# Phyre2

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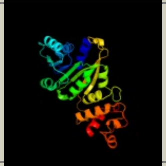
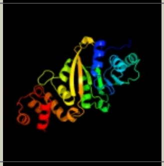
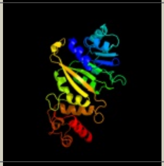
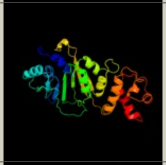
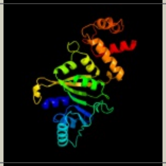
| Email | l.a.kelley@imperial.ac.uk |
| Description | P06992 |
| Date | Thu Jan 5 10:59:48 GMT 2012 |
| Unique Job ID | d7d37e1848855387 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3uzuA_ | Alignment |  | 100.0 | 52 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase a;<br>**PDBTitle:** the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei |
| 2 | d1qyra_ | Alignment |  | 100.0 | 100 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA adenine dimethylase-like |
| 3 | c3tqsB_ | Alignment |  | 100.0 | 48 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**ribosomal rna small subunit methyltransferase a;<br>**PDBTitle:** structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii |
| 4 | c3fuxB_ | Alignment |  | 100.0 | 36 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dimethyladenosine transferase;<br>**PDBTitle:** t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121 |
| 5 | d1zq9a1 | Alignment |  | 100.0 | 28 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA adenine dimethylase-like |
| 6 | c3grrA_ | Alignment |  | 100.0 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dimethyladenosine transferase;<br>**PDBTitle:** crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1. |
| 7 | c3fydA_ | Alignment |  | 100.0 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable dimethyladenosine transferase;<br>**PDBTitle:** crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi |
| 8 | c1i4wA_ | Alignment |  | 100.0 | 14 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**mitochondrial replication protein mtf1;<br>**PDBTitle:** the crystal structure of the transcription factor sc-mttfb2 offers intriguing insights into mitochondrial transcription |
| 9 | d1i4wa_ | Alignment |  | 100.0 | 14 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA adenine dimethylase-like |
| 10 | c2h1rA_ | Alignment |  | 100.0 | 24 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dimethyladenosine transferase, putative;<br>**PDBTitle:** crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum |
| 11 | c3fteA_ | Alignment |  | 100.0 | 35 | **PDB header:**transferase/rna<br>**Chain:** A: **PDB Molecule:**dimethyladenosine transferase;<br>**PDBTitle:** crystal structure of a. aeolicus ksga in complex with rna |

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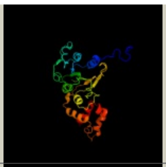
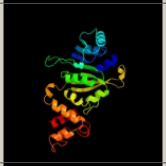
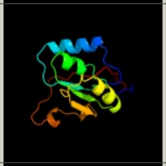
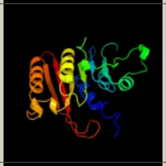
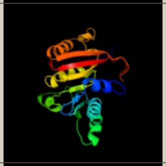
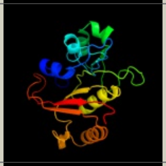
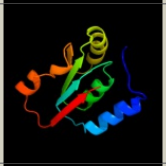
| 12 | d1yuba_ | Alignment |  | 100.0 | 23 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA adenine dimethylase-like |
| 13 | d1qama_ | Alignment |  | 100.0 | 27 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA adenine dimethylase-like |
| 14 | d1wy7a1 | Alignment |  | 99.6 | 15 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Ta1320-like |
| 15 | d2okca1 | Alignment |  | 99.6 | 17 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**N-6 DNA Methylase-like |
| 16 | d2ar0a1 | Alignment |  | 99.6 | 16 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**N-6 DNA Methylase-like |
| 17 | d1uwva2 | Alignment |  | 99.6 | 11 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**(Uracil-5-)-methyltransferase |
| 18 | c3lkdB_ | Alignment |  | 99.5 | 20 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**type i restriction-modification system<br>**PDBTitle:** crystal structure of the type i restriction-modification2 system methyltransferase subunit from streptococcus3 thermophilus, northeast structural genomics consortium4 target sur80 |
| 19 | d1vbfa_ | Alignment |  | 99.5 | 18 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Protein-L-isoaspartyl O-methyltransferase |
| 20 | c3khkA_ | Alignment |  | 99.5 | 14 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**type i restriction-modification system<br>**PDBTitle:** crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazei. |
| 21 | d1m6ya2 | Alignment | not modelled | 99.5 | 9 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**MraW-like putative methyltransferases |
| 22 | c1uwvA_ | Alignment | not modelled | 99.5 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**23s rrna (uracil-5-)-methyltransferase ruma;<br>**PDBTitle:** crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase |
| 23 | c2ozvA_ | Alignment | not modelled | 99.4 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypothetical protein atu0636;<br>**PDBTitle:** crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens. |
| 24 | c3gdhC_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**trimethylguanosine synthase homolog;<br>**PDBTitle:** methyltransferase domain of human trimethylguanosine2 synthase 1 (tgs1) bound to m7gtp and adenosyl-homocysteine3 (active form) |
| 25 | d2f8la1 | Alignment | not modelled | 99.4 | 16 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**N-6 DNA Methylase-like |
| 26 | c2yxdA_ | Alignment | not modelled | 99.4 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable cobalt-precorrin-6y c(15)-methyltransferase<br>**PDBTitle:** crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbit) |
| 27 | c3egiA_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**trimethylguanosine synthase homolog;<br>**PDBTitle:** methyltransferase domain of human trimethylguanosine2 synthase tgs1 bound to m7gpppa (inactive form) |

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| 28 | d1nv8a_ | Alignment | not modelled | 99.4 | 13 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**N5-glutamine methyltransferase, HemK |
| 29 | d1ne2a_ | Alignment | not modelled | 99.4 | 15 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Ta1320-like |
| 30 | c1aqjB_ | Alignment | not modelled | 99.4 | 16 | **PDB header:**methyltransferase<br>**Chain:** B: **PDB Molecule:**adenine-n6-dna-methyltransferase taqi;<br>**PDBTitle:** structure of adenine-n6-dna-methyltransferase taqi |
| 31 | d2fpoa1 | Alignment | not modelled | 99.4 | 21 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**YhhF-like |
| 32 | d1dusa_ | Alignment | not modelled | 99.4 | 10 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Hypothetical protein MJ0882 |
| 33 | c3lbfC_ | Alignment | not modelled | 99.3 | 11 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase;<br>**PDBTitle:** crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli |
| 34 | c1g38A_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**modification methylase taqi;<br>**PDBTitle:** adenine-specific methyltransferase m. taq i/dna complex |
| 35 | c3ku1E_ | Alignment | not modelled | 99.3 | 10 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**sam-dependent methyltransferase;<br>**PDBTitle:** crystal structure of streptococcus pneumoniae sp1610, a2 putative trna (m1a22) methyltransferase, in complex with s-3 adenosyl-l-methionine |
| 36 | d1wg8a2 | Alignment | not modelled | 99.3 | 16 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**MraW-like putative methyltransferases |
| 37 | c3lecA_ | Alignment | not modelled | 99.3 | 10 | **PDB header:**structure genomics, unknown function<br>**Chain:** A: **PDB Molecule:**nadb-rossmann superfamily protein;<br>**PDBTitle:** the crystal structure of a protein in the nadb-rossmann2 superfamily from streptococcus agalactiae to 1.8a |
| 38 | c3gnlB_ | Alignment | not modelled | 99.3 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein, duf633, lmof2365_1472;<br>**PDBTitle:** structure of uncharacterized protein (lmof2365_1472) from2 listeria monocytogenes serotype 4b |
| 39 | d1l3ia_ | Alignment | not modelled | 99.3 | 13 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Precorrin-6Y methyltransferase (CbiT) |
| 40 | c1m6yA_ | Alignment | not modelled | 99.3 | 8 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw;<br>**PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah |
| 41 | c3e05B_ | Alignment | not modelled | 99.3 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**precorrin-6y c5,15-methyltransferase (decarboxylating);<br>**PDBTitle:** crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15 |
| 42 | c2yxeB_ | Alignment | not modelled | 99.3 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase;<br>**PDBTitle:** crystal structure of l-isoaspartyl protein carboxyl methyltranferase |
| 43 | c3bt7A_ | Alignment | not modelled | 99.3 | 16 | **PDB header:**transferase/rna<br>**Chain:** A: **PDB Molecule:**trna (uracil-5-)-methyltransferase;<br>**PDBTitle:** structure of e. coli 5-methyluridine methyltransferase trma2 in complex with 19 nucleotide t-arm analogue |
| 44 | d2fhpa1 | Alignment | not modelled | 99.3 | 17 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**YhhF-like |
| 45 | c2pbfA_ | Alignment | not modelled | 99.3 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase beta-aspartate<br>**PDBTitle:** 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 |
| 46 | c3njrB_ | Alignment | not modelled | 99.3 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**precorrin-6y methylase;<br>**PDBTitle:** crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus |
| 47 | c3evzA_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**methyltransferase;<br>**PDBTitle:** crystal strucure of methyltransferase from pyrococcus furiosus |
| 48 | d1o54a_ | Alignment | not modelled | 99.2 | 16 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**tRNA(1-methyladenosine) methyltransferase-like |
| 49 | c1dl5A_ | Alignment | not modelled | 99.2 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase;<br>**PDBTitle:** protein-l-isoaspartate o-methyltransferase |
| 50 | c2yvlB_ | Alignment | not modelled | 99.2 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus |
| 51 | c3mtiA_ | Alignment | not modelled | 99.2 | 6 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rrna methylase;<br>**PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a |
|  |  |  |  |  |  | **PDB header:**transferase |

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| 52 | c3mb5A_ | Alignment | not modelled | 99.2 | 23 | **Chain:** A: **PDB Molecule:**sam-dependent methyltransferase;<br>**PDBTitle:** crystal structure of p. abyssi trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine |
| 53 | c3lpmA_ | Alignment | not modelled | 99.2 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative methyltransferase;<br>**PDBTitle:** crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes |
| 54 | d1jg1a_ | Alignment | not modelled | 99.2 | 14 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Protein-L-isoaspartyl O-methyltransferase |
| 55 | c3ujcA_ | Alignment | not modelled | 99.2 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase;<br>**PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine |
| 56 | c3g5tA_ | Alignment | not modelled | 99.2 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase;<br>**PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast |
| 57 | d1dl5a1 | Alignment | not modelled | 99.2 | 11 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Protein-L-isoaspartyl O-methyltransferase |
| 58 | c1wg8B_ | Alignment | not modelled | 99.2 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**predicted s-adenosylmethionine-dependent<br>**PDBTitle:** crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8. |
| 59 | d1i1na_ | Alignment | not modelled | 99.2 | 11 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Protein-L-isoaspartyl O-methyltransferase |
| 60 | c1wxwA_ | Alignment | not modelled | 99.2 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypothetical protein ttha1280;<br>**PDBTitle:** crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophillus hb8 |
| 61 | d2esra1 | Alignment | not modelled | 99.2 | 17 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**YhhF-like |
| 62 | c2pjdA_ | Alignment | not modelled | 99.2 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase c;<br>**PDBTitle:** crystal structure of 16s rrna methyltransferase rsmc |
| 63 | c3p9nA_ | Alignment | not modelled | 99.2 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**possible methyltransferase (methylase);<br>**PDBTitle:** rv2966c of m. tuberculosis is a rsmd-like methyltransferase |
| 64 | c2fk8A_ | Alignment | not modelled | 99.2 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**methoxy mycolic acid synthase 4;<br>**PDBTitle:** crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine |
| 65 | d1r18a_ | Alignment | not modelled | 99.2 | 14 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Protein-L-isoaspartyl O-methyltransferase |
| 66 | c3eeyJ_ | Alignment | not modelled | 99.1 | 11 | **PDB header:**transferase<br>**Chain:** J: **PDB Molecule:**putative rrna methylase;<br>**PDBTitle:** crystal structure of putative rrna-methylase from clostridium2 thermocellum |
| 67 | d1yb2a1 | Alignment | not modelled | 99.1 | 18 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**tRNA(1-methyladenosine) methyltransferase-like |
| 68 | c1yb2A_ | Alignment | not modelled | 99.1 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein ta0852;<br>**PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum. |
| 69 | c2esrB_ | Alignment | not modelled | 99.1 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**methyltransferase;<br>**PDBTitle:** conserved hypothetical protein- streptococcus pyogenes |
| 70 | c3bgdB_ | Alignment | not modelled | 99.1 | 11 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**thiopurine s-methyltransferase;<br>**PDBTitle:** thiopurine s-methyltransferase |
| 71 | d1vl5a_ | Alignment | not modelled | 99.1 | 5 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**UbiE/COQ5-like |
| 72 | d1i9ga_ | Alignment | not modelled | 99.1 | 18 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**tRNA(1-methyladenosine) methyltransferase-like |
| 73 | c1vl5B_ | Alignment | not modelled | 99.1 | 5 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**unknown conserved protein bh2331;<br>**PDBTitle:** crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution |
| 74 | d2h00a1 | Alignment | not modelled | 99.1 | 13 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Methyltransferase 10 domain |
| 75 | d2b3ta1 | Alignment | not modelled | 99.1 | 18 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**N5-glutamine methyltransferase, HemK |
| 76 | c2pwyB_ | Alignment | not modelled | 99.1 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase;<br>**PDBTitle:** crystal structure of a m1a58 trna methyltransferase |
| 77 | c3a27A | Alignment | not modelled | 99.1 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein mj1557; |

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| 77 | c3a27A_ | Alignment | not modelled | 99.1 | [illegible] | **PDBTitle:** crystal structure of m. jannaschii tyw2 in complex with2 adomet |
| 78 | c3dmgA_ | Alignment | not modelled | 99.1 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable ribosomal rna small subunit methyltransferase;<br>**PDBTitle:** t. thermophilus 16s rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy |
| 79 | c3lduA_ | Alignment | not modelled | 99.1 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative methylase;<br>**PDBTitle:** the crystal structure of a possible methylase from2 clostridium difficile 630. |
| 80 | c3c0kB_ | Alignment | not modelled | 99.1 | 6 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**upf0064 protein yccw;<br>**PDBTitle:** crystal structure of a ribosomal rna methyltranferase |
| 81 | c3ofkA_ | Alignment | not modelled | 99.1 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nodulation protein s;<br>**PDBTitle:** crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah) |
| 82 | c3a26A_ | Alignment | not modelled | 99.1 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ph0793;<br>**PDBTitle:** crystal structure of p. horikoshii tyw2 in complex with2 mesado |
| 83 | c2yx1A_ | Alignment | not modelled | 99.1 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypothetical protein mj0883;<br>**PDBTitle:** crystal structure of m.jannaschii trna m1g37 methyltransferase |
| 84 | d2as0a2 | Alignment | not modelled | 99.1 | 13 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**hypothetical RNA methyltransferase |
| 85 | d1xxla_ | Alignment | not modelled | 99.1 | 5 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**UbiE/COQ5-like |
| 86 | d2nxca1 | Alignment | not modelled | 99.1 | 9 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Ribosomal protein L11 methyltransferase PrmA |
| 87 | d2ifta1 | Alignment | not modelled | 99.1 | 15 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**YhhF-like |
| 88 | c2ipxA_ | Alignment | not modelled | 99.1 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rrna 2'-o-methyltransferase fibrillarin;<br>**PDBTitle:** human fibrillarin |
| 89 | d1wxxa2 | Alignment | not modelled | 99.1 | 10 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**hypothetical RNA methyltransferase |
| 90 | d2fk8a1 | Alignment | not modelled | 99.1 | 16 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Mycolic acid cyclopropane synthase |
| 91 | c2vs1A_ | Alignment | not modelled | 99.1 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**uncharacterized rna methyltransferase pyrab10780;<br>**PDBTitle:** the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine |
| 92 | c3k0bA_ | Alignment | not modelled | 99.0 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**predicted n6-adenine-specific dna methylase;<br>**PDBTitle:** crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365 |
| 93 | d1l1ea_ | Alignment | not modelled | 99.0 | 18 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Mycolic acid cyclopropane synthase |
| 94 | c3grzA_ | Alignment | not modelled | 99.0 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase;<br>**PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus |
| 95 | d2b25a1 | Alignment | not modelled | 99.0 | 14 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**tRNA(1-methyladenosine) methyltransferase-like |
| 96 | d2frna1 | Alignment | not modelled | 99.0 | 16 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Met-10+ protein-like |
| 97 | c2b78A_ | Alignment | not modelled | 99.0 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein smu.776;<br>**PDBTitle:** a putative sam-dependent methyltransferase from2 streptococcus mutans |
| 98 | d1g8sa_ | Alignment | not modelled | 99.0 | 9 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Fibrillarin homologue |
| 99 | d1pjza_ | Alignment | not modelled | 99.0 | 14 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Thiopurine S-methyltransferase |
| 100 | c3egeA_ | Alignment | not modelled | 99.0 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative methyltransferase from antibiotic biosynthesis<br>**PDBTitle:** crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution |
| 101 | c2yr0A_ | Alignment | not modelled | 99.0 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypothetical protein ttha0223;<br>**PDBTitle:** crystal structure of hypothetical methyltransferase |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | ttha0223 from2 thermus thermophilus hb8 |
| 102 | c3bgvC_ | Alignment | not modelled | 99.0 | 7 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**mrna cap guanine-n7 methyltransferase;<br>**PDBTitle:** crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah |
| 103 | c3e7pA_ | Alignment | not modelled | 99.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative methyltransferase;<br>**PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482 |
| 104 | c3ldgA_ | Alignment | not modelled | 99.0 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.472;<br>**PDBTitle:** crystal structure of smu.472, a putative methyltransferase complexed2 with sah |
| 105 | d1tpya_ | Alignment | not modelled | 99.0 | 19 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Mycolic acid cyclopropane synthase |
| 106 | c3b3jA_ | Alignment | not modelled | 99.0 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1;<br>**PDBTitle:** the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered) |
| 107 | d1xvaa_ | Alignment | not modelled | 99.0 | 9 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Glycine N-methyltransferase |
| 108 | d1kpia_ | Alignment | not modelled | 99.0 | 12 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Mycolic acid cyclopropane synthase |
| 109 | d1prya_ | Alignment | not modelled | 99.0 | 9 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Fibrillarin homologue |
| 110 | c3ccfB_ | Alignment | not modelled | 99.0 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**cyclopropane-fatty-acyl-phospholipid synthase;<br>**PDBTitle:** crystal structure of putative methyltransferase (yp_321342.1) from2 anabaena variabilis atcc 29413 at 1.90 a resolution |
| 111 | d1ws6a1 | Alignment | not modelled | 99.0 | 8 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**YhhF-like |
| 112 | c2v7eB_ | Alignment | not modelled | 99.0 | 10 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**histone-arginine methyltransferase carm1;<br>**PDBTitle:** crystal structure of coactivator-associated arginine2 methyltransferase 1 (carm1), unliganded |
| 113 | d2bzga1 | Alignment | not modelled | 99.0 | 11 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Thiopurine S-methyltransferase |
| 114 | c3q87B_ | Alignment | not modelled | 99.0 | 11 | **PDB header:**transferase activator/transferase<br>**Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase;<br>**PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112 |
| 115 | c3m33B_ | Alignment | not modelled | 99.0 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the crystal structure of a functionally unknown protein from2 deinococcus radiodurans r1 |
| 116 | c3m70A_ | Alignment | not modelled | 99.0 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog;<br>**PDBTitle:** crystal structure of tehb from haemophilus influenzae |
| 117 | c2as0A_ | Alignment | not modelled | 99.0 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypothetical protein ph1915;<br>**PDBTitle:** crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase |
| 118 | d2igta1 | Alignment | not modelled | 99.0 | 8 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**hypothetical RNA methyltransferase |
| 119 | d1kpga_ | Alignment | not modelled | 98.9 | 12 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Mycolic acid cyclopropane synthase |
| 120 | d1wzna1 | Alignment | not modelled | 98.9 | 13 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**CAC2371-like |