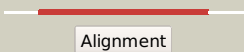

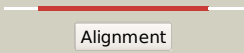

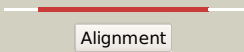

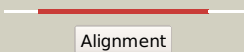

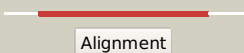

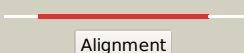

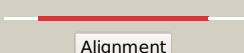





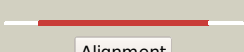

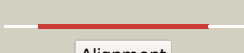



Phyre2

| | |
|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2759c (-) _3070885_3071280 |
| Date | Wed Aug 7 12:50:41 BST 2019 |
| Unique Job ID | cb583297ed071ec3 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4xgrG_ |  Alignment |  | 100.0 | 40 | PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species |
| 2 | d2h1ca1 |  Alignment |  | 99.9 | 17 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 3 | c5wzfB_ |  Alignment |  | 99.8 | 21 | 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 |
| 4 | c3dboB_ |  Alignment |  | 99.8 | 21 | 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 |
| 5 | c3zvkc_ |  Alignment |  | 99.8 | 10 | PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to a dna fragment from their promoter |
| 6 | c3h87B_ |  Alignment |  | 99.8 | 20 | PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis |
| 7 | c5l6mC_ |  Alignment |  | 99.8 | 16 | PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form) |
| 8 | c6nklA_ |  Alignment |  | 99.8 | 16 | PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae |
| 9 | c5sv2A_ |  Alignment |  | 99.8 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis |
| 10 | c3tndC_ |  Alignment |  | 99.8 | 16 | PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex |
| 11 | c6a7vG_ |  Alignment |  | 99.8 | 22 | PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c5x3tD_ | Alignment | | 99.8 | 19 | PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis |
| 13 | d1v96a1 | Alignment | | 99.8 | 15 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 14 | c4chgC_ | Alignment | | 99.7 | 21 | PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis |
| 15 | d1y82a1 | Alignment | | 99.7 | 15 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 16 | 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 |
| 17 | d2fe1a1 | Alignment | | 99.7 | 21 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 18 | d1w8ia_ | Alignment | | 99.5 | 11 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 19 | d1v8pa_ | Alignment | | 99.3 | 18 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 20 | c1v8pK_ | Alignment | | 99.3 | 16 | PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum |
| 21 | c3ix7A_ | Alignment | not modelled | 98.3 | 16 | 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 | c3i8oA_ | Alignment | not modelled | 97.9 | 17 | 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. |
| 23 | c2lcqA_ | Alignment | not modelled | 97.8 | 18 | PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii |
| 24 | d1o4wa_ | Alignment | not modelled | 97.3 | 15 | Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain |
| 25 | c5ywwA_ | Alignment | not modelled | 97.2 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase |
| 26 | c5f4hF_ | Alignment | not modelled | 97.0 | 12 | PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase |
| 27 | c2hwwC_ | Alignment | not modelled | 95.9 | 14 | PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6 |
| 28 | c5jppd_ | Alignment | not modelled | 93.8 | 23 | PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome |
| | | | | | | PDB header: hydrolase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c5yz4A_ | Alignment | not modelled | 92.2 | 16 | Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24 |
| 30 | c6g5iy_ | Alignment | not modelled | 89.8 | 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 |
| 31 | c2hwyB_ | Alignment | not modelled | 81.2 | 11 | PDB header: rna binding protein Chain: B; PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5. |
| 32 | c4mj7B_ | Alignment | not modelled | 79.4 | 17 | 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 | c3v33A_ | Alignment | not modelled | 70.6 | 13 | PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 conserved domain with zinc-finger motif |
| 34 | c3v32B_ | Alignment | not modelled | 69.8 | 13 | PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 n-terminal conserved domain |
| 35 | d1cmwa2 | Alignment | not modelled | 48.5 | 19 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 36 | d1xo1a2 | Alignment | not modelled | 31.8 | 15 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 37 | c3zddA_ | Alignment | not modelled | 23.4 | 15 | 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 |
| 38 | d1tfra2 | Alignment | not modelled | 12.8 | 14 | Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain |
| 39 | c4g94B_ | Alignment | not modelled | 11.8 | 12 | PDB header: dna binding protein Chain: B; PDB Molecule: orf067; PDBTitle: g1 orf67 / staphylococcus aureus sigmaa domain 4 complex |
| 40 | c3rqcB_ | Alignment | not modelled | 11.0 | 8 | PDB header: transferase Chain: B; PDB Molecule: probable lipoamide acyltransferase; PDBTitle: crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum |
| 41 | c4mitG_ | Alignment | not modelled | 10.5 | 21 | PDB header: signaling protein Chain: G; PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpk4 pbd |
| 42 | c4g25A_ | Alignment | not modelled | 10.2 | 19 | 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 |
| 43 | c2ihna_ | Alignment | not modelled | 9.4 | 15 | PDB header: hydrolase/dna Chain: A; PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate |
| 44 | c1ut8B_ | Alignment | not modelled | 7.3 | 15 | PDB header: hydrolase Chain: B; PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease |
| 45 | c1cmwA_ | Alignment | not modelled | 7.3 | 19 | PDB header: transferase Chain: A; PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain |
| 46 | d3eeqa1 | Alignment | not modelled | 6.4 | 6 | Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like |
| 47 | c4pn7A_ | Alignment | not modelled | 5.8 | 19 | PDB header: transcription Chain: A; PDB Molecule: putative transcription factor; PDBTitle: crystal structure of the tfiih p34 n-terminal domain |
| 48 | c1jqsB_ | Alignment | not modelled | 5.4 | 19 | 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 |