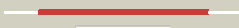
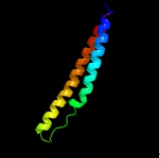



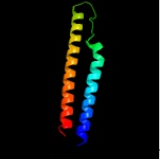
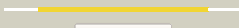
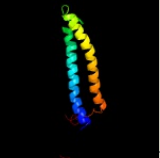
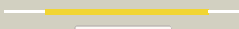
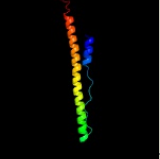
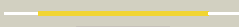
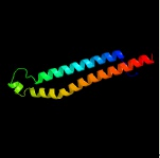

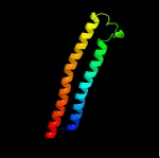

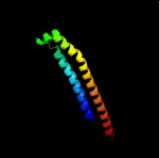

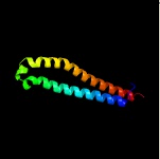



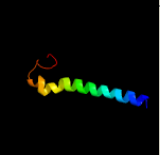

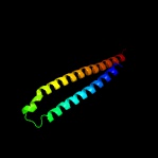
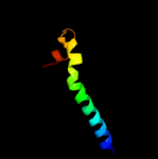
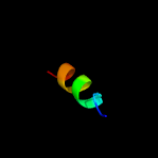




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2107_(PE22)_2367367_2367663
Date	Mon Aug 5 13:25:22 BST 2019
Unique Job ID	d320a800564056f0

Detailed template information

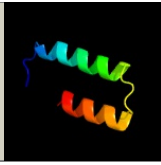
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	40	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38A_	 Alignment		100.0	31	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	31	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	d1wa8a1	 Alignment		79.8	9	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
5	c4wj2A_	 Alignment		78.1	11	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c3gvmA_	 Alignment		74.3	9	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
7	c4iogD_	 Alignment		70.8	8	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	c3zbhC_	 Alignment		66.3	13	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
9	c2vs0B_	 Alignment		58.3	12	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
10	d1lghb_	 Alignment		31.3	23	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
11	d1wa8b1	 Alignment		22.3	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like

12	c1wrgA_	Alignment		21.9	15	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
13	c4lwsA_	Alignment		14.2	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c2kg7B_	Alignment		13.9	9	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
15	c6et5u_	Alignment		12.4	23	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
16	c3onjA_	Alignment		11.8	8	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
17	c4lwsB_	Alignment		9.6	8	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

18

[c4rglA_](#)

Alignment



6.4

18

PDB header: dna binding protein

Chain: A: **PDB Molecule:** filamentation induced by camp protein fic;

PDB title: crystal structure of a fic family protein (dde_2494) from *Desulfovibrio desulfuricans* G20 at 2.70 Å resolution