98.6	22	<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
93	<a href="#">c2vduE</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> structure of trm8-trm82, the yeast trna m7g methylation2 complex
94	<a href="#">c3c3pC</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of a methyltransferase (np_951602.1) from geobacter2 sulfurreducens at 1.90 a resolution
95	<a href="#">c5ccbA</a>	Alignment	not modelled	98.6	22	<b>PDB header:</b> transferase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> trna (adenine(58)-n(1))-methyltransferase catalytic subunit <b>PDBTitle:</b> crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
96	<a href="#">d1xtpa</a>	Alignment	not modelled	98.6	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
97	<a href="#">d1ilna</a>	Alignment	not modelled	98.6	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
98	<a href="#">c6g4wq</a>	Alignment	not modelled	98.6	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
99	<a href="#">c4xcxA</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> small rna 2'-o-methyltransferase; <b>PDBTitle:</b> methyltransferase domain of small rna 2'-o-methyltransferase
100	<a href="#">d1r18a</a>	Alignment	not modelled	98.6	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase
101	<a href="#">d2esra1</a>	Alignment	not modelled	98.6	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
102	<a href="#">d1r74a</a>	Alignment	not modelled	98.6	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="#">c3a26A</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0793; <b>PDBTitle:</b> crystal structure of p. horikoshii tyw2 in complex with2 mesado
104	<a href="#">c3vc2J</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> geranyl diphosphate 2-c-methyltransferase; <b>PDBTitle:</b> crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine
105	<a href="#">c2esrB</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> conserved hypothetical protein- streptococcus pyogenes
106	<a href="#">d1l1ea</a>	Alignment	not modelled	98.6	16	<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
107	<a href="#">c5yacA</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(37)-n1)-methyltransferase trm5b; <b>PDBTitle:</b> crystal structure of wt trm5b from pyrococcus abyssi
108	<a href="#">c2pbfA</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase beta-aspartate <b>PDBTitle:</b> crystal structure of a putative protein-l-isoaspartate o-2 methyltransferase beta-aspartate methyltransferase (pcmt) from3 plasmodium falciparum in complex with s-adenosyl-l-homocysteine
109	<a href="#">c3ofkA</a>	Alignment	not modelled	98.6	14	<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)
110	<a href="#">d2fpoa1</a>	Alignment	not modelled	98.6	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
111	<a href="#">d2b3ta1</a>	Alignment	not modelled	98.5	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N5- glutamine methyltransferase, HemK
112	<a href="#">c3g5tA</a>	Alignment	not modelled	98.5	17	<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
113	<a href="#">c6h1dA</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hemk methyltransferase family member 2; <b>PDBTitle:</b> crystal structure of c21orf127-trmt112 in complex with sah
114	<a href="#">c6ecvB</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> stid protein; <b>PDBTitle:</b> stid o-mt residues 976-1266
115	<a href="#">c3njrB</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y methylase; <b>PDBTitle:</b> crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
116	<a href="#">c2fk8A</a>	Alignment	not modelled	98.5	15	<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
117	<a href="#">d1tpya</a>	Alignment	not modelled	98.5	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
118	<a href="#">c4p7cB</a>	Alignment	not modelled	98.5	18	<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
119	<a href="#">c2yxdA</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cobalt-precorrin-6y c(15)-methyltransferase <b>PDBTitle:</b> crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbt)
120	<a href="#">c4krhB</a>	Alignment	not modelled	98.5	25	<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