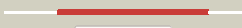



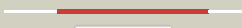
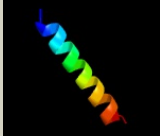

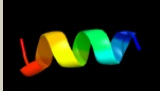

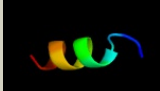



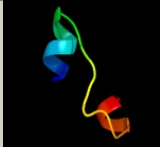








# Phyre2

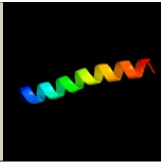
Email mdejesus@rockefeller.edu  
 Description RVBD3372A\_(RVBD3372A)\_3787723\_3787827  
 Date Fri Aug 9 18:20:04 BST 2019  
 Unique Job ID 6268bb76d306a1a9

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c5xfsA_</a> |  Alignment   |    | 95.8       | 48     | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8;<br><b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis          |
| 2  | <a href="#">d2g38a1</a> |  Alignment   |    | 95.7       | 39     | <b>Fold:</b> Ferritin-like<br><b>Superfamily:</b> PE/PPE dimer-like<br><b>Family:</b> PE   |
| 3  | <a href="#">c2g38A_</a> |  Alignment   |    | 95.7       | 39     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein;<br><b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis            |
| 4  | <a href="#">c4proD_</a> |  Alignment   |    | 17.4       | 38     | <b>PDB header:</b> serine protease<br><b>Chain:</b> D: <b>PDB Molecule:</b> alpha-lytic protease;<br><b>PDBTitle:</b> alpha-lytic protease complexed with pro region   |
| 5  | <a href="#">c2n3xA_</a> |  Alignment |  | 13.9       | 54     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> tar dna-binding protein 43;<br><b>PDBTitle:</b> solution structure of tdp-43 amyloidogenic core region                       |
| 6  | <a href="#">c2n2cA_</a> |  Alignment |  | 13.4       | 54     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> tar dna-binding protein 43;<br><b>PDBTitle:</b> nmr structure of tdp-43 prion-like hydrophobic helix in dpc                  |
| 7  | <a href="#">c4mm1E_</a> |  Alignment |  | 8.8        | 57     | <b>PDB header:</b> transferase<br><b>Chain:</b> E: <b>PDB Molecule:</b> geranylgeranylglyceryl phosphate synthase;<br><b>PDBTitle:</b> gggps from methanothermobacter thermautotrophicus                     |
| 8  | <a href="#">d1c9ka_</a> |  Alignment |  | 8.7        | 60     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> RecA protein-like (ATPase-domain)            |
| 9  | <a href="#">c2vs0B_</a> |  Alignment |  | 8.5        | 19     | <b>PDB header:</b> cell invasion<br><b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa;<br><b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa         |
| 10 | <a href="#">c6eluj_</a> |  Alignment |  | 6.7        | 75     | <b>PDB header:</b> antitoxin<br><b>Chain:</b> J: <b>PDB Molecule:</b> serum resistance associated; vsg protein;<br><b>PDBTitle:</b> structure of serum resistance associated protein from t. b.2 rhodesiense |

11 [c4iogD\\_](#)

Alignment



5.5

19

**PDB header:** unknown function

**Chain:** D: **PDB Molecule:** secreted protein esxb;

**PDB Title:** the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne