
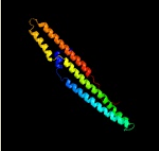

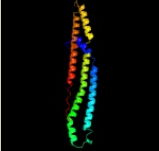

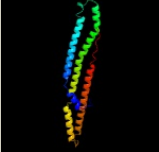

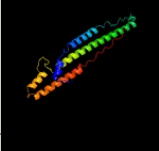

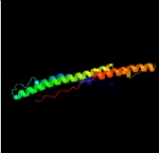





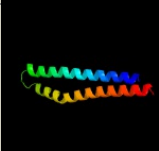



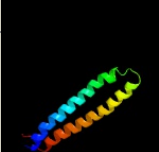

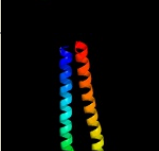


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2768c_(PPE43)_3076904_3078088
 Date Wed Aug 7 12:50:42 BST 2019
 Unique Job ID afa3c1e71f1bc81f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	83	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	30	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	30	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	16	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	16	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.7	13	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.6	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
8	c3gvmA_	 Alignment		97.6	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
9	c3zbhC_	 Alignment		97.4	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.7	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.7	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	Alignment		95.0	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		94.9	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		94.0	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		88.8	12	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		80.6	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	c5frgA_	Alignment		18.6	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
18	d1ui5a2	Alignment		18.5	26	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
19	c1bkvA_	Alignment		14.6	44	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvC_	Alignment		13.9	44	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
21	c1bkvB_	Alignment	not modelled	13.9	44	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
22	c2ke4A_	Alignment	not modelled	11.5	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	c2nviA_	Alignment	not modelled	7.9	40	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit a from2 the yeast proton v-atpase PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
24	c6aokA_	Alignment	not modelled	7.4	22	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	c3h6pB_	Alignment	not modelled	7.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
26	c4xb6D_	Alignment	not modelled	7.3	30	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
27	c1vytF_	Alignment	not modelled	7.2	50	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
28	c6cglA_	Alignment	not modelled	6.8	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

29	c2kg7A_	Alignment	not modelled	6.7	24	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
30	c2iu1A_	Alignment	not modelled	6.6	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
31	c3sjrB_	Alignment	not modelled	6.6	6	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknwn function protein cv_1783 from2 chromobacterium violaceum atcc 12472
32	c1bzgA_	Alignment	not modelled	6.3	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
33	c2lkqA_	Alignment	not modelled	6.1	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
34	c2fulE_	Alignment	not modelled	6.0	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
35	c4i6jB_	Alignment	not modelled	5.6	44	PDB header: transcription Chain: B: PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
36	c4lzxB_	Alignment	not modelled	5.6	35	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
37	c2hfvA_	Alignment	not modelled	5.5	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa1041; PDBTitle: solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
38	c5l85B_	Alignment	not modelled	5.4	18	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
39	d2hfva1	Alignment	not modelled	5.4	50	Fold: Ferredoxin-like Superfamily: GlnB-like Family: RPA1041-like
40	c4mveB_	Alignment	not modelled	5.3	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcur_1030 protein from thermomonospora curvata
41	c2jtwA_	Alignment	not modelled	5.1	50	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
42	c6nbiP_	Alignment	not modelled	5.0	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