







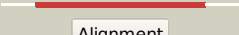

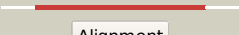






















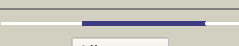
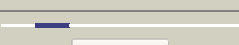
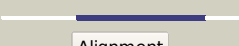
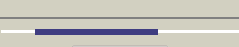
Phyre2

| | |
|---------------|--------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3757c_proW_4202788_4203477 |
| Date | Fri Aug 9 18:20:46 BST 2019 |
| Unique Job ID | 1ae3466db0831c6f |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4ymuC_ |  Alignment |  | 99.9 | 17 | PDB header: protein binding/transport protein Chain: C: PDB Molecule: abc-type amino acid transport system, permease component; PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps |
| 2 | d2onkc1 |  Alignment |  | 99.9 | 19 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 3 | c2onkC_ |  Alignment |  | 99.9 | 19 | PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda |
| 4 | d3d31c1 |  Alignment |  | 99.9 | 18 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 5 | c3d31D_ |  Alignment |  | 99.9 | 18 | PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans |
| 6 | c4tqvI_ |  Alignment |  | 99.9 | 16 | PDB header: transport protein Chain: I: PDB Molecule: algm1; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate |
| 7 | d3dhwa1 |  Alignment |  | 99.9 | 23 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 8 | c2r6gF_ |  Alignment |  | 99.9 | 18 | PDB header: hydrolase/transport protein Chain: F: PDB Molecule: maltose transport system permease protein malF; PDBTitle: the crystal structure of the e. coli maltose transporter |
| 9 | d2r6gf2 |  Alignment |  | 99.9 | 18 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 10 | c4tqvJ_ |  Alignment |  | 99.9 | 15 | PDB header: transport protein Chain: J: PDB Molecule: algm2; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate |
| 11 | c3fh6F_ |  Alignment |  | 99.9 | 17 | PDB header: transport protein Chain: F: PDB Molecule: maltose transport system permease protein malF; PDBTitle: crystal structure of the resting state maltose transporter from e.2 coli |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | d2r6gg1 | Alignment |  | 99.8 | 17 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 13 | c5kbuA | Alignment |  | 93.3 | 14 | PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor 2,voltage-dependent calcium channel PDBTitle: cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution |
| 14 | c2m8gX | Alignment |  | 32.8 | 23 | PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators |
| 15 | d1umqa | Alignment |  | 28.8 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 16 | c1umqA | Alignment |  | 28.8 | 10 | PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity |
| 17 | d1ntca | Alignment |  | 28.4 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 18 | c4l5eA | Alignment |  | 27.1 | 13 | PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain |
| 19 | d1fipa | Alignment |  | 18.0 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 20 | d1etob | Alignment |  | 15.4 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 21 | d1etxa | Alignment | not modelled | 13.4 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 22 | c3e7lD | Alignment | not modelled | 13.0 | 19 | PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain |
| 23 | c1g2hA | Alignment | not modelled | 11.1 | 20 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae |
| 24 | d1g2ha | Alignment | not modelled | 11.1 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 25 | c2ks1A | Alignment | not modelled | 9.3 | 17 | PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation |
| 26 | c2jwaA | Alignment | not modelled | 9.3 | 17 | PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure |
| 27 | c2cw1A | Alignment | not modelled | 9.2 | 26 | PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein |
| 28 | c2lhuA | Alignment | not modelled | 8.6 | 29 | PDB header: structural protein Chain: A: PDB Molecule: mybpc3 protein; PDBTitle: structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain |

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|----|-------------------------|---|--------------|-----|----|--|
| 29 | c2momC_ |  Alignment | not modelled | 8.3 | 17 | PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles |
| 30 | c2momB_ |  Alignment | not modelled | 8.3 | 17 | PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles |
| 31 | c5xu1M_ |  Alignment | not modelled | 7.7 | 11 | PDB header: transport protein Chain: M: PDB Molecule: abc transporter permease; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6 |
| 32 | c5m7nA_ |  Alignment | not modelled | 7.7 | 16 | PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystal direct automated mounting and cryo-cooling3 technology |
| 33 | c6f2dJ_ |  Alignment | not modelled | 5.9 | 22 | PDB header: protein transport Chain: J: PDB Molecule: flagellar biosynthetic protein fliq; PDBTitle: a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus. |
| 34 | c6f2dI_ |  Alignment | not modelled | 5.9 | 22 | PDB header: protein transport Chain: I: PDB Molecule: flagellar biosynthetic protein fliq; PDBTitle: a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus. |
| 35 | c5lj7B_ |  Alignment | not modelled | 5.8 | 13 | PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21) |
| 36 | c1ojlD_ |  Alignment | not modelled | 5.7 | 26 | PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding |
| 37 | c4m48A_ |  Alignment | not modelled | 5.4 | 12 | PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism |