
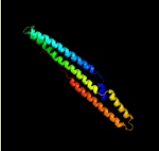

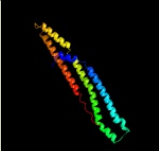

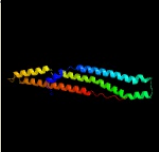

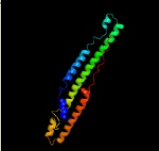

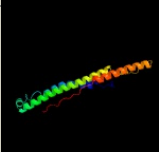

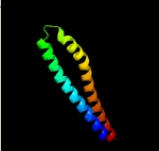

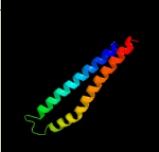

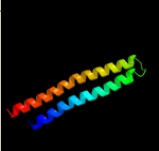

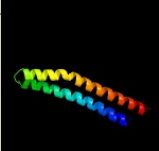

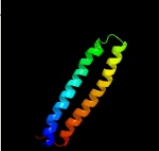

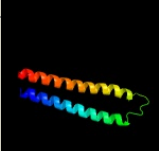
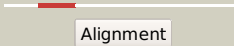

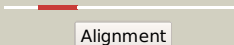

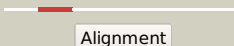
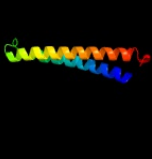
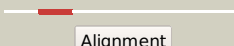
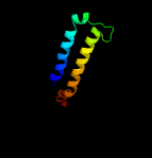
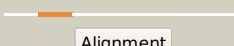
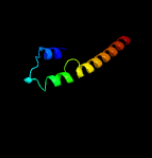
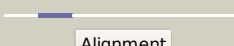
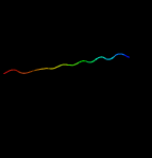
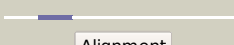
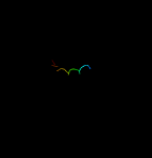

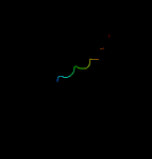


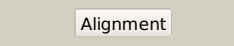
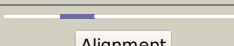


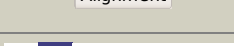
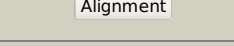
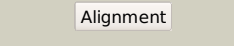

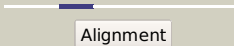


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0096_(PPE1)_105321_106712
 Date Tue Jul 23 14:50:13 BST 2019
 Unique Job ID f822c7e9a8506be0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	38	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	28	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	28	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	22	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	18	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.8	22	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.7	18	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	10	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		97.5	19	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.9	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.8	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	 Alignment		95.4	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	 Alignment		95.2	13	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	 Alignment		92.1	18	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		90.7	19	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		83.1	24	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		15.6	38	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
18	c1bkvC	 Alignment		15.0	38	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvB	 Alignment		15.0	38	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
20	c3h6pB	 Alignment		14.1	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
21	c2kg7A	 Alignment	not modelled	13.3	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
22	d1zeea1	 Alignment	not modelled	12.8	38	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
23	d1ui5a2	 Alignment	not modelled	12.6	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
24	c3q4hB	 Alignment	not modelled	8.5	19	PDB header: metal transport Chain: B; PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esxhg complex2 (msmeg_0620-msmeg_0621)
25	c1vytF	 Alignment	not modelled	7.8	50	PDB header: transport protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
26	c6et5y	 Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: Y; PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
27	c6et5m	 Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: M; PDB Molecule: reaction center protein m chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
28	c6et5j	 Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: J; PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
						PDB header: photosynthesis

29	c6et5R_	Alignment	not modelled	7.1	38	Chain: R: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
30	c6et5p_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: P: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
31	c6et5v_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: V: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
32	c6et5O_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: O: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
33	c6et5a_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: A: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. virids
34	c6et5g_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: G: PDB Molecule: light-harvesting protein b-1015 beta chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
35	c6et5U_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
36	c6et55_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: 5: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
37	c6et52_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: 2: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
38	c6et5s_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: S: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
39	c6et5l_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: l: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
40	c6et5d_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: D: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. virids
41	c6et5X_	Alignment	not modelled	7.1	38	PDB header: photosynthesis Chain: X: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. virids
42	c2iu1A_	Alignment	not modelled	7.0	22	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
43	c4gyxC_	Alignment	not modelled	7.0	38	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
44	d1fcda3	Alignment	not modelled	6.9	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
45	c5vmoB_	Alignment	not modelled	6.8	40	PDB header: viral protein/apoptosis Chain: B: PDB Molecule: bcl-2 interacting mediator of cell death; PDBTitle: crystal structure of grouper iridovirus giv66:bim complex
46	c5l85B_	Alignment	not modelled	6.5	45	PDB header: signaling protein Chain: B: PDB Molecule: nuclear fragile x mental retardation-interacting protein 1; PDBTitle: solution structure of the complex between human znhit3 and nufip12 proteins
47	c4dmtB_	Alignment	not modelled	6.5	36	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
48	c4dmtA_	Alignment	not modelled	6.5	36	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
49	c4dmtC_	Alignment	not modelled	6.5	36	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
50	c2fulE_	Alignment	not modelled	6.4	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
51	d1vifn1	Alignment	not modelled	6.3	100	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
52	c1vytE_	Alignment	not modelled	6.0	50	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
53	c4gyxB_	Alignment	not modelled	6.0	45	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
						PDB header: structural protein, blood clotting Chain: A: PDB Molecule: type iii collagen fragment in a host peptide

54	c4gyxA_	Alignment	not modelled	6.0	45	stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
55	c2fwtA_	Alignment	not modelled	5.9	43	PDB header: electron transport Chain: A: PDB Molecule: dhc, diheme cytochrome c; PDBTitle: crystal structure of dhc purified from rhodobacter2 sphaeroides
56	c3u99A_	Alignment	not modelled	5.9	43	PDB header: electron transport Chain: A: PDB Molecule: diheme cytochrome c; PDBTitle: the experimental x-ray structure of the new diheme cytochrome type c2 from shewanella baltica os155 sb-dhc
57	c6aokA_	Alignment	not modelled	5.8	25	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
58	c6nbiP_	Alignment	not modelled	5.7	50	PDB header: signaling protein Chain: P: PDB Molecule: long-acting parathyroid hormone analog; PDBTitle: cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
59	c6cqiA_	Alignment	not modelled	5.5	38	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
60	c2lkqA_	Alignment	not modelled	5.4	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
61	c4deyB_	Alignment	not modelled	5.3	29	PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker.
62	d1nkt4	Alignment	not modelled	5.2	56	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
63	c1t0jC_	Alignment	not modelled	5.1	57	PDB header: signaling protein Chain: C: PDB Molecule: voltage-dependent l-type calcium channel alpha-1c subunit; PDBTitle: crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
64	c2y5tG_	Alignment	not modelled	5.1	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