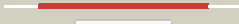
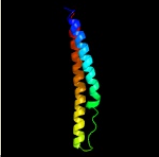

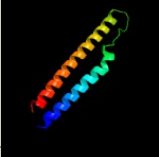
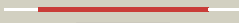
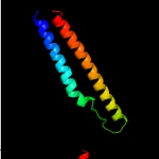

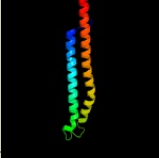

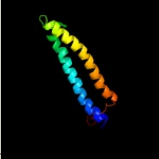

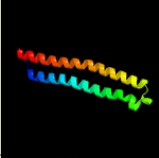
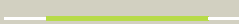
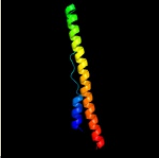

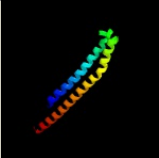

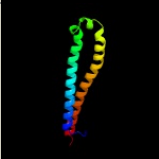

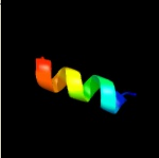




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1788_(PE18)_2026484_2026783
 Date Fri Aug 2 13:30:39 BST 2019
 Unique Job ID 5c2ec3086c57748d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	62	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	35	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		100.0	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c3gvmA_	 Alignment		83.0	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
5	d1wa8a1	 Alignment		73.6	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	c4iogD_	 Alignment		71.4	17	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
7	c4wj2A_	 Alignment		69.8	15	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
8	c3zbhC_	 Alignment		57.8	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
9	c2vs0B_	 Alignment		57.2	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		34.7	38	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
11	c1wrgA_	 Alignment		25.4	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		14.5	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	c3onjA_	Alignment		13.5	13	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
14	c4lwsA_	Alignment		10.5	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
15	c4lwsB_	Alignment		9.9	10	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
16	c2kg7B_	Alignment		9.7	16	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
17	c4rglA_	Alignment		7.5	18	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
18	c2w0cR_	Alignment		6.1	20	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
19	d1wa8b1	Alignment		6.0	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
20	c3fkeB_	Alignment		5.0	31	PDB header: rna binding protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of the ebola vp35 interferon inhibitory domain
21	c2q1kA_	Alignment	not modelled	5.0	31	PDB header: chaperone Chain: A: PDB Molecule: asce; PDBTitle: cyrstal structure of asce from aeromonas hydrophilla