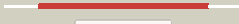
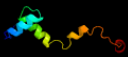

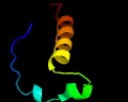
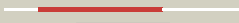












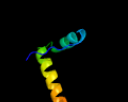




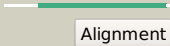

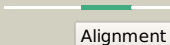
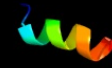
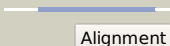
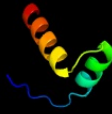
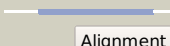
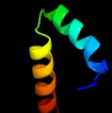


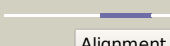

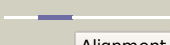


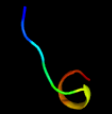
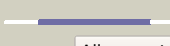

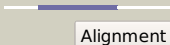

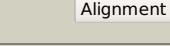
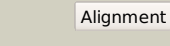
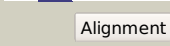
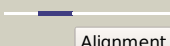
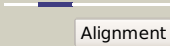



Phyre2

| | |
|------------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1113 (-)_1239421_1239618 |
| Date | Wed Jul 31 22:05:19 BST 2019 |
| Unique Job ID | 8f0188bd07d5621b |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c6a7vU_ |  Alignment |  | 99.7 | 27 | PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapp11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex |
| 2 | c2bj3D_ |  Alignment |  | 95.4 | 17 | PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nkr-apo |
| 3 | d2bj7a1 |  Alignment |  | 94.9 | 18 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 4 | c2ca9B_ |  Alignment |  | 94.6 | 21 | PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation |
| 5 | d2hzaa1 |  Alignment |  | 93.9 | 33 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 6 | c1q5vB_ |  Alignment |  | 93.3 | 33 | PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr |
| 7 | d2hza1 |  Alignment |  | 87.3 | 34 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 8 | c5cegC_ |  Alignment |  | 82.5 | 19 | PDB header: toxin Chain: C: PDB Molecule: addiction module antidote protein, copg/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum |
| 9 | c2k5jB_ |  Alignment |  | 77.6 | 16 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1 |
| 10 | c3kxeD_ |  Alignment |  | 68.8 | 20 | PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex |
| 11 | c4me7E_ |  Alignment |  | 67.1 | 11 | PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | c6iyaD_ |  Alignment |  | 40.5 | 20 | PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso |
| 13 | c5vgtA_ |  Alignment |  | 40.4 | 20 | PDB header: viral protein Chain: A: PDB Molecule: gene 7 protein; PDBTitle: x-ray structure of bacteriophage sf6 tail adaptor protein gp7 |
| 14 | c2rbfB_ |  Alignment |  | 21.0 | 19 | PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2) |
| 15 | c2kelB_ |  Alignment |  | 20.7 | 11 | PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1 |
| 16 | c3fmtF_ |  Alignment |  | 19.7 | 50 | PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna |
| 17 | c1y66D_ |  Alignment |  | 19.0 | 20 | PDB header: de novo protein Chain: D: PDB Molecule: engrailed homeodomain; PDBTitle: dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant |
| 18 | c1rxrD_ |  Alignment |  | 18.5 | 50 | PDB header: replication inhibitor Chain: D: PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein |
| 19 | d1rxra1 |  Alignment |  | 18.5 | 50 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like |
| 20 | c2zq5A_ |  Alignment |  | 16.3 | 33 | PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form) |
| 21 | c2mnqA_ |  Alignment | not modelled | 16.3 | 35 | PDB header: protein binding Chain: A: PDB Molecule: thymosin alpha-1; PDBTitle: 1h, 13c, and 15n chemical shift assignments for thymosin alpha 1 |
| 22 | c2l9iA_ |  Alignment | not modelled | 15.8 | 36 | PDB header: peptide binding protein Chain: A: PDB Molecule: thymosin alpha-1; PDBTitle: nmr structure of thymosin alpha-1 |
| 23 | c2q2kA_ |  Alignment | not modelled | 14.1 | 27 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein |
| 24 | c2q2kB_ |  Alignment | not modelled | 14.0 | 27 | PDB header: dna binding protein/dna Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein |
| 25 | c3plxB_ |  Alignment | not modelled | 9.0 | 27 | PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168 |
| 26 | c1vc3B_ |  Alignment | not modelled | 8.7 | 64 | PDB header: lyase Chain: B: PDB Molecule: l-aspartate-alpha-decarboxylase heavy chain; PDBTitle: crystal structure of l-aspartate-alpha-decarboxylase |
| 27 | c1uheA_ |  Alignment | not modelled | 8.4 | 36 | PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase alpha chain; PDBTitle: crystal structure of aspartate decarboxylase, isoasparagine complex |
| 28 | c1pt1B_ |  Alignment | not modelled | 7.7 | 25 | PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine |
| | | | | | | Fold: Rubredoxin-like |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|---|
| 29 | d1qf8a_ | Alignment | not modelled | 7.4 | 28 | Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit |
| 30 | d1ppya_ | Alignment | not modelled | 7.3 | 25 | Fold: Double psi beta-barrel Superfamily: ADC-like Family: Pyruvoyl dependent aspartate decarboxylase, ADC |
| 31 | d2cpga_ | Alignment | not modelled | 7.1 | 19 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 32 | c1ea4K_ | Alignment | not modelled | 7.1 | 19 | PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex |
| 33 | c2k9iB_ | Alignment | not modelled | 6.7 | 13 | PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus |
| 34 | c3j47P_ | Alignment | not modelled | 6.3 | 19 | PDB header: protein binding Chain: P: PDB Molecule: 26s proteasome regulatory subunit rpn5; PDBTitle: formation of an intricate helical bundle dictates the assembly of the 2 26s proteasome lid |
| 35 | c2c45F_ | Alignment | not modelled | 6.2 | 45 | PDB header: lyase Chain: F: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: native precursor of pyruvoyl dependent aspartate decarboxylase |
| 36 | c3ougA_ | Alignment | not modelled | 6.0 | 25 | PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis |
| 37 | c3ms1l_ | Alignment | not modelled | 5.9 | 50 | PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: recognition of the amber stop codon by release factor rf1. this entry2 3ms1 contains 50s ribosomal subunit. the 30s ribosomal subunit can be3 found in pdb entry 3mr8. molecule b in the same asymmetric unit is4 deposited as 3mrz (50s) and 3ms0 (30s). |
| 38 | c3mrzl_ | Alignment | not modelled | 5.9 | 50 | PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: recognition of the amber stop codon by release factor rf1. this entry2 3mrz contains 50s ribosomal subunit. the 30s ribosomal subunit can be3 found in pdb entry 3ms0. molecule a in the same asymmetric unit is4 deposited as 3mr8 (50s) and 3ms1 (30s). |
| 39 | d1lrqa_ | Alignment | not modelled | 5.8 | 14 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Omega transcriptional repressor |