

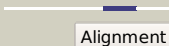

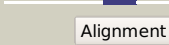
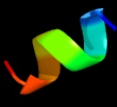
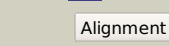



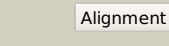

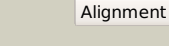

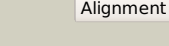

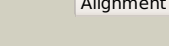

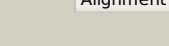



# Phyre2

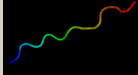
Email	mdejesus@rockefeller.edu
Description	RVBD0426c_(-)_515376_515819
Date	Tue Jul 23 14:50:50 BST 2019
Unique Job ID	df4033ea20947736

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1be3K_</a>	 Alignment		7.6	67	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
2	<a href="#">c5nmiX_</a>	 Alignment		7.6	67	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> arg-asn-trp-val-pro-thr-ala-gln-leu-trp-gly-ala-val-gly- <b>PDBTitle:</b> cytochrome bc1 bound to the inhibitor mjm170
3	<a href="#">c5nmiK_</a>	 Alignment		7.6	67	<b>PDB header:</b> membrane protein <b>Chain:</b> K: <b>PDB Molecule:</b> arg-asn-trp-val-pro-thr-ala-gln-leu-trp-gly-ala-val-gly- <b>PDBTitle:</b> cytochrome bc1 bound to the inhibitor mjm170
4	<a href="#">c2x43S_</a>	 Alignment		7.0	39	<b>PDB header:</b> membrane protein <b>Chain:</b> S: <b>PDB Molecule:</b> sherp; <b>PDBTitle:</b> structural basis of molecular recognition by sherp at membrane2 surfaces
5	<a href="#">c2lj2A_</a>	 Alignment		6.9	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> integral membrane core domain of the mercury transporter merf in lipid2 bilayer membranes
6	<a href="#">c1iflA_</a>	 Alignment		6.7	28	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> inovirus; <b>PDBTitle:</b> molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13),3 if1 and ike
7	<a href="#">c2m67A_</a>	 Alignment		6.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
8	<a href="#">c1wazA_</a>	 Alignment		6.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
9	<a href="#">c4b0tB_</a>	 Alignment		5.9	35	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pup--protein ligase; <b>PDBTitle:</b> structure of the pup ligase pafa of the prokaryotic2 ubiquitin-like modification pathway in complex with adp
10	<a href="#">c4bjrA_</a>	 Alignment		5.8	35	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pup--protein ligase, prokaryotic ubiquitin-like protein <b>PDBTitle:</b> crystal structure of the complex between prokaryotic2 ubiquitin-like protein pup and its ligase pafa

11 [c2w4zB](#)

Alignment



5.6

54

**PDB header:**virus  
**Chain:** B: **PDB Molecule:**caulobacter bacteriophage 5;  
**PDBTitle:** caulobacter bacteriophage 5