


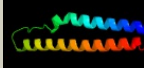

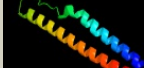


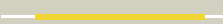
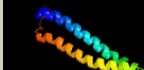
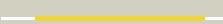






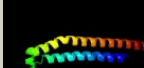




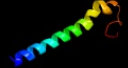



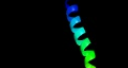

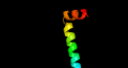



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3477\_(PE31)\_3894272\_3894568  
 Date Fri Aug 9 18:20:15 BST 2019  
 Unique Job ID 3bea43fe84334034

Detailed template information

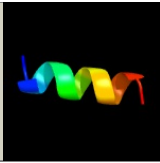
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsA_</a>	 Alignment		100.0	51	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	<a href="#">d2g38a1</a>	 Alignment		100.0	43	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
3	<a href="#">c2g38A_</a>	 Alignment		100.0	43	<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
4	<a href="#">c3gvmA_</a>	 Alignment		85.0	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="#">d1wa8a1</a>	 Alignment		79.4	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
6	<a href="#">c4iogD_</a>	 Alignment		74.6	16	<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
7	<a href="#">c4wj2A_</a>	 Alignment		73.3	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
8	<a href="#">c2vs0B_</a>	 Alignment		64.5	12	<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="#">c3zbcC_</a>	 Alignment		63.5	17	<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		36.1	46	<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		26.9	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="#">d1wa8b1</a>	Alignment		19.5	9	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
13	<a href="#">c4lwsA</a>	Alignment		17.0	12	<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
14	<a href="#">c3onjA</a>	Alignment		16.4	8	<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
15	<a href="#">c6et5u</a>	Alignment		15.2	38	<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
16	<a href="#">c2kg7B</a>	Alignment		11.5	13	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> esat-6-like protein esxh; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
17	<a href="#">c4rglA</a>	Alignment		8.2	24	<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
18	<a href="#">c2w0cR</a>	Alignment		5.9	23	<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
19	<a href="#">c3fkeB</a>	Alignment		5.7	38	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> structure of the ebola vp35 interferon inhibitory domain

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[c2q1kA](#)

Alignment



5.3

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**PDB header:**chaperone

**Chain:** A: **PDB Molecule:**asce;

**PDBTitle:** crystal structure of asce from aeromonas hydrophilla