

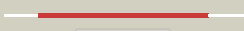


















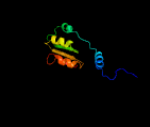











Phyre2

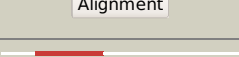
| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1513_(-)_1705064_1705795 |
| Date | Fri Aug 2 13:30:10 BST 2019 |
| Unique Job ID | 2ff2c6188140aa09 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d2py6a1 |  Alignment |  | 100.0 | 18 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: FkbM-like |
| 2 | c4df3B_ |  Alignment |  | 98.8 | 15 | PDB header: transferase Chain: B: PDB Molecule: fibrillarlin-like rrna/trna 2'-o-methyltransferase; PDBTitle: crystal structure of aeropyrum pernix fibrillarlin in complex with2 natively bound s-adenosyl-l-methionine at 1.7a |
| 3 | c3hm2G_ |  Alignment |  | 98.7 | 15 | PDB header: transferase Chain: G: PDB Molecule: precorrin-6y c5,15-methyltransferase; PDBTitle: crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae |
| 4 | d1g8sa_ |  Alignment |  | 98.5 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Fibrillarlin homologue |
| 5 | c3e05B_ |  Alignment |  | 98.5 | 15 | 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 |
| 6 | c3gnlB_ |  Alignment |  | 98.5 | 13 | 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 |
| 7 | c3id5F_ |  Alignment |  | 98.5 | 14 | PDB header: transferase/ribosomal protein/rna Chain: F: PDB Molecule: fibrillarlin-like rrna/trna 2'-o-methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarlin, l7ae and a split half c/d rna |
| 8 | c3a27A_ |  Alignment |  | 98.5 | 17 | PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein mj1557; PDBTitle: crystal structure of m. jannaschii tyw2 in complex with2 adomet |
| 9 | c6ifsB_ |  Alignment |  | 98.4 | 16 | PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168 |
| 10 | c6qe6A_ |  Alignment |  | 98.4 | 7 | 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) |
| 11 | c4gc5A_ |  Alignment |  | 98.4 | 19 | PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase 1, mitochondrial; PDBTitle: crystal structure of murine tfb1m |

| | | | | | | |
|----|-------------------------|-----------|---|------|----|--|
| 12 | c3nrjB_ | Alignment |  | 98.4 | 18 | 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 |
| 13 | c3fuxB_ | Alignment |  | 98.4 | 24 | 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 |
| 14 | c3lecA_ | Alignment |  | 98.4 | 17 | 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 |
| 15 | c6q56C_ | Alignment |  | 98.3 | 15 | 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 |
| 16 | c5xj2C_ | Alignment |  | 98.3 | 15 | PDB header: transferase/rna Chain: C; PDB Molecule: uncharacterized rna methyltransferase sp_1029; PDBTitle: structure of sprlmcid with u747 rna |
| 17 | d1dl5a1 | Alignment |  | 98.3 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 18 | c6h1dA_ | Alignment |  | 98.3 | 13 | PDB header: gene regulation Chain: A; PDB Molecule: hemk methyltransferase family member 2; PDBTitle: crystal structure of c21orf127-trmt112 in complex with sah |
| 19 | c3ku1E_ | Alignment |  | 98.3 | 18 | 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 |
| 20 | d1yzha1 | Alignment |  | 98.2 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like |
| 21 | c3a26A_ | Alignment | not modelled | 98.2 | 14 | PDB header: transferase Chain: A; PDB Molecule: uncharacterized protein ph0793; PDBTitle: crystal structure of p. horikoshii tyw2 in complex with2 mesado |
| 22 | d1qama_ | Alignment | not modelled | 98.2 | 6 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like |
| 23 | c1m6yA_ | Alignment | not modelled | 98.2 | 11 | PDB header: transferase Chain: A; PDB Molecule: s-adenosyl-methyltransferase mraw; PDBTitle: crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah |
| 24 | d1jsxa_ | Alignment | not modelled | 98.2 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glucose-inhibited division protein B (GidB) |
| 25 | c3eeyl_ | Alignment | not modelled | 98.2 | 14 | PDB header: transferase Chain: J; PDB Molecule: putative rrna methylase; PDBTitle: crystal structure of putative rrna-methylase from clostridium2 thermocellum |
| 26 | c2yxdA_ | Alignment | not modelled | 98.2 | 14 | PDB header: transferase Chain: A; PDB Molecule: probable cobalt-precorrin-6y c(15)-methyltransferase PDBTitle: crystal structure of cobalamin biosynthesis precorrin 8w decarboxylase2 (cbt) |
| 27 | c2yxeB_ | Alignment | not modelled | 98.2 | 18 | PDB header: transferase Chain: B; PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of l-isoaspartyl protein carboxyl methyltransferase |
| 28 | c1dl5A_ | Alignment | not modelled | 98.1 | 17 | PDB header: transferase Chain: A; PDB Molecule: protein-l-isoaspartate o- |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 28 | c103A | Alignment | not modelled | 98.1 | 17 | methyltransferase; PDBTitle: protein-l-isoaspartate o-methyltransferase |
| 29 | d1m6ya2 | Alignment | not modelled | 98.1 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: MraW-like putative methyltransferases |
| 30 | c2gpyB | Alignment | not modelled | 98.1 | 18 | PDB header: structural genomics, unknown function Chain: B; PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of putative o-methyltransferase from bacillus2 halodurans |
| 31 | c3grrA | Alignment | not modelled | 98.1 | 11 | PDB header: transferase Chain: A; PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1. |
| 32 | c6gkvB | Alignment | not modelled | 98.1 | 12 | 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 |
| 33 | c3fydA | Alignment | not modelled | 98.1 | 11 | PDB header: transferase Chain: A; PDB Molecule: probable dimethyladenosine transferase; PDBTitle: crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi |
| 34 | c2ipxA | Alignment | not modelled | 98.1 | 19 | PDB header: transferase Chain: A; PDB Molecule: rrna 2'-o-methyltransferase fibrillarin; PDBTitle: human fibrillarin |
| 35 | d1vbfa | Alignment | not modelled | 98.1 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 36 | c3wssA | Alignment | not modelled | 98.0 | 17 | PDB header: transferase Chain: A; PDB Molecule: protein arginine n-methyltransferase 7; PDBTitle: crystal structure of c.elegans prmt7 in complex with sah (p43212) |
| 37 | c5zy5B | Alignment | not modelled | 98.0 | 11 | PDB header: transferase Chain: B; PDB Molecule: probable catechol o-methyltransferase 1; PDBTitle: spcomt apo structure |
| 38 | c5kn4B | Alignment | not modelled | 98.0 | 9 | PDB header: transferase Chain: B; PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0 |
| 39 | d1wy7a1 | Alignment | not modelled | 98.0 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ta1320-like |
| 40 | c4o29A | Alignment | not modelled | 98.0 | 18 | 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 |
| 41 | c4jxA | Alignment | not modelled | 98.0 | 14 | 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 |
| 42 | c4c4aA | Alignment | not modelled | 98.0 | 15 | PDB header: transferase Chain: A; PDB Molecule: protein arginine n-methyltransferase 7; PDBTitle: crystal structure of mouse protein arginine methyltransferase 7 in2 complex with sah |
| 43 | c5ccbA | Alignment | not modelled | 98.0 | 14 | 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 |
| 44 | d2frna1 | Alignment | not modelled | 98.0 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Met-10+ protein-like |
| 45 | c2yx1A | Alignment | not modelled | 98.0 | 11 | PDB header: transferase Chain: A; PDB Molecule: hypothetical protein mj0883; PDBTitle: crystal structure of m.jannaschii trna m1g37 methyltransferase |
| 46 | c3bt7A | Alignment | not modelled | 98.0 | 15 | 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 |
| 47 | d1uwva2 | Alignment | not modelled | 98.0 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: (Uracil-5-)-methyltransferase |
| 48 | d2p7ia1 | Alignment | not modelled | 98.0 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 49 | c3tqsB | Alignment | not modelled | 98.0 | 10 | PDB header: transferase Chain: B; PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii |
| 50 | d1i1na | Alignment | not modelled | 97.9 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase |
| 51 | d1qyra | Alignment | not modelled | 97.9 | 10 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like |
| 52 | c4m38A | Alignment | not modelled | 97.9 | 17 | PDB header: transferase/transferase substrate Chain: A; PDB Molecule: protein arginine n-methyltransferase 7; PDBTitle: crystal structure of trypanosoma brucei protein arginine2 methyltransferase 7 complex with adohcy and histone h4 peptide |

| | | | | | | |
|----|-------------------------|---|--------------|------|----|--|
| 53 | c5ergB |  Alignment | not modelled | 97.9 | 15 | 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 |
| 54 | c2pbfA |  Alignment | not modelled | 97.9 | 15 | 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 |
| 55 | d1prya |  Alignment | not modelled | 97.9 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Fibrillarlin homologue |
| 56 | d1g8aa |  Alignment | not modelled | 97.9 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Fibrillarlin homologue |
| 57 | d1g6q1 |  Alignment | not modelled | 97.9 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase |
| 58 | d1nt2a |  Alignment | not modelled | 97.9 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Fibrillarlin homologue |
| 59 | c5lkjA |  Alignment | not modelled | 97.9 | 18 | PDB header: transferase Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: crystal structure of mouse carm1 in complex with ligand sa684 |
| 60 | c2p7iB |  Alignment | not modelled | 97.9 | 12 | PDB header: transferase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sam dependent methyl-transferase type 12 family2 protein (eca1738) from pectobacterium atrosepticum scri1043 at 1.74 a3 resolution |
| 61 | c5wp5A |  Alignment | not modelled | 97.9 | 13 | PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah |
| 62 | c5hjmA |  Alignment | not modelled | 97.9 | 11 | PDB header: transferase Chain: A: PDB Molecule: trna (guanine(37)-n1)-methyltransferase trm5a; PDBTitle: crystal structure of pyrococcus abyssi trm5a complexed with mta |
| 63 | d1zq9a1 |  Alignment | not modelled | 97.9 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like |
| 64 | d1f3la |  Alignment | not modelled | 97.9 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase |
| 65 | c3mq2A |  Alignment | not modelled | 97.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: 16s rrna methyltransferase; PDBTitle: crystal structure of 16s rrna methyltransferase kamb |
| 66 | c3lbfC |  Alignment | not modelled | 97.9 | 19 | PDB header: transferase Chain: C: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli |
| 67 | c5yacA |  Alignment | not modelled | 97.9 | 11 | PDB header: rna binding protein Chain: A: PDB Molecule: trna (guanine(37)-n1)-methyltransferase trm5b; PDBTitle: crystal structure of wt trm5b from pyrococcus abyssi |
| 68 | d2fcaa1 |  Alignment | not modelled | 97.9 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like |
| 69 | c3g8aF |  Alignment | not modelled | 97.9 | 18 | PDB header: transferase Chain: F: PDB Molecule: ribosomal rna small subunit methyltransferase g; PDBTitle: t. thermophilus 16s rrna g527 methyltransferase in complex with adohcy2 in space group p61 |
| 70 | c3g5tA |  Alignment | not modelled | 97.9 | 9 | PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast |
| 71 | c1vl5B |  Alignment | not modelled | 97.8 | 13 | 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 |
| 72 | c2pwyB |  Alignment | not modelled | 97.8 | 27 | PDB header: transferase Chain: B: PDB Molecule: trna (adenine-n(1))-methyltransferase; PDBTitle: crystal structure of a m1a58 trna methyltransferase |
| 73 | d1vl5a |  Alignment | not modelled | 97.8 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 74 | c2pjdA |  Alignment | not modelled | 97.8 | 17 | PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase c; PDBTitle: crystal structure of 16s rrna methyltransferase rsmc |
| 75 | c5fubA | Alignment | not modelled | 97.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: protein arginine methyltransferase 2; PDBTitle: crystal structure of zebrafish protein arginine methyltransferase 22 catalytic domain with sah |
| 76 | c6dnzB | Alignment | not modelled | 97.8 | 21 | PDB header: gene regulation Chain: B: PDB Molecule: arginine n-methyltransferase, putative; PDBTitle: trypanosoma brucei prmt1 enzyme-prozyme heterotetrameric complex with2 adohcy |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 77 | c1yb2A_ | Alignment | not modelled | 97.8 | 18 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein ta0852; PDBTitle: structure of a putative methyltransferase from thermoplasma2 acidophilum. |
| 78 | d1yb2a1 | Alignment | not modelled | 97.8 | 18 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like |
| 79 | c3evzA_ | Alignment | not modelled | 97.8 | 11 | PDB header: transferase Chain: A; PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from pyrococcus furiosus |
| 80 | d1i9ga_ | Alignment | not modelled | 97.8 | 25 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like |
| 81 | c3mggB_ | Alignment | not modelled | 97.8 | 14 | PDB header: transferase Chain: B; PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei |
| 82 | c1uwvA_ | Alignment | not modelled | 97.8 | 18 | 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 |
| 83 | c5fwaA_ | Alignment | not modelled | 97.8 | 12 | PDB header: transferase Chain: A; PDB Molecule: protein arginine n-methyltransferase 2; PDBTitle: crystal structure of mus musculus protein arginine methyltransferase 22 with cp1 |
| 84 | c2ozvA_ | Alignment | not modelled | 97.8 | 14 | PDB header: transferase Chain: A; PDB Molecule: hypothetical protein atu0636; PDBTitle: crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens. |
| 85 | c3r0qA_ | Alignment | not modelled | 97.8 | 18 | PDB header: transferase Chain: A; PDB Molecule: probable protein arginine n-methyltransferase 4.2; PDBTitle: a uniquely open conformation revealed in the crystal structure of2 arabidopsis thaliana protein arginine methyltransferase 10 |
| 86 | d2b25a1 | Alignment | not modelled | 97.8 | 23 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like |
| 87 | c4l7vA_ | Alignment | not modelled | 97.8 | 11 | PDB header: transferase Chain: A; PDB Molecule: protein-l-isoadpartate o-methyltransferase; PDBTitle: crystal structure of protein l-isoadpartyl-o-methyltransferase of2 vibrio cholerae |
| 88 | c4dcmA_ | Alignment | not modelled | 97.8 | 18 | PDB header: transferase Chain: A; PDB Molecule: ribosomal rna large subunit methyltransferase g; PDBTitle: crystal structure of methyltransferase rlmg modifying g1835 of 23s2 rna in escherichia coli |
| 89 | c3p2kA_ | Alignment | not modelled | 97.8 | 13 | PDB header: transferase Chain: A; PDB Molecule: 16s rna methylase; PDBTitle: structure of an antibiotic related methyltransferase |
| 90 | c3gdhC_ | Alignment | not modelled | 97.8 | 16 | 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) |
| 91 | d2fhpa1 | Alignment | not modelled | 97.8 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like |
| 92 | d1o54a_ | Alignment | not modelled | 97.8 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like |
| 93 | c6ectA_ | Alignment | not modelled | 97.8 | 17 | PDB header: transferase Chain: A; PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257 |
| 94 | d2b3ta1 | Alignment | not modelled | 97.8 | 22 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N5-glutamine methyltransferase, HemK |
| 95 | c3mb5A_ | Alignment | not modelled | 97.7 | 17 | 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 |
| 96 | d1xdza_ | Alignment | not modelled | 97.7 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glucose-inhibited division protein B (GidB) |
| 97 | c4y30B_ | Alignment | not modelled | 97.7 | 21 | PDB header: transferase Chain: B; PDB Molecule: protein arginine n-methyltransferase 6; PDBTitle: crystal structure of human protein arginine methyltransferase prmt62 bound to sah and epz020411 |
| 98 | d1oria_ | Alignment | not modelled | 97.7 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase |
| 99 | d2cl5a1 | Alignment | not modelled | 97.7 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: COMT-like |
| 100 | d1dusa_ | Alignment | not modelled | 97.7 | 9 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein MJ0882 |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| 101 | c4hc4A | Alignment | not modelled | 97.7 | 19 | PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 6; PDBTitle: human hmt1 hrnp methyltransferase-like protein 6 (s. cerevisiae) |
| 102 | c3b3jA | Alignment | not modelled | 97.7 | 20 | PDB header: transferase Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; 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) |
| 103 | c5z9oA | Alignment | not modelled | 97.7 | 13 | 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 |
| 104 | d1xxla | Alignment | not modelled | 97.7 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 105 | c3c3yB | Alignment | not modelled | 97.7 | 9 | PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of pfomt, phenylpropanoid and flavonoid o-2 methyltransferase from m. crystallinum |
| 106 | d2fyta1 | Alignment | not modelled | 97.7 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase |
| 107 | d1pjza | Alignment | not modelled | 97.7 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase |
| 108 | c4ponB | Alignment | not modelled | 97.7 | 14 | PDB header: transferase Chain: B: PDB Molecule: putative rna methylase; PDBTitle: the crystal structure of a putative sam-dependent methyltransferase,2 ytqb, from bacillus subtilis |
| 109 | d2fpoa1 | Alignment | not modelled | 97.7 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like |
| 110 | d2b9ea1 | Alignment | not modelled | 97.7 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: NOL1/NOP2/sun |
| 111 | c4krqB | Alignment | not modelled | 97.7 | 16 | 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 |
| 112 | c4krhB | Alignment | not modelled | 97.7 | 16 | 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 |
| 113 | c3dxyA | Alignment | not modelled | 97.7 | 13 | PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(7)-)-methyltransferase; PDBTitle: crystal structure of ectrmb in complex with sam |
| 114 | c3fzgA | Alignment | not modelled | 97.7 | 14 | PDB header: transferase Chain: A: PDB Molecule: 16s rna methylase; PDBTitle: structure of the 16s rna methylase arma |
| 115 | c3gwzB | Alignment | not modelled | 97.7 | 14 | PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr |
| 116 | c4lwoG | Alignment | not modelled | 97.6 | 19 | PDB header: transferase Chain: G: PDB Molecule: arginine n-methyltransferase, putative; PDBTitle: crystal structure of prmt6 |
| 117 | d2fk8a1 | Alignment | not modelled | 97.6 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 118 | d2ifta1 | Alignment | not modelled | 97.6 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like |
| 119 | c4qttB | Alignment | not modelled | 97.6 | 17 | 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 rna (apo-form) |
| 120 | d1nv8a | Alignment | not modelled | 97.6 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N5-glutamine methyltransferase, HemK |