

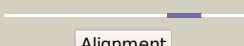

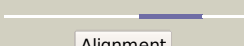
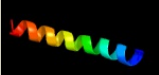
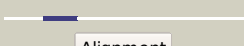
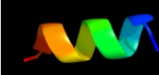

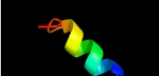






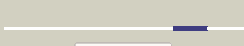







# Phyre2

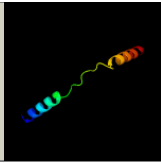
Email	mdejesus@rockefeller.edu
Description	RVBD0968 (-)_1078395_1078691
Date	Wed Jul 31 22:05:03 BST 2019
Unique Job ID	1af37d79fe5bc11c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4x3mB_</a>	 Alignment		38.4	41	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rna 2'-o ribose methyltransferase; <b>PDBTitle:</b> crystal structure of ttha0275 from thermus thermophilus (hb8) in2 complex with adenosine in space group p212121
2	<a href="#">c6mbbB_</a>	 Alignment		14.3	38	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> df1; <b>PDBTitle:</b> human bfl-1 in complex with the designed peptide df1
3	<a href="#">c6mtkA_</a>	 Alignment		11.0	30	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from elizabethkingia2 anophelis nuhp1
4	<a href="#">c3c85D_</a>	 Alignment		9.3	50	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative glutathione-regulated potassium-efflux system <b>PDBTitle:</b> crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
5	<a href="#">d1we3a3</a>	 Alignment		9.2	33	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> GroEL-like chaperone, intermediate domain
6	<a href="#">d1l2pa_</a>	 Alignment		8.7	30	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> F1F0 ATP synthase subunit B, membrane domain <b>Family:</b> F1F0 ATP synthase subunit B, membrane domain
7	<a href="#">c3io9B_</a>	 Alignment		7.4	36	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> biml12y in complex with mcl-1
8	<a href="#">d1kp8a3</a>	 Alignment		7.3	31	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> GroEL-like chaperone, intermediate domain
9	<a href="#">d1ioka3</a>	 Alignment		7.1	40	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> GroEL-like chaperone, intermediate domain
10	<a href="#">c2g9mB_</a>	 Alignment		7.0	21	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> phycoerythrin; <b>PDBTitle:</b> crystal structure of the pigment protein phycoerythrin from2 cyanobacterium at 2.6a resolution
11	<a href="#">d1kl9a1</a>	 Alignment		5.8	38	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> eIF2alpha middle domain-like <b>Family:</b> eIF2alpha middle domain-like

12 [c1vw4Q\\_](#)

Alignment



5.4

20

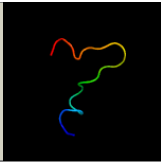
**PDB header:** ribosome  
**Chain:** Q: **PDB Molecule:** 54s ribosomal protein l40, mitochondrial;  
**PDB Title:** structure of the yeast mitochondrial large ribosomal subunit

13

[c2c55A](#)



Alignment



5.4

21

**PDB header:** viral protein  
**Chain:** A: **PDB Molecule:** protein p6;  
**PDB Title:** solution structure of the human immunodeficiency virus type2 1 p6 protein