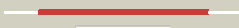
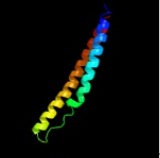

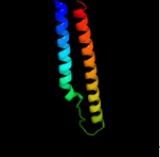

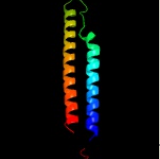
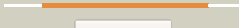


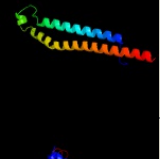
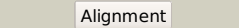
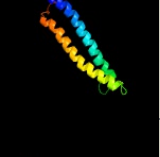
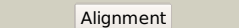
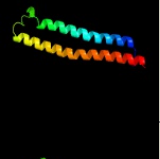
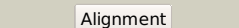
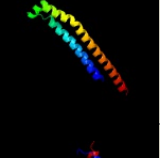
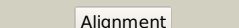
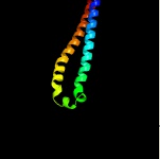
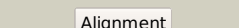
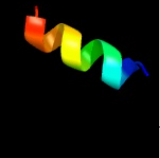
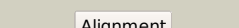
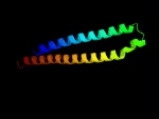

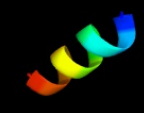

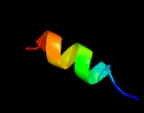
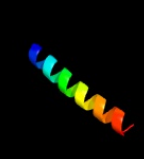


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2431c_(PE25)_2727977_2728276
 Date Wed Aug 7 12:50:05 BST 2019
 Unique Job ID 9fcc55c6beb18610

Detailed template information

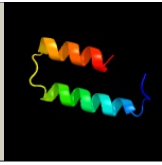
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1	c5xfsA_	 Alignment		100.0	33	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38a1	 Alignment		100.0	100	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		100.0	100	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c4wj2A_	 Alignment		86.9	19	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
5	c3gvmA_	 Alignment		84.5	16	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	d1wa8a1	 Alignment		83.8	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
7	c4iogD_	 Alignment		68.2	15	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		62.6	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
9	c2vs0B_	 Alignment		52.8	17	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
10	d1lghb_	 Alignment		33.6	23	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
11	c4lwsA_	 Alignment		26.3	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		24.4	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c1wrgA_	Alignment		23.5	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
14	c2kg7B_	Alignment		14.4	11	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		13.3	15	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		6.7	26	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain

17

[c4rglA_](#)

Alignment



6.2

24

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