



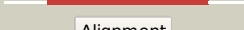

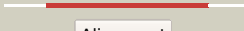









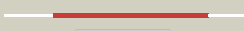
















Phyre2

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|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1515c_(-)_1706636_1707532 |
| Date | Fri Aug 2 13:30:10 BST 2019 |
| Unique Job ID | e809df0de975da4c |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4krhB_ |  Alignment |  | 100.0 | 17 | 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 |
| 2 | c4p7cB_ |  Alignment |  | 100.0 | 22 | PDB header: transferase Chain: B: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato |
| 3 | c5t39A_ |  Alignment |  | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: evdmo1; PDBTitle: crystal structure of the n-terminal domain of evdmo1 in the presence2 of sah and d-fucose |
| 4 | c4ineB_ |  Alignment |  | 100.0 | 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 |
| 5 | c4qnuH_ |  Alignment |  | 99.9 | 21 | PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212 |
| 6 | c5wp5A_ |  Alignment |  | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah |
| 7 | d1r74a_ |  Alignment |  | 99.9 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase |
| 8 | c6gkvB_ |  Alignment |  | 99.9 | 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 |
| 9 | d1xvaa_ |  Alignment |  | 99.9 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase |
| 10 | c5kn4B_ |  Alignment |  | 99.9 | 14 | PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0 |
| 11 | c6ec3C_ |  Alignment |  | 99.9 | 24 | PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdmo1 |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | c3vc2j_ | Alignment |  | 99.9 | 20 | 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 |
| 13 | c5z9oA_ | Alignment |  | 99.9 | 15 | 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 |
| 14 | d1y8ca_ | Alignment |  | 99.9 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like |
| 15 | d1wzna1 | Alignment |  | 99.9 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like |
| 16 | c2fk8A_ | Alignment |  | 99.9 | 15 | 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 |
| 17 | c4hgyC_ | Alignment |  | 99.9 | 11 | PDB header: transferase Chain: C: PDB Molecule: ccbj; PDBTitle: structure of the ccbj methyltransferase from streptomyces caelestis |
| 18 | c3g2qA_ | Alignment |  | 99.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtfA2 complexed with sinefungin |
| 19 | c3pfnD_ | Alignment |  | 99.9 | 18 | PDB header: transferase Chain: D: PDB Molecule: n-methyltransferase; PDBTitle: x-ray crystal structure the n,n-dimethyltransferase tyM1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n |
| 20 | c5hijA_ | Alignment |  | 99.9 | 15 | PDB header: transferase Chain: A: PDB Molecule: glycine sarcosine n-methyltransferase; PDBTitle: crystal structure of glycine sarcosine n-methyltransferase from2 methanohalophilus portucalensis in complex with betaine |
| 21 | c3e7pA_ | Alignment | not modelled | 99.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482 |
| 22 | c1vl5B_ | Alignment | not modelled | 99.9 | 15 | 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 |
| 23 | c5dplB_ | Alignment | not modelled | 99.9 | 19 | PDB header: transferase Chain: B: PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy |
| 24 | c3bxoA_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: n,n-dimethyltransferase; PDBTitle: crystal structure of streptomyces venezuelae desvi |
| 25 | d1vl5a_ | Alignment | not modelled | 99.9 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 26 | d1kpga_ | Alignment | not modelled | 99.9 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 27 | c2yr0A_ | Alignment | not modelled | 99.9 | 10 | PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8 |
| 28 | d2o57a1 | Alignment | not modelled | 99.9 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c4azwA | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: crystal structure of monomeric wbdd. |
| 30 | c5egpB | Alignment | not modelled | 99.9 | 9 | PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmta |
| 31 | c5w7kA | Alignment | not modelled | 99.9 | 12 | PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag |
| 32 | d2gh1a1 | Alignment | not modelled | 99.9 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like |
| 33 | d2fk8a1 | Alignment | not modelled | 99.9 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 34 | c5bszA | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: n-methyltransferase; PDBTitle: x-ray structure of the sugar n-methyltransferase keds8 from2 streptoalloteichus sp atcc 53650 |
| 35 | c4necC | Alignment | not modelled | 99.9 | 18 | PDB header: transferase/antibiotic Chain: C: PDB Molecule: putative sam-dependent methyltransferase; PDBTitle: conversion of a disulfide bond into a thioacetal group during2 echinomycin biosynthesis |
| 36 | c3qnhA | Alignment | not modelled | 99.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: arsenic methyltransferase; PDBTitle: arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii) |
| 37 | c5evjA | Alignment | not modelled | 99.9 | 20 | PDB header: transferase Chain: A: PDB Molecule: arsenite methyltransferase; PDBTitle: x-ray crystal structure of crasm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii |
| 38 | c3f4kA | Alignment | not modelled | 99.9 | 18 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309. |
| 39 | c3g5IA | Alignment | not modelled | 99.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes |
| 40 | d1nkva | Alignment | not modelled | 99.9 | 24 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein Yjhp |
| 41 | c4kdcA | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9 3-methyltransferase; PDBTitle: crystal structure of ubig |
| 42 | d1kpia | Alignment | not modelled | 99.9 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 43 | d1l1ea | Alignment | not modelled | 99.9 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 44 | c3m70A | Alignment | not modelled | 99.9 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae |
| 45 | c5do0A | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii |
| 46 | d1d2ha | Alignment | not modelled | 99.9 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase |
| 47 | c4krkB | Alignment | not modelled | 99.9 | 14 | 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 |
| 48 | c4azsA | Alignment | not modelled | 99.9 | 18 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase wbdd; PDBTitle: high resolution (2.2 a) crystal structure of wbdd. |
| 49 | c3lccA | Alignment | not modelled | 99.9 | 20 | PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana |
| 50 | c3g5tA | Alignment | not modelled | 99.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast |
| 51 | c6ectA | Alignment | not modelled | 99.9 | 12 | PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257 |
| 52 | d1xxla | Alignment | not modelled | 99.9 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 53 | c3bkxB | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of cyclopropane-fatty-acyl-phospholipid |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution |
| 54 | d1tpya_ | Alignment | not modelled | 99.9 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 55 | c3ccfB_ | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: B: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: crystal structure of putative methyltransferase (yp_321342.1) from2 anaebaena variabilis atcc 29413 at 1.90 a resolution |
| 56 | c3ocjA_ | Alignment | not modelled | 99.9 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: the crystal structure of a possilbe exported protein from bordetella2 parapertussis |
| 57 | c5fcdA_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: mccd; PDBTitle: crystal structure of mccd protein |
| 58 | c6bqcA_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli |
| 59 | c3cc8A_ | Alignment | not modelled | 99.9 | 18 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a putative methyltransferase (bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution |
| 60 | c3d2lC_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase Chain: C: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exiguobacterium sp. 255-15 at 1.90 a resolution |
| 61 | c5bp9A_ | Alignment | not modelled | 99.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase protein; PDBTitle: crystal structure of sam-dependent methyltransferase from bacteroides2 fragilis in complex with s-adenosyl-l-homocysteine |
| 62 | c3mggB_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanosarcina2 mazei |
| 63 | c5je0B_ | Alignment | not modelled | 99.9 | 20 | PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of burkholderia glumae toxa with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethyltoxoflavin |
| 64 | d2ex4a1 | Alignment | not modelled | 99.9 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like |
| 65 | c3h2bB_ | Alignment | not modelled | 99.9 | 24 | PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of the sam-dependent methyltransferase cg3271 from2 corynebacterium glutamicum in complex with s-adenosyl-l-homocysteine3 and pyrophosphate. northeast structural genomics consortium target4 cgr113a |
| 66 | c2p35A_ | Alignment | not modelled | 99.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; PDBTitle: crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens |
| 67 | c6ecvB_ | Alignment | not modelled | 99.9 | 12 | PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o-mt residues 976-1266 |
| 68 | d1ve3a1 | Alignment | not modelled | 99.9 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like |
| 69 | c4iscA_ | Alignment | not modelled | 99.9 | 11 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a putative methyltransferase from pseudomonas2 syringae |
| 70 | c3ujcA_ | Alignment | not modelled | 99.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine |
| 71 | c4kvzA_ | Alignment | not modelled | 99.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: baml; PDBTitle: crystal structure of the plantazolicin methyltransferase baml in2 complex with sah |
| 72 | d2a14a1 | Alignment | not modelled | 99.9 | 23 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arylamine N-methyltransferase |
| 73 | c4uw0A_ | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: low resolution structure of wbdd with c-terminal bundle ordered to2 residue 505 |
| 74 | c4x1oA_ | Alignment | not modelled | 99.9 | 21 | 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 |
| 75 | c3dlcA_ | Alignment | not modelled | 99.9 | 15 | PDB header: transferase Chain: A: PDB Molecule: putative s-adenosyl-l-methionine-dependent PDBTitle: crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution |
| 76 | c3l8dA_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis |
| | | | | | | PDB header: transferase |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 77 | c3ofkA_ | Alignment | not modelled | 99.9 | 14 | Chain: A; PDB Molecule: nodulation protein s; PDBTitle: crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah) |
| 78 | c5u18A_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A; PDB Molecule: n-3" methyltransferase; PDBTitle: crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin |
| 79 | c3e23A_ | Alignment | not modelled | 99.9 | 15 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein rpa2492; PDBTitle: crystal structure of the rpa2492 protein in complex with sam from2 rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr299 |
| 80 | c5mgzA_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A; PDB Molecule: 8-demethylnovobiocic acid c(8)-methyltransferase; PDBTitle: streptomycetes spheroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah |
| 81 | d1jqea_ | Alignment | not modelled | 99.9 | 10 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase |
| 82 | c6g4wq_ | Alignment | not modelled | 99.9 | 17 | 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 |
| 83 | c3mtiA_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase Chain: A; PDB Molecule: rrna methylase; PDBTitle: the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a |
| 84 | d1im8a_ | Alignment | not modelled | 99.9 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO) |
| 85 | c3bgdB_ | Alignment | not modelled | 99.9 | 20 | PDB header: transferase Chain: B; PDB Molecule: thiopurine s-methyltransferase; PDBTitle: thiopurine s-methyltransferase |
| 86 | c1z3cA_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase Chain: A; PDB Molecule: mrna capping enzyme; PDBTitle: encephalitozoan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet |
| 87 | d1ri5a_ | Alignment | not modelled | 99.9 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase |
| 88 | c4kwcA_ | Alignment | not modelled | 99.9 | 18 | PDB header: transferase Chain: A; PDB Molecule: bpuml; PDBTitle: structure of the plantazolicin methyltransferase bpuml in complex with2 sah |
| 89 | c3lecA_ | Alignment | not modelled | 99.9 | 19 | 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 |
| 90 | d2bzga1 | Alignment | not modelled | 99.9 | 25 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase |
| 91 | c5ufmB_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase Chain: B; PDB Molecule: methyltransferase domain protein; PDBTitle: crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine |
| 92 | d2p7ia1 | Alignment | not modelled | 99.9 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 93 | c6q56C_ | Alignment | not modelled | 99.9 | 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 |
| 94 | c4htfA_ | Alignment | not modelled | 99.9 | 21 | PDB header: transferase Chain: A; PDB Molecule: s-adenosylmethionine-dependent methyltransferase; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 from escherichia coli in complex with s-adenosylmethionine. |
| 95 | c2xvmB_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: B; PDB Molecule: tellurite resistance protein tehb; PDBTitle: crystal structure of the tellurite detoxification protein2 tehb from e. coli in complex with sah |
| 96 | c3bgvC_ | Alignment | not modelled | 99.9 | 11 | PDB header: transferase Chain: C; PDB Molecule: mrna cap guanine-n7 methyltransferase; PDBTitle: crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah |
| 97 | c4pneA_ | Alignment | not modelled | 99.9 | 22 | PDB header: biosynthetic protein Chain: A; PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf |
| 98 | c3ou7A_ | Alignment | not modelled | 99.8 | 12 | PDB header: transferase Chain: A; PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex |
| 99 | c4obxD_ | Alignment | not modelled | 99.8 | 12 | PDB header: transferase Chain: D; PDB Molecule: 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, PDBTitle: crystal structure of yeast coq5 in the apo form |
| 100 | c4rvgA_ | Alignment | not modelled | 99.8 | 16 | PDB header: transferase Chain: A; PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp |
| 101 | c2p7iB_ | Alignment | not modelled | 99.8 | 11 | PDB header: transferase Chain: B; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sam dependent methyl-transferase |

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|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | type 12 family2 protein (eca1738) from pectobacterium atrosepticum scri1043 at 1.74 a3 resolution |
| 102 | c3g2qB_ | Alignment | not modelled | 99.8 | 15 | PDB header: transferase Chain: B: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin |
| 103 | c3ku1E_ | Alignment | not modelled | 99.8 | 16 | 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 |
| 104 | c4qdkB_ | Alignment | not modelled | 99.8 | 17 | PDB header: transferase Chain: B: PDB Molecule: magnesium-protoporphyrin o-methyltransferase; PDBTitle: crystal structure of magnesium protoporphyrin ix methyltransferase2 (chlml) from synechocystis pcc 6803 with bound sah |
| 105 | c3gnlB_ | Alignment | not modelled | 99.8 | 17 | 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 |
| 106 | c6dcbA_ | Alignment | not modelled | 99.8 | 17 | PDB header: transferase/rna Chain: A: PDB Molecule: 7sk snrna methylphosphate capping enzyme; PDBTitle: structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna |
| 107 | c4iv0B_ | Alignment | not modelled | 99.8 | 20 | PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase, putative; PDBTitle: crystal structure of n-methyl transferase from plasmodium vivax2 complexed with s-adenosyl methionine and phosphate |
| 108 | d1pjza_ | Alignment | not modelled | 99.8 | 10 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase |
| 109 | d1yzha1 | Alignment | not modelled | 99.8 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like |
| 110 | d2avna1 | Alignment | not modelled | 99.8 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 111 | c5mptA_ | Alignment | not modelled | 99.8 | 17 | PDB header: transferase Chain: A: PDB Molecule: citrinin polyketide synthase; PDBTitle: structure of the citrinin polyketide synthase cmet domain |
| 112 | d2fcaa1 | Alignment | not modelled | 99.8 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like |
| 113 | c3egeA_ | Alignment | not modelled | 99.8 | 18 | 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 |
| 114 | c3e8sA_ | Alignment | not modelled | 99.8 | 14 | PDB header: transferase Chain: A: PDB Molecule: putative sam dependent methyltransferase; PDBTitle: crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution |
| 115 | c6f5zB_ | Alignment | not modelled | 99.8 | 15 | PDB header: transferase Chain: B: PDB Molecule: 24-sterol c-methyltransferase; PDBTitle: complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase |
| 116 | d1xtpa_ | Alignment | not modelled | 99.8 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like |
| 117 | d1yb2a1 | Alignment | not modelled | 99.8 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like |
| 118 | c1yb2A_ | Alignment | not modelled | 99.8 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0852; PDBTitle: structure of a putative methyltransferase from thermoplasma2 acidophilum. |
| 119 | c3ndjA_ | Alignment | not modelled | 99.8 | 11 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product |
| 120 | c3bkwb_ | Alignment | not modelled | 99.8 | 14 | PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of s-adenosylmethionine dependent methyltransferase2 (np_104914.1) from mesorhizobium loti at 1.60 a resolution |