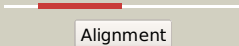
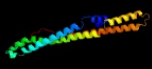


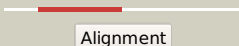
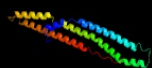

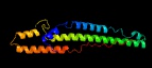

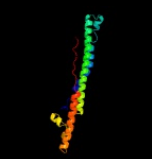
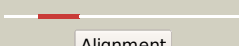

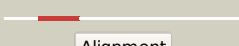

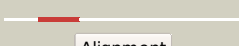


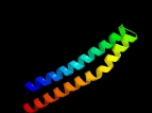



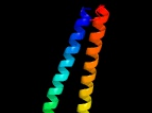


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1801_(PPE29)_2042008_2043279
Date	Fri Aug 2 13:30:41 BST 2019
Unique Job ID	989b67cb04e83ea8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	60	<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 esp95 from m.2 tuberculosis
2	<a href="#">d2g38b1</a>	 Alignment		100.0	35	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
3	<a href="#">c2g38B_</a>	 Alignment		100.0	35	<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
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	14	<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
5	<a href="#">c4wj2A_</a>	 Alignment		98.6	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
6	<a href="#">c2vs0B_</a>	 Alignment		98.0	10	<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
7	<a href="#">c4iogD_</a>	 Alignment		97.9	13	<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
8	<a href="#">c3gvmA_</a>	 Alignment		97.9	13	<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
9	<a href="#">c3zbhC_</a>	 Alignment		97.8	18	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
10	<a href="#">d1wa8a1</a>	 Alignment		97.2	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		96.7	16	<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

12	<a href="#">c4lwsA_</a>	Alignment		96.6	16	<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
13	<a href="#">d1wa8b1</a>	Alignment		96.2	19	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		96.1	15	<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
15	<a href="#">c2kg7B_</a>	Alignment		93.2	21	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein esxh; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	<a href="#">c4i0xJ_</a>	Alignment		87.4	19	<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
17	<a href="#">d1ui5a2</a>	Alignment		37.1	20	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
18	<a href="#">c5frgA_</a>	Alignment		20.1	75	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
19	<a href="#">c1bkvA_</a>	Alignment		17.9	56	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
20	<a href="#">c1bkvC_</a>	Alignment		17.1	56	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
21	<a href="#">c1bkvB_</a>	Alignment	not modelled	17.1	56	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
22	<a href="#">d1fcdA3</a>	Alignment	not modelled	13.0	31	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
23	<a href="#">c2ke4A_</a>	Alignment	not modelled	13.0	75	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cdc42-interacting protein 4; <b>PDBTitle:</b> the nmr structure of the tc10 and cdc42 interacting domain2 of cjp4
24	<a href="#">c1vytF_</a>	Alignment	not modelled	8.9	25	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
25	<a href="#">c2kg7A_</a>	Alignment	not modelled	8.5	28	<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
26	<a href="#">c2iu1A_</a>	Alignment	not modelled	8.3	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of eif5 c-terminal domain
27	<a href="#">c3h6pB_</a>	Alignment	not modelled	8.1	35	<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
28	<a href="#">c2fulE_</a>	Alignment	not modelled	8.0	28	<b>PDB header:</b> translation <b>Chain:</b> E: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of the c-terminal domain of s. cerevisiae

					22	<p>ef5</p> <p><b>PDB header:</b>hydrolase</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>ceg4;</p> <p><b>PDBTitle:</b> crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence</p>
29	<a href="#">c6aokA_</a>	Alignment	not modelled	8.0		
30	<a href="#">c3sjrB_</a>	Alignment	not modelled	8.0	13	<p><b>PDB header:</b>structural genomics, unknown function</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>uncharacterized protein;</p> <p><b>PDBTitle:</b> crystal structure of conserved unknown function protein cv_1783 from2 chromobacterium violaceum atcc 12472</p>
31	<a href="#">c6cgjA_</a>	Alignment	not modelled	7.8	33	<p><b>PDB header:</b>hydrolase</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>effector protein lem4 (lpg1101);</p> <p><b>PDBTitle:</b> structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila</p>
32	<a href="#">c1bzbqA_</a>	Alignment	not modelled	6.9	0	<p><b>PDB header:</b>hormone</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>parathyroid hormone-related protein;</p> <p><b>PDBTitle:</b> the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures</p>
33	<a href="#">c6nbiP_</a>	Alignment	not modelled	6.7	80	<p><b>PDB header:</b>signaling protein</p> <p><b>Chain:</b> P: <b>PDB Molecule:</b>long-acting parathyroid hormone analog;</p> <p><b>PDBTitle:</b> cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein</p>
34	<a href="#">c4deyB_</a>	Alignment	not modelled	6.6	12	<p><b>PDB header:</b>transport protein</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>voltage-dependent l-type calcium channel subunit alpha-1c;</p> <p><b>PDBTitle:</b> crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker.</p>
35	<a href="#">c2i94B_</a>	Alignment	not modelled	6.5	83	<p><b>PDB header:</b>protein binding</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>rhodopsin kinase;</p> <p><b>PDBTitle:</b> nmr structure of recoverin bound to rhodopsin kinase</p>
36	<a href="#">c2y5tG_</a>	Alignment	not modelled	6.4	100	<p><b>PDB header:</b>immune system</p> <p><b>Chain:</b> G: <b>PDB Molecule:</b>c1;</p> <p><b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide</p>
37	<a href="#">d2vk9a1</a>	Alignment	not modelled	6.2	46	<p><b>Fold:</b>Nucleotide-diphospho-sugar transferases</p> <p><b>Superfamily:</b>Nucleotide-diphospho-sugar transferases</p> <p><b>Family:</b>Glycosylating toxin catalytic domain-like</p>
38	<a href="#">c2y5tE_</a>	Alignment	not modelled	6.2	100	<p><b>PDB header:</b>immune system</p> <p><b>Chain:</b> E: <b>PDB Molecule:</b>c1;</p> <p><b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide</p>
39	<a href="#">c5uc0B_</a>	Alignment	not modelled	5.9	80	<p><b>PDB header:</b>hydrolase</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>uncharacterized protein cog5400;</p> <p><b>PDBTitle:</b> crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus</p>
40	<a href="#">c4i6jB_</a>	Alignment	not modelled	5.9	44	<p><b>PDB header:</b>transcription</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>ef-box/lrr-repeat protein 3;</p> <p><b>PDBTitle:</b> a ubiquitin ligase-substrate complex</p>
41	<a href="#">c1t0jC_</a>	Alignment	not modelled	5.7	29	<p><b>PDB header:</b>signaling protein</p> <p><b>Chain:</b> C: <b>PDB Molecule:</b>voltage-dependent l-type calcium channel alpha-1c subunit;</p> <p><b>PDBTitle:</b> crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit</p>
42	<a href="#">d1khba2</a>	Alignment	not modelled	5.6	20	<p><b>Fold:</b>PEP carboxykinase N-terminal domain</p> <p><b>Superfamily:</b>PEP carboxykinase N-terminal domain</p> <p><b>Family:</b>PEP carboxykinase N-terminal domain</p>
43	<a href="#">d1vifn1</a>	Alignment	not modelled	5.6	80	<p><b>Fold:</b>Prealbumin-like</p> <p><b>Superfamily:</b>Cna protein B-type domain</p> <p><b>Family:</b>Cna protein B-type domain</p>
44	<a href="#">c5i4rA_</a>	Alignment	not modelled	5.5	43	<p><b>PDB header:</b>toxin/antitoxin</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>contact-dependent inhibitor a;</p> <p><b>PDBTitle:</b> contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)</p>
45	<a href="#">c2wuhD_</a>	Alignment	not modelled	5.4	100	<p><b>PDB header:</b>receptor/peptide</p> <p><b>Chain:</b> D: <b>PDB Molecule:</b>collagen peptide;</p> <p><b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide</p>
46	<a href="#">d1paqa_</a>	Alignment	not modelled	5.4	12	<p><b>Fold:</b>alpha-alpha superhelix</p> <p><b>Superfamily:</b>ARM repeat</p> <p><b>Family:</b>MIF4G domain-like</p>
47	<a href="#">c1paqA_</a>	Alignment	not modelled	5.4	12	<p><b>PDB header:</b>translation</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>translation initiation factor eif-2b epsilon</p> <p><b>PDBTitle:</b> crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon</p>
48	<a href="#">c2y5tF_</a>	Alignment	not modelled	5.3	100	<p><b>PDB header:</b>immune system</p> <p><b>Chain:</b> F: <b>PDB Molecule:</b>c1;</p> <p><b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide</p>
49	<a href="#">c2qngA_</a>	Alignment	not modelled	5.3	9	<p><b>PDB header:</b>structural genomics, unknown function</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>uncharacterized protein sav2460;</p> <p><b>PDBTitle:</b> crystal structure of unknown function protein sav2460</p>
50	<a href="#">c6a0aA_</a>	Alignment	not modelled	5.3	75	<p><b>PDB header:</b>structural protein</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>collagen type iii peptide;</p> <p><b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii</p>
51	<a href="#">c3trhl_</a>	Alignment	not modelled	5.3	19	<p><b>PDB header:</b>lyase</p> <p><b>Chain:</b> I: <b>PDB Molecule:</b>phosphoribosylaminoimidazole carboxylase</p> <p><b>PDBTitle:</b> structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii</p>
52	<a href="#">c3juiA_</a>	Alignment	not modelled	5.2	8	<p><b>PDB header:</b>translation</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>translation initiation factor eif-2b subunit epsilon;</p> <p><b>PDBTitle:</b> crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit</p>
53	<a href="#">c2wuhC_</a>	Alignment	not modelled	5.2	100	<p><b>PDB header:</b>receptor/peptide</p> <p><b>Chain:</b> C: <b>PDB Molecule:</b>collagen peptide;</p>

53	<a href="#">c2wuhC_</a>	Alignment	not modelled	5.2	100	<b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide <b>PDB header:</b> receptor/peptide
54	<a href="#">c2wuhB_</a>	Alignment	not modelled	5.2	100	<b>Chain:</b> B: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
55	<a href="#">c2f6aj_</a>	Alignment	not modelled	5.2	80	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> J: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
56	<a href="#">d1pp7u_</a>	Alignment	not modelled	5.1	56	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> 39 kda initiator binding protein, IBP39, N-terminal domain
57	<a href="#">c6et5j_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> J: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
58	<a href="#">c6et5y_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> Y: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
59	<a href="#">c6et5d_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
60	<a href="#">c6et5R_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
61	<a href="#">c6et5v_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> V: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
62	<a href="#">c6et5I_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> I: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
63	<a href="#">c6et5p_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> P: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
64	<a href="#">c6et5m_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> reaction center protein m chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
65	<a href="#">c6et52_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
66	<a href="#">c6et5a_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
67	<a href="#">c6et5X_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
68	<a href="#">c6et5U_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> U: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
69	<a href="#">c6et55_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> 5: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
70	<a href="#">c6et5g_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> light-harvesting protein b-1015 beta chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
71	<a href="#">c6et5O_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> O: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids
72	<a href="#">c6et5s_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> S: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. virids