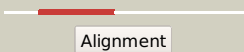

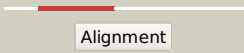

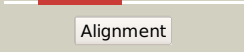

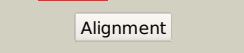



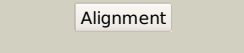

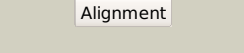


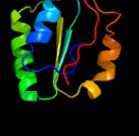
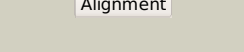

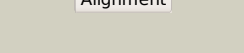

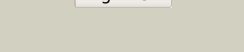



# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD2735c_(-)_3047570_3048562 |
| Date          | Wed Aug 7 12:50:39 BST 2019   |
| Unique Job ID | 1d3cb52265ee9093              |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c4bluB_</a> |  Alignment   |    | 98.7       | 27     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase j;<br><b>PDBTitle:</b> crystal structure of escherichia coli 23s rrna (a2030-n6)-2 methyltransferase rimj  |
| 2  | <a href="#">d2oo3a1</a> |  Alignment   |    | 98.6       | 23     | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> LPG1296-like   |
| 3  | <a href="#">d2fhpa1</a> |  Alignment   |    | 97.0       | 15     | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> YhhF-like  |
| 4  | <a href="#">d2dula1</a> |  Alignment   |   | 96.8       | 18     | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> TRM1-like  |
| 5  | <a href="#">c3axtA_</a> |  Alignment |  | 96.4       | 13     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable n(2),n(2)-dimethylguanosine trna methyltransferase<br><b>PDBTitle:</b> complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine                       |
| 6  | <a href="#">c5xj2C_</a> |  Alignment |  | 96.3       | 16     | <b>PDB header:</b> transferase/rna<br><b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized rna methyltransferase sp_1029;<br><b>PDBTitle:</b> structure of sprlmcid with u747 rna   |
| 7  | <a href="#">c1m6yA_</a> |  Alignment |  | 96.3       | 19     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-methyltransferase mraw;<br><b>PDBTitle:</b> crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah   |
| 8  | <a href="#">c3ll7A_</a> |  Alignment |  | 96.1       | 16     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative methyltransferase pg_1098 from2 porphyromonas gingivalis w83   |
| 9  | <a href="#">c1wg8B_</a> |  Alignment |  | 95.5       | 21     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> predicted s-adenosylmethionine-dependent<br><b>PDBTitle:</b> crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.                    |
| 10 | <a href="#">c2r6zA_</a> |  Alignment |  | 95.3       | 20     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> upf0341 protein in rsp 3' region;<br><b>PDBTitle:</b> crystal structure of the sam-dependent methyltransferase ngo1261 from2 neisseria gonorrhoeae, northeast structural genomics consortium3 target ngr48 |
| 11 | <a href="#">d2as0a2</a> |  Alignment |  | 95.3       | 13     | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> hypothetical RNA methyltransferase   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | <a href="#">c2esrB_</a> | Alignment |              | 95.3 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase;<br><b>PDBTitle:</b> conserved hypothetical protein- streptococcus pyogenes  |
| 13 | <a href="#">c1uwvA_</a> | Alignment |              | 95.2 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 23s rna (uracil-5-)-methyltransferase ruma;<br><b>PDBTitle:</b> crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase              |
| 14 | <a href="#">d1uwva2</a> | Alignment |              | 95.1 | 11 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> (Uracil-5-)-methyltransferase  |
| 15 | <a href="#">c4gf5S_</a> | Alignment |              | 94.8 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> S: <b>PDB Molecule:</b> cals11;<br><b>PDBTitle:</b> crystal structure of calicheamicin methyltransferase, cals11   |
| 16 | <a href="#">c5zy5B_</a> | Alignment |              | 94.6 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable catechol o-methyltransferase 1;<br><b>PDBTitle:</b> spcomt apo structure  |
| 17 | <a href="#">d2cl5a1</a> | Alignment |              | 94.5 | 17 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> COMT-like  |
| 18 | <a href="#">d2avda1</a> | Alignment |              | 94.2 | 19 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> COMT-like  |
| 19 | <a href="#">d2fpoa1</a> | Alignment |              | 94.2 | 22 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> YhhF-like  |
| 20 | <a href="#">c3v8vB_</a> | Alignment |              | 94.1 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase I;<br><b>PDBTitle:</b> crystal structure of bifunctional methyltransferase ycby (rlmlk) from2 escherichia coli, sam binding                                |
| 21 | <a href="#">d1ws6a1</a> | Alignment | not modelled | 93.9 | 19 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> YhhF-like  |
| 22 | <a href="#">c3bt7A_</a> | Alignment | not modelled | 93.9 | 16 | <b>PDB header:</b> transferase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna (uracil-5-)-methyltransferase;<br><b>PDBTitle:</b> structure of e. coli 5-methyluridine methyltransferase trna in complex2 with 19 nucleotide t-arm analogue                                    |
| 23 | <a href="#">c3k0bA_</a> | Alignment | not modelled | 93.8 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> predicted n6-adenine-specific dna methylase;<br><b>PDBTitle:</b> crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365 |
| 24 | <a href="#">c3lduA_</a> | Alignment | not modelled | 93.8 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methylase;<br><b>PDBTitle:</b> the crystal structure of a possible methylase from2 clostridium difficile 630.   |
| 25 | <a href="#">c3p9nA_</a> | Alignment | not modelled | 93.7 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> possible methyltransferase (methylase);<br><b>PDBTitle:</b> rv2966c of m. tuberculosis is a rsm-d-like methyltransferase   |
| 26 | <a href="#">c1wxwA_</a> | Alignment | not modelled | 93.2 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1280;<br><b>PDBTitle:</b> crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophilus hb8  |
| 27 | <a href="#">c2as0A_</a> | Alignment | not modelled | 92.8 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1915;<br><b>PDBTitle:</b> crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase   |
| 28 | <a href="#">c3vseA_</a> | Alignment | not modelled | 92.7 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of methyltransferase   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | <a href="#">d1wxax2</a> | Alignment | not modelled | 92.6 | 15 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> hypothetical RNA methyltransferase  |
| 30 | <a href="#">c5hjmA</a>  | Alignment | not modelled | 92.6 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(37)-n1)-methyltransferase trm5a;<br><b>PDBTitle:</b> crystal structure of pyrococcus abyssii trm5a complexed with mta   |
| 31 | <a href="#">c2b78A</a>  | Alignment | not modelled | 92.5 | 11 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein smu.776;<br><b>PDBTitle:</b> a putative sam-dependent methyltransferase from streptococcus mutans  |
| 32 | <a href="#">c3pt6B</a>  | Alignment | not modelled | 92.5 | 23 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 1;<br><b>PDBTitle:</b> crystal structure of mouse dnmt1(650-1602) in complex with dna  |
| 33 | <a href="#">c3tr6A</a>  | Alignment | not modelled | 92.5 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase;<br><b>PDBTitle:</b> structure of a o-methyltransferase from coxiella burnetii  |
| 34 | <a href="#">d2pkwa1</a> | Alignment | not modelled | 92.5 | 26 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> YhiQ-like   |
| 35 | <a href="#">c3ldgA</a>  | Alignment | not modelled | 91.9 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.472;<br><b>PDBTitle:</b> crystal structure of smu.472, a putative methyltransferase complexed2 with sah  |
| 36 | <a href="#">c4ce0A</a>  | Alignment | not modelled | 91.3 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase;<br><b>PDBTitle:</b> crystal structure of sah-bound spinosyn rhamnosyl 4'-o-2 methyltransferase spnh from saccharopolyspora spinosa                                   |
| 37 | <a href="#">c3pt9A</a>  | Alignment | not modelled | 91.2 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 1;<br><b>PDBTitle:</b> crystal structure of mouse dnmt1(731-1602) in the free state  |
| 38 | <a href="#">c3me5A</a>  | Alignment | not modelled | 91.1 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytosine-specific methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 2457t                                       |
| 39 | <a href="#">d2igta1</a> | Alignment | not modelled | 90.9 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> hypothetical RNA methyltransferase  |
| 40 | <a href="#">c3c0kB</a>  | Alignment | not modelled | 90.9 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> upf0064 protein yccw;<br><b>PDBTitle:</b> crystal structure of a ribosomal rna methyltransferase  |
| 41 | <a href="#">c3cbgA</a>  | Alignment | not modelled | 90.6 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase;<br><b>PDBTitle:</b> functional and structural characterization of a cationdependent o-2 methyltransferase from the cyanobacterium synechocystis sp. strain3 pcc 6803 |
| 42 | <a href="#">c3swrA</a>  | Alignment | not modelled | 90.6 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 1;<br><b>PDBTitle:</b> structure of human dnmt1 (601-1600) in complex with sinefungin  |
| 43 | <a href="#">c3tm4A</a>  | Alignment | not modelled | 90.4 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine n2-)-methyltransferase trm14;<br><b>PDBTitle:</b> crystal structure of trm14 from pyrococcus furiosus in complex with s-2 adenosylmethionine                                |
| 44 | <a href="#">c3tkaA</a>  | Alignment | not modelled | 90.4 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase h;<br><b>PDBTitle:</b> crystal structure and solution saxs of methyltransferase rsmh from2 e.coli   |
| 45 | <a href="#">c3a26A</a>  | Alignment | not modelled | 89.8 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0793;<br><b>PDBTitle:</b> crystal structure of p. horikoshii tyw2 in complex with2 mesado   |
| 46 | <a href="#">c4g56C</a>  | Alignment | not modelled | 89.7 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> hsl7 protein;<br><b>PDBTitle:</b> crystal structure of full length prmt5/mep50 complexes from xenopus2 laevis   |
| 47 | <a href="#">c2wk1A</a>  | Alignment | not modelled | 89.7 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> novp;<br><b>PDBTitle:</b> structure of the o-methyltransferase novp   |
| 48 | <a href="#">c5lhmA</a>  | Alignment | not modelled | 89.6 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase;<br><b>PDBTitle:</b> crystal structure of safc from myxococcus xanthus apo-form  |
| 49 | <a href="#">d2oyra1</a> | Alignment | not modelled | 89.4 | 28 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> YhiQ-like   |
| 50 | <a href="#">c3r3hA</a>  | Alignment | not modelled | 89.1 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase, sam-dependent;<br><b>PDBTitle:</b> crystal structure of o-methyltransferase from legionella pneumophila  |
| 51 | <a href="#">c2yx1A</a>  | Alignment | not modelled | 89.1 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mj0883;<br><b>PDBTitle:</b> crystal structure of m.jannaschii trna m1g37 methyltransferase   |
| 52 | <a href="#">c4ponB</a>  | Alignment | not modelled | 89.1 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative rna methylase;<br><b>PDBTitle:</b> the crystal structure of a putative sam-dependent methyltransferase,2 ytbq, from bacillus subtilis  |
| 53 | <a href="#">c3egiA</a>  | Alignment | not modelled | 89.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trimethylguanosine synthase homolog;<br><b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine synthase tgs12 bound to m7gpppa (inactive form)                             |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 54 | <a href="#">c3a27A</a>  | Alignment | not modelled | 88.8 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj1557;<br><b>PDBTitle:</b> crystal structure of m. jannaschii tyw2 in complex with2 adomet  |
| 55 | <a href="#">d2b78a2</a> | Alignment | not modelled | 88.6 | 11 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> hypothetical RNA methyltransferase   |
| 56 | <a href="#">c2zifB</a>  | Alignment | not modelled | 87.9 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative modification methylase;<br><b>PDBTitle:</b> crystal structure of ttha0409, putative dna modification methylase2 from thermus thermophilus hb8- complexed with s-adenosyl-l-methionine |
| 57 | <a href="#">c3a4tA</a>  | Alignment | not modelled | 87.8 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase mj0026;<br><b>PDBTitle:</b> crystal structure of atrm4 from m.jannaschii with sinefungin  |
| 58 | <a href="#">c2hncC</a>  | Alignment | not modelled | 87.6 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent o-methyltransferase;<br><b>PDBTitle:</b> crystal structure of sam-dependent o-methyltransferase from pathogenic2 bacterium leptospira interrogans                                |
| 59 | <a href="#">c1nw6A</a>  | Alignment | not modelled | 87.5 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> modification methylase rsri;<br><b>PDBTitle:</b> structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin  |
| 60 | <a href="#">d1susa1</a> | Alignment | not modelled | 87.1 | 17 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> COMT-like  |
| 61 | <a href="#">c3av6A</a>  | Alignment | not modelled | 87.1 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 1;<br><b>PDBTitle:</b> crystal structure of mouse dna methyltransferase 1 with adomet   |
| 62 | <a href="#">d2frna1</a> | Alignment | not modelled | 86.9 | 18 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Met-10+ protein-like   |
| 63 | <a href="#">c5zvdB</a>  | Alignment | not modelled | 86.7 | 12 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> 389aa long hypothetical nucleolar protein;<br><b>PDBTitle:</b> the crystal structure of nsun6 from pyrococcus horikoshii   |
| 64 | <a href="#">c3lbyA</a>  | Alignment | not modelled | 86.6 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1697c;<br><b>PDBTitle:</b> crystal structure of smu.1697c, a putative methyltransferase from2 streptococcus mutans in complex with sah                    |
| 65 | <a href="#">d1xdza</a>  | Alignment | not modelled | 86.1 | 10 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Glucose-inhibited division protein B (GidB)  |
| 66 | <a href="#">d2ifta1</a> | Alignment | not modelled | 85.3 | 14 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> YhhF-like  |
| 67 | <a href="#">c3c3yB</a>  | Alignment | not modelled | 85.3 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase;<br><b>PDBTitle:</b> crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum  |
| 68 | <a href="#">c5yacA</a>  | Alignment | not modelled | 84.6 | 18 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(37)-n1)-methyltransferase trm5b;<br><b>PDBTitle:</b> crystal structure of wt trm5b from pyrococcus abyssi  |
| 69 | <a href="#">d1g60a</a>  | Alignment | not modelled | 84.6 | 19 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Type II DNA methylase  |
| 70 | <a href="#">d1zq9a1</a> | Alignment | not modelled | 84.3 | 15 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> rRNA adenine dimethylase-like  |
| 71 | <a href="#">c3lx6B</a>  | Alignment | not modelled | 82.9 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytosine-specific methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 2457t  |
| 72 | <a href="#">d2esra1</a> | Alignment | not modelled | 82.9 | 22 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> YhhF-like  |
| 73 | <a href="#">c4xvzB</a>  | Alignment | not modelled | 82.2 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> mycinamicin iii 3''-o-methyltransferase;<br><b>PDBTitle:</b> mycf mycinamicin iii 3'-o-methyltransferase in complex with mg  |
| 74 | <a href="#">c3duwB</a>  | Alignment | not modelled | 82.2 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase, putative;<br><b>PDBTitle:</b> crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah   |
| 75 | <a href="#">c2gpyB</a>  | Alignment | not modelled | 81.3 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative o-methyltransferase from bacillus2 halodurans   |
| 76 | <a href="#">c4fsxB</a>  | Alignment | not modelled | 81.2 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 1;<br><b>PDBTitle:</b> crystal structure of se-substituted zea mays zmet2 in complex with sah   |
| 77 | <a href="#">c3mtiA</a>  | Alignment | not modelled | 81.1 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase;<br><b>PDBTitle:</b> the crystal structure of a rna methylase from streptococcus2 thermophilus to 1.95a   |
| 78 | <a href="#">c3gdhC</a>  | Alignment | not modelled | 81.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> trimethylguanosine synthase homolog;<br><b>PDBTitle:</b> methyltransferase domain of human trimethylguanosine synthase 1 (tgs1)2 bound to m7gtp and adenosyl-homocysteine (active form)        |

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| 79  | <a href="#">c3g8aF_</a> | Alignment | not modelled | 81.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> F: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase g;<br><b>PDBTitle:</b> t. thermophilus 16s rrna g527 methyltransferase in complex with adohcy2 in space group p61   |
| 80  | <a href="#">d1jsxa_</a> | Alignment | not modelled | 80.4 | 12 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Glucose-inhibited division protein B (GidB)   |
| 81  | <a href="#">c5hjfF_</a> | Alignment | not modelled | 79.9 | 21 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> adenine specific dna methyltransferase (dpna);<br><b>PDBTitle:</b> crystal structure of m1.hpyavi-sam complex   |
| 82  | <a href="#">c6em5q_</a> | Alignment | not modelled | 79.5 | 18 | <b>PDB header:</b> ribosome<br><b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l18-a;<br><b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes   |
| 83  | <a href="#">c3eeyl_</a> | Alignment | not modelled | 79.2 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> J: <b>PDB Molecule:</b> putative rrna methylase;<br><b>PDBTitle:</b> crystal structure of putative rrna-methylase from clostridium2 thermocellum  |
| 84  | <a href="#">c2g1pB_</a> | Alignment | not modelled | 77.6 | 21 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna adenine methylase;<br><b>PDBTitle:</b> structure of e. coli dna adenine methyltransferase (dam)   |
| 85  | <a href="#">c3g7uA_</a> | Alignment | not modelled | 77.2 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytosine-specific methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative dna modification methyltransferase2 encoded within prophage cp-933r (e.coli)   |
| 86  | <a href="#">c6q56C_</a> | Alignment | not modelled | 75.7 | 9  | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> trna (adenine(22)-n(1))-methyltransferase;<br><b>PDBTitle:</b> crystal structure of the b. subtilis m1a22 trna methyltransferase trmk   |
| 87  | <a href="#">d1wy7a1</a> | Alignment | not modelled | 75.5 | 24 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Ta1320-like   |
| 88  | <a href="#">c5zw3B_</a> | Alignment | not modelled | 73.5 | 25 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative o-methyltransferase yrrm;<br><b>PDBTitle:</b> crystal structure of trmr from b. subtilis   |
| 89  | <a href="#">c3tmaA_</a> | Alignment | not modelled | 73.4 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase;<br><b>PDBTitle:</b> crystal structure of trmn from thermus thermophilus  |
| 90  | <a href="#">c2vs1A_</a> | Alignment | not modelled | 73.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rna methyltransferase pyrab10780;<br><b>PDBTitle:</b> the crystal structure of pyrococcus abyssi trna (uracil-54, c5)-2 methyltransferase in complex with s-adenosyl-l-homocysteine   |
| 91  | <a href="#">c3njrB_</a> | Alignment | not modelled | 71.9 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-6y methylase;<br><b>PDBTitle:</b> crystal structure of c-terminal domain of precocorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus  |
| 92  | <a href="#">c5e72A_</a> | Alignment | not modelled | 71.3 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n2, n2-dimethylguanosine trna methyltransferase;<br><b>PDBTitle:</b> crystal structure of the archaeal trna m2g/m22g10 methyltransferase2 (atrm11) in complex with s-adenosyl-l-methionine (sam) from3 thermococcus kodakarensis                                    |
| 93  | <a href="#">d1o9ga_</a> | Alignment | not modelled | 71.1 | 7  | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> rRNA methyltransferase AviRa  |
| 94  | <a href="#">c6qe6A_</a> | Alignment | not modelled | 69.2 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna (adenine(22)-n(1))-methyltransferase;<br><b>PDBTitle:</b> structure of m. capricolum trmk in complex with the natural cofactor2 product s-adenosyl-homocysteine (sah)  |
| 95  | <a href="#">c3dmgA_</a> | Alignment | not modelled | 68.9 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable ribosomal rna small subunit methyltransferase;<br><b>PDBTitle:</b> t. thermophilus 16s rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy  |
| 96  | <a href="#">d1l3ia_</a> | Alignment | not modelled | 68.4 | 19 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Precocorrin-6Y methyltransferase (CbIT)   |
| 97  | <a href="#">c6b92A_</a> | Alignment | not modelled | 68.2 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> u6 small nuclear rna (adenine-(43)-n(6))-methyltransferase;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of human mettl16 in complex2 with sah  |
| 98  | <a href="#">d1dcta_</a> | Alignment | not modelled | 67.0 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> C5 cytosine-specific DNA methylase, DCM   |
| 99  | <a href="#">d1yzha1</a> | Alignment | not modelled | 66.6 | 7  | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> TrmB-like   |
| 100 | <a href="#">c3ua4A_</a> | Alignment | not modelled | 66.5 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 5;<br><b>PDBTitle:</b> crystal structure of protein arginine methyltransferase prmt5   |
| 101 | <a href="#">d1booa_</a> | Alignment | not modelled | 65.2 | 18 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Type II DNA methylase   |
| 102 | <a href="#">c3ku1E_</a> | Alignment | not modelled | 65.1 | 9  | <b>PDB header:</b> transferase<br><b>Chain:</b> E: <b>PDB Molecule:</b> sam-dependent methyltransferase;<br><b>PDBTitle:</b> crystal structure of streptococcus pneumoniae sp1610, a putative trna2 (m1a22) methyltransferase, in complex with s-adenosyl-l-methionine<br><b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases |



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| 103 | <a href="#">d1eg2a_</a> | Alignment | not modelled | 64.9 | 18 | <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Type II DNA methylase  |
| 104 | <a href="#">c5n5dA_</a> | Alignment | not modelled | 63.6 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase;<br><b>PDBTitle:</b> crystal structure of the o-methyltransferase tomg from streptomyces2 achromogenes involved in tomaymycin synthesis in complex with sam               |
| 105 | <a href="#">d1nv8a_</a> | Alignment | not modelled | 63.5 | 13 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> N5-glutamine methyltransferase, HemK  |
| 106 | <a href="#">d1o54a_</a> | Alignment | not modelled | 63.3 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like  |
| 107 | <a href="#">c2ozvA_</a> | Alignment | not modelled | 62.8 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0636;<br><b>PDBTitle:</b> crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.                                     |
| 108 | <a href="#">c2yx1A_</a> | Alignment | not modelled | 61.1 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 450aa long hypothetical fmu protein;<br><b>PDBTitle:</b> crystal structure of ph0851  |
| 109 | <a href="#">c3fydA_</a> | Alignment | not modelled | 60.4 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable dimethyladenosine transferase;<br><b>PDBTitle:</b> crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi  |
| 110 | <a href="#">c3grrA_</a> | Alignment | not modelled | 60.4 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dimethyladenosine transferase;<br><b>PDBTitle:</b> crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.                                 |
| 111 | <a href="#">c1sqgA_</a> | Alignment | not modelled | 60.2 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sun protein;<br><b>PDBTitle:</b> the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution   |
| 112 | <a href="#">c3e05B_</a> | Alignment | not modelled | 59.7 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase (decarboxylating);<br><b>PDBTitle:</b> crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15                 |
| 113 | <a href="#">c3hm2G_</a> | Alignment | not modelled | 58.7 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> G: <b>PDB Molecule:</b> precorrin-6y c5,15-methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae            |
| 114 | <a href="#">d2b9ea1</a> | Alignment | not modelled | 57.1 | 11 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> NOL1/NOP2/sun   |
| 115 | <a href="#">c3gn1B_</a> | Alignment | not modelled | 56.8 | 8  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmof2365_1472;<br><b>PDBTitle:</b> structure of uncharacterized protein (lmof2365_1472) from listeria2 monocytogenes serotype 4b |
| 116 | <a href="#">c6h2uA_</a> | Alignment | not modelled | 56.7 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein 5;<br><b>PDBTitle:</b> crystal structure of human mettl5-trmt112 complex, the 18s rrna2 m6a1832 methyltransferase at 1.6a resolution                         |
| 117 | <a href="#">c4dmgA_</a> | Alignment | not modelled | 56.1 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1493;<br><b>PDBTitle:</b> thermus thermophilus m5c1942 methyltransferase rlmo  |
| 118 | <a href="#">c3tqsB_</a> | Alignment | not modelled | 55.6 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase a;<br><b>PDBTitle:</b> structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii  |
| 119 | <a href="#">c3lpmA_</a> | Alignment | not modelled | 55.0 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes   |
| 120 | <a href="#">c4onqA_</a> | Alignment | not modelled | 54.7 | 16 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna methyltransferase;<br><b>PDBTitle:</b> crystal structure of ntrdm e283s/r309s/f310s/y590s/d591s mutant  |