
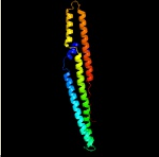

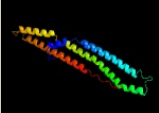

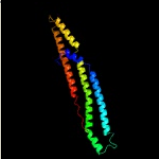

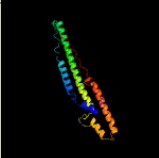

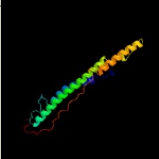



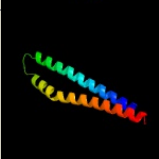

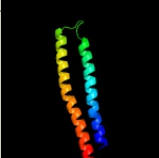

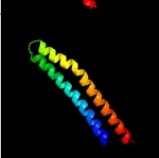

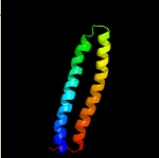

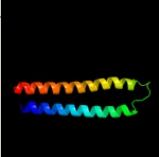


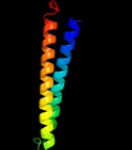


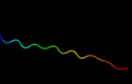
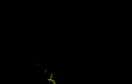
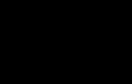



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1196_(PPE18)_1339355_1340530
 Date Wed Jul 31 22:05:28 BST 2019
 Unique Job ID 6876b3893a32fe53

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	53	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	d2g38b1	 Alignment		100.0	36	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	36	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c4xy3A_	 Alignment		100.0	20	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		98.6	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	15	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	13	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		97.6	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.0	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		96.1	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		95.7	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		95.5	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		95.3	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		90.5	13	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		83.4	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	c1bkvA	Alignment		17.3	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
18	c1bkvB	Alignment		16.5	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvC	Alignment		16.5	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
20	c4yk3B	Alignment		11.0	31	PDB header: protein binding Chain: B: PDB Molecule: bepe protein; PDBTitle: crystal structure of the bid domain of bepe from bartonella henselae
21	c5frgA	Alignment	not modelled	10.8	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
22	c4yk2B	Alignment	not modelled	9.9	14	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
23	c5kq4F	Alignment	not modelled	9.2	50	PDB header: hydrolase Chain: F: PDB Molecule: proline-rich nuclear receptor coactivator 2; PDBTitle: crystal structure of s. pombe dcp1/dcp2 in complex with h. sapiens2 pnrc2 and synthetic cap analog
24	c5kq1C	Alignment	not modelled	9.2	50	PDB header: hydrolase Chain: C: PDB Molecule: proline-rich nuclear receptor coactivator 2; PDBTitle: crystal structure of s. pombe dcp1/dcp2 in complex with h. sapiens2 pnrc2
25	c5kq1F	Alignment	not modelled	9.1	50	PDB header: hydrolase Chain: F: PDB Molecule: proline-rich nuclear receptor coactivator 2; PDBTitle: crystal structure of s. pombe dcp1/dcp2 in complex with h. sapiens2 pnrc2
26	d1zeea1	Alignment	not modelled	8.7	32	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
27	d1ui5a2	Alignment	not modelled	8.4	15	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
28	c5kq4C	Alignment	not modelled	8.1	43	PDB header: hydrolase Chain: C: PDB Molecule: proline-rich nuclear receptor coactivator 2;

						PDBTitle: crystal structure of s. pombe dcp1/dcp2 in complex with h. sapiens2 pnrc2 and synthetic cap analog
29	c2iu1A_	Alignment	not modelled	8.0	22	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
30	c2fulE_	Alignment	not modelled	7.7	22	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
31	c1vytF_	Alignment	not modelled	7.0	25	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
32	c4gyxC_	Alignment	not modelled	6.6	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
33	c4grdA_	Alignment	not modelled	6.5	28	PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
34	c4dmtA_	Alignment	not modelled	6.5	31	PDB header: structural protein Chain: A: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
35	c4dmtB_	Alignment	not modelled	6.5	31	PDB header: structural protein Chain: B: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
36	c4dmtC_	Alignment	not modelled	6.5	31	PDB header: structural protein Chain: C: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
37	c2lkqA_	Alignment	not modelled	6.5	56	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
38	c4gyxA_	Alignment	not modelled	6.4	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
39	c4gyxB_	Alignment	not modelled	6.4	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
40	c3h6pB_	Alignment	not modelled	6.3	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
41	c4lzxB_	Alignment	not modelled	6.1	29	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
42	c2kg7A_	Alignment	not modelled	5.9	35	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
43	c4m1lB_	Alignment	not modelled	5.5	36	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-bound cam
44	c2ke4A_	Alignment	not modelled	5.2	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 cip4