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| Description | RVBD1962c_(-)_2204873_2205280 |
| Date | Mon Aug 5 13:25:06 BST 2019 |
| Unique Job ID | beac800aeb7052db |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | d1v8pa_ |  Alignment |  | 99.7 | 21 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 2 | c1v8pK_ |  Alignment |  | 99.7 | 21 | PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum |
| 3 | d2fe1a1 |  Alignment |  | 99.7 | 21 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 4 | c2fe1A_ |  Alignment |  | 99.7 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum |
| 5 | c5wzfb_ |  Alignment |  | 99.6 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: 23s rna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin |
| 6 | c4xgrG_ |  Alignment |  | 99.5 | 21 | PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species |
| 7 | d2h1ca1 |  Alignment |  | 99.5 | 26 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 8 | c6a7vG_ |  Alignment |  | 99.4 | 17 | PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex |
| 9 | c3h87B_ |  Alignment |  | 99.4 | 17 | PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis |
| 10 | c3zvkc_ |  Alignment |  | 99.4 | 17 | 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 |
| 11 | d1y82a1 |  Alignment |  | 99.3 | 15 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c6nklA_ | Alignment | | 99.2 | 14 | PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae |
| 13 | c5x3tD_ | Alignment | | 99.2 | 18 | PDB header: antitoxin/toxin Chain: D; PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis |
| 14 | c4chgC_ | Alignment | | 99.2 | 13 | PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis |
| 15 | d1v96a1 | Alignment | | 99.2 | 19 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 16 | c5l6mC_ | Alignment | | 99.1 | 16 | PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form) |
| 17 | c3tndC_ | Alignment | | 99.1 | 17 | PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex |
| 18 | c5sv2A_ | Alignment | | 99.0 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis |
| 19 | c3dboB_ | Alignment | | 98.9 | 19 | 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 |
| 20 | c3i8oA_ | Alignment | | 98.7 | 16 | 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. |
| 21 | c3ix7A_ | Alignment | not modelled | 98.5 | 27 | 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 |
| 22 | d1w8ia_ | Alignment | not modelled | 98.3 | 14 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 23 | d1o4wa_ | Alignment | not modelled | 97.9 | 17 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 24 | c5ywwA_ | Alignment | not modelled | 97.9 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase |
| 25 | c2hwwC_ | Alignment | not modelled | 97.9 | 16 | PDB header: rna binding protein Chain: C; PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6 |
| 26 | c5f4hF_ | Alignment | not modelled | 97.8 | 16 | PDB header: hydrolase Chain: F; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase |
| 27 | c2lcqA_ | Alignment | not modelled | 97.8 | 16 | PDB header: metal binding protein Chain: A; PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii |
| 28 | c5jpdq_ | Alignment | not modelled | 96.3 | 15 | PDB header: ribosome Chain: D; PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome |
| 29 | c6n5iv_ | Alignment | not modelled | 95.5 | 17 | PDB header: ribosome Chain: Y; PDB Molecule: 40s ribosomal protein s24; |

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| 29 | c0g9ly_ | Alignment | not modelled | 93.3 | 17 | PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r |
| 30 | c5yz4A_ | Alignment | not modelled | 95.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24 |
| 31 | c2mdtA_ | Alignment | not modelled | 93.0 | 18 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus solfataricus p2 |
| 32 | c4mj7B_ | Alignment | not modelled | 92.5 | 9 | PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23 |
| 33 | c2hwyB_ | Alignment | not modelled | 72.2 | 17 | PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5. |
| 34 | d1tfra2 | Alignment | not modelled | 69.2 | 7 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 35 | c4mwaA_ | Alignment | not modelled | 46.4 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis |
| 36 | c2zkr9_ | Alignment | not modelled | 41.2 | 29 | PDB header: ribosomal protein/rna Chain: 9: PDB Molecule: 60s ribosomal protein l32; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 37 | c4a1cX_ | Alignment | not modelled | 39.3 | 16 | PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l32; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4. |
| 38 | c3j3be_ | Alignment | not modelled | 38.6 | 26 | PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein l6; PDBTitle: structure of the human 60s ribosomal proteins |
| 39 | c3zf7i_ | Alignment | not modelled | 34.4 | 11 | PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l18; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 40 | c3cceY_ | Alignment | not modelled | 34.2 | 33 | PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l32e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535a |
| 41 | d1vqoy1 | Alignment | not modelled | 34.2 | 33 | Fold: Barstar-like Superfamily: Ribosomal protein L32e Family: Ribosomal protein L32e |
| 42 | c5mq9A_ | Alignment | not modelled | 32.4 | 16 | PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant) |
| 43 | d3eeqa1 | Alignment | not modelled | 32.0 | 10 | Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like |
| 44 | d1y81a1 | Alignment | not modelled | 26.8 | 5 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 45 | c3j21b_ | Alignment | not modelled | 24.5 | 29 | PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l2p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |
| 46 | c3lotC_ | Alignment | not modelled | 23.6 | 14 | PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution |
| 47 | c3c6cA_ | Alignment | not modelled | 23.2 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution |
| 48 | c2duwA_ | Alignment | not modelled | 22.9 | 20 | PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae |
| 49 | c3no5C_ | Alignment | not modelled | 22.6 | 29 | PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution |
| 50 | d1ulza2 | Alignment | not modelled | 22.4 | 13 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like |
| 51 | c3e02A_ | Alignment | not modelled | 21.5 | 33 | PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution |
| 52 | c3iz5h_ | Alignment | not modelled | 21.4 | 21 | PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l7a (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 53 | d2j9ga2 | Alignment | not modelled | 20.9 | 18 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like |

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|----|--------------------------|-----------|--------------|------|----|--|
| 54 | d1iuka_ | Alignment | not modelled | 20.6 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 55 | c5zmyf_ | Alignment | not modelled | 20.5 | 14 | PDB header: hydrolase Chain: F; PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids |
| 56 | c3e49A_ | Alignment | not modelled | 18.5 | 38 | PDB header: metal binding protein Chain: A; PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution |
| 57 | c3chvA_ | Alignment | not modelled | 18.1 | 29 | PDB header: metal binding protein Chain: A; PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution |
| 58 | c2ihnA_ | Alignment | not modelled | 17.8 | 5 | PDB header: hydrolase/dna Chain: A; PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate |
| 59 | c2y7eA_ | Alignment | not modelled | 17.7 | 33 | PDB header: lyase Chain: A; PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form) |
| 60 | c4nncA_ | Alignment | not modelled | 17.0 | 14 | PDB header: lyase Chain: A; PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate |
| 61 | d2w6ka1 | Alignment | not modelled | 14.8 | 27 | Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like |
| 62 | d1xoia2 | Alignment | not modelled | 14.5 | 11 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 63 | d1cmwa2 | Alignment | not modelled | 13.6 | 20 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 64 | c3v33A_ | Alignment | not modelled | 13.3 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif |
| 65 | c3v32B_ | Alignment | not modelled | 13.0 | 20 | PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain |
| 66 | c1s1i0_ | Alignment | not modelled | 11.8 | 45 | PDB header: ribosome Chain: 0; PDB Molecule: 60s ribosomal protein l32; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h. |
| 67 | d1kzyc2 | Alignment | not modelled | 9.9 | 33 | Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1 |
| 68 | d2csua1 | Alignment | not modelled | 9.2 | 24 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 69 | d1w96a2 | Alignment | not modelled | 8.4 | 16 | Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like |
| 70 | c2cokA_ | Alignment | not modelled | 7.7 | 20 | PDB header: transferase Chain: A; PDB Molecule: poly [adp-ribose] polymerase-1; PDBTitle: solution structure of brct domain of poly(adp-ribose)2 polymerase-1 |
| 71 | c3eeqB_ | Alignment | not modelled | 6.7 | 10 | PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative cobalamin biosynthesis protein g homolog; PDBTitle: crystal structure of a putative cobalamin biosynthesis protein g2 homolog from sulfolobus solfataricus |
| 72 | c3ghfA_ | Alignment | not modelled | 6.7 | 16 | PDB header: cell cycle Chain: A; PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium |
| 73 | c1gr0A_ | Alignment | not modelled | 6.6 | 13 | PDB header: isomerase Chain: A; PDB Molecule: inositol-3-phosphate synthase; PDBTitle: myo-inositol 1-phosphate synthase from mycobacterium2 tuberculosis in complex with nad and zinc. |
| 74 | d1j6ua1 | Alignment | not modelled | 6.5 | 20 | Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain |
| 75 | d1xmx_a_ | Alignment | not modelled | 5.5 | 24 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899 |
| 76 | c3ff4A_ | Alignment | not modelled | 5.4 | 20 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412 |
| 77 | c1u1iC_ | Alignment | not modelled | 5.3 | 21 | PDB header: isomerase Chain: C; PDB Molecule: myo-inositol-1-phosphate synthase; PDBTitle: myo-inositol phosphate synthase mips from a. fulgidus |