
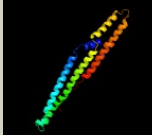

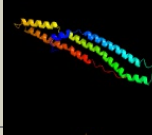



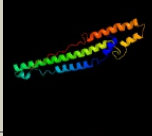

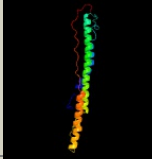

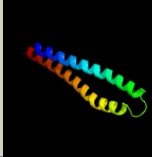



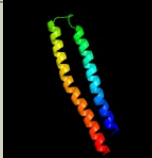

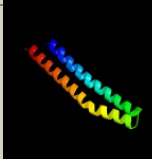

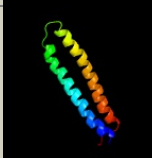

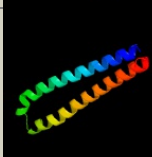


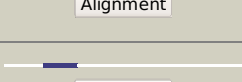
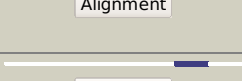
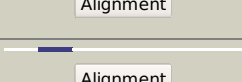
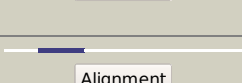
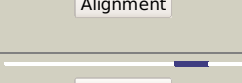
Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3873_(PPE68)_4351253_4352359
 Date Sat Aug 10 22:05:05 BST 2019
 Unique Job ID 979e034e021b23a5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	41	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	29	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	29	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	18	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	16	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.9	13	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	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
8	c4iogD_	 Alignment		97.8	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	13	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.1	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		96.8	11	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	Alignment		96.7	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		96.4	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		95.7	19	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		93.8	13	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
16	c4i0xJ_	Alignment		89.2	16	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	d1ui5a2	Alignment		32.1	18	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c1bkvA_	Alignment		14.1	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvB_	Alignment		13.3	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvC_	Alignment		13.3	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
21	c4dcia_	Alignment	not modelled	12.4	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of unknown function protein from synechococcus sp.2 wh 8102
22	c2kg7A_	Alignment	not modelled	10.2	20	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
23	c2iu1A_	Alignment	not modelled	10.2	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
24	c2fulE_	Alignment	not modelled	9.6	50	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
25	c3ay5A_	Alignment	not modelled	9.3	27	PDB header: cell cycle Chain: A: PDB Molecule: cyclin-d1-binding protein 1; PDBTitle: crystal structure of hhm (human homologue of murine maternal id-like2 molecule)
26	d1k91a_	Alignment	not modelled	6.8	40	Fold: P-domain of calnexin/calreticulin Superfamily: P-domain of calnexin/calreticulin Family: P-domain of calnexin/calreticulin
27	c3ukxC_	Alignment	not modelled	6.8	57	PDB header: protein transport/inhibitor Chain: C: PDB Molecule: bimax2 peptide; PDBTitle: mouse importin alpha: bimax2 peptide complex
28	c4yk3B_	Alignment	not modelled	6.1	22	PDB header: protein binding Chain: B: PDB Molecule: bepe protein; PDBTitle: crystal structure of the bid domain of bepe from bartonella henselae

29	c4yk2B_	 Alignment	not modelled	5.8	18	PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
30	c2kp7A_	 Alignment	not modelled	5.8	20	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
31	c4behB_	 Alignment	not modelled	5.6	27	PDB header: translation Chain: B: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: solution structure of human ribosomal protein p1.p2 heterodimer
32	d1paqa_	 Alignment	not modelled	5.6	35	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
33	c1paqA_	 Alignment	not modelled	5.6	35	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
34	c3juia_	 Alignment	not modelled	5.5	23	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
35	d1x4ka2	 Alignment	not modelled	5.4	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
36	d1dipa1	 Alignment	not modelled	5.4	18	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
37	c4grdA_	 Alignment	not modelled	5.4	26	PDB header: lyase, isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
38	c3q4hB_	 Alignment	not modelled	5.3	23	PDB header: metal transport Chain: B: PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esxh complex2 (msmeg_0620-msmeg_0621)
39	c4gyxC_	 Alignment	not modelled	5.2	36	PDB header: structural protein, blood clotting Chain: C: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
40	c2y5tG_	 Alignment	not modelled	5.2	67	PDB header: immune system Chain: G: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
41	c4gyxB_	 Alignment	not modelled	5.0	36	PDB header: structural protein, blood clotting Chain: B: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
42	c4gyxA_	 Alignment	not modelled	5.0	36	PDB header: structural protein, blood clotting Chain: A: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
43	c4fprC_	 Alignment	not modelled	5.0	36	PDB header: protein binding Chain: C: PDB Molecule: avirulence effector avrlm4-7; PDBTitle: structure of a fungal protein