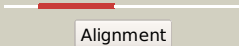
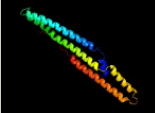



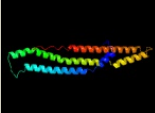


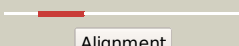
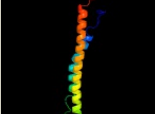
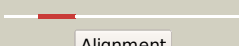

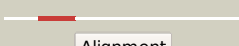
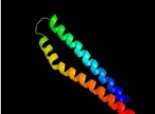
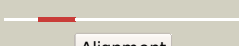


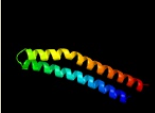



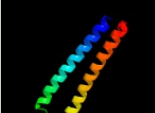


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2123_(PPE37)_2381079_2382500
Date	Mon Aug 5 13:25:24 BST 2019
Unique Job ID	78dbb1bf08baf60

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	37	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	29	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	29	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	19	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		98.2	17	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.8	16	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.6	20	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c4iogD_	 Alignment		97.6	12	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
9	c3zbhC_	 Alignment		97.4	20	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.7	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.7	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	Alignment		95.2	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	c4i0xA_	Alignment		95.0	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
14	d1wa8b1_	Alignment		94.6	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
15	c2kg7B_	Alignment		88.8	19	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		83.8	22	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	c4mveB_	Alignment		19.7	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcur_1030 protein from thermomonospora curvata
18	d1zeea1_	Alignment		13.9	27	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
19	c6et5O_	Alignment		13.1	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
20	c6et5R_	Alignment		13.1	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
21	c6et5U_	Alignment	not modelled	13.1	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
22	c6et5p_	Alignment	not modelled	13.1	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
23	c6et5X_	Alignment	not modelled	13.1	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
24	c6et5I_	Alignment	not modelled	13.1	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
25	c6et5d_	Alignment	not modelled	13.1	44	PDB header: photosynthesis Chain: D: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
26	c6et5j_	Alignment	not modelled	13.1	44	PDB header: photosynthesis Chain: J: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
27	c6et5s_	Alignment	not modelled	13.1	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
28	c6et5y_	Alignment	not modelled	13.1	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
						PDB header: photosynthesis

29	c6et5g_	Alignment	not modelled	13.1	44	Chain: G; PDB Molecule: light-harvesting protein b-1015 beta chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
30	c6et5a_	Alignment	not modelled	13.1	44	PDB header: photosynthesis Chain: A; PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
31	c6et52_	Alignment	not modelled	13.1	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
32	c6et5v_	Alignment	not modelled	13.1	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
33	c6et55_	Alignment	not modelled	13.1	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
34	c6et5m_	Alignment	not modelled	13.1	44	PDB header: photosynthesis Chain: M; PDB Molecule: reaction center protein m chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
35	c1bkvA_	Alignment	not modelled	11.8	44	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
36	c1bkvC_	Alignment	not modelled	11.3	44	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
37	c1bkvB_	Alignment	not modelled	11.3	44	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
38	c1vytF_	Alignment	not modelled	10.1	38	PDB header: transport protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
39	c2kg7A_	Alignment	not modelled	9.5	30	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
40	c4xb6D_	Alignment	not modelled	9.1	22	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
41	c4gyxC_	Alignment	not modelled	8.8	45	PDB header: structural protein, blood clotting stabilized by Chain: C; PDB Molecule: type iii collagen fragment in a host peptide PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
42	c4dmtA_	Alignment	not modelled	8.7	45	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
43	c4dmtC_	Alignment	not modelled	8.7	45	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
44	c4dmtB_	Alignment	not modelled	8.7	45	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
45	c3h6pB_	Alignment	not modelled	8.4	47	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
46	c5l85B_	Alignment	not modelled	8.4	36	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
47	c4gyxA_	Alignment	not modelled	8.4	56	PDB header: structural protein, blood clotting stabilized by Chain: A; PDB Molecule: type iii collagen fragment in a host peptide PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
48	c4gyxB_	Alignment	not modelled	8.4	56	PDB header: structural protein, blood clotting stabilized by Chain: B; PDB Molecule: type iii collagen fragment in a host peptide PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
49	c1vytE_	Alignment	not modelled	8.3	38	PDB header: transport protein Chain: E; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
50	d1dlpa1	Alignment	not modelled	8.0	18	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
51	d1vfn1	Alignment	not modelled	7.6	100	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
52	c3sjrB_	Alignment	not modelled	7.5	20	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknwon function protein cv_1783 from2 chromobacterium violaceum atcc 12472
53	c2nvjA_	Alignment	not modelled	7.3	50	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
						Fold: Tetracyclin repressor-like, C-terminal domain

54	d1ui5a2	Alignment	not modelled	6.9	18	Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
55	c2y5tG	Alignment	not modelled	6.7	83	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
56	c2y5tE	Alignment	not modelled	6.3	83	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
57	c4u39O	Alignment	not modelled	6.3	45	PDB header: cell cycle Chain: Q: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
58	c2lkqA	Alignment	not modelled	6.1	56	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
59	c6q5IA	Alignment	not modelled	6.0	27	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
60	c6q5IB	Alignment	not modelled	6.0	27	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
61	c2wseE	Alignment	not modelled	6.0	25	PDB header: photosynthesis Chain: E: PDB Molecule: photosystem i reaction center subunit iv a, chloroplastic; PDBTitle: improved model of plant photosystem i
62	c6q5hA	Alignment	not modelled	5.9	27	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
63	c3j00Z	Alignment	not modelled	5.9	4	PDB header: ribosome/ribosomal protein Chain: Z: PDB Molecule: cell division protein ftsq; PDBTitle: structure of the ribosome-secye complex in the membrane environment
64	c6q5mB	Alignment	not modelled	5.9	27	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
65	c6q5iB	Alignment	not modelled	5.9	27	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
66	c6q5kA	Alignment	not modelled	5.9	27	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
67	c2iu1A	Alignment	not modelled	5.8	39	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
68	c6q5mA	Alignment	not modelled	5.8	27	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
69	c6aokA	Alignment	not modelled	5.8	25	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
70	c1t0jC	Alignment	not modelled	5.8	29	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
71	c6a0aA	Alignment	not modelled	5.8	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
72	c1bzgA	Alignment	not modelled	5.7	14	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
73	c2y5tF	Alignment	not modelled	5.7	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
74	d1fcdA3	Alignment	not modelled	5.6	23	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
75	c2fulE	Alignment	not modelled	5.6	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
76	c6q5jE	Alignment	not modelled	5.6	27	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
77	c2wuhD	Alignment	not modelled	5.6	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
78	c4f3fC	Alignment	not modelled	5.6	44	PDB header: immune system Chain: C: PDB Molecule: mesothelin; PDBTitle: crystal structure of msln7-64 morab-009 fab complex
						PDB header: de novo protein

79	c3r47B_	Alignment	not modelled	5.6	27	Chain: B: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
80	c3r47J_	Alignment	not modelled	5.6	27	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
81	c3r47I_	Alignment	not modelled	5.6	27	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
82	c6q5jF_	Alignment	not modelled	5.5	27	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
83	c6q5kB_	Alignment	not modelled	5.5	27	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
84	c5dn4A_	Alignment	not modelled	5.4	57	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan hydrolase flgj; PDBTitle: structure of the glycoside hydrolase domain from salmonella2 typhimurium flgj
85	c6a0cB_	Alignment	not modelled	5.4	63	PDB header: structural protein Chain: B: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
86	c6cglA_	Alignment	not modelled	5.4	38	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
87	c3r47F_	Alignment	not modelled	5.4	27	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
88	c3r47C_	Alignment	not modelled	5.4	27	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
89	c3r47M_	Alignment	not modelled	5.4	27	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
90	c3r47L_	Alignment	not modelled	5.4	27	PDB header: de novo protein Chain: L: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
91	c2wuhB_	Alignment	not modelled	5.3	83	PDB header: receptor/peptide Chain: B: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
92	c2wuhC_	Alignment	not modelled	5.3	83	PDB header: receptor/peptide Chain: C: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
93	c6q5hB_	Alignment	not modelled	5.3	27	PDB header: de novo protein Chain: B: 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
94	c5hl8B_	Alignment	not modelled	5.3	30	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein I; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuH-k2044
95	c1qsuC_	Alignment	not modelled	5.3	63	PDB header: structural protein Chain: C: PDB Molecule: protein ((pro-hyp-gly)4- glu-lys-gly(pro-hyp-gly)5); PDBTitle: crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly(pro-hyp-gly)5
96	c3ponA_	Alignment	not modelled	5.3	46	PDB header: unknown function Chain: A: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of mbl collagen-like peptide
97	c3pobC_	Alignment	not modelled	5.3	46	PDB header: hydrolase Chain: C: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
98	c3pobB_	Alignment	not modelled	5.3	46	PDB header: hydrolase Chain: B: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
99	c3ponB_	Alignment	not modelled	5.3	46	PDB header: unknown function Chain: B: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of mbl collagen-like peptide