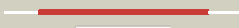
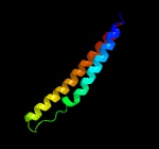







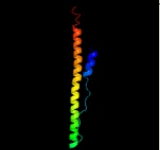

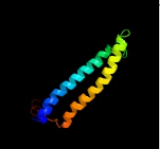

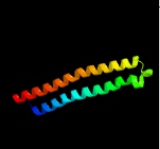

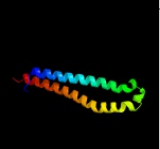
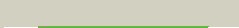




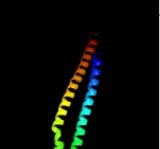


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1806_(PE20)_2048079_2048378
 Date Fri Aug 2 13:30:41 BST 2019
 Unique Job ID e37fff2f47f0cdae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	50	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	c2g38A_	 Alignment		100.0	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38a1	 Alignment		100.0	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c3gvmA_	 Alignment		86.1	14	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
5	c4wj2A_	 Alignment		85.1	16	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	d1wa8a1	 Alignment		84.1	11	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
7	c4iogD_	 Alignment		71.7	19	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
8	c2vs0B_	 Alignment		57.6	12	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
9	c3zbhC_	 Alignment		53.0	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1lghb_	 Alignment		35.4	31	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
11	c4lwsA_	 Alignment		27.5	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c1wrgA_	Alignment		25.9	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		14.6	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	c4lwsB_	Alignment		9.9	7	<p>PDB header:unknown function Chain: B: PDB Molecule:uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata</p>
15	d1wa8b1	Alignment		8.8	9	<p>Fold:Ferritin-like Superfamily:EsxAB dimer-like Family:ESAT-6 like</p>
16	c3onjA_	Alignment		7.8	13	<p>PDB header:protein transport Chain: A: PDB Molecule:t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain</p>
17	c4rglA_	Alignment		7.1	16	<p>PDB header:dna binding protein Chain: A: PDB Molecule:filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution</p>

18 [c2w0cR_](#)

Alignment



LQVWV

6.3

17

PDB header:virus
Chain: R: **PDB Molecule:**protein p3;
PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2