
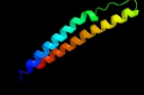






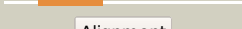

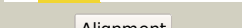

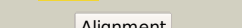

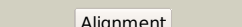

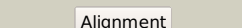





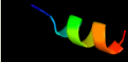
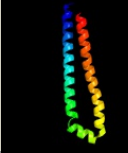







Phyre2

Email mdejesus@rockefeller.edu
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 Date Fri Aug 2 13:30:24 BST 2019
 Unique Job ID 5fa71375e4576cf6

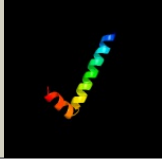
Detailed template information

#	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	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	c4wj2A_	 Alignment		85.6	19	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
5	c3gvmA_	 Alignment		81.0	12	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		77.3	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
7	c4iogD_	 Alignment		71.0	12	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		66.8	10	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
9	c3zbhC_	 Alignment		49.8	13	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1lghb_	 Alignment		27.7	23	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
11	c1wrgA_	 Alignment		16.6	23	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

12	c6et5u_	Alignment		11.6	31	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
13	c4lwsB_	Alignment		11.2	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c2kg7B_	Alignment		10.7	12	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	c3onjA_	Alignment		9.8	21	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
16	c3by7E_	Alignment		7.6	21	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein structurally similar to sm/lsm-like2 rna-binding proteins (jcvl_pep_1096686650277) from uncultured marine3 organism at 2.60 a resolution
17	c4lwsA_	Alignment		6.7	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
18	c4rglA_	Alignment		5.2	29	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

19 [c2w0cR_](#)

Alignment



5.1

22

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