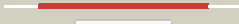



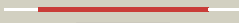




















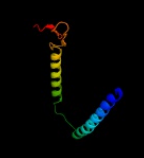

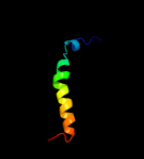







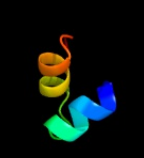





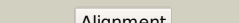
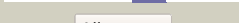




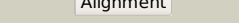


# Phyre2

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD1237_(sugB)_1379861_1380685 |
| Date          | Wed Jul 31 22:05:32 BST 2019    |
| Unique Job ID | 187334c69e0e591b                |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">d2r6gg1</a> |  Alignment   |    | 100.0      | 31     | <b>Fold:</b> MetI-like<br><b>Superfamily:</b> MetI-like<br><b>Family:</b> MetI-like   |
| 2  | <a href="#">c4tqvj_</a> |  Alignment   |    | 100.0      | 25     | <b>PDB header:</b> transport protein<br><b>Chain:</b> J; <b>PDB Molecule:</b> algm2;<br><b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate   |
| 3  | <a href="#">c3fh6F_</a> |  Alignment   |    | 100.0      | 19     | <b>PDB header:</b> transport protein<br><b>Chain:</b> F; <b>PDB Molecule:</b> maltose transport system permease protein malf;<br><b>PDBTitle:</b> crystal structure of the resting state maltose transporter from e.2 coli                                      |
| 4  | <a href="#">c4tqvj_</a> |  Alignment   |    | 100.0      | 14     | <b>PDB header:</b> transport protein<br><b>Chain:</b> I; <b>PDB Molecule:</b> algm1;<br><b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate   |
| 5  | <a href="#">c2r6gF_</a> |  Alignment |  | 100.0      | 22     | <b>PDB header:</b> hydrolase/transport protein<br><b>Chain:</b> F; <b>PDB Molecule:</b> maltose transport system permease protein malf;<br><b>PDBTitle:</b> the crystal structure of the e. coli maltose transporter  |
| 6  | <a href="#">d2onkc1</a> |  Alignment |  | 100.0      | 21     | <b>Fold:</b> MetI-like<br><b>Superfamily:</b> MetI-like<br><b>Family:</b> MetI-like   |
| 7  | <a href="#">c2onkC_</a> |  Alignment |  | 100.0      | 21     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C; <b>PDB Molecule:</b> molybdate/tungstate abc transporter, permease<br><b>PDBTitle:</b> abc transporter modbc in complex with its binding protein2 moda  |
| 8  | <a href="#">d2r6gf2</a> |  Alignment |  | 100.0      | 24     | <b>Fold:</b> MetI-like<br><b>Superfamily:</b> MetI-like<br><b>Family:</b> MetI-like   |
| 9  | <a href="#">d3d31c1</a> |  Alignment |  | 100.0      | 21     | <b>Fold:</b> MetI-like<br><b>Superfamily:</b> MetI-like<br><b>Family:</b> MetI-like   |
| 10 | <a href="#">c3d31D_</a> |  Alignment |  | 100.0      | 21     | <b>PDB header:</b> transport protein<br><b>Chain:</b> D; <b>PDB Molecule:</b> sulfate/molybdate abc transporter, permease protein;<br><b>PDBTitle:</b> modbc from methanosarcina acetivorans  |
| 11 | <a href="#">c4ymuC_</a> |  Alignment |  | 99.9       | 17     | <b>PDB header:</b> protein binding/transport protein<br><b>Chain:</b> C; <b>PDB Molecule:</b> abc-type amino acid transport system, permease component;<br><b>PDBTitle:</b> crystal structure of an amino acid abc transporter complex with2 arginines and atps |

|    |                         |   |   |      |    |  |
|----|-------------------------|---|---|------|----|--|
| 12 | <a href="#">d3dhwa1</a> |  Alignment   |     | 99.9 | 18 | <b>Fold:</b> MetI-like<br><b>Superfamily:</b> MetI-like<br><b>Family:</b> MetI-like  |
| 13 | <a href="#">c5kbuA</a>  |  Alignment   |    | 78.5 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor 2,voltage-dependent calcium channel<br><b>PDBTitle:</b> cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution   |
| 14 | <a href="#">d2r6gf1</a> |  Alignment   |    | 75.2 | 18 | <b>Fold:</b> MalF N-terminal region-like<br><b>Superfamily:</b> MalF N-terminal region-like<br><b>Family:</b> MalF N-terminal region-like  |
| 15 | <a href="#">c2hx6A</a>  |  Alignment   |    | 30.8 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease;<br><b>PDBTitle:</b> solution structure analysis of the phage t42 endoribonuclease regb   |
| 16 | <a href="#">c2jwaA</a>  |  Alignment   |    | 27.9 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2;<br><b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure   |
| 17 | <a href="#">c2ks1A</a>  |  Alignment   |   | 27.9 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2;<br><b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation  |
| 18 | <a href="#">c2m8gX</a>  |  Alignment |  | 21.5 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> X: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> structure, function, and tethering of dna-binding domains in 542 transcriptional activators   |
| 19 | <a href="#">c4l5eA</a>  |  Alignment |  | 16.9 | 13 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family);<br><b>PDBTitle:</b> crystal structure of a. aeolicus ntrc1 dna binding domain   |
| 20 | <a href="#">d1umqa</a>  |  Alignment |  | 14.8 | 4  | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> FIS-like   |
| 21 | <a href="#">c1umqA</a>  |  Alignment | not modelled  | 14.8 | 4  | <b>PDB header:</b> dna-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein;<br><b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity |
| 22 | <a href="#">d1fipa</a>  |  Alignment | not modelled  | 12.7 | 21 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> FIS-like   |
| 23 | <a href="#">d1ntca</a>  |  Alignment | not modelled  | 10.7 | 19 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> FIS-like   |
| 24 | <a href="#">d1etxa</a>  |  Alignment | not modelled  | 9.2  | 21 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> FIS-like   |
| 25 | <a href="#">d1etob</a>  |  Alignment | not modelled  | 8.7  | 21 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> FIS-like   |
| 26 | <a href="#">c3e7lD</a>  |  Alignment | not modelled  | 7.5  | 25 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family);<br><b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain  |
| 27 | <a href="#">c5lr6A</a>  |  Alignment | not modelled  | 7.3  | 8  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bd-type quinol oxidase subunit i;<br><b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans  |
| 28 | <a href="#">c2n2aA</a>  |  Alignment | not modelled  | 7.2  | 21 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2;<br><b>PDBTitle:</b> spatial structure of her2/erbb2 dimeric transmembrane domain in the2 presence of cytoplasmic jxtamembrane domains  |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
| 29 | <a href="#">c1bctA_</a> | Alignment | not modelled | 7.1 | 21 | <b>PDB header:</b> photoreceptor<br><b>Chain:</b> A: <b>PDB Molecule:</b> bacteriorhodopsin;<br><b>PDBTitle:</b> three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution |
| 30 | <a href="#">c1pyuD_</a> | Alignment | not modelled | 6.0 | 31 | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> aspartate 1-decarboxylase alfa chain;<br><b>PDBTitle:</b> processed aspartate decarboxylase mutant with ser25 mutated to cys  |
| 31 | <a href="#">c1g2hA_</a> | Alignment | not modelled | 6.0 | 30 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein tyrr homolog;<br><b>PDBTitle:</b> solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae                  |
| 32 | <a href="#">d1g2ha_</a> | Alignment | not modelled | 6.0 | 30 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> FIS-like  |
| 33 | <a href="#">d2ns0a1</a> | Alignment | not modelled | 5.2 | 8  | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> RHA1 ro06458-like  |