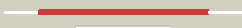









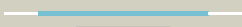






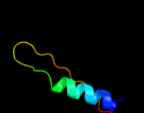

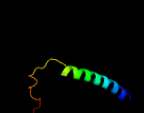

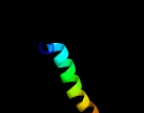
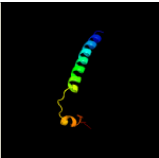
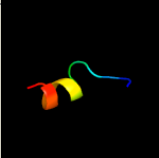
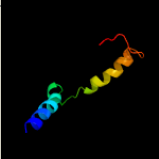


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1822\_(pgsA2)\_2069087\_2069716  
 Date Fri Aug 2 13:30:43 BST 2019  
 Unique Job ID 0f2c26fd55251cb9

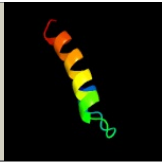
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6h59B_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cdp-diacylglycerol--inositol 3-phosphatidyltransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphatidylinositol2 phosphate synthase (pgsa1) with cdp-dag bound
2	<a href="#">c5d92B_</a>	 Alignment		99.9	20	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> af2299 protein,phosphatidylinositol synthase; <b>PDBTitle:</b> structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
3	<a href="#">c4mndA_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l- <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
4	<a href="#">c4o6mA_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> af2299, a cdp-alcohol phosphotransferase; <b>PDBTitle:</b> structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
5	<a href="#">c4k1cB_</a>	 Alignment		48.8	11	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger
6	<a href="#">c4k1cA_</a>	 Alignment		38.0	11	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger
7	<a href="#">c6mjbC_</a>	 Alignment		28.6	33	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> kinetochore-associated protein dsn1; <b>PDBTitle:</b> structure of candida glabrata csm1:dsn1(14-72) complex
8	<a href="#">c5gufA_</a>	 Alignment		17.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cdp-archaeol synthase; <b>PDBTitle:</b> structural insight into an intramembrane enzyme for archaeal membrane2 lipids biosynthesis
9	<a href="#">c2rkhA_</a>	 Alignment		11.0	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative apha-like transcription factor; <b>PDBTitle:</b> crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution
10	<a href="#">c3eh4A_</a>	 Alignment		10.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase subunit 1; <b>PDBTitle:</b> structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
11	<a href="#">c2voyG_</a>	 Alignment		10.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus

12	<a href="#">d1xmea1</a>	Alignment		9.5	17	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
13	<a href="#">c2le7A_</a>	Alignment		8.2	43	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 2; <b>PDBTitle:</b> solution nmr structure of the s4s5 linker of herg potassium channel
14	<a href="#">c2n28A_</a>	Alignment		7.2	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein vpu; <b>PDBTitle:</b> solid-state nmr structure of vpu

15 [c4arpB\\_](#)

Alignment



5.6

13

**PDB header:**hydrolase  
**Chain:** B: **PDB Molecule:**pesticin;  
**PDBTitle:** structure of the inactive pesticin e178a mutant