
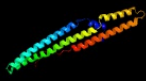





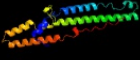

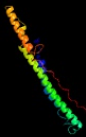











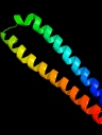


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1802_(PPE30)_2043391_2044782
 Date Fri Aug 2 13:30:41 BST 2019
 Unique Job ID 337c52c5edab37d7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	64	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	35	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	35	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	16	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		98.7	20	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.9	14	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.8	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
8	c4iogD_	 Alignment		97.7	15	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
9	c3zbhC_	 Alignment		97.7	18	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.1	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		96.4	13	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	Alignment		96.3	17	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		96.1	21	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		94.8	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
15	c2kg7B_	Alignment		92.3	22	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		79.4	20	PDB header: structural genomics, unknown function Chain: J; PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	c5frgA_	Alignment		20.7	75	PDB header: protein binding Chain: A; PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
18	c1bkvA_	Alignment		13.2	56	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvC_	Alignment		12.6	56	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvB_	Alignment		12.6	56	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
21	c2ke4A_	Alignment	not modelled	11.8	75	PDB header: membrane protein Chain: A; PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cjp4
22	c2i94B_	Alignment	not modelled	11.8	83	PDB header: protein binding Chain: B; PDB Molecule: rhodopsin kinase; PDBTitle: nmr structure of recoverin bound to rhodopsin kinase
23	d1khba2	Alignment	not modelled	10.5	20	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
24	c2iu1A_	Alignment	not modelled	9.9	17	PDB header: transcription Chain: A; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
25	c2fulE_	Alignment	not modelled	9.4	28	PDB header: translation Chain: E; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
26	d1xkna_	Alignment	not modelled	7.4	15	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
27	c1bcvA_	Alignment	not modelled	7.1	56	PDB header: synthetic peptide Chain: A; PDB Molecule: peptide corresponding to the major immunogen site of fmd PDBTitle: synthetic peptide corresponding to the major immunogen site of fmd2 virus, nmr, 10 structures
28	c4i6jB_	Alignment	not modelled	7.0	44	PDB header: transcription Chain: B; PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex PDB header: lyase,isomerase

29	c4grdA_	Alignment	not modelled	6.1	30	Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
30	c3juiA_	Alignment	not modelled	6.0	8	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
31	c1paqA_	Alignment	not modelled	5.7	12	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
32	d1paqa_	Alignment	not modelled	5.7	12	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
33	c5c3IA_	Alignment	not modelled	5.6	18	PDB header: transport protein Chain: A: PDB Molecule: nup54; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
34	d1ui5a2	Alignment	not modelled	5.5	28	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
35	c2qsrA_	Alignment	not modelled	5.4	20	PDB header: transcription Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of c-terminal domain of transcription-repair2 coupling factor
36	c4yh8B_	Alignment	not modelled	5.4	18	PDB header: splicing Chain: B: PDB Molecule: splicing factor u2af 59 kda subunit; PDBTitle: structure of yeast u2af complex