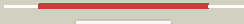


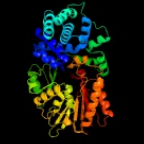
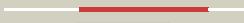



















# Phyre2

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 Description RVBD1407\_fmU\_1583107\_1584480  
 Date Wed Jul 31 22:05:51 BST 2019  
 Unique Job ID 0303081a3bce777a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1sqgA_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sun protein; <b>PDBTitle:</b> the crystal structure of the e. coli fmU apoenzyme at 1.652 Å resolution
2	<a href="#">c2yxlA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 450aa long hypothetical fmU protein; <b>PDBTitle:</b> crystal structure of ph0851
3	<a href="#">c3m6wA_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> multi-site-specific 16S rRNA methyltransferase Rsmf from Thermus2 thermophilus in space group P21212 in complex with S-adenosyl-L-methionine
4	<a href="#">c3m4xA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> noL1/nop2/sun family protein; <b>PDBTitle:</b> structure of a ribosomal methyltransferase
5	<a href="#">c2frxD_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein yebU; <b>PDBTitle:</b> crystal structure of yebU, a m5C rRNA methyltransferase from E. coli
6	<a href="#">c6em5q_</a>	 Alignment		100.0	23	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60S ribosomal protein L18-a; <b>PDBTitle:</b> state D architectural model (NSA1-TAP flag-YTM1) - visualizing the 2 assembly pathway of nucleolar pre-60S ribosomes
7	<a href="#">d1ixka_</a>	 Alignment		100.0	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
8	<a href="#">c5zvdB_</a>	 Alignment		100.0	30	<b>PDB header:</b> rRNA binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> 389aa long hypothetical nucleolar protein; <b>PDBTitle:</b> the crystal structure of nsun6 from Pyrococcus horikoshii
9	<a href="#">c5wwrA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase/rRNA <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase nsun6; <b>PDBTitle:</b> crystal structure of human nsun6/tRNA/sfg
10	<a href="#">d1sqga2</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> NOL1/NOP2/sun
11	<a href="#">c4fp9F_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> methyltransferase nsun4; <b>PDBTitle:</b> human mterf4-nsun4 protein complex

12	<a href="#">c3a4tA_</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase mj0026; <b>PDBTitle:</b> crystal structure of atm4 from m.jannaschii with sinefungin
13	<a href="#">d2b9ea1</a>	Alignment		100.0	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
14	<a href="#">d1sqa1</a>	Alignment		100.0	30	<b>Fold:</b> NusB-like <b>Superfamily:</b> NusB-like <b>Family:</b> RmsB N-terminal domain-like
15	<a href="#">c6ckqA_</a>	Alignment		99.9	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusb; <b>PDBTitle:</b> solution structure of the burkholderia thailandensis transcription2 antitermination protein nusb (bth_i1529) - seattle structural3 genomics center for infectious disease target butha.17903.a
16	<a href="#">d1ey1a_</a>	Alignment		99.9	26	<b>Fold:</b> NusB-like <b>Superfamily:</b> NusB-like <b>Family:</b> Antitermination factor NusB
17	<a href="#">d1tzva_</a>	Alignment		99.9	24	<b>Fold:</b> NusB-like <b>Superfamily:</b> NusB-like <b>Family:</b> Antitermination factor NusB
18	<a href="#">c2jr0A_</a>	Alignment		99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> n utilization substance protein b homolog; <b>PDBTitle:</b> solution structure of nusb from aquifex aeolicus
19	<a href="#">d1eyva_</a>	Alignment		99.9	25	<b>Fold:</b> NusB-like <b>Superfamily:</b> NusB-like <b>Family:</b> Antitermination factor NusB
20	<a href="#">c1eyvA_</a>	Alignment		99.9	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> n-utilizing substance protein b homolog; <b>PDBTitle:</b> the crystal structure of nusb from mycobacterium tuberculosis
21	<a href="#">c4dmgA_</a>	Alignment	not modelled	99.9	20	<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
22	<a href="#">d2as0a2</a>	Alignment	not modelled	99.9	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
23	<a href="#">d1wxxa2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> hypothetical RNA methyltransferase
24	<a href="#">c2as0A_</a>	Alignment	not modelled	99.9	18	<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
25	<a href="#">d2b78a2</a>	Alignment	not modelled	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 RNA methyltransferase
26	<a href="#">c1wxwA_</a>	Alignment	not modelled	99.8	26	<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
27	<a href="#">c3c0kB_</a>	Alignment	not modelled	99.8	22	<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
28	<a href="#">c2nyuA_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ribosomal rna methyltransferase 2; <b>PDBTitle:</b> crystal structure of human ftsj homolog 2 (e.coli) protein in complex2 with s-adenosylmethionine

29	<a href="#">c3vseA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of methyltransferase
30	<a href="#">c2b78A</a>	Alignment	not modelled	99.8	13	<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
31	<a href="#">d2b3ta1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N5- glutamine methyltransferase, HemK
32	<a href="#">d2igta1</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 RNA methyltransferase
33	<a href="#">c2plwA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna methyltransferase, putative; <b>PDBTitle:</b> crystal structure of a ribosomal rna methyltransferase, putative, from2 plasmodium falciparum (pf13_0052).
34	<a href="#">c3mb5A</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of p. abyss trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine
35	<a href="#">d1g8aa</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> Fibrillarlin homologue
36	<a href="#">c3lbyA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1697c; <b>PDBTitle:</b> crystal structure of smu.1697c, a putative methyltransferase from2 streptococcus mutans in complex with sah
37	<a href="#">c3douA</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase ; <b>PDBTitle:</b> crystal structure of methyltransferase involved in cell division from2 thermoplasma volcanicum gss1
38	<a href="#">d1ej0a</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> RNA methyltransferase FtsJ
39	<a href="#">d1m6ya2</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> MraW-like putative methyltransferases
40	<a href="#">d1o54a</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> tRNA(1-methyladenosine) methyltransferase-like
41	<a href="#">c6j27D</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n(4)-bis(aminopropyl)spermidine synthase; <b>PDBTitle:</b> crystal structure of the branched-chain polyamine synthase from2 thermus thermophilus (tth-bpsa) in complex with n4-3 aminopropylspermidine and 5'-methylthioadenosine
42	<a href="#">c3id5F</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase/ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> fibrillarlin-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarlin, l7ae and a split half c/d rna
43	<a href="#">c5ccbA</a>	Alignment	not modelled	99.6	20	<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
44	<a href="#">d1i9ga</a>	Alignment	not modelled	99.6	25	<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
45	<a href="#">c6h1dA</a>	Alignment	not modelled	99.6	16	<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
46	<a href="#">c4df3B</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fibrillarlin-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of aeropyrum pernix fibrillarlin in complex with2 natively bound s-adenosyl-l-methionine at 1.7a
47	<a href="#">c5yacA</a>	Alignment	not modelled	99.6	24	<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
48	<a href="#">d2b25a1</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> tRNA(1-methyladenosine) methyltransferase-like
49	<a href="#">d1prya</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> Fibrillarlin homologue
50	<a href="#">d2frna1</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> Met-10+ protein-like
51	<a href="#">d1yb2a1</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> tRNA(1-methyladenosine) methyltransferase-like
52	<a href="#">c1yb2A</a>	Alignment	not modelled	99.5	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.

53	<a href="#">c3e05B</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-6y c5,15-methyltransferase (decarboxylating); <b>PDBTitle:</b> crystal structure of precocorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
54	<a href="#">c2pwyB</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (adenine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of a m1a58 trna methyltransferase
55	<a href="#">d1wg8a2</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> MraW-like putative methyltransferases
56	<a href="#">c3tmaA</a>	Alignment	not modelled	99.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of trmN from thermus thermophilus
57	<a href="#">c3mtiA</a>	Alignment	not modelled	99.5	18	<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
58	<a href="#">d1l3ia</a>	Alignment	not modelled	99.5	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Precocorrin-6Y methyltransferase (CbiT)
59	<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
60	<a href="#">c2yvlB</a>	Alignment	not modelled	99.5	19	<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
61	<a href="#">c3a26A</a>	Alignment	not modelled	99.5	18	<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
62	<a href="#">c3bt7A</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna (uracil-5-)-methyltransferase; <b>PDBTitle:</b> structure of e. coli 5-methyluridine methyltransferase trna in complex2 with 19 nucleotide t-arm analogue
63	<a href="#">c2pjdA</a>	Alignment	not modelled	99.5	23	<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
64	<a href="#">c3v8vB</a>	Alignment	not modelled	99.5	19	<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 ycbY (rlmlk) from2 escherichia coli, sam binding
65	<a href="#">c2ipxA</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna 2'-o-methyltransferase fibrillarin; <b>PDBTitle:</b> human fibrillarlin
66	<a href="#">d1nt2a</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> Fibrillarlin homologue
67	<a href="#">d1uwva2</a>	Alignment	not modelled	99.5	32	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> (Uracil-5-)-methyltransferase
68	<a href="#">c2vs1A</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rna methyltransferase pyrab10780; <b>PDBTitle:</b> the crystal structure of pyrococcus abyssi trna (uracil-54, c5)-2 methyltransferase in complex with s-adenosyl-l-homocysteine
69	<a href="#">c3njb</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-6y methylase; <b>PDBTitle:</b> crystal structure of c-terminal domain of precocorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
70	<a href="#">d1yzha1</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
71	<a href="#">c5xj2C</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized rna methyltransferase sp_1029; <b>PDBTitle:</b> structure of sprlmcD with u747 rna
72	<a href="#">c3dmgA</a>	Alignment	not modelled	99.4	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribosomal rna small subunit methyltransferase; <b>PDBTitle:</b> t. thermophilus 16s rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy
73	<a href="#">c1uwvA</a>	Alignment	not modelled	99.4	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 23s rrna (uracil-5-)-methyltransferase ruma; <b>PDBTitle:</b> crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
74	<a href="#">d1g8sa</a>	Alignment	not modelled	99.4	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Fibrillarlin homologue
75	<a href="#">c5hjmA</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(37)-n1)-methyltransferase trm5a; <b>PDBTitle:</b> crystal structure of pyrococcus abyssi trm5a complexed with mta
76	<a href="#">c5kn4B</a>	Alignment	not modelled	99.4	16	<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
						<b>PDB header:</b> transferase

77	<a href="#">c2yxdA_</a>	Alignment	not modelled	99.4	13	<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 (cbit)
78	<a href="#">c5wp5A_</a>	Alignment	not modelled	99.4	21	<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
79	<a href="#">d1dusa_</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Hypothetical protein MJ0882
80	<a href="#">c3hm2G_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> transferase <b>Chain:</b> G; <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase; <b>PDBTitle:</b> crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
81	<a href="#">c3gdhC_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine synthase 1 (tgs1)2 bound to m7gtp and adenosyl-homocysteine (active form)
82	<a href="#">d1dl5a1</a>	Alignment	not modelled	99.4	22	<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
83	<a href="#">c3a27A_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein mj1557; <b>PDBTitle:</b> crystal structure of m. jannaschii tyw2 in complex with2 adomet
84	<a href="#">c5dplB_</a>	Alignment	not modelled	99.4	17	<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
85	<a href="#">d1nv8a_</a>	Alignment	not modelled	99.4	14	<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
86	<a href="#">c3tkaA_</a>	Alignment	not modelled	99.4	30	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase h; <b>PDBTitle:</b> crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
87	<a href="#">c1m6yA_</a>	Alignment	not modelled	99.4	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> s-adenosyl-methyltransferase mraw; <b>PDBTitle:</b> crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah
88	<a href="#">c1dl5A_</a>	Alignment	not modelled	99.3	22	<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
89	<a href="#">c5e72A_</a>	Alignment	not modelled	99.3	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> n2, n2-dimethylguanosine trna methyltransferase; <b>PDBTitle:</b> crystal structure of the archaeal trna m2g/m22g10 methyltransferase2 (atrm11) in complex with s-adenosyl-l-methionine (sam) from3 thermococcus kodakarensis
90	<a href="#">d1wy7a1</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
91	<a href="#">c3grzA_</a>	Alignment	not modelled	99.3	19	<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="#">c2yx1A_</a>	Alignment	not modelled	99.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein mj0883; <b>PDBTitle:</b> crystal structure of m.jannaschii trna m1g37 methyltransferase
93	<a href="#">c2ozvA_</a>	Alignment	not modelled	99.3	28	<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.
94	<a href="#">c4dcmA_</a>	Alignment	not modelled	99.3	24	<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 rimg modifying g1835 of 23s2 rrna in escherichia coli
95	<a href="#">c3egiA_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> trimethylguanosine synthase homolog; <b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine synthase tgs12 bound to m7gpppa (inactive form)
96	<a href="#">c4qttB_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> transferase <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)
97	<a href="#">c5ergB_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> trna (adenine(58)-n(1))-methyltransferase catalytic subunit <b>PDBTitle:</b> crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam
98	<a href="#">c3tm4A_</a>	Alignment	not modelled	99.3	18	<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
99	<a href="#">c6gkvB_</a>	Alignment	not modelled	99.3	23	<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
100	<a href="#">c3gnhA_</a>	Alignment	not modelled	99.3	10	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> arsenic methyltransferase;



100	<a href="#">c3qmlA</a>	Alignment	not modelled	99.3	19	<b>PDBTitle:</b> arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii) <b>PDB header:</b> transferase
101	<a href="#">c5n5dA</a>	Alignment	not modelled	99.3	22	<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
102	<a href="#">c4krhB</a>	Alignment	not modelled	99.3	17	<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
103	<a href="#">d1xcla</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Guanidinoacetate methyltransferase
104	<a href="#">c5do0A</a>	Alignment	not modelled	99.3	18	<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
105	<a href="#">d1ilna</a>	Alignment	not modelled	99.3	25	<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
106	<a href="#">c3duwB</a>	Alignment	not modelled	99.3	21	<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
107	<a href="#">d2fcaa1</a>	Alignment	not modelled	99.3	10	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
108	<a href="#">c3e7pA</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
109	<a href="#">c5u18A</a>	Alignment	not modelled	99.2	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
110	<a href="#">c4ineB</a>	Alignment	not modelled	99.2	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
111	<a href="#">c3f4kA</a>	Alignment	not modelled	99.2	15	<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.
112	<a href="#">c6g4wq</a>	Alignment	not modelled	99.2	13	<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
113	<a href="#">c5zw3B</a>	Alignment	not modelled	99.2	16	<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
114	<a href="#">c4o29A</a>	Alignment	not modelled	99.2	24	<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 from pyrobaculum aerophilum2 in complex with s-adenosyl-l-homocysteine
115	<a href="#">c3evzA</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of methyltransferase from pyrococcus furiosus
116	<a href="#">c2yxeB</a>	Alignment	not modelled	99.2	25	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> crystal structure of l-isoaspartyl protein carboxyl methyltransferase
117	<a href="#">c3lecA</a>	Alignment	not modelled	99.2	18	<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
118	<a href="#">c3dxyA</a>	Alignment	not modelled	99.2	13	<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
119	<a href="#">c3ntvB</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> mw1564 protein; <b>PDBTitle:</b> crystal structure of a putative coffeoyl-coa o-methyltransferase from2 staphylococcus aureus
120	<a href="#">c5evjA</a>	Alignment	not modelled	99.2	22	<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