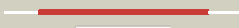


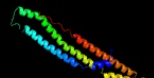

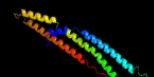



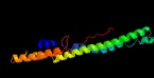

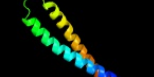












# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2430c\_(PPE41)\_2727346\_2727930  
 Date Wed Aug 7 12:50:05 BST 2019  
 Unique Job ID 0d6b0e59e4b6cd91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	33	<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	100	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
3	<a href="#">c2g38B_</a>	 Alignment		100.0	100	<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	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
5	<a href="#">c4wj2A_</a>	 Alignment		99.2	16	<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		98.4	13	<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="#">c3gvmA_</a>	 Alignment		98.3	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
8	<a href="#">c4iogD_</a>	 Alignment		98.2	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
9	<a href="#">c3zbhC_</a>	 Alignment		98.2	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		97.7	16	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		97.3	12	<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		97.3	13	<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		97.0	21	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		96.4	19	<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		95.4	13	<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		70.4	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="#">c3q4hB_</a>	Alignment		13.4	15	<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 esxhg complex2 (msmeg_0620-msmeg_0621)
18	<a href="#">c2iu1A_</a>	Alignment		12.0	23	<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
19	<a href="#">c2fulE_</a>	Alignment		9.3	39	<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 eif5
20	<a href="#">c1bkvA_</a>	Alignment		9.0	44	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
21	<a href="#">c1bkvC_</a>	Alignment	not modelled	8.3	44	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
22	<a href="#">c1bkvB_</a>	Alignment	not modelled	8.3	44	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
23	<a href="#">c2y5tG_</a>	Alignment	not modelled	6.6	67	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
24	<a href="#">c2y5tE_</a>	Alignment	not modelled	6.2	67	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
25	<a href="#">d1paqa_</a>	Alignment	not modelled	6.0	18	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
26	<a href="#">c1paqA_</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor eif-2b epsilon <b>PDBTitle:</b> crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
27	<a href="#">c2f6aJ_</a>	Alignment	not modelled	5.8	57	<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
28	<a href="#">c2f6aE_</a>	Alignment	not modelled	5.4	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
						<b>PDB header:</b> cell adhesion/structural protein

29	<a href="#">c2f6aI_</a>	Alignment	not modelled	5.4	57	<b>Chain:</b> I: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
30	<a href="#">c2f6aF_</a>	Alignment	not modelled	5.4	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
31	<a href="#">c2f6aG_</a>	Alignment	not modelled	5.4	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> G: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
32	<a href="#">c2f6aH_</a>	Alignment	not modelled	5.4	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
33	<a href="#">c2nbaA_</a>	Alignment	not modelled	5.4	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> prepilin-type cleavage/methylation n-terminal domain <b>PDBTitle:</b> solution nmr structure of the minor dna-uptake pilin comp from2 neisseri subflava
34	<a href="#">c4gyxC_</a>	Alignment	not modelled	5.3	36	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
35	<a href="#">c2wuhD_</a>	Alignment	not modelled	5.2	67	<b>PDB header:</b> receptor/peptide <b>Chain:</b> D: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
36	<a href="#">c2y5tF_</a>	Alignment	not modelled	5.1	67	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody cic1 in complex with2 the triple-helical c1 peptide