
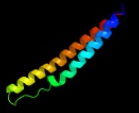



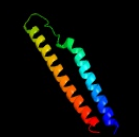





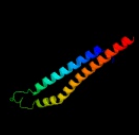


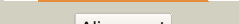






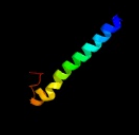

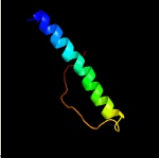
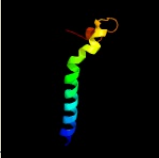
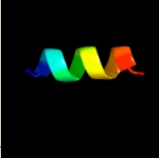



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0285_(PE5)_349624_349932
 Date Tue Jul 23 14:50:35 BST 2019
 Unique Job ID 941d5a7242c30b4a

Detailed template information

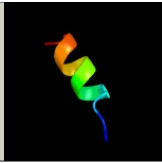
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	38	PDB header: protein transport Chain: A; PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38A_	 Alignment		100.0	29	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	29	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c4wj2A_	 Alignment		96.0	12	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
5	d1wa8a1	 Alignment		95.1	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	c3gvmA_	 Alignment		87.7	15	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	c2vs0B_	 Alignment		87.7	12	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	c3zbhC_	 Alignment		84.7	13	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
9	c4iogD_	 Alignment		78.1	10	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
10	c4lwsA_	 Alignment		58.6	17	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
11	d1wa8b1	 Alignment		29.2	9	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like

12	d1lghb_	Alignment		21.3	8	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
13	c2kg7A_	Alignment		19.4	36	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
14	c2kg7B_	Alignment		18.3	18	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	c1wrgA_	Alignment		13.3	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
16	c3onjA_	Alignment		9.4	9	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain

17

[c6et5u_](#)

Alignment



8.6

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