










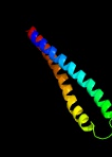







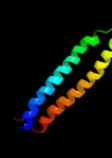


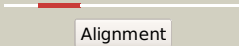





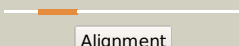
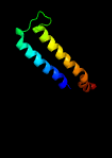


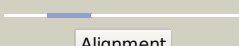

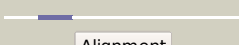
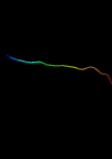







Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3892c_(PPE69)_4374662_4375861
 Date Sat Aug 10 22:05:07 BST 2019
 Unique Job ID b5bf654c558f0a92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	26	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38B_	 Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	22	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	11	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		97.5	16	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.5	10	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.3	5	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	c3gvmA_	 Alignment		97.2	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
9	c3zbhC_	 Alignment		97.1	9	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.1	9	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		92.9	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	 Alignment		92.5	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	 Alignment		92.0	22	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	 Alignment		86.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B_	 Alignment		80.3	13	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ_	 Alignment		31.2	11	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
17	d1ui5a2	 Alignment		27.0	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c1bkvA_	 Alignment		17.8	31	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvB_	 Alignment		16.8	31	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvC_	 Alignment		16.8	31	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
21	c5h2sA_	 Alignment	not modelled	5.4	38	PDB header: antimicrobial protein Chain: A: PDB Molecule: piscidin-4; PDBTitle: solution structure of tilapia piscidin 4 (tp4) from oreochromis2 niloticus