
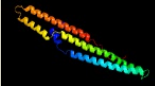

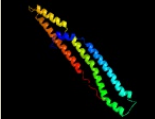

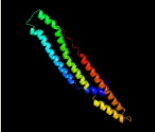

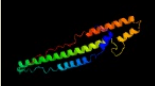

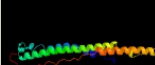

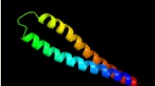

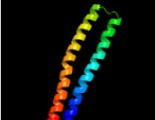








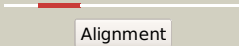




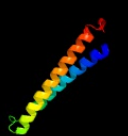
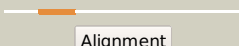
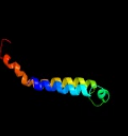
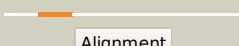

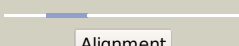

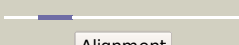
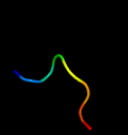

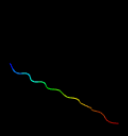



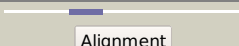

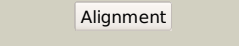

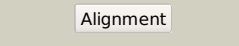




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1808_(PPE32)_2049928_2051157
 Date Fri Aug 2 13:30:42 BST 2019
 Unique Job ID 61fc79690c716eee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	64	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	32	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	32	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		98.5	16	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.7	10	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		97.6	15	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	16	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.7	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.7	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	 Alignment		95.3	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	 Alignment		95.1	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	 Alignment		93.4	11	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		89.7	16	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		80.2	15	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		20.0	22	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c5frgA	 Alignment		18.9	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
19	c1bkvA	 Alignment		15.0	56	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvB	 Alignment		14.3	56	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
21	c1bkvC	 Alignment	not modelled	14.3	56	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
22	d1zeea1	 Alignment	not modelled	12.8	29	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
23	c2ke4A	 Alignment	not modelled	11.4	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
24	c1vytF	 Alignment	not modelled	10.7	38	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
25	c3h6pB	 Alignment	not modelled	9.0	35	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	c2lkqA	 Alignment	not modelled	8.6	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
27	c2nvjA	 Alignment	not modelled	8.5	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
28	c2kg7A	 Alignment	not modelled	8.3	47	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
29	c1bzgA	Alignment	not modelled	8.2	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
30	c2iu1A	Alignment	not modelled	7.6	11	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
31	c1vytE	Alignment	not modelled	7.5	38	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
32	c4lzxB	Alignment	not modelled	7.3	31	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
33	c4dexB	Alignment	not modelled	7.3	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.
34	c3ub0D	Alignment	not modelled	7.2	21	PDB header: replication Chain: D: PDB Molecule: non-structural protein 6, nsp6,; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of2 feline coronavirus
35	c2fulE	Alignment	not modelled	7.2	22	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
36	c5i4rA	Alignment	not modelled	7.1	43	PDB header: toxin/antitoxin 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)
37	c6aokA	Alignment	not modelled	7.0	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
38	c6et5m	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: M: PDB Molecule: reaction center protein m chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
39	c6et5s	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: S: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
40	c6et5O	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: O: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
41	c6et5R	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: R: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
42	c6et5U	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
43	c6et55	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: 5: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
44	c6et52	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: 2: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
45	c6et5I	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: I: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
46	c6et5X	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: X: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
47	c6et5a	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: A: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
48	c6et5y	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: Y: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
49	c6et5v	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: V: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
50	c6et5j	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: J: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
51	c6et5d	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: D: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
52	c6et5g	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: G: PDB Molecule: light-harvesting protein b-1015 beta chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
53	c6et5p	Alignment	not modelled	7.0	44	PDB header: photosynthesis Chain: P: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
54	c6cniA	Alignment	not modelled	6.9	38	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101);

54	c0cgjA	Alignment	not modelled	6.9	30	PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from <i>Legionella pneumophila</i> PDB header: hydrolase
55	c5uc0B	Alignment	not modelled	6.9	80	Chain: B; PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from <i>Brucella abortus</i>
56	c2jtwA	Alignment	not modelled	6.8	50	PDB header: membrane protein Chain: A; PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
57	c5l85B	Alignment	not modelled	6.7	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
58	c3sjrB	Alignment	not modelled	6.3	6	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknown function protein cv_1783 from <i>Chromobacterium violaceum</i> atcc 12472
59	c4m1lB	Alignment	not modelled	6.2	36	PDB header: metal binding protein Chain: B; PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-bound cam
60	d1khba2	Alignment	not modelled	6.2	20	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
61	c1t0jC	Alignment	not modelled	6.2	43	PDB header: signaling protein Chain: C; PDB Molecule: voltage-dependent l-type calcium channel alpha-1c subunit; PDBTitle: crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
62	c2y5tG	Alignment	not modelled	6.1	83	PDB header: immune system Chain: G; PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody cic1 in complex with2 the triple-helical c1 peptide
63	d1vfn1	Alignment	not modelled	6.1	80	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
64	c1nauA	Alignment	not modelled	6.1	25	PDB header: hormone/growth factor Chain: A; PDB Molecule: glucagon; PDBTitle: nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
65	c4xb6D	Alignment	not modelled	5.9	11	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
66	c2y5tE	Alignment	not modelled	5.9	83	PDB header: immune system Chain: E; PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody cic1 in complex with2 the triple-helical c1 peptide
67	c5lzkB	Alignment	not modelled	5.6	4	PDB header: structural genomics Chain: B; PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
68	c4mveB	Alignment	not modelled	5.6	26	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcu_1030 protein from <i>Thermomonospora curvata</i>
69	d1fcda3	Alignment	not modelled	5.6	19	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
70	c3juia	Alignment	not modelled	5.5	8	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
71	c6nblP	Alignment	not modelled	5.3	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
72	c6q5lA	Alignment	not modelled	5.3	23	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-l24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-l24h
73	c6q5lB	Alignment	not modelled	5.3	23	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-l24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-l24h
74	c2i94B	Alignment	not modelled	5.3	67	PDB header: protein binding Chain: B; PDB Molecule: rhodopsin kinase; PDBTitle: nmr structure of recoverin bound to rhodopsin kinase
75	c6q5hA	Alignment	not modelled	5.3	23	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-l24d; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-l24d
76	c2l5ba	Alignment	not modelled	5.3	31	PDB header: apoptosis Chain: A; PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
77	c6q5iB	Alignment	not modelled	5.2	23	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-l24e; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-l24e
78	c6q5mB	Alignment	not modelled	5.2	23	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-l24dab; PDBTitle: crystal structure of a cc-hex mutant that forms an

						antiparallel four-2 helix coiled coil cc-hex*-I24dab
79	c6q5kA_	Alignment	not modelled	5.2	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
80	c2qngA_	Alignment	not modelled	5.2	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sav2460; PDBTitle: crystal structure of unknown function protein sav2460
81	c6q5mA_	Alignment	not modelled	5.2	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
82	c2wuhD_	Alignment	not modelled	5.1	83	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
83	c4yk2B_	Alignment	not modelled	5.1	14	PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
84	c2y5tF_	Alignment	not modelled	5.1	83	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
85	c6a0aA_	Alignment	not modelled	5.1	63	PDB header: structural protein Chain: A: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii