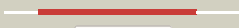
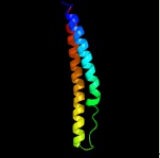

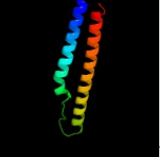

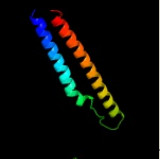

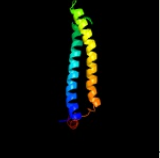

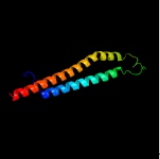
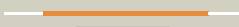
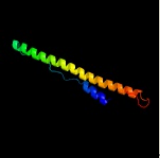

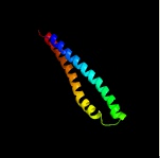
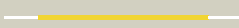
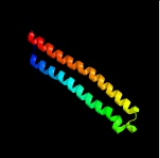

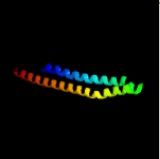
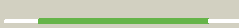
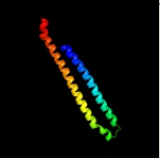

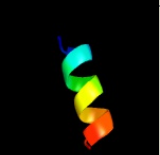
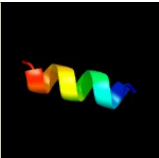
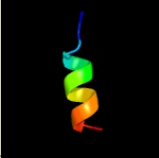
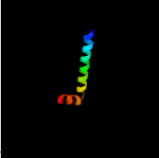
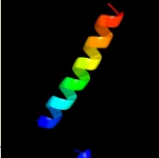
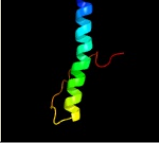


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3022A_(PE29)_3380690_3381007
 Date Thu Aug 8 16:20:19 BST 2019
 Unique Job ID 93c1ae701b12ee0e

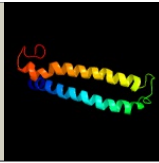
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	33	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38a1	 Alignment		100.0	27	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		100.0	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	d1wa8a1	 Alignment		94.0	12	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
5	c3gvmA_	 Alignment		85.9	13	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
6	c4wj2A_	 Alignment		84.2	13	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
7	c2vs0B_	 Alignment		77.2	12	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	c4iogD_	 Alignment		77.2	7	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
9	c3zbhC_	 Alignment		63.9	13	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	c4lwsA_	 Alignment		54.4	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
11	d1lghb_	 Alignment		31.2	8	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits

12	c1wrgA_	Alignment		22.9	15	<p>PDB header:membrane protein Chain: A: PDB Molecule:light-harvesting protein b-880, beta chain; PDBTitle: light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum</p>
13	c6et5u_	Alignment		13.4	23	<p>PDB header:photosynthesis Chain: U: PDB Molecule:light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis</p>
14	c2w0cR_	Alignment		8.9	20	<p>PDB header:virus Chain: R: PDB Molecule:protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2</p>
15	c3onjA_	Alignment		8.6	9	<p>PDB header:protein transport Chain: A: PDB Molecule:t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain</p>
16	c2kg7A_	Alignment		8.1	32	<p>PDB header:unknown function Chain: A: PDB Molecule:uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288</p>

17 [d1wa8b1](#)

Alignment



6.7

17

Fold: Ferritin-like
Superfamily: EsxAB dimer-like
Family: ESAT-6 like