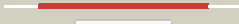
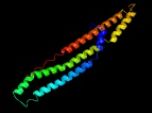

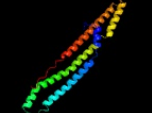
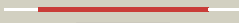
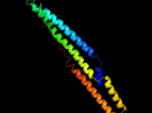

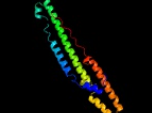

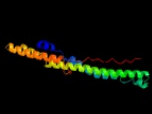

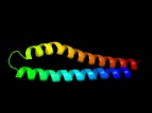









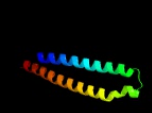


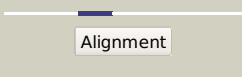
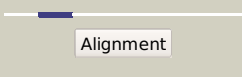
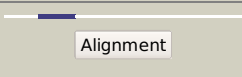
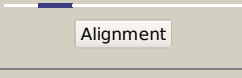
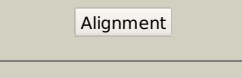
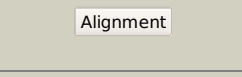
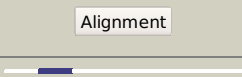
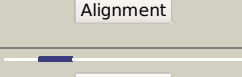
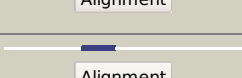
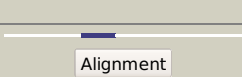
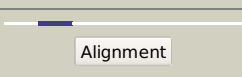

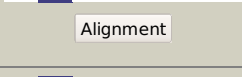
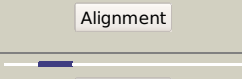
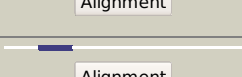
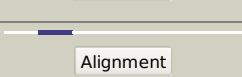
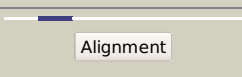
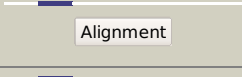
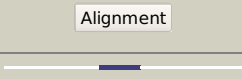
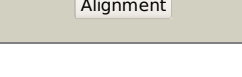


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3429\_(PPE59)\_3847345\_3847881  
 Date Fri Aug 9 18:20:10 BST 2019  
 Unique Job ID 39a130a869781768

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2g38b1</a>	 Alignment		100.0	34	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
2	<a href="#">c2g38B_</a>	 Alignment		100.0	34	<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
3	<a href="#">c5xfsB_</a>	 Alignment		100.0	31	<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 espG5 from m.2 tuberculosis
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	15	<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	14	<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		98.3	15	<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		98.2	18	<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="#">c3zbcC_</a>	 Alignment		98.1	19	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
9	<a href="#">c4iogD_</a>	 Alignment		98.1	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="#">d1wa8a1</a>	 Alignment		97.5	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsA_</a>	 Alignment		97.3	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

12	<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
13	<a href="#">d1wa8b1</a>	Alignment		97.1	18	<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	20	<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	8	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein eshx; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	<a href="#">c4i0xJ_</a>	Alignment		76.9	13	<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="#">d2ix0a4</a>	Alignment		19.4	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> RNB domain-like
18	<a href="#">d2vnud4</a>	Alignment		14.9	11	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> RNB domain-like
19	<a href="#">c1xyr6_</a>	Alignment		14.8	31	<b>PDB header:</b> virus <b>Chain:</b> 6: <b>PDB Molecule:</b> genome polyprotein, coat protein vp3; <b>PDB Fragment:</b> residues 620-630 <b>PDBTitle:</b> poliovirus 135s cell entry intermediate
20	<a href="#">d2r7da2</a>	Alignment		14.7	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> RNB domain-like
21	<a href="#">c3p5tE_</a>	Alignment	not modelled	13.4	40	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor subunit 5; <b>PDBTitle:</b> cfim25-cfim68 complex
22	<a href="#">c3q4hB_</a>	Alignment	not modelled	12.2	10	<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 esxgh complex2 (msmeg_0620-msmeg_0621)
23	<a href="#">c1bkvA_</a>	Alignment	not modelled	12.0	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
24	<a href="#">c2r7fA_</a>	Alignment	not modelled	11.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease ii family protein; <b>PDBTitle:</b> crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63
25	<a href="#">c2iu1A_</a>	Alignment	not modelled	11.3	14	<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
26	<a href="#">c1bkvB_</a>	Alignment	not modelled	11.2	19	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
27	<a href="#">c1bkvC_</a>	Alignment	not modelled	11.2	19	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
28	<a href="#">c2ahmG_</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> viral protein, replication <b>Chain:</b> G: <b>PDB Molecule:</b> replicase polyprotein 1ab, heavy chain; <b>PDBTitle:</b> crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer

29	<a href="#">c2fulE_</a>	 Alignment	not modelled	8.7	24	<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
30	<a href="#">c2j8qB_</a>	 Alignment	not modelled	7.5	40	<b>PDB header:</b> nuclear protein <b>Chain:</b> B; <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor 5; <b>PDBTitle:</b> crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
31	<a href="#">c1vw45_</a>	 Alignment	not modelled	7.5	13	<b>PDB header:</b> ribosome <b>Chain:</b> 5; <b>PDB Molecule:</b> 54s ribosomal protein l3, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
32	<a href="#">c2vnuD_</a>	 Alignment	not modelled	6.6	11	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> D; <b>PDB Molecule:</b> exosome complex exonuclease rrp44; <b>PDBTitle:</b> crystal structure of sc rrp44
33	<a href="#">c3ub0D_</a>	 Alignment	not modelled	6.5	18	<b>PDB header:</b> replication <b>Chain:</b> D; <b>PDB Molecule:</b> non-structural protein 6, nsp6,; <b>PDBTitle:</b> crystal structure of the nonstructural protein 7 and 8 complex of2 feline coronavirus
34	<a href="#">c3juia_</a>	 Alignment	not modelled	6.4	20	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
35	<a href="#">c5xguB_</a>	 Alignment	not modelled	6.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ribonuclease r; <b>PDBTitle:</b> escherichia coli. rnase r
36	<a href="#">c6iczX_</a>	 Alignment	not modelled	5.8	30	<b>PDB header:</b> splicing <b>Chain:</b> X; <b>PDB Molecule:</b> prkr-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
37	<a href="#">c2f6aJ_</a>	 Alignment	not modelled	5.8	43	<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
38	<a href="#">c1paqA_</a>	 Alignment	not modelled	5.8	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
39	<a href="#">d1paqa_</a>	 Alignment	not modelled	5.8	18	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
40	<a href="#">c2y5tG_</a>	 Alignment	not modelled	5.7	50	<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
41	<a href="#">c5x2dA_</a>	 Alignment	not modelled	5.5	50	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> tegumental protein 20.8 kda; <b>PDBTitle:</b> crystal structure of dlc like domain of cstal3 (83-177aa)
42	<a href="#">c2y5tE_</a>	 Alignment	not modelled	5.4	50	<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
43	<a href="#">c2f6aF_</a>	 Alignment	not modelled	5.4	43	<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
44	<a href="#">c2f6aI_</a>	 Alignment	not modelled	5.4	43	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> I; <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
45	<a href="#">c2f6aE_</a>	 Alignment	not modelled	5.4	43	<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
46	<a href="#">c2f6aH_</a>	 Alignment	not modelled	5.4	43	<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
47	<a href="#">c2f6aG_</a>	 Alignment	not modelled	5.4	43	<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
48	<a href="#">d2vk9a1</a>	 Alignment	not modelled	5.2	31	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Glycosylating toxin catalytic domain-like
49	<a href="#">c4ro1B_</a>	 Alignment	not modelled	5.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dis3-like exonuclease 2; <b>PDBTitle:</b> an 3'-5'-exoribonuclease that specifically recognizes rnas.
50	<a href="#">c2kp7A_</a>	 Alignment	not modelled	5.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> crossover junction endonuclease mus81; <b>PDBTitle:</b> solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a