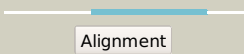
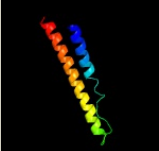
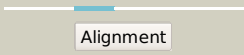

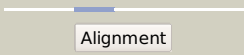
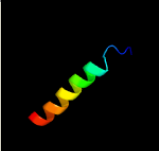
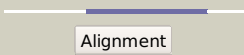
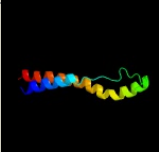
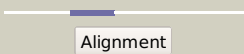
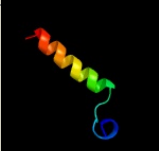
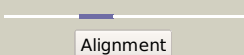
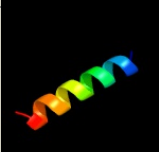
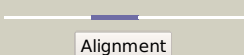
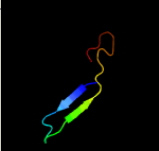


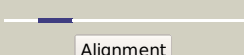

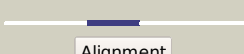
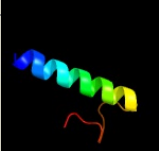


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2541_(-)_2864437_2864844
Date	Wed Aug 7 12:50:17 BST 2019
Unique Job ID	8a39779c5ab81c93

Detailed template information

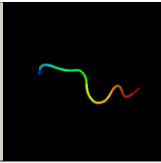
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4xy3A_</a>	 Alignment		31.4	18	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
2	<a href="#">d1wa8a1</a>	 Alignment		31.0	29	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
3	<a href="#">c4iogD_</a>	 Alignment		28.6	33	<b>PDB header:</b> unknown function <b>Chain:</b> D; <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
4	<a href="#">c5xfsB_</a>	 Alignment		13.1	22	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with espG5 from m.2 tuberculosis
5	<a href="#">c3gvmA_</a>	 Alignment		12.5	15	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
6	<a href="#">c2vs0B_</a>	 Alignment		12.1	5	<b>PDB header:</b> cell invasion <b>Chain:</b> B; <b>PDB Molecule:</b> virulence factor esxA; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxA
7	<a href="#">c3dzmB_</a>	 Alignment		11.6	21	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical conserved protein; <b>PDBTitle:</b> crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
8	<a href="#">d1khba2</a>	 Alignment		6.7	46	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
9	<a href="#">c1ic9A_</a>	 Alignment		6.1	60	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> th10aox; <b>PDBTitle:</b> nmr solution structure of the designed beta-sheet mini-2 protein th10aox
10	<a href="#">c5cmoB_</a>	 Alignment		5.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> crystal structure of holo-[acyl-carrier-protein] synthase (acps) from2 neisseria meningitidis

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[c1icA\\_](#)



Alignment



5.6

60

**PDB header:** de novo protein  
**Chain:** A: **PDB Molecule:** th1ox;  
**PDB Title:** solution structure of designed beta-sheet mini-protein th1ox