







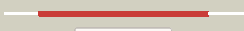
























Phyre2

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|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1988 (-) _2231688_2232227 |
| Date | Mon Aug 5 13:25:09 BST 2019 |
| Unique Job ID | 8fb7fb64d4735789 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3fuxB_ |  Alignment |  | 100.0 | 30 | PDB header: transferase Chain: B; PDB Molecule: dimethyladenosine transferase; PDBTitle: t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121 |
| 2 | c4gc5A_ |  Alignment |  | 100.0 | 22 | PDB header: transferase Chain: A; PDB Molecule: dimethyladenosine transferase 1, mitochondrial; PDBTitle: crystal structure of murine tfb1m |
| 3 | c6ifsB_ |  Alignment |  | 100.0 | 28 | PDB header: transferase Chain: B; PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168 |
| 4 | c3uzuA_ |  Alignment |  | 100.0 | 30 | PDB header: transferase Chain: A; PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei |
| 5 | c3tqsB_ |  Alignment |  | 100.0 | 29 | PDB header: transferase Chain: B; PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii |
| 6 | d1qyra_ |  Alignment |  | 100.0 | 28 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like |
| 7 | d1zq9a1 |  Alignment |  | 100.0 | 30 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like |
| 8 | d1yuba_ |  Alignment |  | 100.0 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like |
| 9 | c3grrA_ |  Alignment |  | 100.0 | 27 | PDB header: transferase Chain: A; PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1. |
| 10 | c3fydA_ |  Alignment |  | 100.0 | 27 | PDB header: transferase Chain: A; PDB Molecule: probable dimethyladenosine transferase; PDBTitle: crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi |
| 11 | c2h1rA_ |  Alignment |  | 100.0 | 23 | PDB header: transferase Chain: A; PDB Molecule: dimethyladenosine transferase, putative; PDBTitle: crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c4jxA | Alignment |  | 100.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: crystal structure of ribosomal rna small subunit methyltransferase a2 from rickettsia bellii determined by iodide sad phasing |
| 13 | c3fteA | Alignment |  | 100.0 | 22 | PDB header: transferase/rna Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of a. aeolicus ksga in complex with rna |
| 14 | d1qama | Alignment |  | 100.0 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like |
| 15 | c1i4wA | Alignment |  | 100.0 | 17 | PDB header: transcription Chain: A: PDB Molecule: mitochondrial replication protein mtf1; PDBTitle: the crystal structure of the transcription factor sc-mttfb2 offers intriguing insights into mitochondrial transcription |
| 16 | d1i4wa | Alignment |  | 100.0 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like |
| 17 | c6erpJ | Alignment |  | 100.0 | 23 | PDB header: transcription Chain: J: PDB Molecule: dimethyladenosine transferase 2, mitochondrial; PDBTitle: structure of the human mitochondrial transcription initiation complex2 at the lsp promoter |
| 18 | d1wy7a1 | Alignment |  | 99.8 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ta1320-like |
| 19 | c6h2uA | Alignment |  | 99.8 | 18 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase-like protein 5; PDBTitle: crystal structure of human mettl5-trmt112 complex, the 18s rna2 m6a1832 methyltransferase at 1.6a resolution |
| 20 | d1ne2a | Alignment |  | 99.7 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ta1320-like |
| 21 | d2okca1 | Alignment | not modelled | 99.7 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like |
| 22 | d1uwva2 | Alignment | not modelled | 99.7 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: (Uracil-5-)-methyltransferase |
| 23 | c5ybbA | Alignment | not modelled | 99.7 | 19 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: type i restriction-modification system methyltransferase PDBTitle: structural basis underlying complex assembly and conformational2 transition of the type i r-m system |
| 24 | c5xj2C | Alignment | not modelled | 99.7 | 15 | PDB header: transferase/rna Chain: C: PDB Molecule: uncharacterized rna methyltransferase sp_1029; PDBTitle: structure of sprlmcD with u747 rna |
| 25 | c1uwvA | Alignment | not modelled | 99.7 | 21 | PDB header: transferase Chain: A: PDB Molecule: 23s rna (uracil-5-)-methyltransferase ruma; PDBTitle: crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase |
| 26 | c3ufbA | Alignment | not modelled | 99.7 | 17 | PDB header: transferase Chain: A: PDB Molecule: type i restriction-modification system methyltransferase PDBTitle: crystal structure of a modification subunit of a putative type i2 restriction enzyme from vibrio vulnificus vj016 |
| 27 | d2ar0a1 | Alignment | not modelled | 99.7 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like |

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|----|-------------------------|-----------|--------------|------|----|---|
| 28 | d1vbfa_ | Alignment | not modelled | 99.7 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 29 | c3bt7A_ | Alignment | not modelled | 99.7 | 13 | PDB header: transferase/rna Chain: A: PDB Molecule: trna (uracil-5-)-methyltransferase; PDBTitle: structure of e. coli 5-methyluridine methyltransferase trna in complex2 with 19 nucleotide t-arm analogue |
| 30 | c4krhB_ | Alignment | not modelled | 99.7 | 18 | PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 2; PDBTitle: semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine |
| 31 | c4ineB_ | Alignment | not modelled | 99.7 | 17 | PDB header: transferase Chain: B: PDB Molecule: protein pmt-2; PDBTitle: crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine |
| 32 | c2yxdA_ | Alignment | not modelled | 99.6 | 13 | PDB header: transferase Chain: A: PDB Molecule: probable cobalt-precorrin-6y c(15)-methyltransferase PDBTitle: crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbt) |
| 33 | c6q56C_ | Alignment | not modelled | 99.6 | 16 | PDB header: rna binding protein Chain: C: PDB Molecule: trna (adenine(22)-n(1))-methyltransferase; PDBTitle: crystal structure of the b. subtilis m1a22 trna methyltransferase trmk |
| 34 | c2vs1A_ | Alignment | not modelled | 99.6 | 16 | PDB header: transferase Chain: A: PDB Molecule: uncharacterized rna methyltransferase pyrab10780; PDBTitle: the crystal structure of pyrococcus abyssi trna (uracil-54, c5)-2 methyltransferase in complex with s-adenosyl-l-homocysteine |
| 35 | c3lkdB_ | Alignment | not modelled | 99.6 | 21 | PDB header: transferase Chain: B: PDB Molecule: type i restriction-modification system methyltransferase PDBTitle: crystal structure of the type i restriction-modification system2 methyltransferase subunit from streptococcus thermophilus, northeast3 structural genomics consortium target sur80 |
| 36 | d1dusa_ | Alignment | not modelled | 99.6 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein MJ0882 |
| 37 | c5wp5A_ | Alignment | not modelled | 99.6 | 18 | PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah |
| 38 | c3lbfC_ | Alignment | not modelled | 99.6 | 21 | PDB header: transferase Chain: C: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli |
| 39 | c3khkA_ | Alignment | not modelled | 99.6 | 16 | PDB header: dna binding protein Chain: A: PDB Molecule: type i restriction-modification system methylation subunit; PDBTitle: crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazel. |
| 40 | c2fk8A_ | Alignment | not modelled | 99.6 | 14 | PDB header: transferase Chain: A: PDB Molecule: methoxy mycolic acid synthase 4; PDBTitle: crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine |
| 41 | c2ozvA_ | Alignment | not modelled | 99.6 | 22 | PDB header: transferase Chain: A: PDB Molecule: hypothetical protein atu0636; PDBTitle: crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens. |
| 42 | d2f8la1 | Alignment | not modelled | 99.6 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like |
| 43 | c6gkvB_ | Alignment | not modelled | 99.6 | 22 | PDB header: transferase Chain: B: PDB Molecule: coclaurine n-methyltransferase; PDBTitle: crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah |
| 44 | c1g38A_ | Alignment | not modelled | 99.6 | 24 | PDB header: transferase/dna Chain: A: PDB Molecule: modification methylase taqi; PDBTitle: adenine-specific methyltransferase m. taqi /dna complex |
| 45 | c2yxeB_ | Alignment | not modelled | 99.6 | 19 | PDB header: transferase Chain: B: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of l-isoaspartyl protein carboxyl methyltransferase |
| 46 | d1jg1a_ | Alignment | not modelled | 99.6 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 47 | c3gdhC_ | Alignment | not modelled | 99.6 | 20 | PDB header: transferase Chain: C: PDB Molecule: trimethylguanosine synthase homolog; PDBTitle: methyltransferase domain of human trimethylguanosine synthase 1 (tgs1)2 bound to m7gtp and adenosyl-homocysteine (active form) |
| 48 | c3ccfB_ | Alignment | not modelled | 99.6 | 21 | PDB header: transferase Chain: B: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: crystal structure of putative methyltransferase (yp_321342.1) from2 anabaena variabilis atcc 29413 at 1.90 a resolution |
| 49 | c5bxyB_ | Alignment | not modelled | 99.5 | 18 | PDB header: transferase Chain: B: PDB Molecule: rna methyltransferase; PDBTitle: crystal structure of rna methyltransferase from salinibacter ruber in2 complex with s-adenosyl-l-homocysteine |
| | | | | | | PDB header: transferase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 50 | c5u18A | Alignment | not modelled | 99.5 | 24 | Chain: A: PDB Molecule: n-3" methyltransferase; PDBTitle: crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin |
| 51 | c3egiA | Alignment | not modelled | 99.5 | 19 | PDB header: transferase Chain: A: PDB Molecule: trimethylguanosine synthase homolog; PDBTitle: methyltransferase domain of human trimethylguanosine synthase tgs12 bound to m7gpppa (inactive form) |
| 52 | d1i1na | Alignment | not modelled | 99.5 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 53 | c1dl5A | Alignment | not modelled | 99.5 | 17 | PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: protein-l-isoaspartate o-methyltransferase |
| 54 | c5kn4B | Alignment | not modelled | 99.5 | 13 | PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0 |
| 55 | c4l7vA | Alignment | not modelled | 99.5 | 20 | PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of protein l-isoaspartyl-o-methyltransferase of2 vibrio cholerae |
| 56 | d1r18a | Alignment | not modelled | 99.5 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 57 | c4o29A | Alignment | not modelled | 99.5 | 16 | PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: protein-l-isoaspartate o-methyltransferase from pyrobaculum aerophilum2 in complex with s-adenosyl-l-homocysteine |
| 58 | c2pjdA | Alignment | not modelled | 99.5 | 20 | PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase c; PDBTitle: crystal structure of 16s rrna methyltransferase rsmc |
| 59 | c5z9oA | Alignment | not modelled | 99.5 | 16 | PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus |
| 60 | c3vc2J | Alignment | not modelled | 99.5 | 17 | PDB header: transferase Chain: J: PDB Molecule: geranyl diphosphate 2-c-methyltransferase; PDBTitle: crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine |
| 61 | d2fk8a1 | Alignment | not modelled | 99.5 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 62 | c5fcdA | Alignment | not modelled | 99.5 | 11 | PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein |
| 63 | d1yb2a1 | Alignment | not modelled | 99.5 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like |
| 64 | c1yb2A | Alignment | not modelled | 99.5 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0852; PDBTitle: structure of a putative methyltransferase from thermoplasma2 acidophilum. |
| 65 | c3e05B | Alignment | not modelled | 99.5 | 19 | PDB header: transferase Chain: B: PDB Molecule: precorrin-6y c5,15-methyltransferase (decarboxylating); PDBTitle: crystal structure of precorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15 |
| 66 | c4krkB | Alignment | not modelled | 99.5 | 22 | PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 1; PDBTitle: semet haemonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine |
| 67 | c5e72A | Alignment | not modelled | 99.5 | 20 | PDB header: transferase Chain: A: PDB Molecule: n2, n2-dimethylguanosine trna methyltransferase; PDBTitle: crystal structure of the archaeal trna m2g/m22g10 methyltransferase2 (atrm11) in complex with s-adenosyl-l-methionine (sam) from3 thermococcus kodakarensis |
| 68 | d1nv8a | Alignment | not modelled | 99.5 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N5- glutamine methyltransferase, HemK |
| 69 | c6bqcA | Alignment | not modelled | 99.5 | 23 | PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli |
| 70 | d1dl5a1 | Alignment | not modelled | 99.5 | 18 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 71 | d1m6ya2 | Alignment | not modelled | 99.5 | 10 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: MraW-like putative methyltransferases |
| 72 | c3tmaA | Alignment | not modelled | 99.5 | 27 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of trmn from thermus thermophilus |
| | | | | | | PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n- |

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|----|------------------------|-----------|--------------|------|----|--|
| 73 | c3ujcA | Alignment | not modelled | 99.5 | 18 | methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine |
| 74 | c6qe6A | Alignment | not modelled | 99.5 | 13 | PDB header: transferase Chain: A: PDB Molecule: trna (adenine(22)-n(1))-methyltransferase; PDBTitle: structure of m. capricolum trmk in complex with the natural cofactor2 product s-adenosyl-homocysteine (sah) |
| 75 | c3mb5A | Alignment | not modelled | 99.5 | 27 | PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of p. abyssi trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine |
| 76 | c3lecA | Alignment | not modelled | 99.5 | 16 | PDB header: structure genomics, unknown function Chain: A: PDB Molecule: nadb-rossmann superfamily protein; PDBTitle: the crystal structure of a protein in the nadb-rossmann superfamily2 from streptococcus agalactiae to 1.8a |
| 77 | c1vl5B | Alignment | not modelled | 99.5 | 18 | PDB header: transferase Chain: B: PDB Molecule: unknown conserved protein bh2331; PDBTitle: crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution |
| 78 | c3mtiA | Alignment | not modelled | 99.5 | 11 | PDB header: transferase Chain: A: PDB Molecule: rrna methylase; PDBTitle: the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a |
| 79 | d1vl5a | Alignment | not modelled | 99.5 | 18 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 80 | c3ku1E | Alignment | not modelled | 99.5 | 19 | PDB header: transferase Chain: E: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of streptococcus pneumoniae sp1610, a putative trna2 (m1a22) methyltransferase, in complex with s-adenosyl-l-methionine |
| 81 | c6g4wq | Alignment | not modelled | 99.5 | 18 | PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s16; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a |
| 82 | d1o54a | Alignment | not modelled | 99.5 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like |
| 83 | d1pjza | Alignment | not modelled | 99.5 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase |
| 84 | c3g5tA | Alignment | not modelled | 99.5 | 11 | PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast |
| 85 | c1aqjB | Alignment | not modelled | 99.5 | 24 | PDB header: methyltransferase Chain: B: PDB Molecule: adenine-n6-dna-methyltransferase taqi; PDBTitle: structure of adenine-n6-dna-methyltransferase taqi |
| 86 | d1l3ia | Alignment | not modelled | 99.5 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Precorrin-6Y methyltransferase (CbiT) |
| 87 | c3a26A | Alignment | not modelled | 99.5 | 21 | PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein ph0793; PDBTitle: crystal structure of p. horikoshii tyw2 in complex with2 mesado |
| 88 | c2yvlB | Alignment | not modelled | 99.5 | 16 | PDB header: transferase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of trna (m1a58) methyltransferase trmi from aquifex2 aeolicus |
| 89 | c5ccbA | Alignment | not modelled | 99.5 | 22 | PDB header: transferase/rna Chain: A: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase catalytic subunit PDBTitle: crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah |
| 90 | c3evzA | Alignment | not modelled | 99.5 | 18 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from pyrococcus furiosus |
| 91 | d1l1ea | Alignment | not modelled | 99.5 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 92 | c5ergB | Alignment | not modelled | 99.5 | 16 | PDB header: transferase Chain: B: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase catalytic subunit PDBTitle: crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam |
| 93 | d1tpya | Alignment | not modelled | 99.5 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 94 | c3njrB | Alignment | not modelled | 99.5 | 23 | PDB header: transferase Chain: B: PDB Molecule: precorrin-6y methylase; PDBTitle: crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus |
| 95 | c4pneA | Alignment | not modelled | 99.5 | 13 | PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf |
| 96 | d1kpga | Alignment | not modelled | 99.5 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 97 | c3gnlB | Alignment | not modelled | 99.5 | 15 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein, duf633, lmof2365_1472; PDBTitle: structure of uncharacterized protein (lmof2365_1472) from listeria2 monocytogenes serotype 4b |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 98 | d1xxla_ | Alignment | not modelled | 99.5 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 99 | c3lpmA_ | Alignment | not modelled | 99.4 | 17 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes |
| 100 | d2frna1 | Alignment | not modelled | 99.4 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Met-10+ protein-like |
| 101 | d1nkva_ | Alignment | not modelled | 99.4 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein YjHP |
| 102 | c2yr0A_ | Alignment | not modelled | 99.4 | 20 | PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8 |
| 103 | c3lbyA_ | Alignment | not modelled | 99.4 | 12 | PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein smu.1697c; PDBTitle: crystal structure of smu.1697c, a putative methyltransferase from2 streptococcus mutans in complex with sah |
| 104 | c5egpB_ | Alignment | not modelled | 99.4 | 16 | PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta |
| 105 | c4qnuH_ | Alignment | not modelled | 99.4 | 18 | PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212 |
| 106 | c3lduA_ | Alignment | not modelled | 99.4 | 16 | PDB header: transferase Chain: A: PDB Molecule: putative methylase; PDBTitle: the crystal structure of a possible methylase from2 clostridium difficile 630. |
| 107 | c3cggB_ | Alignment | not modelled | 99.4 | 25 | PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution |
| 108 | d2nxca1 | Alignment | not modelled | 99.4 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ribosomal protein L11 methyltransferase PrmA |
| 109 | d2fpoa1 | Alignment | not modelled | 99.4 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like |
| 110 | c4dcmA_ | Alignment | not modelled | 99.4 | 20 | PDB header: transferase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase g; PDBTitle: crystal structure of methyltransferase rlmg modifying g1835 of 23s2 rrna in escherichia coli |
| 111 | c2pbfA_ | Alignment | not modelled | 99.4 | 19 | PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase beta-aspartate 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 |
| 112 | d1kpia_ | Alignment | not modelled | 99.4 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 113 | d1wzna1 | Alignment | not modelled | 99.4 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like |
| 114 | c3m33B_ | Alignment | not modelled | 99.4 | 19 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein from2 deinococcus radiodurans r1 |
| 115 | c4azwA_ | Alignment | not modelled | 99.4 | 20 | PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: crystal structure of monomeric wbdd. |
| 116 | c4qttB_ | Alignment | not modelled | 99.4 | 15 | PDB header: transferase Chain: B: PDB Molecule: putative methyltransferase bud23; PDBTitle: structure of s. cerevisiae bud23-trm112 complex involved in formation2 of m7g1575 on 18s rrna (apo-form) |
| 117 | d2o57a1 | Alignment | not modelled | 99.4 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 118 | c3eeyl_ | Alignment | not modelled | 99.4 | 15 | PDB header: transferase Chain: J: PDB Molecule: putative rrna methylase; PDBTitle: crystal structure of putative rrna-methylase from clostridium2 thermocellum |
| 119 | c3egeA_ | Alignment | not modelled | 99.4 | 17 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase from antibiotic biosynthesis PDBTitle: crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution |
| 120 | c4x1oA_ | Alignment | not modelled | 99.4 | 22 | PDB header: transferase Chain: A: PDB Molecule: 16s rrna (adenine(1408)-n(1))-methyltransferase; PDBTitle: crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia |