
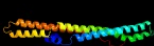

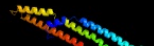

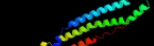



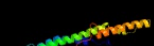









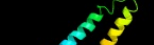


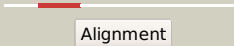

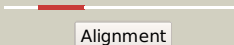

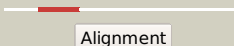

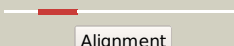

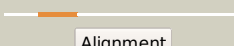

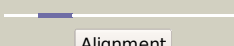
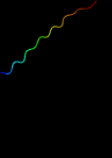
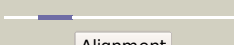





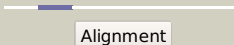
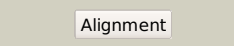
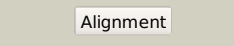
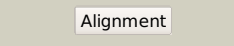
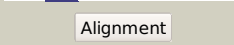
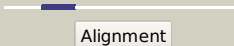
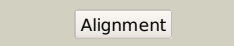
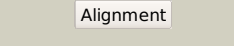


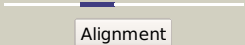


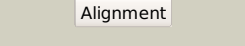



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3478_(PPE60)_3894605_3895786
 Date Fri Aug 9 18:20:15 BST 2019
 Unique Job ID ec23aa5e9e6713a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	50	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	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	34	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	21	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	17	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.9	10	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		97.8	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		97.7	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.1	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		96.2	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	 Alignment		95.8	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	 Alignment		95.7	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	 Alignment		95.1	20	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		90.3	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		81.1	17	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		16.3	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
18	c1bkvC	 Alignment		15.5	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvB	 Alignment		15.5	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
20	c5frgA	 Alignment		11.3	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
21	c3h6pB	 Alignment	not modelled	10.2	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
22	d1zeea1	 Alignment	not modelled	9.2	38	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
23	c2kg7A	 Alignment	not modelled	9.1	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
24	d1ui5a2	 Alignment	not modelled	8.6	11	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
25	c1vytF	 Alignment	not modelled	8.0	25	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
26	c2iu1A	 Alignment	not modelled	7.8	22	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
27	c2fulE	 Alignment	not modelled	7.8	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
28	c2ke4A	 Alignment	not modelled	5.6	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

29	d1fcda3	 Alignment	not modelled	5.2	15	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
30	c6aokA_	 Alignment	not modelled	5.2	11	PDB header: hydrolase Chain: A; PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
31	c4lzxB_	 Alignment	not modelled	5.1	29	PDB header: metal binding protein Chain: B; PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
32	c2lkqA_	 Alignment	not modelled	5.1	56	PDB header: immune system Chain: A; PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
33	c1vytE_	 Alignment	not modelled	5.1	25	PDB header: transport protein Chain: E; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
34	c5kq1C_	 Alignment	not modelled	5.1	25	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
35	c5kq4F_	 Alignment	not modelled	5.1	25	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