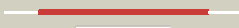
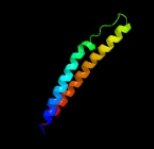

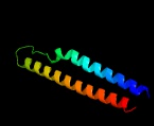

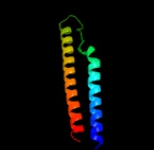

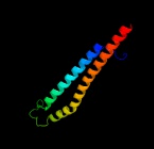
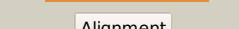
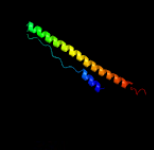
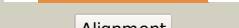
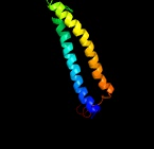
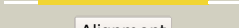

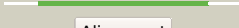
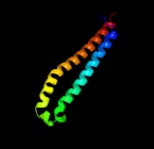

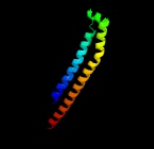

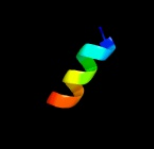




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1195_(PE13)_1339009_1339308
Date	Wed Jul 31 22:05:28 BST 2019
Unique Job ID	c9741d184ff66eb7

Detailed template information

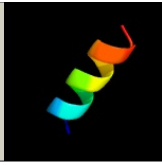
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsA_</a>	 Alignment		100.0	60	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	<a href="#">c2g38A_</a>	 Alignment		100.0	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
3	<a href="#">d2g38a1</a>	 Alignment		100.0	36	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
4	<a href="#">c3gvmA_</a>	 Alignment		87.1	14	<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
5	<a href="#">c4wj2A_</a>	 Alignment		82.8	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
6	<a href="#">d1wa8a1</a>	 Alignment		81.4	11	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
7	<a href="#">c4iogD_</a>	 Alignment		72.2	13	<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
8	<a href="#">c2vs0B_</a>	 Alignment		58.4	11	<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
9	<a href="#">c3zbhC_</a>	 Alignment		53.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
10	<a href="#">d1lghb_</a>	 Alignment		34.7	54	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
11	<a href="#">c1wrgA_</a>	 Alignment		25.4	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> light-harvesting protein b-880, beta chain; <b>PDBTitle:</b> light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum

12	<a href="#">c4lwsA_</a>	Alignment		22.9	18	<p><b>PDB header:</b>unknown function  <b>Chain:</b> A: <b>PDB Molecule:</b>uncharacterized protein;  <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata</p>
13	<a href="#">c6et5u_</a>	Alignment		14.4	31	<p><b>PDB header:</b>photosynthesis  <b>Chain:</b> U: <b>PDB Molecule:</b>light-harvesting protein b-1015 gamma chain;  <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis</p>
14	<a href="#">c4lwsB_</a>	Alignment		10.0	10	<p><b>PDB header:</b>unknown function  <b>Chain:</b> B: <b>PDB Molecule:</b>uncharacterized protein;  <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata</p>
15	<a href="#">d1wa8b1</a>	Alignment		8.9	9	<p><b>Fold:</b>Ferritin-like  <b>Superfamily:</b>EsxAB dimer-like  <b>Family:</b>ESAT-6 like</p>
16	<a href="#">c3onjA_</a>	Alignment		8.4	9	<p><b>PDB header:</b>protein transport  <b>Chain:</b> A: <b>PDB Molecule:</b>t-snare vti1;  <b>PDBTitle:</b> crystal structure of yeast vti1p_habc domain</p>
17	<a href="#">c4rglA_</a>	Alignment		7.9	21	<p><b>PDB header:</b>dna binding protein  <b>Chain:</b> A: <b>PDB Molecule:</b>filamentation induced by camp protein fic;  <b>PDBTitle:</b> crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution</p>
18	<a href="#">c2w0cR_</a>	Alignment		6.2	20	<p><b>PDB header:</b>virus  <b>Chain:</b> R: <b>PDB Molecule:</b>protein p3;  <b>PDBTitle:</b> x-ray structure of the entire lipid-containing bacteriophage pm2</p>

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[c3fkeB\\_](#)

Alignment



5.3

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**PDB header:** rna binding protein  
**Chain:** B: **PDB Molecule:** polymerase cofactor vp35;  
**PDBTitle:** structure of the ebola vp35 interferon inhibitory domain