
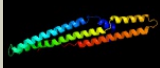

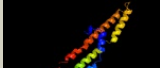

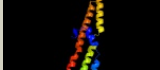

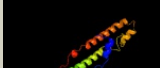

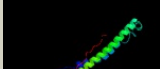











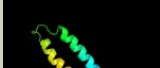
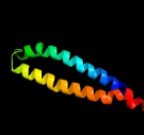
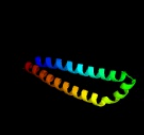


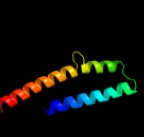



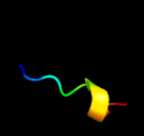


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0915c_(PPE14)_1020062_1021333
 Date Fri Jul 26 01:50:50 BST 2019
 Unique Job ID 116896f498553256

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	58	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	36	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	36	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	19	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		98.5	23	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.9	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.7	17	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		97.7	14	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		97.6	18	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		95.9	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		95.6	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		95.5	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		92.8	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		90.1	14	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		58.9	28	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		39.0	19	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c5frgA	Alignment		16.1	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
19	c1bkvA	Alignment		13.7	38	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
20	c4xb6D	Alignment		13.4	33	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
21	c1bkvB	Alignment	not modelled	13.0	38	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
22	c1bkvC	Alignment	not modelled	13.0	38	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
23	c2nvjA	Alignment	not modelled	10.8	40	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
24	c6aokA	Alignment	not modelled	10.5	33	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
25	c6cgjA	Alignment	not modelled	9.8	22	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
26	d1fcda3	Alignment	not modelled	9.2	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
27	c2ke4A	Alignment	not modelled	8.8	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
28	c6et5s	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: S: PDB Molecule: light-harvesting protein b-1015 alpha chain;

						PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
29	c6et5p_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: P: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
30	c6et5O_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: O: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
31	c6et5R_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: R: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
32	c6et5j_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: J: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
33	c6et5I_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: I: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
34	c6et55_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: 5: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
35	c6et5X_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: X: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
36	c6et5g_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: G: PDB Molecule: light-harvesting protein b-1015 beta chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
37	c6et5m_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: M: PDB Molecule: reaction center protein m chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
38	c6et5v_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: V: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
39	c6et52_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: 2: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
40	c6et5U_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
41	c6et5a_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: A: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
42	c6et5y_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: Y: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
43	c6et5d_	Alignment	not modelled	8.8	44	PDB header: photosynthesis Chain: D: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
44	c2kg7A_	Alignment	not modelled	8.6	26	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
45	c2iu1A_	Alignment	not modelled	8.5	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
46	c1bzgA_	Alignment	not modelled	7.5	0	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone-related protein; PDBTitle: the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
47	c2fulE_	Alignment	not modelled	7.4	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
48	c1vytF_	Alignment	not modelled	7.3	25	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
49	c2lkqA_	Alignment	not modelled	6.5	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
50	c6nbiP_	Alignment	not modelled	6.3	80	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
51	c3h6pB_	Alignment	not modelled	6.2	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
52	c5I85B_	Alignment	not modelled	6.2	9	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
53	c5IzkB_	Alignment	not modelled	6.1	9	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b

54	d1xkna_	Alignment	not modelled	6.0	11	Fold: Pentein, beta/alpha-propeller Superfamily: Pentein Family: Porphyromonas-type peptidylarginine deiminase
55	c2jtwA_	Alignment	not modelled	5.8	50	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
56	c1vytE_	Alignment	not modelled	5.7	25	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
57	c3trhI_	Alignment	not modelled	5.6	19	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
58	d1zea1	Alignment	not modelled	5.6	25	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
59	c4dexB_	Alignment	not modelled	5.5	25	PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent n-type calcium channel subunit alpha-1b; PDBTitle: crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav2.2 i-ii linker.
60	d1vifn1	Alignment	not modelled	5.1	40	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain