
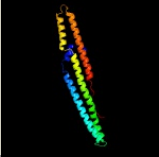



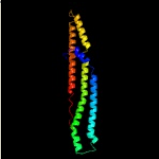

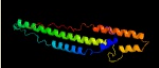

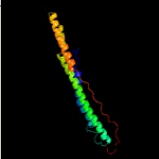





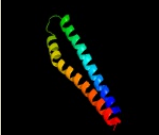





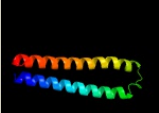


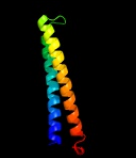
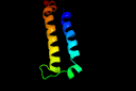
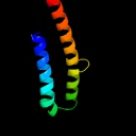

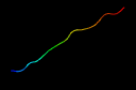
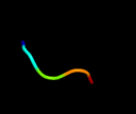



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3532_(PPE61)_3969522_3970742
 Date Fri Aug 9 18:20:21 BST 2019
 Unique Job ID 6499fcd1aaf6a5a5

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	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
3	d2g38b1	 Alignment		100.0	33	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	18	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		98.8	16	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.7	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.5	19	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	16	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	18	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.6	25	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.7	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		95.0	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		94.9	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		93.8	12	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		89.4	13	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		82.2	18	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		22.4	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c1bkvA	Alignment		13.4	38	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
19	c2knuA	Alignment		13.4	40	PDB header: membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of the transmembrane proximal region of2 the hepatitis c virus e1 glycoprotein
20	c5frgA	Alignment		13.1	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
21	c1bkvC	Alignment	not modelled	12.8	38	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
22	c1bkvB	Alignment	not modelled	12.8	38	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
23	d1zeeal	Alignment	not modelled	11.8	29	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
24	c2iu1A	Alignment	not modelled	9.3	17	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
25	c2fulE	Alignment	not modelled	8.6	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
26	c2nviA	Alignment	not modelled	8.0	20	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
27	c4lzxB	Alignment	not modelled	7.6	41	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
28	c2ke4A	Alignment	not modelled	7.0	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 Fold: CO dehydrogenase flavoprotein C-domain-like

29	d1fcd3	Alignment	not modelled	6.8	38	Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
30	c4m1B	Alignment	not modelled	6.8	50	PDB header: metal binding protein Chain: B: PDB Molecule: iqq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-bound cam
31	c5kj3A	Alignment	not modelled	6.6	50	PDB header: transport protein Chain: A: PDB Molecule: gap junction beta-2 protein; PDBTitle: connexin 26 wt peptide nmr structure
32	c4i6jB	Alignment	not modelled	6.4	22	PDB header: transcription Chain: B: PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
33	c2lkqA	Alignment	not modelled	6.2	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	c3juia	Alignment	not modelled	6.1	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
35	c1vytF	Alignment	not modelled	5.8	38	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
36	c6nbiP	Alignment	not modelled	5.7	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
37	c6q5IA	Alignment	not modelled	5.6	23	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
38	c6q5IB	Alignment	not modelled	5.6	23	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
39	c6q5hA	Alignment	not modelled	5.6	23	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
40	c6q5iB	Alignment	not modelled	5.5	23	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
41	c6q5mB	Alignment	not modelled	5.5	23	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
42	c6q5kA	Alignment	not modelled	5.5	23	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
43	c1paqA	Alignment	not modelled	5.5	24	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
44	d1paqa	Alignment	not modelled	5.5	24	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
45	d1vfn1	Alignment	not modelled	5.5	100	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
46	c6q5mA	Alignment	not modelled	5.5	23	PDB header: de novo protein Chain: A: 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
47	c3sjrB	Alignment	not modelled	5.4	19	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
48	c1bzqA	Alignment	not modelled	5.4	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
49	c6aokA	Alignment	not modelled	5.4	50	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
50	c2jtwA	Alignment	not modelled	5.3	25	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
51	c3r47B	Alignment	not modelled	5.3	23	PDB header: de novo protein Chain: B: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
52	c3r47J	Alignment	not modelled	5.3	23	PDB header: de novo protein Chain: J: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
53	c3r47I	Alignment	not modelled	5.3	23	PDB header: de novo protein Chain: I: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
54	c6q5jE	Alignment	not modelled	5.3	23	PDB header: de novo protein Chain: E: PDB Molecule: cc-hex*-I24e; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel

						six-helix2 coiled coil cc-hex*-I24e PDB header: de novo protein Chain: B: 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
55	c6q5kB_	Alignment	not modelled	5.2	23	PDB header: de novo protein Chain: F: PDB Molecule: cc-hex*-I24e; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24e
56	c6q5jF_	Alignment	not modelled	5.2	23	PDB header: de novo protein Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
57	c6cgjA_	Alignment	not modelled	5.2	38	PDB header: hydrolase Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
58	c5i4rA_	Alignment	not modelled	5.2	57	PDB header: toxin/antitoxin Chain: L: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
59	c3r47L_	Alignment	not modelled	5.1	23	PDB header: de novo protein Chain: F: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
60	c3r47F_	Alignment	not modelled	5.1	23	PDB header: de novo protein Chain: C: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
61	c3r47C_	Alignment	not modelled	5.1	23	PDB header: de novo protein Chain: M: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
62	c3r47M_	Alignment	not modelled	5.1	23	PDB header: de novo protein Chain: M: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24