
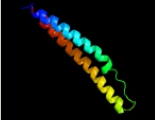

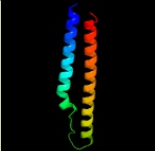

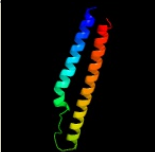


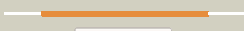


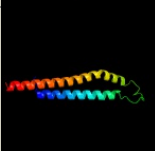

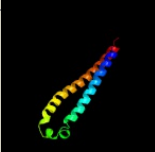



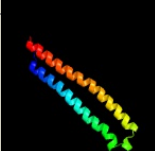






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1386_(PE15)_1561470_1561778
Date	Wed Jul 31 22:05:49 BST 2019
Unique Job ID	32eac30b6550cec8

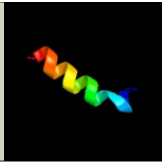
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	29	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	23	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	d1wa8a1	 Alignment		91.4	11	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
5	c4wj2A_	 Alignment		89.3	10	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c3gvmA_	 Alignment		88.4	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
7	c2vs0B_	 Alignment		87.7	10	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	c3zbhC_	 Alignment		82.4	13	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
9	c4iogD_	 Alignment		82.3	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		48.4	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
11	d1lghb_	 Alignment		25.3	0	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits

12	c1wrgA_	Alignment		16.8	8	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
13	c3onjA_	Alignment		12.5	13	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
14	d1wa8b1	Alignment		11.0	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
15	c6et5u_	Alignment		10.8	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	c4lwsB_	Alignment		10.3	15	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
17	c2w0cR_	Alignment		6.3	20	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
18	d1iwpa_	Alignment		6.2	9	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
19	c2kg7A_	Alignment		5.5	30	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

20 [d1v54k_](#)

Alignment



5.4

26

Fold:Single transmembrane helix

Superfamily:Mitochondrial cytochrome c oxidase subunit VIIb

Family:Mitochondrial cytochrome c oxidase subunit VIIb