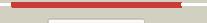
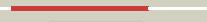


Phyre²

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0089 (-) _97755_98348 |
| Date | Tue Jul 23 14:50:12 BST 2019 |
| Unique Job ID | 4952baac1ee19212 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4p7cB_ |  Alignment |  | 99.9 | 26 | PDB header: transferase Chain: B: PDB Molecule: tRNA (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato |
| 2 | c4ineB_ |  Alignment |  | 99.9 | 23 | PDB header: transferase Chain: B: PDB Molecule: protein pmt-2; PDBTitle: crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegans complexed with s-adenosyl homocysteine and3 phosphoethanolamine |
| 3 | c5wp5A_ |  Alignment |  | 99.9 | 23 | PDB header: transferase Chain: A: PDB Molecule: phosphomethylethanolamine n-methyltransferase 2; PDBTitle: arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah |
| 4 | c4krhB_ |  Alignment |  | 99.9 | 26 | 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 |
| 5 | c3bkxB_ |  Alignment |  | 99.9 | 16 | PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution |
| 6 | c4kwca_ |  Alignment |  | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: bpuml; PDBTitle: structure of the plantazolicin methyltransferase bpuml in complex with2 sah |
| 7 | c2yr0A_ |  Alignment |  | 99.9 | 22 | PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8 |
| 8 | c4necC_ |  Alignment |  | 99.9 | 23 | 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 |
| 9 | c4qnuH_ |  Alignment |  | 99.9 | 22 | PDB header: transferase Chain: H: PDB Molecule: tRNA (mo5u34)-methyltransferase; PDBTitle: crystal structure of cmob bound with cx-sam in p21212 |
| 10 | c3ofkA_ |  Alignment |  | 99.9 | 24 | PDB header: transferase 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) |
| 11 | c3l8dA_ |  Alignment |  | 99.9 | 21 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from bacillus thuringiensis |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | c6f5zB | Alignment |  | 99.9 | 18 | 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 |
| 13 | c3vc2j | Alignment |  | 99.9 | 15 | 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 |
| 14 | c5mgzA | Alignment |  | 99.9 | 23 | PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobioc acid c(8)-methyltransferase; PDBTitle: streptomyces sphaeroides novo (8-demethylnovobioc acid2 methyltransferase) with sah |
| 15 | c3cc8A | Alignment |  | 99.9 | 16 | 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 |
| 16 | d1xxla | Alignment |  | 99.9 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 17 | c4kvzA | Alignment |  | 99.9 | 20 | PDB header: transferase Chain: A: PDB Molecule: baml; PDBTitle: crystal structure of the plantazolicin methyltransferase baml in2 complex with sah |
| 18 | c4iscA | Alignment |  | 99.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a putative methyltransferase from pseudomonas2 syringae |
| 19 | c1vl5B | Alignment |  | 99.9 | 20 | 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 |
| 20 | d1vl5a | Alignment |  | 99.9 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 21 | c5z9oA | Alignment | not modelled | 99.9 | 17 | 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 |
| 22 | c4htfA | Alignment | not modelled | 99.9 | 24 | 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. |
| 23 | c5egpB | Alignment | not modelled | 99.9 | 15 | PDB header: transferase Chain: B: PDB Molecule: ubie/coq5 family methyltransferase, putative; PDBTitle: crystal structure of the s-methyltransferase tmata |
| 24 | c3egeA | Alignment | not modelled | 99.9 | 19 | 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 |
| 25 | c4kdcA | Alignment | not modelled | 99.9 | 23 | PDB header: transferase Chain: A: PDB Molecule: 3-demethylubiquinone-9-3-methyltransferase; PDBTitle: crystal structure of ubig |
| 26 | c6gkvB | Alignment | not modelled | 99.9 | 17 | 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 |
| 27 | d2o57a1 | Alignment | not modelled | 99.9 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase PDB header: transferase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 28 | c3ujcA | Alignment | not modelled | 99.9 | 22 | Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmidium2 falciparum in complex with phosphocholine |
| 29 | c6ecvB | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: B: PDB Molecule: stid protein; PDBTitle: stid o- <i>mt</i> residues 976-1266 |
| 30 | c3lccA | Alignment | not modelled | 99.9 | 21 | PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabiopsis2 thaliana |
| 31 | c4hg2B | Alignment | not modelled | 99.9 | 24 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase type 11; PDBTitle: the structure of a putative type ii methyltransferase from2 anaeromyxobacter dehalogenans. |
| 32 | c2fk8A | Alignment | not modelled | 99.9 | 21 | 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 |
| 33 | c5kn4B | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: B: PDB Molecule: pavine n-methyltransferase; PDBTitle: pavine n-methyltransferase apoenzyme ph 6.0 |
| 34 | c5w7kA | Alignment | not modelled | 99.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag |
| 35 | c6bqcA | Alignment | not modelled | 99.9 | 24 | PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli |
| 36 | c3g5IA | Alignment | not modelled | 99.9 | 21 | PDB header: transferase Chain: A: PDB Molecule: putative s-adenosylmethionine dependent methyltransferase; PDBTitle: crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes |
| 37 | d1nkva | Alignment | not modelled | 99.9 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical Protein YjhP |
| 38 | c3e7pA | Alignment | not modelled | 99.9 | 18 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase from bacteroides2 vulgatus atcc 8482 |
| 39 | c6ectA | Alignment | not modelled | 99.9 | 20 | PDB header: transferase Chain: A: PDB Molecule: stie protein; PDBTitle: stie o- <i>mt</i> residues 961-1257 |
| 40 | d1kpga | Alignment | not modelled | 99.9 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 41 | d2fk8a1 | Alignment | not modelled | 99.9 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 42 | d1l1ea | Alignment | not modelled | 99.9 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 43 | d1ve3a1 | Alignment | not modelled | 99.9 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: CAC2371-like |
| 44 | c5fcda | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: mccc; PDBTitle: crystal structure of mccc protein |
| 45 | c4pneA | Alignment | not modelled | 99.9 | 26 | PDB header: biosynthetic protein Chain: A: PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase snpf |
| 46 | c3f4kA | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309. |
| 47 | c3ggdA | Alignment | not modelled | 99.9 | 20 | PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anaabaena variabilis atcc 29413 at 2.11 a resolution |
| 48 | d1d2ha | Alignment | not modelled | 99.9 | 23 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase |
| 49 | c2gs9A | Alignment | not modelled | 99.9 | 21 | PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tt1324; PDBTitle: crystal structure of tt1324 from thermus thermophilis hb8 |
| 50 | c6g4wq | Alignment | not modelled | 99.9 | 20 | 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 |
| 51 | d2i6ga1 | Alignment | not modelled | 99.8 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TehB-like |
| 52 | c3g5tA | Alignment | not modelled | 99.8 | 15 | PDB header: transferase Chain: A: PDB Molecule: trans-aconitate 3-methyltransferase; PDBTitle: crystal structure of trans-aconitate 3-methyltransferase from yeast |
| | | | | | | PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n- |

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|----|-------------------------|-----------|--------------|------|----|--|
| 53 | c4iv0B_ | Alignment | not modelled | 99.8 | 18 | methyltransferase, putative; PDBTitle: crystal structure of n-methyl transferase from plasmodium vivax2 complexed with s-adenosyl methionine and phosphate |
| 54 | d1xcla_ | Alignment | not modelled | 99.8 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase |
| 55 | c3mggB_ | Alignment | not modelled | 99.8 | 26 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyl transferase from methanoscarcina2 mazei |
| 56 | d2gh1a1 | Alignment | not modelled | 99.8 | 25 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like |
| 57 | c3bkwB_ | Alignment | not modelled | 99.8 | 29 | 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 |
| 58 | c4qttB_ | Alignment | not modelled | 99.8 | 19 | PDB header: transferase Chain: B: PDB Molecule: putative methyltransferase bud23; PDBTitle: structure of s. cerevisiae bud23-trm112 complex involved in formation of m7g1575 on 18s rrna (apo-form) |
| 59 | d1xvaa_ | Alignment | not modelled | 99.8 | 29 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase |
| 60 | d2avna1 | Alignment | not modelled | 99.8 | 23 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: UbiE/COQ5-like |
| 61 | d1r74a_ | Alignment | not modelled | 99.8 | 29 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase |
| 62 | c3ccfB_ | Alignment | not modelled | 99.8 | 23 | 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 |
| 63 | c1z3cA_ | Alignment | not modelled | 99.8 | 24 | PDB header: transferase Chain: A: PDB Molecule: mRNA capping enzyme; PDBTitle: encephalitozoan cuniculi mRNA cap (guanine-n7)2 methyltransferasein complexed with azoadomet |
| 64 | c3ou7A_ | Alignment | not modelled | 99.8 | 18 | PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: dhpi-sam-hep complex |
| 65 | c5bp9A_ | Alignment | not modelled | 99.8 | 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 |
| 66 | c3dlbI_ | Alignment | not modelled | 99.8 | 20 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus |
| 67 | d1ri5a_ | Alignment | not modelled | 99.8 | 24 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: mRNA cap (Guanine N-7) methyltransferase |
| 68 | d1kpia_ | Alignment | not modelled | 99.8 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 69 | c3e8sA_ | Alignment | not modelled | 99.8 | 27 | PDB header: transferase Chain: A: PDB Molecule: putative sam dependent methyltransferase; PDBTitle: crystal structure of putative sam dependent methyltransferasein2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution |
| 70 | d1jqa_ | Alignment | not modelled | 99.8 | 14 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Histamine methyltransferase |
| 71 | d1zx0a1 | Alignment | not modelled | 99.8 | 18 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase |
| 72 | c4krgB_ | Alignment | not modelled | 99.8 | 20 | PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 1; PDBTitle: semet haemomonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine |
| 73 | c3bgvC_ | Alignment | not modelled | 99.8 | 23 | 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 |
| 74 | c3pfhD_ | Alignment | not modelled | 99.8 | 20 | 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-quip3n |
| 75 | d1tpya_ | Alignment | not modelled | 99.8 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase |
| 76 | d2p7ia1 | Alignment | not modelled | 99.8 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | Family: UbiE/COQ5-like |
| 77 | c4x1oA_ | Alignment | not modelled | 99.8 | 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 <i>Catenulisporales acidiphilia</i> |
| | | | | | | PDB header: transferase |
| 78 | c3dlcA_ | Alignment | not modelled | 99.8 | 20 | Chain: A: PDB Molecule: putative S-adenosyl-L-methionine-dependent |
| | | | | | | PDBTitle: crystal structure of a putative S-adenosyl-L-methionine-dependent 2-methyltransferase (mmp1179) from <i>Methanococcus maripaludis</i> at 1.15 Å resolution |
| | | | | | | PDB header: transferase |
| 79 | c3qnhA_ | Alignment | not modelled | 99.8 | 21 | Chain: A: PDB Molecule: arsenic methyltransferase; |
| | | | | | | PDBTitle: arsm arsenic(iii) S-adenosylmethionine methyltransferase with as(iii) |
| | | | | | | Fold: S-adenosyl-L-methionine-dependent methyltransferases |
| 80 | d1pjza_ | Alignment | not modelled | 99.8 | 14 | Superfamily: S-adenosyl-L-methionine-dependent methyltransferases |
| | | | | | | Family: Thiopurine S-methyltransferase |
| | | | | | | PDB header: transferase |
| 81 | c3cggb_ | Alignment | not modelled | 99.8 | 19 | Chain: B: PDB Molecule: sam-dependent methyltransferase; |
| | | | | | | PDBTitle: crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from <i>Corynebacterium glutamicum</i> ATCC 13032 <i>kitasato</i> at 3.200 Å resolution |
| | | | | | | PDB header: transferase |
| 82 | c6mroA_ | Alignment | not modelled | 99.8 | 19 | Chain: A: PDB Molecule: methyl transferase from <i>Methanoscincus acetivorans</i> ; |
| | | | | | | PDBTitle: crystal structure of methyl transferase from <i>Methanoscincus acetivorans</i> at 1.6 Å resolution, northeast structural genomics consortium (nsg) target mvr53. |
| | | | | | | PDB header: transferase |
| 83 | c3bxoA_ | Alignment | not modelled | 99.8 | 18 | Chain: A: PDB Molecule: n,n-dimethyltransferase; |
| | | | | | | PDBTitle: crystal structure of <i>Streptomyces venezuelae</i> desvi |
| | | | | | | PDB header: transferase |
| 84 | c2xvmB_ | Alignment | not modelled | 99.8 | 18 | Chain: B: PDB Molecule: tellurite resistance protein tehb; |
| | | | | | | PDBTitle: crystal structure of the tellurite detoxification protein2 tehb from <i>E. coli</i> in complex with sah |
| | | | | | | PDB header: transferase |
| 85 | c2p35A_ | Alignment | not modelled | 99.8 | 20 | Chain: A: PDB Molecule: trans-aconitate 2-methyltransferase; |
| | | | | | | PDBTitle: crystal structure of trans-aconitate methyltransferase from <i>Agrobacterium tumefaciens</i> |
| | | | | | | PDB header: structural genomics, unknown function |
| 86 | c3e23A_ | Alignment | not modelled | 99.8 | 23 | Chain: A: PDB Molecule: uncharacterized protein rpa2492; |
| | | | | | | PDBTitle: crystal structure of the rpa2492 protein in complex with sam from <i>Rhodopseudomonas palustris</i> , northeast structural genomics consortium3 target rpr299 |
| | | | | | | PDB header: transferase |
| 87 | c2p7ib_ | Alignment | not modelled | 99.8 | 20 | Chain: B: PDB Molecule: hypothetical protein; |
| | | | | | | PDBTitle: crystal structure of a sam dependent methyl-transferase type 12 family2 protein (eca1738) from <i>Pectobacterium atrosepticum</i> scri1043 at 1.74 Å resolution |
| | | | | | | PDB header: transferase |
| 88 | c3h2bB_ | Alignment | not modelled | 99.8 | 22 | Chain: B: PDB Molecule: sam-dependent methyltransferase; |
| | | | | | | PDBTitle: crystal structure of the sam-dependent methyltransferase cg3271 from <i>Corynebacterium glutamicum</i> in complex with S-adenosyl-L-homocysteine and pyrophosphate. northeast structural genomics consortium target4 cgr113a |
| | | | | | | PDB header: transferase |
| 89 | c3hnra_ | Alignment | not modelled | 99.8 | 11 | Chain: A: PDB Molecule: probable methyltransferase bt9727_4108; |
| | | | | | | PDBTitle: crystal structure of a probable methyltransferase2 bt9727_4108 from <i>Bacillus thuringiensis</i> subsp. northeast3 structural genomics consortium target id bur219 |
| | | | | | | PDB header: transferase |
| 90 | c5evja_ | Alignment | not modelled | 99.8 | 27 | Chain: A: PDB Molecule: arsenite methyltransferase; |
| | | | | | | PDBTitle: x-ray crystal structure of crarsm, an arsenic (iii) S-adenosylmethionine methyltransferase from <i>Chlamydomonas reinhardtii</i> |
| | | | | | | Fold: S-adenosyl-L-methionine-dependent methyltransferases |
| 91 | d1p91a_ | Alignment | not modelled | 99.8 | 21 | Superfamily: S-adenosyl-L-methionine-dependent methyltransferases |
| | | | | | | Family: rRNA methyltransferase RlmA |
| | | | | | | PDB header: protein binding |
| 92 | c4xrpF_ | Alignment | not modelled | 99.8 | 16 | Chain: F: PDB Molecule: hen1; |
| | | | | | | PDBTitle: structure of the pnkp1/rnl/hen1 RNA repair complex |
| | | | | | | Fold: S-adenosyl-L-methionine-dependent methyltransferases |
| 93 | d1wzna1 | Alignment | not modelled | 99.8 | 22 | Superfamily: S-adenosyl-L-methionine-dependent methyltransferases |
| | | | | | | Family: CAC2371-like |
| | | | | | | PDB header: transferase |
| 94 | c5bszA_ | Alignment | not modelled | 99.8 | 18 | Chain: A: PDB Molecule: n-methyltransferase; |
| | | | | | | PDBTitle: x-ray structure of the sugar n-methyltransferase keds8 from <i>Streptallocteichus</i> sp. ATCC 53650 |
| | | | | | | PDB header: transferase/rna |
| 95 | c6dcba_ | Alignment | not modelled | 99.8 | 20 | Chain: A: PDB Molecule: 7sk snrRNA methylphosphate capping enzyme; |
| | | | | | | PDBTitle: structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk RNA |
| | | | | | | PDB header: structural genomics, unknown function |
| 96 | c3mera_ | Alignment | not modelled | 99.8 | 19 | Chain: A: PDB Molecule: slr1183 protein; |
| | | | | | | PDBTitle: crystal structure of the methyltransferase slr1183 from <i>Synechocystis</i> sp. PCC 6803, northeast structural genomics consortium target sgr145 |
| | | | | | | PDB header: transferase |
| 97 | c3busB_ | Alignment | not modelled | 99.8 | 30 | Chain: B: PDB Molecule: methyltransferase; |
| | | | | | | PDBTitle: crystal structure of rebm |
| | | | | | | PDB header: transferase |
| 98 | c5je0B_ | Alignment | not modelled | 99.8 | 18 | Chain: B: PDB Molecule: methyl transferase; |
| | | | | | | PDBTitle: crystal structure of <i>Burkholderia glumae</i> tox with bound S-2 adenosylhomocysteine (sah) and 1,6-didemethyltoxoflavin |
| | | | | | | PDB header: transferase |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 99 | c5ufmB | Alignment | not modelled | 99.8 | 24 | 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 |
| 100 | c5u18A | Alignment | not modelled | 99.8 | 20 | 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 |
| 101 | c3g2qA | Alignment | not modelled | 99.8 | 21 | PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin |
| 102 | c3m70A | Alignment | not modelled | 99.8 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stellirule resistance protein tehb homolog; PDBTitle: crystal structure of tehb from haemophilus influenzae |
| 103 | c4xcxA | Alignment | not modelled | 99.8 | 23 | PDB header: transferase Chain: A: PDB Molecule: small rna 2'-o-methyltransferase; PDBTitle: methyltransferase domain of small rna 2'-o-methyltransferase |
| 104 | c5gm2E | Alignment | not modelled | 99.8 | 21 | PDB header: transferase Chain: E: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1 |
| 105 | c2pxxA | Alignment | not modelled | 99.8 | 27 | PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein mgc2408; PDBTitle: human putative methyltransferase mgc2408 |
| 106 | c4rvgA | Alignment | not modelled | 99.8 | 13 | PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp |
| 107 | d2bzga1 | Alignment | not modelled | 99.8 | 13 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase |
| 108 | c5mpmA | Alignment | not modelled | 99.8 | 13 | PDB header: transferase Chain: A: PDB Molecule: citrinin polyketide synthase; PDBTitle: structure of the citrinin polyketide synthase cmet domain |
| 109 | c3mq2A | Alignment | not modelled | 99.8 | 22 | PDB header: transferase Chain: A: PDB Molecule: 16s rrna methyltransferase; PDBTitle: crystal structure of 16s rrna methyltransferase kamb |
| 110 | d2ex4a1 | Alignment | not modelled | 99.8 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like |
| 111 | c3m33B | Alignment | not modelled | 99.8 | 22 | 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 |
| 112 | d1xtpa | Alignment | not modelled | 99.8 | 20 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like |
| 113 | c3bgdB | Alignment | not modelled | 99.8 | 15 | PDB header: transferase Chain: B: PDB Molecule: thiopurine s-methyltransferase; PDBTitle: thiopurine s-methyltransferase |
| 114 | c5t39A | Alignment | not modelled | 99.8 | 16 | PDB header: transferase Chain: A: PDB Molecule: evdm01; PDBTitle: crystal structure of the n-terminal domain of evdm01 in the presence2 of sah and d-fucose |
| 115 | d1yzha1 | Alignment | not modelled | 99.8 | 17 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like |
| 116 | c6d6yA | Alignment | not modelled | 99.8 | 15 | PDB header: transferase Chain: A: PDB Molecule: apra methyltransferase 2; PDBTitle: apra methyltransferase 2 - gnat didomain in complex with sah |
| 117 | c4hgyC | Alignment | not modelled | 99.8 | 22 | PDB header: transferase Chain: C: PDB Molecule: ccbj; PDBTitle: structure of the ccbj methyltransferase from streptomyces caelestis |
| 118 | c3dtmA | Alignment | not modelled | 99.8 | 22 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methyltransferase mm_2633; PDBTitle: crystal structure of putative methyltransferase-mm_2633 from2 methanoscarsina maezi . |
| 119 | d1wg8a2 | Alignment | not modelled | 99.8 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: MraW-like putative methyltransferases |
| 120 | d1p1ca | Alignment | not modelled | 99.8 | 21 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Guanidinoacetate methyltransferase |