
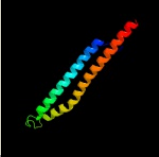

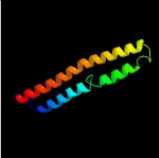

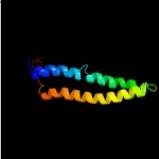
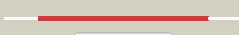


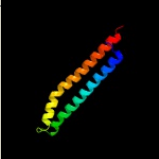

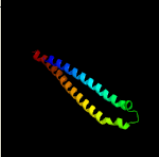

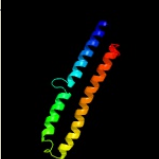

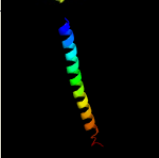



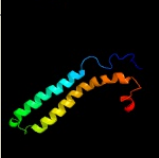

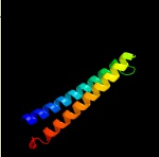


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3615c_(-)_4054991_4055302
Date	Fri Aug 9 18:20:30 BST 2019
Unique Job ID	b7c96208d19a7ae3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gvmA_	 Alignment		97.7	13	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
2	c4iogD_	 Alignment		97.7	16	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
3	d1wa8a1	 Alignment		97.5	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
4	c3zbhC_	 Alignment		97.3	12	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
5	c2vs0B_	 Alignment		97.1	10	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
6	c4lwsA_	 Alignment		96.5	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
7	c4lwsB_	 Alignment		96.0	11	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
8	c4wj2A_	 Alignment		91.7	21	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
9	d1wa8b1	 Alignment		90.9	10	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
10	c2kg7B_	 Alignment		83.8	12	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
11	c4i0xA_	 Alignment		63.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex

12	c4xy3A_	Alignment		60.5	30	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
13	c2kg7A_	Alignment		12.0	21	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	c3jywM_	Alignment		10.9	15	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l16(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
15	c2ixsB_	Alignment		7.8	30	PDB header: hydrolase Chain: B: PDB Molecule: sdai restriction endonuclease; PDBTitle: structure of sdai restriction endonuclease
16	d1zcza1	Alignment		6.6	45	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
17	c6nkoA_	Alignment		6.4	45	PDB header: unknown function Chain: A: PDB Molecule: forh; PDBTitle: crystal structure of forh
18	c5jx6C_	Alignment		6.4	7	PDB header: hydrolase Chain: C: PDB Molecule: glucanase; PDBTitle: gh6 orpinomyces sp. y102 enzyme

19 [d1pkxa1](#)

Alignment



6.1

45

Fold: Methylglyoxal synthase-like
Superfamily: Methylglyoxal synthase-like
Family: Inosicase