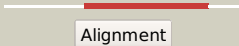



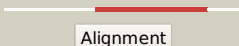

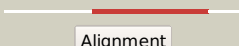

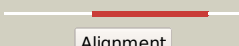

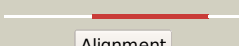

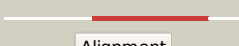











Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2143 (-) _2402985_2404043 |
| Date | Mon Aug 5 13:25:26 BST 2019 |
| Unique Job ID | 1c3d8e0d41fd3d09 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | d1wd5a_ |  Alignment |  | 100.0 | 44 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 2 | c1ecjB_ |  Alignment |  | 99.7 | 20 | PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer |
| 3 | c1gph1_ |  Alignment |  | 99.7 | 23 | PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis |
| 4 | d1hgxa_ |  Alignment |  | 99.6 | 20 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 5 | c5eswB_ |  Alignment |  | 99.6 | 22 | PDB header: transferase Chain: B: PDB Molecule: purine/pyrimidine phosphoribosyltransferase; PDBTitle: crystal structure of apo hypoxanthine-guanine2 phosphoribosyltransferase from legionella pneumophila |
| 6 | c1yfaA_ |  Alignment |  | 99.6 | 20 | PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis |
| 7 | d1yfa1 |  Alignment |  | 99.6 | 20 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 8 | d1ecfa1 |  Alignment |  | 99.5 | 23 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 9 | d1gph11 |  Alignment |  | 99.5 | 23 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 10 | c2ywtA_ |  Alignment |  | 99.5 | 18 | PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8 |
| 11 | d1j7ja_ |  Alignment |  | 99.5 | 20 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c3kb8A_ | Alignment | | 99.5 | 23 | PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp |
| 13 | c4rhyC_ | Alignment | | 99.5 | 22 | PDB header: transferase/transferase inhibitor Chain: C: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structures of mycobacterium tuberculosis 6-oxopurine2 phosphoribosyltransferase which is a potential target for drug3 development against this disease |
| 14 | d1tc1a_ | Alignment | | 99.5 | 17 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 15 | c4lyyA_ | Alignment | | 99.5 | 21 | PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 shewanela pealeana atcc 700345, nysgrc target 029677. |
| 16 | c3o7mD_ | Alignment | | 99.5 | 15 | PDB header: transferase Chain: D: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor' |
| 17 | c4pfqF_ | Alignment | | 99.4 | 24 | PDB header: transferase Chain: F: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 brachybacterium faecium dsm 4810, nysgrc target 029763. |
| 18 | c5t3oB_ | Alignment | | 99.4 | 22 | PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate synthetase ii2 from thermus thermophilus |
| 19 | d1xtta1 | Alignment | | 99.4 | 19 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 20 | c3lpnB_ | Alignment | | 99.4 | 23 | PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp). |
| 21 | d1zn7a1 | Alignment | not modelled | 99.4 | 30 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 22 | c5zgoB_ | Alignment | not modelled | 99.3 | 20 | PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of apt2 from thermus thermophilus hb8 |
| 23 | c4rqbB_ | Alignment | not modelled | 99.3 | 14 | PDB header: transferase Chain: B: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of a hypoxanthine phosphoribosyltransferase (target2 id nysgrc-029686) from staphylococcus aureus (tetragonal space group) |
| 24 | c1pzmB_ | Alignment | not modelled | 99.3 | 23 | PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp |
| 25 | d1g9sa_ | Alignment | not modelled | 99.3 | 19 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 26 | c2dy0A_ | Alignment | not modelled | 99.3 | 26 | PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli |
| 27 | c4z1oB_ | Alignment | not modelled | 99.3 | 18 | PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpirt) from2 sulfolobus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium |
| 28 | c3dezA_ | Alignment | not modelled | 99.3 | 19 | PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | from2 streptococcus mutans |
| 29 | c4lzaB_ | Alignment | not modelled | 99.3 | 24 | PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 thermoanaerobacter pseudethanolicus atcc 33223, nysgrc target 029700. |
| 30 | dlz7ga1 | Alignment | not modelled | 99.3 | 23 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 31 | diy0ba1 | Alignment | not modelled | 99.3 | 16 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 32 | dlpzma_ | Alignment | not modelled | 99.2 | 22 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 33 | d2aeaa1 | Alignment | not modelled | 99.2 | 17 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 34 | dlvdma1 | Alignment | not modelled | 99.2 | 25 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 35 | c5yw2D_ | Alignment | not modelled | 99.2 | 26 | PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis. |
| 36 | dlg2qa_ | Alignment | not modelled | 99.2 | 27 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 37 | c5vogA_ | Alignment | not modelled | 99.2 | 16 | PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound ppppp |
| 38 | c3efhB_ | Alignment | not modelled | 99.2 | 20 | PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1 |
| 39 | dlvcha1 | Alignment | not modelled | 99.2 | 17 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 40 | c5ipfA_ | Alignment | not modelled | 99.2 | 19 | PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase (hgprt); PDBTitle: crystal structure of hypoxanthine-guanine phosphoribosyltransferase2 from schistosoma mansoni in complex with imp |
| 41 | c2c4kD_ | Alignment | not modelled | 99.1 | 23 | PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase-associated protein PDBTitle: crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39) |
| 42 | dl1lqa_ | Alignment | not modelled | 99.1 | 19 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 43 | c5mp7C_ | Alignment | not modelled | 99.1 | 27 | PDB header: transferase Chain: C: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosylpyrophosphate synthetase from2 mycobacterium smegmatis |
| 44 | c4s2uA_ | Alignment | not modelled | 99.1 | 23 | PDB header: transferase Chain: A: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli |
| 45 | dl15ea_ | Alignment | not modelled | 99.1 | 21 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 46 | c4trbA_ | Alignment | not modelled | 99.1 | 19 | PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfobolus solfataricus adenine phosphoribosyltransferase |
| 47 | c2ehjA_ | Alignment | not modelled | 99.1 | 26 | PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase |
| 48 | dlu9ya2 | Alignment | not modelled | 99.1 | 29 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like |
| 49 | dlp17b_ | Alignment | not modelled | 99.1 | 21 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 50 | d2c4ka2 | Alignment | not modelled | 99.1 | 25 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like |
| 51 | dl05oa_ | Alignment | not modelled | 99.1 | 22 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 52 | dlw30a_ | Alignment | not modelled | 99.1 | 29 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 53 | c2wnsB_ | Alignment | not modelled | 99.1 | 16 | PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (oprtae) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp) |
| | | | | | | PDB header: ligase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; |

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|----|-------------------------|-----------|--------------|------|----|---|
| 54 | c6nfeB | Alignment | not modelled | 99.1 | 27 | PDBTitle: crystal structure of ribose-phosphate pyrophosphokinase from2 legionella pneumophila with bound amp, adp, and ribose-5-phosphate |
| 55 | c5kapA | Alignment | not modelled | 99.0 | 26 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: trypanosoma brucei hypoxanthine-guanine phosphoribosyltransferase in2 complex with a 9-(4-(phosphonobutyl)hypoxanthine |
| 56 | c2p1zA | Alignment | not modelled | 99.0 | 33 | PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase; PDBTitle: crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae |
| 57 | c4m0kD | Alignment | not modelled | 99.0 | 27 | PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 rhodothermus marinus dsm 4252, nysgrc target 029775. |
| 58 | c5hkiD | Alignment | not modelled | 99.0 | 30 | PDB header: transferase Chain: D: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis h37rv orotate2 phosphoribosyltransferase in complex with fe(iii) dicitrate |
| 59 | c1u9yD | Alignment | not modelled | 99.0 | 34 | PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii |
| 60 | d1o57a2 | Alignment | not modelled | 99.0 | 20 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 61 | c1o57A | Alignment | not modelled | 99.0 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis |
| 62 | c1dkrB | Alignment | not modelled | 99.0 | 19 | PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation. |
| 63 | d1a3ca | Alignment | not modelled | 99.0 | 31 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 64 | d2igba1 | Alignment | not modelled | 99.0 | 26 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 65 | d1cjbA | Alignment | not modelled | 99.0 | 18 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 66 | c4pawA | Alignment | not modelled | 98.9 | 20 | PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: structure of hypothetical protein hp1257. |
| 67 | d1dkua2 | Alignment | not modelled | 98.9 | 21 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like |
| 68 | c3dahB | Alignment | not modelled | 98.9 | 30 | PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei |
| 69 | c4twbB | Alignment | not modelled | 98.9 | 18 | PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: sulfobolus solfataricus ribose-phosphate pyrophosphokinase |
| 70 | c5e38D | Alignment | not modelled | 98.9 | 23 | PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structural basis of mapping the spontaneous mutations with 5-2 flourouracil in uracil phosphoribosyltransferase from mycobacterium3 tuberculosis |
| 71 | d1ufra | Alignment | not modelled | 98.9 | 29 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 72 | d1fsga | Alignment | not modelled | 98.9 | 28 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 73 | c5vn4A | Alignment | not modelled | 98.8 | 28 | PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase, putative; PDBTitle: crystal structure of adenine phosphoribosyl transferase from2 trypanosoma brucei in complex with amp, pyrophosphate, and ribose-5-3 phosphate |
| 74 | c6apsA | Alignment | not modelled | 98.8 | 22 | PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: trypanosoma brucei hypoxanthine guanine phosphoribosyltransferase in2 complex with [(2-((guanine-9h-yl)methyl)propane-1,3 diyl)bis(oxy)3]bis(methylene)diphosphonic acid |
| 75 | c3m3hA | Alignment | not modelled | 98.7 | 20 | PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor' |
| 76 | c2yzkC | Alignment | not modelled | 98.7 | 28 | PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix |
| 77 | d1qb7a | Alignment | not modelled | 98.7 | 21 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| 78 | c2e55D_ | Alignment | not modelled | 98.7 | 19 | PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus |
| 79 | d1mzva_ | Alignment | not modelled | 98.6 | 24 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 80 | c6ar9A_ | Alignment | not modelled | 98.5 | 25 | PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase, putative; PDBTitle: crystal structure of hypoxanthine-guanine-xanthine2 phosphoribosyltransferase in complex with [(2-{{[2-(2-amino-6-oxo-1,6,3 dihydro-9h-purin-9-yl)ethyl]}(e)-2-phosphonoethyl]amino}ethoxy)4 methyl]phosphonic acid |
| 81 | c2jbhA_ | Alignment | not modelled | 98.5 | 24 | PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase domain-containing protein 1; PDBTitle: human phosphoribosyl transferase domain containing 1 |
| 82 | d1v9sa1 | Alignment | not modelled | 98.5 | 22 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 83 | c3mjdA_ | Alignment | not modelled | 98.5 | 15 | PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis. |
| 84 | d1lh0a_ | Alignment | not modelled | 98.5 | 36 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 85 | c3qw4B_ | Alignment | not modelled | 98.4 | 22 | PDB header: transferase, lyase Chain: B: PDB Molecule: ump synthase; PDBTitle: structure of leishmania donovani ump synthase |
| 86 | d1nula_ | Alignment | not modelled | 98.4 | 22 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 87 | c3n2IA_ | Alignment | not modelled | 98.3 | 28 | PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961 |
| 88 | c2przB_ | Alignment | not modelled | 98.3 | 14 | PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed with omp |
| 89 | d1bd3a_ | Alignment | not modelled | 98.0 | 18 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 90 | c2jkzB_ | Alignment | not modelled | 98.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'-3 monophosphate) (orthorhombic crystal form) |
| 91 | c3dmpD_ | Alignment | not modelled | 97.9 | 29 | PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase from2 burkholderia pseudomallei |
| 92 | d1dqna_ | Alignment | not modelled | 97.5 | 19 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases) |
| 93 | c4fymA_ | Alignment | not modelled | 97.5 | 16 | PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of plasmodium falciparum orotate2 phosphoribosyltransferase |
| 94 | c2qahA_ | Alignment | not modelled | 97.3 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: 2-pyrone-4,6-dicarboxylic acid hydrolase; PDBTitle: crystal structure of the 2-pyrone-4,6-dicarboxylic acid hydrolase from2 sphingomonas paucimobiliis |
| 95 | c4do7B_ | Alignment | not modelled | 97.2 | 32 | PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase 2; PDBTitle: crystal structure of an amidohydrolase (cog3618) from burkholderia2 multivorans (target efi-500235) with bound zn, space group c2 |
| 96 | c4mupC_ | Alignment | not modelled | 96.7 | 17 | PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of agrobacterium tumefaciens atu3138 (efi target2 505157), apo structure |
| 97 | d2dvtA1 | Alignment | not modelled | 96.1 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like |
| 98 | c4i6kA_ | Alignment | not modelled | 95.8 | 9 | PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase family protein; PDBTitle: crystal structure of probable 2-pyrone-4,6-dicarboxylic acid hydrolase2 abaye1769 (target efi-505029) from acinetobacter baumannii with3 citric acid bound |
| 99 | c2wm1A_ | Alignment | not modelled | 95.6 | 15 | PDB header: lyase Chain: A: PDB Molecule: 2-amino-3-carboxymuconate-6-semialdehyde PDBTitle: the crystal structure of human alpha-amino-beta-2 carboxymuconate-epsilon-semialdehyde decarboxylase in3 complex with 1,3- dihydroxyacetonephosphate suggests a4 regulatory link between nad synthesis and glycolysis |
| 100 | d2hbva1 | Alignment | not modelled | 95.6 | 26 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like |
| 101 | c3irsB_ | Alignment | not modelled | 95.5 | 15 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bb4693; PDBTitle: crystal structure of uncharacterized tim-barrel protein |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | bb4693 from2 bordetella bronchiseptica |
| 102 | d2ffia1 | Alignment | not modelled | 95.4 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like |
| 103 | c4l5pD | Alignment | not modelled | 95.0 | 15 | PDB header: lyase Chain: D: PDB Molecule: 5-carboxyvanillate decarboxylase; PDBTitle: crystal structure of 5-carboxyvanillate decarboxylase from2 sphingomonas paucimobilis complexed with 4-hydroxy-3-methoxy-5-3 nitrobenzoic acid |
| 104 | d2f6ka1 | Alignment | not modelled | 94.4 | 11 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like |
| 105 | c3lj6A | Alignment | not modelled | 94.0 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 lactobacillus acidophilus |
| 106 | c4infA | Alignment | not modelled | 93.4 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: metal-dependent hydrolase; PDBTitle: crystal structure of amidohydrolase saro_0799 (target efi-505250) from2 novosphingobium aromaticivorans dsm 12444 with bound calcium |
| 107 | c3nurA | Alignment | not modelled | 93.1 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus |
| 108 | c4hk6D | Alignment | not modelled | 92.7 | 17 | PDB header: lyase Chain: D: PDB Molecule: uracil-5-carboxylate decarboxylase; PDBTitle: crystal structure of cordyceps militaris idcase in complex with 5-2 nitro-uracil |
| 109 | d2gwga1 | Alignment | not modelled | 90.8 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like |
| 110 | d2c4ka1 | Alignment | not modelled | 90.6 | 17 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like |
| 111 | c6omqA | Alignment | not modelled | 89.5 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: ptmu3; PDBTitle: crystal structure of ptmu3 complexed with ptm substrate |
| 112 | d1dkua1 | Alignment | not modelled | 89.4 | 17 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like |
| 113 | d1u9ya1 | Alignment | not modelled | 89.2 | 10 | Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like |
| 114 | c6dxsB | Alignment | not modelled | 88.8 | 18 | PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: 4-oxalomesaconate hydratase; PDBTitle: crystal structure of the ligj hydratase e284q mutant substrate complex2 with (3z)-2-keto-4-carboxy-3-hexenedioate |
| 115 | c3gg7A | Alignment | not modelled | 87.6 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized metalloprotein; PDBTitle: crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans |
| 116 | c5vn5A | Alignment | not modelled | 85.1 | 7 | PDB header: hydrolase Chain: A: PDB Molecule: 2,2',3-trihydroxy-3'-methoxy-5,5'-dicarboxybiphenyl meta- PDBTitle: crystal structure of ligy from sphingobium sp. strain syk-6 |
| 117 | d1vi2a1 | Alignment | not modelled | 84.9 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain |
| 118 | d1xwya1 | Alignment | not modelled | 83.5 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like |
| 119 | c1e8cB | Alignment | not modelled | 81.8 | 18 | PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamate-2,6-diaminopimelate PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli |
| 120 | d1m1na | Alignment | not modelled | 81.7 | 11 | Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein |