



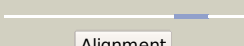
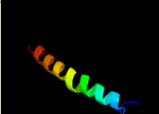
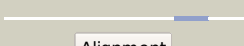
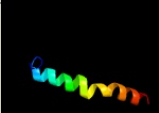

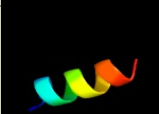






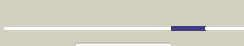
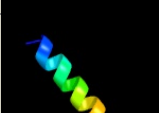



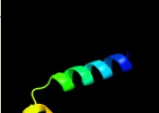

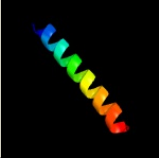
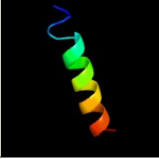


# Phyre2

Email	mdejesus@rockefeller.edu
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Date	Wed Jul 31 22:05:14 BST 2019
Unique Job ID	2ba8be6632f8d55f

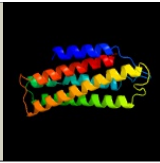
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4pguA_</a>	 Alignment		100.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein yetj; <b>PDBTitle:</b> crystal structure of yetj from bacillus subtilis at ph 7 by soaking
2	<a href="#">c4pgwA_</a>	 Alignment		100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein yetj; <b>PDBTitle:</b> crystal structure of yetj from bacillus subtilis at ph 6 by pt-sad
3	<a href="#">c5vylA_</a>	 Alignment		28.5	6	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> inner tegument protein; <b>PDBTitle:</b> crystal structure of n-terminal half of herpes simplex virus type 12 ul37 protein
4	<a href="#">c4k70B_</a>	 Alignment		20.3	25	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> ul37; <b>PDBTitle:</b> crystal structure of n-terminal half of pseudorabiesvirus ul37 protein
5	<a href="#">c4z6yD_</a>	 Alignment		10.7	38	<b>PDB header:</b> hydrolase inhibitor/protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> hamartin; <b>PDBTitle:</b> structure of the tbc1d7-tsc1 complex
6	<a href="#">c4z6yC_</a>	 Alignment		10.7	38	<b>PDB header:</b> hydrolase inhibitor/protein binding <b>Chain:</b> C; <b>PDB Molecule:</b> hamartin; <b>PDBTitle:</b> structure of the tbc1d7-tsc1 complex
7	<a href="#">c5oqtC_</a>	 Alignment		10.4	6	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> uncharacterized protein ynem; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
8	<a href="#">c4z6yF_</a>	 Alignment		9.9	38	<b>PDB header:</b> hydrolase inhibitor/protein binding <b>Chain:</b> F; <b>PDB Molecule:</b> hamartin; <b>PDBTitle:</b> structure of the tbc1d7-tsc1 complex
9	<a href="#">c6f34C_</a>	 Alignment		9.6	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> mgts; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue bound to arginine.
10	<a href="#">c6hwhW_</a>	 Alignment		9.4	12	<b>PDB header:</b> electron transport <b>Chain:</b> W; <b>PDB Molecule:</b> cytochrome c oxidase subunit 3; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
11	<a href="#">d1m47a_</a>	 Alignment		9.2	13	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines

12	<a href="#">c5ejcC_</a>	Alignment		8.7	50	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> hamartin; <b>PDBTitle:</b> crystal structural of the tsc1-tbc1d7 complex
13	<a href="#">c6ithA_</a>	Alignment		7.8	31	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> syndecan-2; <b>PDBTitle:</b> structure of the transmembrane domain of syndecan 2 in micelles
14	<a href="#">c5z1L_</a>	Alignment		6.4	14	<b>PDB header:</b> protein fibril <b>Chain:</b> L: <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> cryo-em structure of methanoccus maripaludis archaellum

15 [d1v54c\\_](#)

Alignment



5.6

12

**Fold:**Cytochrome c oxidase subunit III-like  
**Superfamily:**Cytochrome c oxidase subunit III-like  
**Family:**Cytochrome c oxidase subunit III-like