
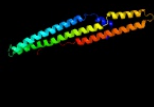

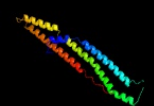

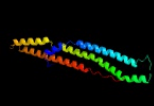



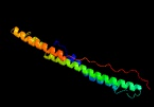





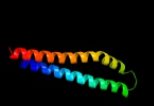

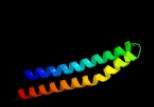






Phyre2


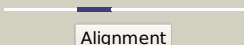

Email mdejesus@rockefeller.edu
 Description RVBD1039c_(PPE15)_1161301_1162476
 Date Wed Jul 31 22:05:11 BST 2019
 Unique Job ID 6447f71383864137

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	100	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	31	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	31	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	17	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	17	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.9	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		97.7	10	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	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
9	c3zbhC_	 Alignment		97.5	18	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.8	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.4	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	Alignment		94.5	18	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		94.4	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		93.2	20	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		88.2	18	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		63.0	20	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		17.5	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		17.4	24	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
19	c1bkvA_	Alignment		16.8	56	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvC_	Alignment		16.0	56	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
21	c1bkvB_	Alignment	not modelled	16.0	56	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
22	c2ke4A_	Alignment	not modelled	10.3	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	c1vytF_	Alignment	not modelled	7.1	50	PDB header: transport protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
24	c4xb6D_	Alignment	not modelled	7.0	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
25	c4gyxC_	Alignment	not modelled	6.9	45	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
26	c2iu1A_	Alignment	not modelled	6.7	22	PDB header: transcription Chain: A; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
27	c4dmtC_	Alignment	not modelled	6.7	38	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
28	c4dmtB_	Alignment	not modelled	6.7	38	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

29	c4dmtA	Alignment	not modelled	6.7	38	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
30	c4gyxA	Alignment	not modelled	6.6	45	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
31	c4gyxB	Alignment	not modelled	6.6	45	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
32	d1fcdA3	Alignment	not modelled	6.4	31	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
33	c2fulE	Alignment	not modelled	6.1	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
34	c2kg7A	Alignment	not modelled	6.0	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
35	c1vytE	Alignment	not modelled	5.7	50	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
36	c2lkqA	Alignment	not modelled	5.6	56	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
37	c2y5tG	Alignment	not modelled	5.6	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
38	c6q5IA	Alignment	not modelled	5.5	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
39	c6q5IB	Alignment	not modelled	5.5	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
40	c6q5hA	Alignment	not modelled	5.5	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
41	c6q5mB	Alignment	not modelled	5.4	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	c6q5iB	Alignment	not modelled	5.4	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
43	c6q5kA	Alignment	not modelled	5.4	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
44	d1zeeA1	Alignment	not modelled	5.4	33	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
45	c4lzxB	Alignment	not modelled	5.3	38	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
46	c6q5mA	Alignment	not modelled	5.3	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	c5ucOB	Alignment	not modelled	5.3	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
48	c2y5tE	Alignment	not modelled	5.3	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
49	c6q5IE	Alignment	not modelled	5.1	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
50	c3r47J	Alignment	not modelled	5.1	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
51	c3r47B	Alignment	not modelled	5.1	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	c3r47I	Alignment	not modelled	5.1	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
53	c5I85B	Alignment	not modelled	5.1	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

54	c4dexB_	 Alignment	not modelled	5.1	38	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.
55	c6aokA_	 Alignment	not modelled	5.1	38	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
56	c6q5jF_	 Alignment	not modelled	5.1	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