
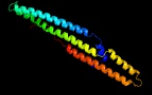

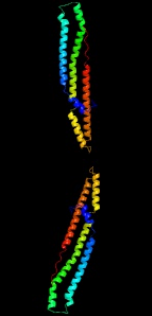

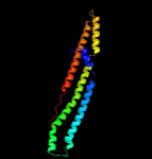

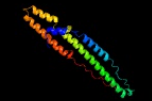

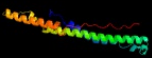

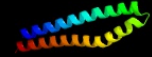









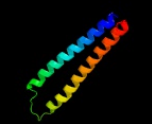
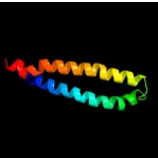

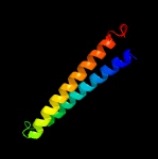
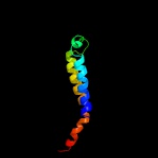
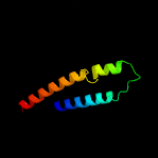

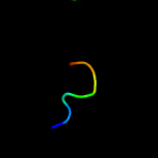
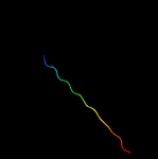
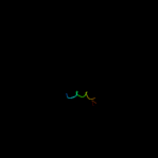


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2352c_(PPE38)_2632933_2634108
 Date Mon Aug 5 13:25:50 BST 2019
 Unique Job ID cc025e5e2113d58b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	54	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	33	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	33	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	21	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	21	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.7	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		97.6	15	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		97.5	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		97.3	18	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.6	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.1	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		94.7	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		94.3	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		93.1	22	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		86.0	15	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		44.4	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		26.0	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		16.8	88	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	56	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvC	Alignment		13.0	56	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
21	c1bkvB	Alignment	not modelled	13.0	56	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
22	c2ke4A	Alignment	not modelled	10.1	88	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	c4lzxB	Alignment	not modelled	7.7	38	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
24	c3jygB	Alignment	not modelled	6.5	38	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein ws1659 from wolinnella2 succinogenes
25	c4xb6D	Alignment	not modelled	6.1	20	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
26	c2kg7A	Alignment	not modelled	6.1	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
27	c2lkqA	Alignment	not modelled	6.0	56	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
28	c2iu1A	Alignment	not modelled	5.7	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain

29	c2i94B_	Alignment	not modelled	5.7	50	PDB header: protein binding Chain: B: PDB Molecule: rhodopsin kinase; PDBTitle: nmr structure of recoverin bound to rhodopsin kinase
30	c6aokA_	Alignment	not modelled	5.6	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
31	c1vytF_	Alignment	not modelled	5.6	38	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
32	c4m1IB_	Alignment	not modelled	5.6	43	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-bound cam
33	c3sjrB_	Alignment	not modelled	5.5	6	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unkown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
34	c2fulE_	Alignment	not modelled	5.5	39	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	c6cgjA_	Alignment	not modelled	5.4	44	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
36	c6nbiP_	Alignment	not modelled	5.3	60	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
37	d2a0sa1	Alignment	not modelled	5.3	29	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
38	c5lzkB_	Alignment	not modelled	5.3	4	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
39	c2nvjA_	Alignment	not modelled	5.2	30	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
40	c6q5IA_	Alignment	not modelled	5.2	32	PDB header: de novo protein Chain: A: PDB Molecule: cc-hex*-I24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24h
41	c6q5IB_	Alignment	not modelled	5.2	32	PDB header: de novo protein Chain: B: PDB Molecule: cc-hex*-I24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24h
42	c6q5hA_	Alignment	not modelled	5.1	32	PDB header: de novo protein Chain: A: PDB Molecule: cc-hex*-I24d; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24d
43	c6q5iB_	Alignment	not modelled	5.1	32	PDB header: de novo protein Chain: B: PDB Molecule: cc-hex*-I24e; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24e
44	c6q5mB_	Alignment	not modelled	5.1	32	PDB header: de novo protein Chain: B: PDB Molecule: cc-hex*-I24dab; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24dab
45	c6q5kA_	Alignment	not modelled	5.1	32	PDB header: de novo protein Chain: A: PDB Molecule: cc-hex*-I24k; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24k
46	d1y13a_	Alignment	not modelled	5.1	50	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: 6-pyruvoyl tetrahydropterin synthase
47	d1khba2	Alignment	not modelled	5.1	20	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain