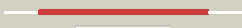
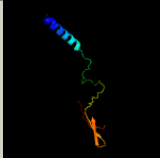

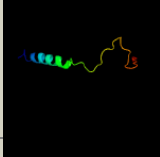

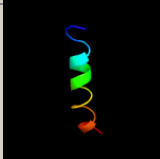

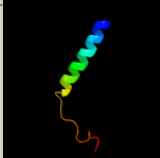

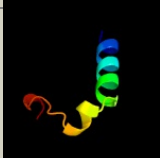
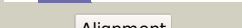
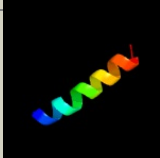
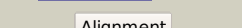
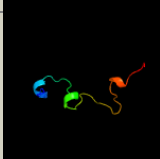
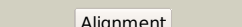
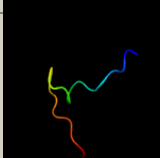
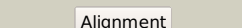

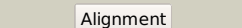
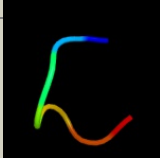

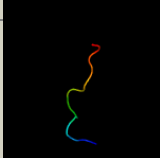

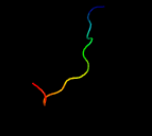

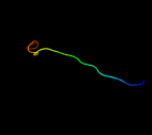

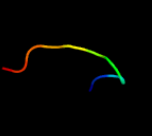
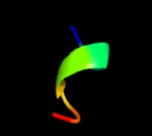

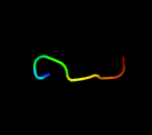


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2468A\_(RVBD2468A)\_2772108\_2772341  
 Date Wed Aug 7 12:50:09 BST 2019  
 Unique Job ID ea392de40531df9f

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">c6adql_</a> | <br>Alignment   |    | 99.9       | 56     | <b>PDB header:</b> electron transport<br><b>Chain:</b> I: <b>PDB Molecule:</b> cytochrome c oxidase subunit ctaj;<br><b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis  |
| 2  | <a href="#">c6hwhR_</a> | <br>Alignment   |    | 99.6       | 56     | <b>PDB header:</b> electron transport<br><b>Chain:</b> R: <b>PDB Molecule:</b> msmeg_4693;<br><b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis                                    |
| 3  | <a href="#">d1fftb2</a> | <br>Alignment   |    | 23.0       | 32     | <b>Fold:</b> Transmembrane helix hairpin<br><b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region<br><b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region                                     |
| 4  | <a href="#">c6hu9e_</a> | <br>Alignment   |   | 19.5       | 12     | <b>PDB header:</b> oxidoreductase/electron transport<br><b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial;<br><b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae |
| 5  | <a href="#">c6h3wA_</a> | <br>Alignment |  | 17.1       | 25     | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein;<br><b>PDBTitle:</b> la crosse virus glycoprotein gc head domain  |
| 6  | <a href="#">c6e3yE_</a> | <br>Alignment |  | 14.8       | 20     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> receptor activity-modifying protein 1;<br><b>PDBTitle:</b> cryo-em structure of the active, gs-protein complexed, human cgrp2 receptor                        |
| 7  | <a href="#">d1gph11</a> | <br>Alignment |  | 12.0       | 20     | <b>Fold:</b> PRTase-like<br><b>Superfamily:</b> PRTase-like<br><b>Family:</b> Phosphoribosyltransferases (PRTases)  |
| 8  | <a href="#">c3nk4C_</a> | <br>Alignment |  | 10.4       | 36     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> C: <b>PDB Molecule:</b> zona pellucida 3;<br><b>PDBTitle:</b> crystal structure of full-length sperm receptor zp3 at 2.0 a2 resolution  |
| 9  | <a href="#">c3nk3C_</a> | <br>Alignment |  | 10.3       | 36     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> C: <b>PDB Molecule:</b> zona pellucida 3;<br><b>PDBTitle:</b> crystal structure of full-length sperm receptor zp3 at 2.6 a2 resolution  |
| 10 | <a href="#">c2gesA_</a> | <br>Alignment |  | 10.2       | 43     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase;<br><b>PDBTitle:</b> pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)         |
| 11 | <a href="#">c2iifA_</a> | <br>Alignment |  | 10.0       | 36     | <b>PDB header:</b> recombination/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> integration host factor;<br><b>PDBTitle:</b> single chain integration host factor mutant protein (scihf2-k45ae) in2 complex with dna                          |

|    |                         |           |   |     |    |   |
|----|-------------------------|-----------|---|-----|----|---|
| 12 | <a href="#">c3tqcB_</a> | Alignment |    | 9.5 | 43 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate kinase;<br><b>PDBTitle:</b> structure of the pantothenate kinase (coaa) from coxiella burnetii   |
| 13 | <a href="#">c2lfwA_</a> | Alignment |    | 9.2 | 33 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> phyr sigma-like domain;<br><b>PDBTitle:</b> nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1  |
| 14 | <a href="#">d1o9aa1</a> | Alignment |    | 9.1 | 17 | <b>Fold:</b> Fnl-like domain<br><b>Superfamily:</b> Fnl-like domain<br><b>Family:</b> Fibronectin type I module   |
| 15 | <a href="#">c3vu1A_</a> | Alignment |    | 8.7 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0242;<br><b>PDBTitle:</b> crystal structure of the c-terminal globular domain of f2 oligosaccharyltransferase (phaglb-l, o74088_pyrho) from pyrococcus3 horikoshii |
| 16 | <a href="#">d1sq5a_</a> | Alignment |    | 8.7 | 43 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Phosphoribulokinase/pantothenate kinase   |
| 17 | <a href="#">d2cg7a2</a> | Alignment |   | 8.2 | 27 | <b>Fold:</b> Fnl-like domain<br><b>Superfamily:</b> Fnl-like domain<br><b>Family:</b> Fibronectin type I module   |
| 18 | <a href="#">c2bzwB_</a> | Alignment |  | 7.8 | 86 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> bcl2-antagonist of cell death;<br><b>PDBTitle:</b> the crystal structure of bcl-xl in complex with full-length bad  |
| 19 | <a href="#">c3c8uA_</a> | Alignment |  | 7.3 | 33 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fructokinase;<br><b>PDBTitle:</b> crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution                                     |
| 20 | <a href="#">c2ec3A_</a> | Alignment |  | 6.4 | 40 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> fibronectin;<br><b>PDBTitle:</b> solution structure of the 11th fn1 domain from human2 fibronectin 1  |
| 21 | <a href="#">d1v54d_</a> | Alignment | not modelled  | 6.4 | 28 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV<br><b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV  |
| 22 | <a href="#">c1gph1_</a> | Alignment | not modelled  | 6.4 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> 1: <b>PDB Molecule:</b> glutamine phosphoribosyl-pyrophosphate amidotransferase;<br><b>PDBTitle:</b> structure of the allosteric regulatory enzyme of purine biosynthesis   |
| 23 | <a href="#">c5b3fB_</a> | Alignment | not modelled  | 6.2 | 43 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribulokinase/uridine kinase;<br><b>PDBTitle:</b> crystal structure of phosphoribulokinase from methanospirillum2 hungatei  |
| 24 | <a href="#">d2rkya1</a> | Alignment | not modelled  | 6.1 | 36 | <b>Fold:</b> Fnl-like domain<br><b>Superfamily:</b> Fnl-like domain<br><b>Family:</b> Fibronectin type I module   |
| 25 | <a href="#">d1f2fa_</a> | Alignment | not modelled  | 6.1 | 30 | <b>Fold:</b> SH2-like<br><b>Superfamily:</b> SH2 domain<br><b>Family:</b> SH2 domain  |
| 26 | <a href="#">d2cg7a1</a> | Alignment | not modelled  | 5.9 | 36 | <b>Fold:</b> Fnl-like domain<br><b>Superfamily:</b> Fnl-like domain<br><b>Family:</b> Fibronectin type I module   |
| 27 | <a href="#">c3ejhB_</a> | Alignment | not modelled  | 5.7 | 20 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B: <b>PDB Molecule:</b> fibronectin;<br><b>PDBTitle:</b> crystal structure of the fibronectin 8-9fni domain pair in complex2 with a type-i collagen peptide   |
| 28 | <a href="#">d1gwma_</a> | Alignment | not modelled  | 5.6 | 31 | <b>Fold:</b> Galactose-binding domain-like<br><b>Superfamily:</b> Galactose-binding domain-like<br><b>Family:</b> Family 29 carbohydrate binding module, CBM29  |
|    |                         |           |   |     |    | <b>PDB header:</b> electron transport   |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
| 29 | <a href="#">c2y69Q_</a> | Alignment | not modelled | 5.6 | 28 | <b>Chain:</b> Q; <b>PDB Molecule:</b> cytochrome c oxidase subunit 4 isoform 1;<br><b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen   |
| 30 | <a href="#">d1v54g_</a> | Alignment | not modelled | 5.3 | 20 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIa<br><b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIa   |
| 31 | <a href="#">c3wg7T_</a> | Alignment | not modelled | 5.3 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> T; <b>PDB Molecule:</b> cytochrome c oxidase subunit 6a2, mitochondrial;<br><b>PDBTitle:</b> a 1.9 angstrom radiation damage free x-ray structure of large (420kda)2 protein by femtosecond crystallography |
| 32 | <a href="#">c1m57H_</a> | Alignment | not modelled | 5.1 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H; <b>PDB Molecule:</b> cytochrome c oxidase;<br><b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))   |
| 33 | <a href="#">d2i1sa1</a> | Alignment | not modelled | 5.1 | 30 | <b>Fold:</b> MM3350-like<br><b>Superfamily:</b> MM3350-like<br><b>Family:</b> MM3350-like  |
| 34 | <a href="#">d1ecfa1</a> | Alignment | not modelled | 5.0 | 15 | <b>Fold:</b> PRTase-like<br><b>Superfamily:</b> PRTase-like<br><b>Family:</b> Phosphoribosyltransferases (PRTases)   |