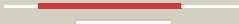
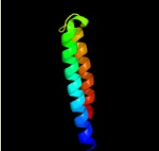


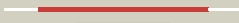


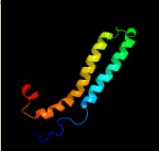

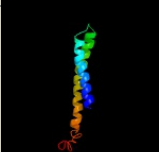

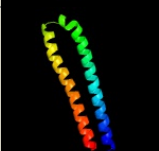
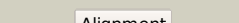


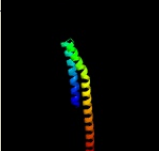





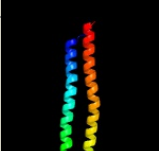
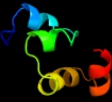

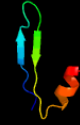
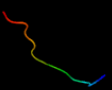







# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1198\_(esxL)\_1341012\_1341296  
 Date Wed Jul 31 22:05:28 BST 2019  
 Unique Job ID 3b73700b9727c9f2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4gzaA_</a>	 Alignment		100.0	91	<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 esxop2 (rv2346c-rv2347c) complex in space group c2221
2	<a href="#">c3ogiC_</a>	 Alignment		100.0	89	<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 esxop2 complex (rv2346c-rv2347c)
3	<a href="#">d1wa8b1</a>	 Alignment		96.2	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
4	<a href="#">c2kg7B_</a>	 Alignment		95.4	18	<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
5	<a href="#">d1wa8a1</a>	 Alignment		84.7	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
6	<a href="#">c4lwsB_</a>	 Alignment		69.2	18	<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
7	<a href="#">c3gvmA_</a>	 Alignment		65.0	11	<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="#">c3zbhC_</a>	 Alignment		63.3	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
9	<a href="#">c2vs0B_</a>	 Alignment		61.2	11	<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
10	<a href="#">c4lwsA_</a>	 Alignment		58.8	12	<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
11	<a href="#">c4iogD_</a>	 Alignment		16.8	14	<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

12	<a href="#">d1b4ua_</a>	Alignment		9.1	31	<b>Fold:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Superfamily:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Family:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB
13	<a href="#">d2evra1</a>	Alignment		8.7	35	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Prokaryotic SH3-related domain <b>Family:</b> Spr N-terminal domain-like
14	<a href="#">c2kwaA_</a>	Alignment		8.5	24	<b>PDB header:</b> transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> kinase a inhibitor; <b>PDBTitle:</b> 1h, 13c and 15n backbone and side chain resonance assignments of the2 n-terminal domain of the histidine kinase inhibitor kipi from3 bacillus subtilis
15	<a href="#">d1njha_</a>	Alignment		8.2	50	<b>Fold:</b> Hypothetical protein YojF <b>Superfamily:</b> Hypothetical protein YojF <b>Family:</b> Hypothetical protein YojF
16	<a href="#">c4ui9D_</a>	Alignment		8.2	33	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> anaphase-promoting complex subunit 15; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
17	<a href="#">c2hjqA_</a>	Alignment		7.4	43	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yqbf; <b>PDBTitle:</b> nmr structure of bacillus subtilis protein yqbf, northeast2 structural genomics target sr449
18	<a href="#">c4rs7R_</a>	Alignment		7.4	60	<b>PDB header:</b> dna binding protein <b>Chain:</b> R: <b>PDB Molecule:</b> parb-c; <b>PDBTitle:</b> structure of pnob8 parb-c
19	<a href="#">c4btpl_</a>	Alignment		7.2	41	<b>PDB header:</b> viral protein <b>Chain:</b> I: <b>PDB Molecule:</b> p1; <b>PDBTitle:</b> structure of the capsid protein p1 of the bacteriophage phi8
20	<a href="#">c2ds2A_</a>	Alignment		6.1	83	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> sweet protein mabinlin-2 chain a; <b>PDBTitle:</b> crystal structure of mabinlin ii
21	<a href="#">c2dtuA_</a>	Alignment	not modelled	5.9	30	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> crystal structure of the beta hairpin loop deletion variant of rb692 gp43 in complex with dna containing an abasic site analog
22	<a href="#">c2ds2C_</a>	Alignment	not modelled	5.9	83	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> sweet protein mabinlin-2 chain a; <b>PDBTitle:</b> crystal structure of mabinlin ii
23	<a href="#">c5oqj1_</a>	Alignment	not modelled	5.8	18	<b>PDB header:</b> transcription <b>Chain:</b> 1: <b>PDB Molecule:</b> rna polymerase ii transcription factor b subunit 1; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih
24	<a href="#">c3zh6B_</a>	Alignment	not modelled	5.7	60	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> protein e; <b>PDBTitle:</b> the structure of haemophilus influenzae se_met form of protein e
25	<a href="#">c3g5pB_</a>	Alignment	not modelled	5.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide deformylase, mitochondrial; <b>PDBTitle:</b> structure and activity of human mitochondrial peptide deformylase, a2 novel cancer target
26	<a href="#">c5oqm1_</a>	Alignment	not modelled	5.6	18	<b>PDB header:</b> transcription <b>Chain:</b> 1: <b>PDB Molecule:</b> general transcription and dna repair factor iih subunit <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
27	<a href="#">c6hqaJ_</a>	Alignment	not modelled	5.5	45	<b>PDB header:</b> transcription <b>Chain:</b> J: <b>PDB Molecule:</b> tfiid subunit (48 kda); <b>PDBTitle:</b> molecular structure of promoter-bound yeast tfiid
28	<a href="#">d2fzpa1</a>	Alignment	not modelled	5.3	40	<b>Fold:</b> NRDP1 C-terminal domain-like <b>Superfamily:</b> NRDP1 C-terminal domain-like <b>Family:</b> USP8 interacting domain

