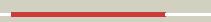
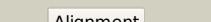
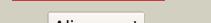
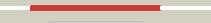


Phyre²

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0726c_(-)_818540_819643 |
| Date | Fri Jul 26 01:50:30 BST 2019 |
| Unique Job ID | 66a92fed09454576 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d2uyoA1 |  |  | 100.0 | 45 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: ML2640-like |
| 2 | c3ieiD |  |  | 100.0 | 21 | PDB header: transferase Chain: D: PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine |
| 3 | d1rjda |  |  | 100.0 | 18 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Leucine carboxy methyltransferase Ppm1 |
| 4 | c3mntA |  |  | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxyl methyltransferase 1 |
| 5 | c2zwaA |  |  | 99.9 | 15 | PDB header: transferase Chain: A: PDB Molecule: leucine carboxyl methyltransferase 2; PDBTitle: crystal structure of trna wybutosine synthesizing enzyme2 tyw4 |
| 6 | c2qe6B |  |  | 99.8 | 23 | PDB header: transferase Chain: B: PDB Molecule: uncharacterized protein tfu_2867; PDBTitle: crystal structure of a putative methyltransferase (tfu_2867) from2 thermobifida fusca yx at 1.95 a resolution |
| 7 | c3giwA |  |  | 99.4 | 19 | PDB header: unknown function Chain: A: PDB Molecule: protein of unknown function duf574; PDBTitle: crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution |
| 8 | c3gwzB |  |  | 98.1 | 15 | PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr |
| 9 | c4qvgC |  |  | 98.1 | 15 | PDB header: transferase Chain: C: PDB Molecule: sibl; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 sibl in its apo form |
| 10 | c6clwA |  |  | 98.0 | 12 | PDB header: biosynthetic protein Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of tnmh |
| 11 | c3mczB |  |  | 97.8 | 12 | PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase; PDBTitle: the structure of an o-methyltransferase family protein from2 burkholderia thailandensis. |

| 12 | c4uy5A | Alignment |  | 97.8 | 17 | PDB header: transferase Chain: A: PDB Molecule: histidine-specific methyltransferase egtd; PDBTitle: crystal structure of histidine-specific methyltransferase egtd from <i>Mycobacterium smegmatis</i> |
|----|-------------------------|-----------|---|------|----|---|
| 13 | d1tw3a2 | Alignment |  | 97.7 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain |
| 14 | c3p9kD | Alignment |  | 97.6 | 12 | PDB header: transferase Chain: D: PDB Molecule: caffic acid o-methyltransferase; PDBTitle: crystal structure of perennial ryegrass lpmot1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde |
| 15 | c1tw3A | Alignment |  | 97.6 | 17 | PDB header: transferase Chain: A: PDB Molecule: carminomycin 4-o-methyltransferase; PDBTitle: crystal structure of carminomycin-4-o-methyltransferase (dnrk) in2 complex with s-adenosyl-l-homocystein (sah) and 4-methoxy-e-3 rhodomycin t (m-et) |
| 16 | c1xdmA | Alignment |  | 97.5 | 17 | PDB header: transferase Chain: A: PDB Molecule: protein rdmb; PDBTitle: crystal structure of aclacinomycin-10-hydroxylase (rdmb) in complex2 with sinefungin (sfg) |
| 17 | c3dp7B | Alignment |  | 97.5 | 16 | PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase from <i>bacteroides vulgatus</i> atcc 8482 |
| 18 | c2ip2B | Alignment |  | 97.5 | 15 | PDB header: transferase Chain: B: PDB Molecule: probable phenazine-specific methyltransferase; PDBTitle: structure of the pyocyanin biosynthetic protein phzm |
| 19 | c6i5zA | Alignment |  | 97.3 | 15 | PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase 1; PDBTitle: papaver somniferum o-methyltransferase |
| 20 | c5i2hB | Alignment |  | 97.3 | 11 | PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase family 2; PDBTitle: crystal structure of o-methyltransferase family 2 protein plim_11472 from <i>planctomyces limnophilus</i> dsm 3776 complex with apigenin |
| 21 | c3g2qA | Alignment | not modelled | 97.2 | 20 | PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin |
| 22 | c6c5bB | Alignment | not modelled | 97.2 | 16 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure analysis of laphzm |
| 23 | c5cvvB | Alignment | not modelled | 97.2 | 14 | PDB header: transferase Chain: B: PDB Molecule: (iso)eugenol o-methyltransferase; PDBTitle: coniferyl alcohol bound monolignol 4-o-methyltransferase 9 |
| 24 | d1r74a | Alignment | not modelled | 97.1 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferases; PDBTitle: crystal structure of n,n-8-amino-8-demethyl-d-riboflavin2 dimethyltransferase (rosa) from <i>streptomyces davawensis</i> |
| 25 | c4d7kB | Alignment | not modelled | 97.1 | 15 | PDB header: transferase Chain: A: PDB Molecule: crtf-related protein; PDBTitle: crystal structure of bchu complexed with s-adenosyl-l-methionine |
| 26 | c1xlaA | Alignment | not modelled | 97.1 | 12 | PDB header: transferase Chain: A: PDB Molecule: hydroxyindole o-methyltransferase; PDBTitle: crystal structure of human n-acetylserotonin2 methyltransferase (asmt) in complex with sam |
| 27 | c4a6dA | Alignment | not modelled | 97.0 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain PDB header: transferase |
| 28 | d1qzza2 | Alignment | not modelled | 97.0 | 14 | PDB header: transferase |

| | | | | | | | |
|----|-------------------------|--|-----------|--------------|------|----|--|
| 29 | c4krhB | | Alignment | not modelled | 97.0 | 12 | Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 2; PDBTitle: semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah) |
| 30 | d1kyza2 | | Alignment | not modelled | 97.0 | 10 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain PDB header: transferase Chain: A: PDB Molecule: putative exported protein; PDBTitle: the crystal structure of a possilbe exported protein from bordetella2 parapertussis |
| 31 | d1fp1d2 | | Alignment | not modelled | 96.9 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah) |
| 32 | c3i53A | | Alignment | not modelled | 96.9 | 15 | 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 |
| 33 | c3ocjA | | Alignment | not modelled | 96.9 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase PDB header: transferase Chain: A: PDB Molecule: methoxy mycolic acid synthase 4; PDBTitle: crystal structure of hma (mma4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine |
| 34 | d1fp2a2 | | Alignment | not modelled | 96.8 | 13 | PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii |
| 35 | d1xvaa | | Alignment | not modelled | 96.8 | 16 | PDB header: transferase Chain: A: PDB Molecule: isoliquiritinigen 2'-o-methyltransferase; PDBTitle: crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase |
| 36 | c2fk8A | | Alignment | not modelled | 96.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: bergaptol o-methyltransferase; PDBTitle: crystal structure of bergaptol o-methyltransferase complex |
| 37 | c5do0A | | Alignment | not modelled | 96.8 | 7 | PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii |
| 38 | c1fpqA | | Alignment | not modelled | 96.8 | 16 | PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana |
| 39 | c3lccA | | Alignment | not modelled | 96.8 | 13 | PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana |
| 40 | c5xohA | | Alignment | not modelled | 96.8 | 13 | PDB header: transferase Chain: A: PDB Molecule: bergaptol o-methyltransferase; PDBTitle: crystal structure of bergaptol o-methyltransferase complex |
| 41 | c3g2qB | | Alignment | not modelled | 96.7 | 21 | PDB header: transferase Chain: B: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin |
| 42 | c5wp5A | | Alignment | not modelled | 96.7 | 14 | PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah |
| 43 | c4p7cb | | Alignment | not modelled | 96.7 | 10 | PDB header: transferase Chain: B: PDB Molecule: tRNA (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato |
| 44 | c5dpIB | | Alignment | not modelled | 96.6 | 13 | PDB header: transferase Chain: B: PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy |
| 45 | c2r3sA | | Alignment | not modelled | 96.5 | 9 | PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative o-methyltransferase (pnun_r0239) from nostoc punctiforme pcc 73102 at 2.15 a resolution |
| 46 | c3bgvC | | Alignment | not modelled | 96.5 | 10 | 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 |
| 47 | d2fk8a1 | | Alignment | not modelled | 96.5 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like |
| 48 | d1wzna1 | | Alignment | not modelled | 96.4 | 21 | PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of burkholderia glumiae tox a with bound s-2 adenylhomocysteine (sah) and 1,6-didemethyltoxoflavin |
| 49 | c5je0B | | Alignment | not modelled | 96.3 | 15 | PDB header: transferase Chain: A: PDB Molecule: coniferyl alcohol 9-o-methyltransferase; PDBTitle: crystal structure analysis of coniferyl alcohol 9-o-methyltransferase2 from linum nodiflorum in complex with coniferyl alcohol |
| 50 | c4e70A | | Alignment | not modelled | 96.3 | 12 | PDB header: plant protein, transferase Chain: A: PDB Molecule: isoflavanone 4'-o-methyltransferase'; PDBTitle: crystal structure of isoflavanone 4'-o-methyltransferase complexed2 with (+)-6a-hydroxymaackiain |
| 51 | c1zgaA | | Alignment | not modelled | 96.3 | 15 | 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 |
| 52 | c4necC | | Alignment | not modelled | 96.2 | 18 | PDB header: transferase Chain: C: PDB Molecule: caffein acid 3-o-methyltransferase; |
| 53 | c1kvzC | | Alignment | not modelled | 96.2 | 12 | PDB header: transferase Chain: C: PDB Molecule: caffein acid 3-o-methyltransferase; |

| | | | | | | |
|----|------------------------|-----------|--------------|------|----|--|
| 53 | c1ky2 | Alignment | not modelled | 96.2 | 12 | PDBTitle: crystal structure analysis of caffeic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase 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 |
| 54 | d1tpya | Alignment | not modelled | 96.2 | 13 | PDB header: transferase Chain: B: PDB Molecule: cur; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase |
| 55 | c5z9oA | Alignment | not modelled | 96.2 | 11 | 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 |
| 56 | c5thyB | Alignment | not modelled | 96.1 | 14 | PDB header: transferase,lyase Chain: B: PDB Molecule: cur; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase |
| 57 | c4ineB | Alignment | not modelled | 96.1 | 13 | 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 |
| 58 | c6pi9A | Alignment | not modelled | 96.1 | 18 | PDB header: transferase Chain: A: PDB Molecule: 16s rrna (guanine(1405)-n(7))-methyltransferase; PDBTitle: crystal structure of 16s rrna methylase rmtf in complex with s-2 adenosyl-l-homocysteine |
| 59 | d1l1ea | Alignment | not modelled | 96.1 | 9 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase PDB header: transferase |
| 60 | c6mroA | Alignment | not modelled | 96.1 | 14 | Chain: A: PDB Molecule: methyl transferase from methanoscincina acetylivors; PDBTitle: crystal structure of methyl transferase from methanoscincina2 acetylivors at 1.6 angstroms resolution, northeast structural3 genomics consortium (nsg) target mvr53. |
| 61 | c4krqB | Alignment | not modelled | 96.0 | 15 | 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 |
| 62 | c3lstB | Alignment | not modelled | 96.0 | 13 | PDB header: transferase Chain: B: PDB Molecule: calo1 methyltransferase; PDBTitle: crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form |
| 63 | c3cgB | Alignment | not modelled | 96.0 | 14 | 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 at 3.00 a resolution |
| 64 | c4htfA | Alignment | not modelled | 96.0 | 13 | 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. |
| 65 | d1im8a | Alignment | not modelled | 95.9 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO) |
| 66 | c4z2yA | Alignment | not modelled | 95.9 | 20 | PDB header: transferase Chain: A: PDB Molecule: calo6; PDBTitle: crystal structure of methyltransferase calo6 |
| 67 | c3h2bB | Alignment | not modelled | 95.8 | 15 | 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 |
| 68 | c3ofkA | Alignment | not modelled | 95.8 | 14 | PDB header: transferase Chain: A: PDB Molecule: nodulation protein s; PDBTitle: crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wmp9 in complex with s-adenosyl-l-homocysteine (sah) |
| 69 | c3pfhD | Alignment | not modelled | 95.8 | 13 | PDB header: transferase Chain: D: PDB Molecule: n-methyltransferase; PDBTitle: x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quin3n |
| 70 | c5ufmB | Alignment | not modelled | 95.8 | 16 | 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 |
| 71 | d1oria | Alignment | not modelled | 95.7 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase |
| 72 | c3dtmA | Alignment | not modelled | 95.7 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methyltransferase mm_2633; PDBTitle: crystal structure of putative methyltransferase-mm_2633 from2 methanoscincina mazei . |
| 73 | c6iv7B | Alignment | not modelled | 95.7 | 20 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase lepi; PDBTitle: the crystal structure of a sam-dependent enzyme from aspergillus2 flavus |
| 74 | c4kifB | Alignment | not modelled | 95.5 | 15 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase mppj; PDBTitle: crystal structure of methyltransferase from streptomyces hygroscopicus2 complexed with phenylpyruvic acid |
| 75 | c3m70A | Alignment | not modelled | 95.4 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae |

| | | | | | | |
|----|-------------------------|--|--------------|------|----|--|
| 76 | c5lkjA | | not modelled | 95.4 | 13 | PDB header: transferase Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: crystal structure of mouse carm1 in complex with ligand sa684 |
| 77 | c2p8jA | | not modelled | 95.4 | 12 | PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine-dependent methyltransferase; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 (np_349143.1) from clostridium acetobutylicum at 2.00 a resolution |
| 78 | c3lcvB | | not modelled | 95.3 | 23 | PDB header: transferase Chain: B: PDB Molecule: sisomicin-gentamicin resistance methylase sgm; PDBTitle: crystal structure of antibiotic related methyltransferase |
| 79 | c3f4kA | | not modelled | 95.3 | 13 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309. |
| 80 | d1f3la | | not modelled | 95.3 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase PDB header: transferase Chain: A: PDB Molecule: n-methyltransferase; PDBTitle: x-ray structure of the sugar n-methyltransferase keds8 from2 streptococcus sp atcc 53650 |
| 81 | c5bszA | | not modelled | 95.3 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase PDB header: transferase Chain: A: PDB Molecule: n-methyltransferase; PDBTitle: x-ray structure of the sugar n-methyltransferase keds8 from2 streptococcus sp atcc 53650 |
| 82 | d2o57a1 | | not modelled | 95.3 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 1; PDBTitle: structure of the predominant protein arginine methyltransferase prmt1 |
| 83 | c1orhA | | not modelled | 95.3 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 1; PDBTitle: structure of the predominant protein arginine methyltransferase prmt1 |
| 84 | d2ex4a1 | | not modelled | 95.2 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like PDB header: transferase Chain: A: PDB Molecule: 16s rrna methylase; PDBTitle: crystal structure of rrna methylase from escherichia coli |
| 85 | c3b89A | | not modelled | 95.1 | 20 | PDB header: transferase Chain: A: PDB Molecule: protein arginine methyltransferase 2; PDBTitle: crystal structure of zebrafish protein arginine methyltransferase 22 catalytic domain with sah |
| 86 | c5fubA | | not modelled | 95.1 | 17 | PDB header: transferase Chain: A: PDB Molecule: protein arginine methyltransferase 2; PDBTitle: crystal structure of zebrafish protein arginine methyltransferase 22 catalytic domain with sah |
| 87 | c4qnuH | | not modelled | 95.0 | 11 | PDB header: transferase Chain: H: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212 |
| 88 | c4x1oA | | not modelled | 94.9 | 15 | 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 |
| 89 | c4iv0B | | not modelled | 94.9 | 10 | 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 |
| 90 | c5iceA | | not modelled | 94.9 | 15 | PDB header: transferase Chain: A: PDB Molecule: (s)-noroclaurine 6-o-methyltransferase; PDBTitle: crystal structure of (s)-noroclaurine 6-o-methyltransferase with s-2 adenosyl-l-homocysteine and norlaudanosoline |
| 91 | c3e7pA | | not modelled | 94.9 | 13 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase from bacteroides2 vulgatus atcc 8482 |
| 92 | c5ubbA | | not modelled | 94.8 | 14 | PDB header: transferase Chain: A: PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b |
| 93 | d1kpga | | not modelled | 94.8 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anaerobic variabilis atcc 29413 at 2.11 a resolution |
| 94 | c3ggdA | | not modelled | 94.7 | 10 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae |
| 95 | c4iscA | | not modelled | 94.7 | 20 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a putative methyltransferase from pseudomonas2 syringae |
| 96 | c5hijA | | not modelled | 94.7 | 13 | PDB header: transferase Chain: A: PDB Molecule: glycine sarcosine n-methyltransferase; PDBTitle: crystal structure of glycine sarcosine n-methyltransferase from2 methanohalophilus portcalensis in complex with betaine |
| 97 | c5fwaA | | not modelled | 94.6 | 13 | PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 2; PDBTitle: crystal structure of mus musculus protein arginine methyltransferase 22 with cp1 |
| 98 | d1ve3a1 | | not modelled | 94.6 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; |
| 99 | d1y8ca | | not modelled | 94.6 | 12 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; |

| | | | | | | |
|-----|-------------------------|--|--------------|------|----|--|
| | | | | | | |
| 100 | c5x1xD | | not modelled | 94.6 | 14 | Family: CAC2371-like PDB header: transferase Chain: D: PDB Molecule: chemotaxis protein methyltransferase 1; PDBTitle: crystal structure of the c-terminal domain of cher1 containing sah |
| 101 | d1d2ha | | not modelled | 94.5 | 15 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase |
| 102 | d1g6q1 | | not modelled | 94.5 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase |
| 103 | c3ou7A | | not modelled | 94.4 | 17 | PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dphi-sam-hep complex |
| 104 | c2v7eB | | not modelled | 94.4 | 13 | PDB header: transferase Chain: B: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: crystal structure of coactivator-associated arginine2 methyltransferase 1 (carm1), unliganded |
| 105 | d1nkva | | not modelled | 94.3 | 11 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein YjhP |
| 106 | c3g5tA | | not modelled | 94.3 | 13 | PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast |
| 107 | c5bp9A | | not modelled | 94.3 | 16 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase protein; PDBTitle: crystal structure of sam-dependent methyltransferase from bacteroides fragilis in complex with s-adenosyl-l-homocysteine |
| 108 | d1xtpa | | not modelled | 94.3 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like |
| 109 | c6ecvB | | not modelled | 94.2 | 15 | PDB header: transferase Chain: B: PDB Molecule: std protein; PDBTitle: std o-mt residues 976-1266 |
| 110 | c6ccaA | | not modelled | 94.1 | 11 | PDB header: transferase Chain: A: PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase |
| 111 | c3ujcA | | not modelled | 94.1 | 14 | PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine |
| 112 | d1pjza | | not modelled | 94.0 | 12 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase |
| 113 | c1fp2A | | not modelled | 94.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: isoflavone o-methyltransferase; PDBTitle: crystal structure analysis of isoflavone o-methyltransferase |
| 114 | c6dnzA | | not modelled | 93.9 | 14 | PDB header: gene regulation Chain: A: PDB Molecule: arginine n-methyltransferase, putative; PDBTitle: trypanosoma brucei prmt1 enzyme-prozyme heterotetrameric complex with2 adohcy |
| 115 | c3tfwB | | not modelled | 93.8 | 9 | PDB header: transferase Chain: B: PDB Molecule: putative o-methyltransferase; PDBTitle: crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae |
| 116 | c6ectA | | not modelled | 93.8 | 16 | PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o-mt residues 961-1257 |
| 117 | d1af7a2 | | not modelled | 93.7 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Chemotaxis receptor methyltransferase CheR, C-terminal domain |
| 118 | c3vc2j | | not modelled | 93.6 | 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 |
| 119 | c4pneA | | not modelled | 93.6 | 14 | PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase snf |
| 120 | c4hgyC | | not modelled | 93.6 | 18 | PDB header: transferase Chain: C: PDB Molecule: ccb; PDBTitle: structure of the ccbj methyltransferase from streptomyces caelestis |