



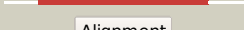

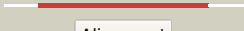









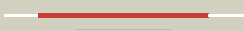
















# Phyre2

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD0503c_(cmaA2)_593874_594782 |
| Date          | Fri Jul 26 01:50:05 BST 2019    |
| Unique Job ID | 1c7fc5dfc08c8cf1                |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">d1kpia_</a> | <br>Alignment   |    | 100.0      | 100    | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Mycolic acid cyclopropane synthase  |
| 2  | <a href="#">c5z9oA_</a> | <br>Alignment   |    | 100.0      | 36     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase;<br><b>PDBTitle:</b> the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus |
| 3  | <a href="#">c6bqcA_</a> | <br>Alignment   |    | 100.0      | 35     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase;<br><b>PDBTitle:</b> cyclopropane fatty acid synthase from e. coli  |
| 4  | <a href="#">d1kpga_</a> | <br>Alignment   |   | 100.0      | 55     | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Mycolic acid cyclopropane synthase  |
| 5  | <a href="#">d1tpya_</a> | <br>Alignment |  | 100.0      | 57     | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Mycolic acid cyclopropane synthase  |
| 6  | <a href="#">c2fk8A_</a> | <br>Alignment |  | 100.0      | 52     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methoxy mycolic acid synthase 4;<br><b>PDBTitle:</b> crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine                |
| 7  | <a href="#">d1l1ea_</a> | <br>Alignment |  | 100.0      | 61     | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Mycolic acid cyclopropane synthase  |
| 8  | <a href="#">d2fk8a1</a> | <br>Alignment |  | 100.0      | 52     | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Mycolic acid cyclopropane synthase  |
| 9  | <a href="#">c6gkvB_</a> | <br>Alignment |  | 100.0      | 22     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> coclaurine n-methyltransferase;<br><b>PDBTitle:</b> crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah                       |
| 10 | <a href="#">c5kn4B_</a> | <br>Alignment |  | 100.0      | 21     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pavine n-methyltransferase;<br><b>PDBTitle:</b> pavine n-methyltransferase apoenzyme ph 6.0   |
| 11 | <a href="#">c4pneA_</a> | <br>Alignment |  | 100.0      | 16     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein;<br><b>PDBTitle:</b> crystal structure of the [4+2]-cyclase spnf  |

|    |                         |           |   |       |    |   |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | <a href="#">c5gm2E_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> E: <b>PDB Molecule:</b> o-methyltransferase;<br><b>PDBTitle:</b> crystal structure of methyltransferase tled complexed with sah and2 teleocidin a1  |
| 13 | <a href="#">d2o57a1</a> | Alignment |    | 100.0 | 17 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Mycolic acid cyclopropane synthase  |
| 14 | <a href="#">c5wp5A_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphomethylethanolamine n-methyltransferase 2;<br><b>PDBTitle:</b> arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah   |
| 15 | <a href="#">c4krhB_</a> | Alignment |    | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 2;<br><b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine  |
| 16 | <a href="#">c4ineB_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein pmt-2;<br><b>PDBTitle:</b> crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine   |
| 17 | <a href="#">c3busB_</a> | Alignment |    | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase;<br><b>PDBTitle:</b> crystal structure of rebm  |
| 18 | <a href="#">c3vc2J_</a> | Alignment |  | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> J: <b>PDB Molecule:</b> geranyl diphosphate 2-c-methyltransferase;<br><b>PDBTitle:</b> crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine |
| 19 | <a href="#">c3ujcA_</a> | Alignment |  | 100.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase;<br><b>PDBTitle:</b> phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine  |
| 20 | <a href="#">c4iv0B_</a> | Alignment |  | 100.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase, putative;<br><b>PDBTitle:</b> crystal structure of n-methyl transferase from plasmodium vivax2 complexed with s-adenosyl methionine and phosphate  |
| 21 | <a href="#">c6ectA_</a> | Alignment | not modelled  | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> stie protein;<br><b>PDBTitle:</b> stie o-mt residues 961-1257   |
| 22 | <a href="#">d1nkva_</a> | Alignment | not modelled  | 100.0 | 15 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Hypothetical Protein YjhP   |
| 23 | <a href="#">c3f4kA_</a> | Alignment | not modelled  | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;<br><b>PDBTitle:</b> crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.   |
| 24 | <a href="#">c3e7pA_</a> | Alignment | not modelled  | 100.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;<br><b>PDBTitle:</b> crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482   |
| 25 | <a href="#">c6ecvB_</a> | Alignment | not modelled  | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> stid protein;<br><b>PDBTitle:</b> stid o-mt residues 976-1266   |
| 26 | <a href="#">c3bkxB_</a> | Alignment | not modelled  | 99.9  | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase;<br><b>PDBTitle:</b> crystal structure of cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution                              |
| 27 | <a href="#">c4qnuH_</a> | Alignment | not modelled  | 99.9  | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> H: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase;<br><b>PDBTitle:</b> crystal structure of cmob bound with cx-sam in p21212  |
| 28 | <a href="#">c4p7cB_</a> | Alignment | not modelled  | 99.9  | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> trna (mo5u34)-methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative methyltransferase from   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | pseudomonas2 syringae pv. tomato<br><b>PDB header:</b> transferase   |
| 29 | <a href="#">c5egpB_</a> | Alignment | not modelled | 99.9 | 13 | <b>Chain:</b> B: <b>PDB Molecule:</b> ubie/coq5 family methyltransferase, putative;<br><b>PDBTitle:</b> crystal structure of the s-methyltransferase tmta  |
| 30 | <a href="#">c3ocjA_</a> | Alignment | not modelled | 99.9 | 14 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein;<br><b>PDBTitle:</b> the crystal structure of a possilbe exported protein from bordetella2 parapertussis   |
| 31 | <a href="#">c2yr0A_</a> | Alignment | not modelled | 99.9 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha0223;<br><b>PDBTitle:</b> crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8   |
| 32 | <a href="#">c4kdcA_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-demethylubiquinone-9 3-methyltransferase;<br><b>PDBTitle:</b> crystal structure of ubig  |
| 33 | <a href="#">c5fcdA_</a> | Alignment | not modelled | 99.9 | 9  | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mccd;<br><b>PDBTitle:</b> crystal structure of mccd protein  |
| 34 | <a href="#">d1vl5a_</a> | Alignment | not modelled | 99.9 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> UbiE/COQ5-like   |
| 35 | <a href="#">c1vl5B_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> unknown conserved protein bh2331;<br><b>PDBTitle:</b> crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution  |
| 36 | <a href="#">c1z3cA_</a> | Alignment | not modelled | 99.9 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme;<br><b>PDBTitle:</b> encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet   |
| 37 | <a href="#">d1ri5a_</a> | Alignment | not modelled | 99.9 | 14 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> mRNA cap (Guanine N-7) methyltransferase   |
| 38 | <a href="#">d2ex4a1</a> | Alignment | not modelled | 99.9 | 14 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> AD-003 protein-like  |
| 39 | <a href="#">c6f5zB_</a> | Alignment | not modelled | 99.9 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 24-sterol c-methyltransferase;<br><b>PDBTitle:</b> complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase  |
| 40 | <a href="#">c3bgvC_</a> | Alignment | not modelled | 99.9 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> mrna cap guanine-n7 methyltransferase;<br><b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah   |
| 41 | <a href="#">c5bp9A_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase protein;<br><b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from bacteroides2 fragilis in complex with s-adenosyl-l-homocysteine                                  |
| 42 | <a href="#">c3mggB_</a> | Alignment | not modelled | 99.9 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase;<br><b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 mazei  |
| 43 | <a href="#">c5w7kA_</a> | Alignment | not modelled | 99.9 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxag;<br><b>PDBTitle:</b> crystal structure of oxag  |
| 44 | <a href="#">d1xxla_</a> | Alignment | not modelled | 99.9 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> UbiE/COQ5-like   |
| 45 | <a href="#">c5je0B_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methyl transferase;<br><b>PDBTitle:</b> crystal structure of burkholderia glumae toxa with bound s-2 adenosylhomocysteine (sah) and 1,6-didemethyltoxoflavin   |
| 46 | <a href="#">d1xtpa_</a> | Alignment | not modelled | 99.9 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> AD-003 protein-like  |
| 47 | <a href="#">c3qnhA_</a> | Alignment | not modelled | 99.9 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arsenic methyltransferase;<br><b>PDBTitle:</b> arsm arsenic(iii) s-adenosylmethionine methyltransferase with as(iii)   |
| 48 | <a href="#">c3dlcA_</a> | Alignment | not modelled | 99.9 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosyl-l-methionine-dependent<br><b>PDBTitle:</b> crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution |
| 49 | <a href="#">c6g4wq_</a> | Alignment | not modelled | 99.9 | 21 | <b>PDB header:</b> ribosome<br><b>Chain:</b> Q: <b>PDB Molecule:</b> 40s ribosomal protein s16;<br><b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state a  |
| 50 | <a href="#">c3mq2A_</a> | Alignment | not modelled | 99.9 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methyltransferase;<br><b>PDBTitle:</b> crystal structure of 16s rrna methyltransferase kamb   |
| 51 | <a href="#">c3lccA_</a> | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methyl chloride transferase;<br><b>PDBTitle:</b> structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana   |
| 52 | <a href="#">d1r74a_</a> | Alignment | not modelled | 99.9 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Glycine N-methyltransferase  |
| 53 | <a href="#">c4qttB_</a> | Alignment | not modelled | 99.9 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative methyltransferase bud23;<br><b>PDBTitle:</b> structure of s. cerevisiae bud23-trm112 complex involved in formation2 of m7g1575 on 18s rrna (apo-form)   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 54 | <a href="#">c4obxD</a>  | Alignment | not modelled | 99.9 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase,<br><b>PDBTitle:</b> crystal structure of yeast coq5 in the apo form  |
| 55 | <a href="#">c5evjA</a>  | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arsenite methyltransferase;<br><b>PDBTitle:</b> x-ray crystal structure of crasm, an arsenic (iii) s-2 adenosylmethionine methyltransferase from chlamydomonas reinhardtii   |
| 56 | <a href="#">d1xvaa</a>  | Alignment | not modelled | 99.9 | 17 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Glycine N-methyltransferase  |
| 57 | <a href="#">d1jqea</a>  | Alignment | not modelled | 99.9 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Histamine methyltransferase  |
| 58 | <a href="#">c4x1oA</a>  | Alignment | not modelled | 99.9 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna (adenine(1408)-n(1))-methyltransferase;<br><b>PDBTitle:</b> crystal structure of the 16s rrna (adenine(1408)-n(1))-2 methyltransferase from catenulisporales acidiphilia  |
| 59 | <a href="#">c4necC</a>  | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transferase/antibiotic<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative sam-dependent methyltransferase;<br><b>PDBTitle:</b> conversion of a disulfide bond into a thioacetal group during2 echinomycin biosynthesis   |
| 60 | <a href="#">d2gh1a1</a> | Alignment | not modelled | 99.9 | 15 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> BC2162-like  |
| 61 | <a href="#">c3e8sA</a>  | Alignment | not modelled | 99.9 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative sam dependent methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution  |
| 62 | <a href="#">c3ou7A</a>  | Alignment | not modelled | 99.9 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sam-dependent methyltransferase;<br><b>PDBTitle:</b> dhpi-sam-hep complex  |
| 63 | <a href="#">c5t39A</a>  | Alignment | not modelled | 99.9 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> evdmo1;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of evdmo1 in the presence2 of sah and d-fucose  |
| 64 | <a href="#">c5mgzA</a>  | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 8-demethylnovobiocic acid c(8)-methyltransferase;<br><b>PDBTitle:</b> streptomyces spheroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah   |
| 65 | <a href="#">c4qdkB</a>  | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> magnesium-protoporphyrin o-methyltransferase;<br><b>PDBTitle:</b> crystal structure of magnesium protoporphyrin ix methyltransferase2 (chlm) from synechocystis pcc 6803 with bound sah  |
| 66 | <a href="#">d1wzna1</a> | Alignment | not modelled | 99.9 | 12 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> CAC2371-like   |
| 67 | <a href="#">c3ccfB</a>  | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase;<br><b>PDBTitle:</b> crystal structure of putative methyltransferase (yp_321342.1) from2 anaabaena variabilis atcc 29413 at 1.90 a resolution  |
| 68 | <a href="#">c5u18A</a>  | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-3" methyltransferase;<br><b>PDBTitle:</b> crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin   |
| 69 | <a href="#">d1im8a</a>  | Alignment | not modelled | 99.9 | 12 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Hypothetical protein HI0319 (YecO)   |
| 70 | <a href="#">c3g2qA</a>  | Alignment | not modelled | 99.9 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.24;<br><b>PDBTitle:</b> crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin   |
| 71 | <a href="#">c2gs9A</a>  | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tt1324;<br><b>PDBTitle:</b> crystal structure of tt1324 from thermus thermophilis hb8   |
| 72 | <a href="#">c5ubbA</a>  | Alignment | not modelled | 99.9 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha n-terminal protein methyltransferase 1b;<br><b>PDBTitle:</b> crystal structure of human alpha n-terminal protein methyltransferase2 1b   |
| 73 | <a href="#">c4htfA</a>  | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine-dependent methyltransferase;<br><b>PDBTitle:</b> crystal structure of s-adenosylmethionine-dependent methyltransferase2 from escherichia coli in complex with s-adenosylmethionine.   |
| 74 | <a href="#">c3h2bB</a>  | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase;<br><b>PDBTitle:</b> 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 |
| 75 | <a href="#">c3g5tA</a>  | Alignment | not modelled | 99.9 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trans-aconitate 3-methyltransferase;<br><b>PDBTitle:</b> crystal structure of trans-aconitate 3-methyltransferase from yeast   |

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| 76 | <a href="#">c4rvgA_</a> | Alignment | not modelled | 99.9 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-mycarose 3-c-methyltransferase;<br><b>PDBTitle:</b> crystal structure of mtmc in complex with sam and tdp  |
| 77 | <a href="#">d1xcla_</a> | Alignment | not modelled | 99.9 | 12 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Guanidinoacetate methyltransferase   |
| 78 | <a href="#">c3lecA_</a> | Alignment | not modelled | 99.9 | 14 | <b>PDB header:</b> structure genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadb-rossmann superfamily protein;<br><b>PDBTitle:</b> the crystal structure of a protein in the nadb-rossmann superfamily2 from streptococcus agalactiae to 1.8a   |
| 79 | <a href="#">c6ccaA_</a> | Alignment | not modelled | 99.9 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> disa protein;<br><b>PDBTitle:</b> crystal structure of dsza carbon methyltransferase   |
| 80 | <a href="#">c4hgyC_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> ccbj;<br><b>PDBTitle:</b> structure of the ccbj methyltransferase from streptomyces caelestis  |
| 81 | <a href="#">c3e23A_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rpa2492;<br><b>PDBTitle:</b> crystal structure of the rpa2492 protein in complex with sam from2 rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr299  |
| 82 | <a href="#">d2a14a1</a> | Alignment | not modelled | 99.9 | 15 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Arylamine N-methyltransferase  |
| 83 | <a href="#">c4krqB_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoethanolamine n-methyltransferase 1;<br><b>PDBTitle:</b> semet haemonchus contortus phosphoethanolamine n-methyltransferase 12 in complex with phosphoethanolamine and s-adenosylhomocysteine                                    |
| 84 | <a href="#">c3g5IA_</a> | Alignment | not modelled | 99.9 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative s-adenosylmethionine dependent methyltransferase;<br><b>PDBTitle:</b> crystal structure of putative s-adenosylmethionine dependent2 methyltransferase from listeria monocytogenes   |
| 85 | <a href="#">c5bxyB_</a> | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> rna methyltransferase;<br><b>PDBTitle:</b> crystal structure of rna methyltransferase from salinibacter ruber in2 complex with s-adenosyl-l-homocysteine   |
| 86 | <a href="#">c3ofkA_</a> | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nodulation protein s;<br><b>PDBTitle:</b> crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah)   |
| 87 | <a href="#">d1pjza_</a> | Alignment | not modelled | 99.8 | 18 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Thiopurine S-methyltransferase   |
| 88 | <a href="#">d1zx0a1</a> | Alignment | not modelled | 99.8 | 11 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Guanidinoacetate methyltransferase   |
| 89 | <a href="#">d1l3ia_</a> | Alignment | not modelled | 99.8 | 17 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Precorin-6Y methyltransferase (CbiT)   |
| 90 | <a href="#">c6ec3C_</a> | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> transferase, oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> methyltransferase domain-containing protein;<br><b>PDBTitle:</b> crystal structure of evdm01   |
| 91 | <a href="#">c3ku1E_</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> E: <b>PDB Molecule:</b> sam-dependent methyltransferase;<br><b>PDBTitle:</b> crystal structure of streptococcus pneumoniae sp1610, a putative trna2 (m1a22) methyltransferase, in complex with s-adenosyl-l-methionine   |
| 92 | <a href="#">d1ve3a1</a> | Alignment | not modelled | 99.8 | 13 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> CAC2371-like   |
| 93 | <a href="#">c5eovA_</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 16s/23s rrna (cytidine-2'-o)-methyltransferase tlya;<br><b>PDBTitle:</b> c-terminal domain of the 16s/23s rrna (cytidine-2'-o)-2 methyltransferase tlya.   |
| 94 | <a href="#">c3e05B_</a> | Alignment | not modelled | 99.8 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> precorin-6y c5,15-methyltransferase (decarboxylating);<br><b>PDBTitle:</b> crystal structure of precorin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15  |
| 95 | <a href="#">c5mptA_</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> citrinin polyketide synthase;<br><b>PDBTitle:</b> structure of the citrinin polyketide synthase cmet domain  |
| 96 | <a href="#">c3cc8A_</a> | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase;<br><b>PDBTitle:</b> crystal structure of a putative methyltransferase (bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution   |
| 97 | <a href="#">c3bxoA_</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethyltransferase;<br><b>PDBTitle:</b> crystal structure of streptomyces venezuelae desvi  |
| 98 | <a href="#">c3m70A_</a> | Alignment | not modelled | 99.8 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein tehb homolog;<br><b>PDBTitle:</b> crystal structure of tehb from haemophilus influenzae   |
| 99 | <a href="#">c3pfdD_</a> | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> n-methyltransferase;<br><b>PDBTitle:</b> x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n<br><b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases |

|     |                         |           |              |      |    |  |
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| 100 | <a href="#">d1y8ca_</a> | Alignment | not modelled | 99.8 | 13 | <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> CAC2371-like  |
| 101 | <a href="#">c3l8dA_</a> | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase;<br><b>PDBTitle:</b> crystal structure of methyltransferase from bacillus thuringiensis  |
| 102 | <a href="#">c6mroA_</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyl transferase from methanosarcina acetivorans;<br><b>PDBTitle:</b> crystal structure of methyl transferase from methanosarcina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53. |
| 103 | <a href="#">c2p35A_</a> | Alignment | not modelled | 99.8 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trans-aconitate 2-methyltransferase;<br><b>PDBTitle:</b> crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens  |
| 104 | <a href="#">d1yzha1</a> | Alignment | not modelled | 99.8 | 16 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> TrmB-like  |
| 105 | <a href="#">c5hijA_</a> | Alignment | not modelled | 99.8 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine sarcosine n-methyltransferase;<br><b>PDBTitle:</b> crystal structure of glycine sarcosine n-methyltransferase from2 methanohalophilus portucalensis in complex with betaine  |
| 106 | <a href="#">c3eeyL_</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> J: <b>PDB Molecule:</b> putative rrna methylase;<br><b>PDBTitle:</b> crystal structure of putative rrna-methylase from clostridium2 thermocellum   |
| 107 | <a href="#">c6d6yA_</a> | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> apra methyltransferase 2;<br><b>PDBTitle:</b> apra methyltransferase 2 - gnat didomain in complex with sah   |
| 108 | <a href="#">c3ndjA_</a> | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase;<br><b>PDBTitle:</b> x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product   |
| 109 | <a href="#">c3opnA_</a> | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative hemolysin;<br><b>PDBTitle:</b> the crystal structure of a putative hemolysin from lactococcus lactis  |
| 110 | <a href="#">c5do0A_</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein lysine methyltransferase 1;<br><b>PDBTitle:</b> the structure of pkmt1 from rickettsia prowazekii  |
| 111 | <a href="#">c5ufmB_</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase domain protein;<br><b>PDBTitle:</b> crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine                       |
| 112 | <a href="#">c6q56C_</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> trna (adenine(22)-n(1))-methyltransferase;<br><b>PDBTitle:</b> crystal structure of the b. subtilis m1a22 trna methyltransferase trmk  |
| 113 | <a href="#">c5dplB_</a> | Alignment | not modelled | 99.8 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein lysine methyltransferase 2;<br><b>PDBTitle:</b> the structure of pkmt2 from rickettsia typhi in complex with adohcy  |
| 114 | <a href="#">c3gwzB_</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> mmcr;<br><b>PDBTitle:</b> structure of the mitomycin 7-o-methyltransferase mmcr  |
| 115 | <a href="#">d2bzga1</a> | Alignment | not modelled | 99.8 | 13 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Thiopurine S-methyltransferase   |
| 116 | <a href="#">c4kvzA_</a> | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> baml;<br><b>PDBTitle:</b> crystal structure of the plantazolicin methyltransferase baml in2 complex with sah   |
| 117 | <a href="#">c6dcbA_</a> | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> transferase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> 7sk snrna methylphosphate capping enzyme;<br><b>PDBTitle:</b> structure of methylphosphate capping enzyme methyltransferase domain2 in complex with 5' end of 7sk rna  |
| 118 | <a href="#">c3gnlB_</a> | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein, duf633, lmf2365_1472;<br><b>PDBTitle:</b> structure of uncharacterized protein (lmf2365_1472) from listeria2 monocytogenes serotype 4b  |
| 119 | <a href="#">d1m6ya2</a> | Alignment | not modelled | 99.8 | 20 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> MraW-like putative methyltransferases  |
| 120 | <a href="#">c2pxxA_</a> | Alignment | not modelled | 99.8 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mgc2408;<br><b>PDBTitle:</b> human putative methyltransferase mgc2408  |