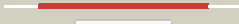
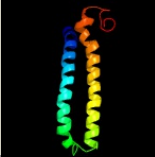

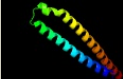
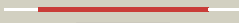






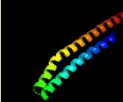

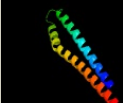

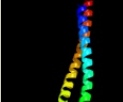








# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3904c\_(esxE)\_4390615\_4390887  
 Date Sat Aug 10 22:05:09 BST 2019  
 Unique Job ID 8c14f3c664319460

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1wa8b1</a>	 Alignment		99.8	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
2	<a href="#">c4lwsA_</a>	 Alignment		99.8	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
3	<a href="#">c4lwsB_</a>	 Alignment		99.8	24	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
4	<a href="#">d1wa8a1</a>	 Alignment		99.7	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
5	<a href="#">c2kg7B_</a>	 Alignment		99.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein esxb; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
6	<a href="#">c3zbhC_</a>	 Alignment		99.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
7	<a href="#">c3gvmA_</a>	 Alignment		99.7	10	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	<a href="#">c2vs0B_</a>	 Alignment		99.6	9	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
9	<a href="#">c4iogD_</a>	 Alignment		99.6	10	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
10	<a href="#">c4i0xl_</a>	 Alignment		99.4	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J: <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
11	<a href="#">c4i0xA_</a>	 Alignment		98.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein mab_3112; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex

12	<a href="#">c2g38B_</a>	Alignment		97.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
13	<a href="#">d2g38b1</a>	Alignment		97.5	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
14	<a href="#">c3q4hB_</a>	Alignment		97.1	11	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> low molecular weight protein antigen 7; <b>PDBTitle:</b> crystal structure of the mycobacterium smegmatis esxg complex2 (msmeg_0620-msmeg_0621)
15	<a href="#">c5xfsB_</a>	Alignment		96.8	23	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp5 from m.2 tuberculosis
16	<a href="#">d2gtsa1</a>	Alignment		96.8	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> HP0062-like <b>Family:</b> HP0062-like
17	<a href="#">c3h6pD_</a>	Alignment		94.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> esat-6-like protein esxr; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
18	<a href="#">c4wj2A_</a>	Alignment		90.2	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
19	<a href="#">c2kg7A_</a>	Alignment		83.4	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein esxg (pe family protein); <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
20	<a href="#">c4xy3A_</a>	Alignment		82.9	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
21	<a href="#">d1aepa_</a>	Alignment	not modelled	59.8	21	<b>Fold:</b> Apolipoprotein-III <b>Superfamily:</b> Apolipoprotein-III <b>Family:</b> Apolipoprotein-III
22	<a href="#">c3h6pB_</a>	Alignment	not modelled	59.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6 like protein esxs; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
23	<a href="#">c3n8uB_</a>	Alignment	not modelled	57.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> imelysin peptidase; <b>PDBTitle:</b> crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution
24	<a href="#">c3ogiD_</a>	Alignment	not modelled	54.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative esat-6-like protein 7; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
25	<a href="#">c1ls4A_</a>	Alignment	not modelled	42.4	17	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein-iii; <b>PDBTitle:</b> nmr structure of apolipoprotein-iii from locusta migratoria
26	<a href="#">d2j0na1</a>	Alignment	not modelled	42.2	12	<b>Fold:</b> lpaD-like <b>Superfamily:</b> lpaD-like <b>Family:</b> lpaD-like
27	<a href="#">c5uxtA_</a>	Alignment	not modelled	33.9	26	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad; <b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad
28	<a href="#">c2ym0B_</a>	Alignment	not modelled	31.0	21	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> cell invasion protein sipd; <b>PDBTitle:</b> truncated sipd from salmonella typhimurium
						<b>PDB header:</b> transcription

29	<a href="#">c3ci9B_</a>	Alignment	not modelled	30.5	12	<b>Chain:</b> B: <b>PDB Molecule:</b> heat shock factor-binding protein 1; <b>PDBTitle:</b> crystal structure of the human hsbp1
30	<a href="#">c1p68A_</a>	Alignment	not modelled	23.0	24	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed protein s-824; <b>PDBTitle:</b> solution structure of s-824, a de novo designed four helix2 bundle
31	<a href="#">d1st6a6</a>	Alignment	not modelled	22.9	11	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
32	<a href="#">c4ug1A_</a>	Alignment	not modelled	22.2	9	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> gpsb n-terminal domain
33	<a href="#">c3ogiC_</a>	Alignment	not modelled	21.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative esat-6-like protein 6; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esoxp2 complex (rv2346c-rv2347c)
34	<a href="#">c4qzrA_</a>	Alignment	not modelled	19.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein 6; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esoxp2 (rv2346c-rv2347c) complex in space group c2221
35	<a href="#">d1h6ga1</a>	Alignment	not modelled	18.5	10	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
36	<a href="#">c4y66D_</a>	Alignment	not modelled	17.7	6	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> putative tbpip family protein; <b>PDBTitle:</b> crystal structure of giardia lamblia hop2-mnd1 complex
37	<a href="#">c5xuaB_</a>	Alignment	not modelled	16.0	9	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> methyl-accepting chemotaxis sensory transducer; <b>PDBTitle:</b> the ligand-free dimer of chemoreceptor mcp2201 ligand binding domain
38	<a href="#">d2j0oa1</a>	Alignment	not modelled	16.0	12	<b>Fold:</b> IpaD-like <b>Superfamily:</b> IpaD-like <b>Family:</b> IpaD-like
39	<a href="#">c2j0oA_</a>	Alignment	not modelled	16.0	12	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> invasin ipad; <b>PDBTitle:</b> shigella flexneri ipad
40	<a href="#">c3f1iS_</a>	Alignment	not modelled	15.6	20	<b>PDB header:</b> protein binding <b>Chain:</b> S: <b>PDB Molecule:</b> signal transducing adapter molecule 1; <b>PDBTitle:</b> human escrt-0 core complex
41	<a href="#">c6gqaD_</a>	Alignment	not modelled	15.4	9	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> cell division regulator s. pneumoniae gpsb
42	<a href="#">c2wukD_</a>	Alignment	not modelled	15.3	21	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> septum site-determining protein diviva; <b>PDBTitle:</b> diviva n-terminal domain, f17a mutant
43	<a href="#">c2pybC_</a>	Alignment	not modelled	14.8	8	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> neutrophil activating protein; <b>PDBTitle:</b> napa protein from borrelia burgdorferi
44	<a href="#">c2yy0D_</a>	Alignment	not modelled	13.7	16	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> c-myc-binding protein; <b>PDBTitle:</b> crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
45	<a href="#">c3swfA_</a>	Alignment	not modelled	13.7	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-gated cation channel alpha-1; <b>PDBTitle:</b> cnga1 621-690 containing clz domain
46	<a href="#">c2of5K_</a>	Alignment	not modelled	13.2	13	<b>PDB header:</b> apoptosis <b>Chain:</b> K: <b>PDB Molecule:</b> leucine-rich repeat and death domain-containing protein; <b>PDBTitle:</b> oligomeric death domain complex
47	<a href="#">c3swyB_</a>	Alignment	not modelled	12.3	27	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic nucleotide-gated cation channel alpha-3; <b>PDBTitle:</b> cnga3 626-672 containing clz domain
48	<a href="#">c5ijnS_</a>	Alignment	not modelled	11.5	8	<b>PDB header:</b> transport protein <b>Chain:</b> S: <b>PDB Molecule:</b> nuclear pore complex protein nup58; <b>PDBTitle:</b> composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
49	<a href="#">d1lvfa_</a>	Alignment	not modelled	11.4	11	<b>Fold:</b> STAT-like <b>Superfamily:</b> t-snare proteins <b>Family:</b> t-snare proteins
50	<a href="#">c6cfzC_</a>	Alignment	not modelled	11.3	16	<b>PDB header:</b> nuclear protein <b>Chain:</b> C: <b>PDB Molecule:</b> dad2; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
51	<a href="#">d1h6gb1</a>	Alignment	not modelled	10.2	10	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
52	<a href="#">c1l4aD_</a>	Alignment	not modelled	9.9	6	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> D: <b>PDB Molecule:</b> s-snap25 fusion protein; <b>PDBTitle:</b> x-ray structure of the neuronal complex/snare complex2 from the squid loligo pealei
53	<a href="#">c3iv1F_</a>	Alignment	not modelled	9.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> tumor susceptibility gene 101 protein; <b>PDBTitle:</b> coiled-coil domain of tumor susceptibility gene 101
54	<a href="#">c1ichA_</a>	Alignment	not modelled	9.0	13	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor-1; <b>PDBTitle:</b> solution structure of the tumor necrosis factor receptor-12 death domain
55	<a href="#">d1icha_</a>	Alignment	not modelled	9.0	13	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH domain, DD

56	<a href="#">c2pnvA_</a>	Alignment	not modelled	8.8	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> small conductance calcium-activated potassium <b>PDBTitle:</b> crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
57	<a href="#">c5xefA_</a>	Alignment	not modelled	8.4	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flis; <b>PDBTitle:</b> crystal structure of flagellar chaperone from bacteria
58	<a href="#">c2c6rA_</a>	Alignment	not modelled	8.4	8	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding stress response protein, dps family; <b>PDBTitle:</b> fe-soaked crystal structure of the dps92 from deinococcus2 radiodurans
59	<a href="#">c2d5kC_</a>	Alignment	not modelled	7.8	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dps family protein; <b>PDBTitle:</b> crystal structure of dps from staphylococcus aureus
60	<a href="#">c4iozC_</a>	Alignment	not modelled	7.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> stromal interaction molecule 1; <b>PDBTitle:</b> the structure of cc1-ih in human stim1.
61	<a href="#">d1st6a7</a>	Alignment	not modelled	7.6	13	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
62	<a href="#">c5t58N_</a>	Alignment	not modelled	7.4	8	<b>PDB header:</b> cell cycle <b>Chain:</b> N: <b>PDB Molecule:</b> klla0c15939p; <b>PDBTitle:</b> structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
63	<a href="#">d2p90a1</a>	Alignment	not modelled	7.3	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Cgl1923-like <b>Family:</b> Cgl1923-like
64	<a href="#">c2oszA_</a>	Alignment	not modelled	6.6	8	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin p58/p45; <b>PDBTitle:</b> structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
65	<a href="#">d1st6a5</a>	Alignment	not modelled	6.4	27	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
66	<a href="#">c1sfcD_</a>	Alignment	not modelled	6.4	4	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> protein (snap-25b); <b>PDBTitle:</b> neuronal synaptic fusion complex
67	<a href="#">c2p90B_</a>	Alignment	not modelled	6.4	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein cgl1923; <b>PDBTitle:</b> the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
68	<a href="#">c6aozD_</a>	Alignment	not modelled	6.3	8	<b>PDB header:</b> gene regulation <b>Chain:</b> D: <b>PDB Molecule:</b> casp8-associated protein 2; <b>PDBTitle:</b> crystal structure of human flash n-terminal domain c54s/c83a (crystal2 form 1)
69	<a href="#">d1orja_</a>	Alignment	not modelled	6.3	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Flagellar export chaperone FlIS <b>Family:</b> Flagellar export chaperone FlIS
70	<a href="#">c3tnuA_</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> keratin, type i cytoskeletal 14; <b>PDBTitle:</b> heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
71	<a href="#">c5lkdB_</a>	Alignment	not modelled	6.3	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase omega-like 2; <b>PDBTitle:</b> crystal structure of the xi glutathione transferase ecm4 from2 saccharomyces cerevisiae in complex with glutathione
72	<a href="#">c3wmjB_</a>	Alignment	not modelled	6.1	13	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> eiaiv vaccine gp45; <b>PDBTitle:</b> crystal structure of eiaiv vaccine gp45
73	<a href="#">c6ckoD_</a>	Alignment	not modelled	6.1	14	<b>PDB header:</b> dna binding protein/transferase <b>Chain:</b> D: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-79 specific; <b>PDBTitle:</b> crystal structure of an af10 fragment
74	<a href="#">c6ckoC_</a>	Alignment	not modelled	6.1	14	<b>PDB header:</b> dna binding protein/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-79 specific; <b>PDBTitle:</b> crystal structure of an af10 fragment
75	<a href="#">d2fjca1</a>	Alignment	not modelled	5.7	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin