
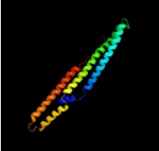

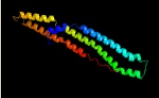

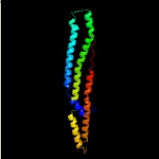

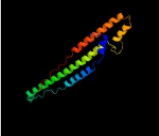

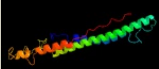



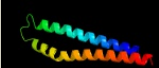

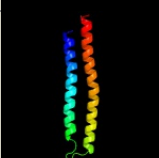



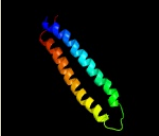

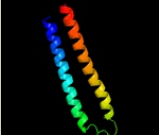


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1705c_(PPE22)_1931504_1932661
 Date Fri Aug 2 13:30:30 BST 2019
 Unique Job ID aac28d022a66e12a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	62	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		98.2	18	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.6	14	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.4	11	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		97.4	14	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		97.2	15	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.4	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		93.7	14	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	Alignment		92.1	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		91.0	21	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		90.6	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		82.3	18	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		58.7	23	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		30.2	24	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c1bkvA_	Alignment		19.5	38	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
19	c5frgA_	Alignment		19.2	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
20	c1bkvC_	Alignment		18.6	38	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
21	c1bkvB_	Alignment	not modelled	18.6	38	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
22	c2ke4A_	Alignment	not modelled	12.3	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
23	c4xb6D_	Alignment	not modelled	10.9	22	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
24	c6aokA_	Alignment	not modelled	9.8	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	c2nviA_	Alignment	not modelled	9.6	40	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit a from2 the yeast proton v-atpase
26	c6cgjA_	Alignment	not modelled	9.1	33	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
27	c6nbiP_	Alignment	not modelled	7.1	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
28	d1zeeal	Alianment	not modelled	7.0	27	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like

						Family: Indoleamine 2,3-dioxygenase-like
29	c5ucOB_	Alignment	not modelled	6.8	60	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
30	c1bzgA_	Alignment	not modelled	6.8	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
31	c2lkqA_	Alignment	not modelled	6.7	56	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
32	d1vfn1	Alignment	not modelled	6.6	60	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
33	c2kg7A_	Alignment	not modelled	6.6	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
34	c2y5tG_	Alignment	not modelled	6.6	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
35	c2y5tE_	Alignment	not modelled	6.3	67	PDB header: immune system Chain: E: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
36	c4gyxC_	Alignment	not modelled	6.3	55	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
37	c1vytF_	Alignment	not modelled	6.2	25	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
38	c5lzkB_	Alignment	not modelled	6.0	9	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
39	c4dmtA_	Alignment	not modelled	6.0	46	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
40	c4dmtC_	Alignment	not modelled	6.0	46	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
41	c4dmtB_	Alignment	not modelled	6.0	46	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
42	c4gyxB_	Alignment	not modelled	5.9	55	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
43	c4gyxA_	Alignment	not modelled	5.9	55	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
44	c2iu1A_	Alignment	not modelled	5.8	11	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
45	c5l85B_	Alignment	not modelled	5.8	27	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
46	c5hl8B_	Alignment	not modelled	5.7	33	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein I; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
47	c2y5tF_	Alignment	not modelled	5.5	67	PDB header: immune system Chain: F: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
48	c2wuhD_	Alignment	not modelled	5.5	67	PDB header: receptor/peptide Chain: D: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
49	d1fcd3	Alignment	not modelled	5.4	38	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
50	c3qi7A_	Alignment	not modelled	5.4	56	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
51	c6a0aA_	Alignment	not modelled	5.3	50	PDB header: structural protein Chain: A: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
						PDB header: membrane protein

52	c2jtwA_	Alignment	not modelled	5.3	50	Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
53	c6dzsD_	Alignment	not modelled	5.3	25	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
54	c2wuhB_	Alignment	not modelled	5.2	67	PDB header: receptor/peptide Chain: B: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
55	c2wuhC_	Alignment	not modelled	5.2	67	PDB header: receptor/peptide Chain: C: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
56	c4i6jB_	Alignment	not modelled	5.1	33	PDB header: transcription Chain: B: PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
57	c4auoE_	Alignment	not modelled	5.0	67	PDB header: hydrolase/peptide Chain: E: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
58	c4auoH_	Alignment	not modelled	5.0	67	PDB header: hydrolase/peptide Chain: H: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide