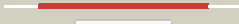



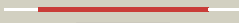



















Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2829c_(-)_3136630_3137022 |
| Date | Wed Aug 7 12:50:49 BST 2019 |
| Unique Job ID | 542e7c4ca6490861 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3zvkc_ |  Alignment |  | 99.9 | 13 | PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter |
| 2 | c6nklA_ |  Alignment |  | 99.9 | 14 | PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae |
| 3 | c3tndC_ |  Alignment |  | 99.9 | 16 | PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex |
| 4 | c5l6mC_ |  Alignment |  | 99.9 | 20 | PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form) |
| 5 | d2h1ca1 |  Alignment |  | 99.9 | 20 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 6 | c4xgrG_ |  Alignment |  | 99.9 | 16 | PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species |
| 7 | c3h87B_ |  Alignment |  | 99.8 | 16 | PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis |
| 8 | c2fe1A_ |  Alignment |  | 99.8 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum |
| 9 | d2fe1a1 |  Alignment |  | 99.8 | 21 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 10 | c3dboB_ |  Alignment |  | 99.8 | 17 | PDB header: toxin/antitoxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis |
| 11 | c6a7vG_ |  Alignment |  | 99.8 | 14 | PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c5wzfB_ | Alignment | | 99.8 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: 23s rrna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin |
| 13 | c5sv2A_ | Alignment | | 99.8 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis |
| 14 | d1v96a1 | Alignment | | 99.8 | 16 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 15 | c4chgC_ | Alignment | | 99.8 | 13 | PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis |
| 16 | d1y82a1 | Alignment | | 99.8 | 16 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 17 | c5x3tD_ | Alignment | | 99.8 | 16 | PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis |
| 18 | d1v8pa_ | Alignment | | 99.3 | 19 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 19 | c1v8pK_ | Alignment | | 99.3 | 19 | PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum |
| 20 | d1w8ia_ | Alignment | | 99.1 | 13 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 21 | c3i8oA_ | Alignment | not modelled | 98.8 | 14 | PDB header: rna binding protein Chain: A: PDB Molecule: kh domain-containing protein mj1533; PDBTitle: a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661. |
| 22 | c3ix7A_ | Alignment | not modelled | 98.7 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ttha0540; PDBTitle: crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8 |
| 23 | c5ywwA_ | Alignment | not modelled | 98.5 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase |
| 24 | d1o4wa_ | Alignment | not modelled | 98.4 | 17 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 25 | c5f4hF_ | Alignment | not modelled | 98.4 | 17 | PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase |
| 26 | c2lcqA_ | Alignment | not modelled | 97.7 | 14 | PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii |
| 27 | c5yz4A_ | Alignment | not modelled | 97.4 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24 |
| 28 | c5jppd_ | Alignment | not modelled | 97.4 | 21 | PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome |
| | | | | | | PDB header: rna binding protein |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c2hwwC_ | Alignment | not modelled | 96.9 | 22 | Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6 |
| 30 | c4mj7B_ | Alignment | not modelled | 95.7 | 13 | PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23 |
| 31 | c3v33A_ | Alignment | not modelled | 81.3 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif |
| 32 | c3v32B_ | Alignment | not modelled | 80.2 | 35 | PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain |
| 33 | c2hwyB_ | Alignment | not modelled | 70.0 | 7 | PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5. |
| 34 | d1tfra2 | Alignment | not modelled | 56.2 | 20 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 35 | c6g5iy_ | Alignment | not modelled | 55.8 | 16 | PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r |
| 36 | d1a77a2 | Alignment | not modelled | 41.0 | 21 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 37 | c4hecB_ | Alignment | not modelled | 35.5 | 25 | PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis |
| 38 | d1cmwa2 | Alignment | not modelled | 34.1 | 39 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 39 | c3q8lA_ | Alignment | not modelled | 27.3 | 14 | PDB header: hydrolase/dna Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+ |
| 40 | c3zddA_ | Alignment | not modelled | 23.8 | 14 | PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium |
| 41 | c2izoA_ | Alignment | not modelled | 23.5 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex |
| 42 | d1rxwa2 | Alignment | not modelled | 22.1 | 12 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 43 | d1ul1x2 | Alignment | not modelled | 21.9 | 14 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 44 | c2ihnA_ | Alignment | not modelled | 20.0 | 17 | PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate |
| 45 | c3qeaZ_ | Alignment | not modelled | 19.4 | 19 | PDB header: hydrolase/dna Chain: Z: PDB Molecule: exonuclease 1; PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii) |
| 46 | d1mc8a2 | Alignment | not modelled | 17.0 | 13 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 47 | c1b43A_ | Alignment | not modelled | 14.6 | 14 | PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus |
| 48 | c1jqsB_ | Alignment | not modelled | 14.3 | 11 | PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog |
| 49 | c2mdtA_ | Alignment | not modelled | 14.1 | 13 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfobolus solfataricus p2 |
| 50 | c1rxvA_ | Alignment | not modelled | 11.5 | 11 | PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna |
| 51 | c1ut8B_ | Alignment | not modelled | 10.9 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease |
| 52 | c4g25A_ | Alignment | not modelled | 9.9 | 32 | PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rnase p 1 (prorp1) from a.2 thaliana, semet substituted form with sr |
| 53 | c1a77A_ | Alignment | not modelled | 9.0 | 20 | PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii |
| 54 | d1xo1a2 | Alignment | not modelled | 8.4 | 17 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 55 | c5dizB_ | Alignment | not modelled | 7.4 | 30 | PDB header: hydrolase Chain: B: PDB Molecule: proteinaceous rnase p 2; PDBTitle: crystal structure of nuclear proteinaceous rnase p 2 |

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| | | | | | (prorp2) from a.2 thaliana |
| 56 | c4wa8A_ | Alignment | not modelled | 6.9 | 18 PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease |
| 57 | c5br9C_ | Alignment | not modelled | 6.7 | 56 PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein with similarity to2 peptidase yeaz from pseudomonas aeruginosa |
| 58 | c4pn7A_ | Alignment | not modelled | 6.4 | 15 PDB header: transcription Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of the tfiih p34 n-terminal domain |
| 59 | c2hsnA_ | Alignment | not modelled | 5.4 | 14 PDB header: ligase/rna binding protein Chain: A: PDB Molecule: methionyl-trna synthetase, cytoplasmic; PDBTitle: structural basis of yeast aminoacyl-trna synthetase complex2 formation revealed by crystal structures of two binary sub-3 complexes |