
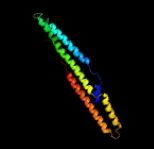

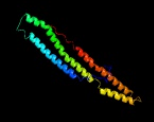

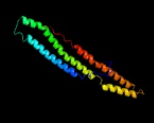

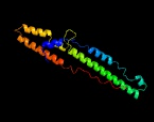





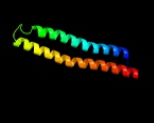
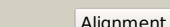

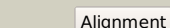


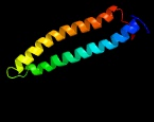


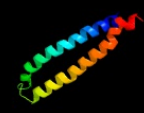


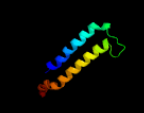
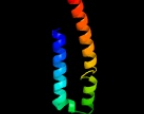
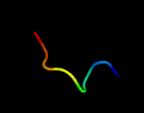





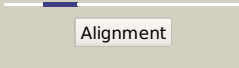
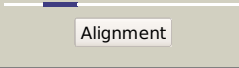
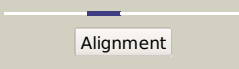
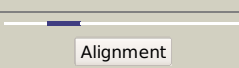
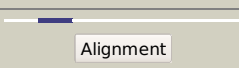
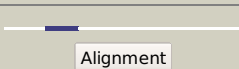
Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1168c_(PPE17)_1298769_1299809
 Date Wed Jul 31 22:05:25 BST 2019
 Unique Job ID ff25c5eb8146fb6c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	45	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	35	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	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
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		98.4	18	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		98.0	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.9	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
8	c3gvmA_	 Alignment		97.9	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
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		97.3	21	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		96.9	9	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		96.6	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		96.6	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		96.1	10	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		94.3	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		81.0	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	c5frgA	Alignment		19.4	63	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	c6epiC	Alignment		14.8	18	PDB header: toxin Chain: C: PDB Molecule: epsilon_1 antitoxin; PDBTitle: structure of the epsilon_1 / zeta_1 antitoxin / toxin system from2 neisseria gonorrhoeae in complex with unam-4p.
19	c2ke4A	Alignment		12.5	63	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
20	d1ui5a2	Alignment		9.3	17	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
21	c2iu1A	Alignment	not modelled	9.3	17	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
22	c3h6pB	Alignment	not modelled	9.2	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
23	c2kg7A	Alignment	not modelled	8.8	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	c2fulE	Alignment	not modelled	8.8	33	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	c5d5pC	Alignment	not modelled	8.0	7	PDB header: transferase Chain: C: PDB Molecule: hcgB; PDBTitle: hcgB from methanococcus maripaludis
26	c3brcA	Alignment	not modelled	7.1	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
27	d1zeeA1	Alignment	not modelled	7.0	32	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
28	c2i94B	Alignment	not modelled	6.8	50	PDB header: protein binding Chain: B: PDB Molecule: rhodopsin kinase; PDBTitle: nmr structure of recoverin bound to rhodopsin kinase

29	c1paqA_	 Alignment	not modelled	5.3	6	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
30	d1paqa_	 Alignment	not modelled	5.3	6	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
31	d1fcda3	 Alignment	not modelled	5.3	23	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
32	c1vytF_	 Alignment	not modelled	5.3	25	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
33	d1kha2	 Alignment	not modelled	5.2	10	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
34	c3luiA_	 Alignment	not modelled	5.1	15	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