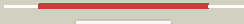
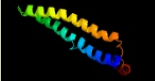


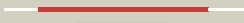


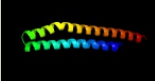





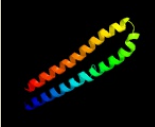

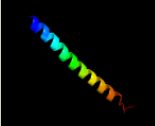



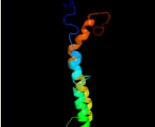

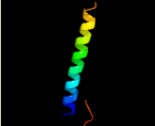
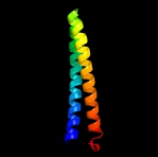
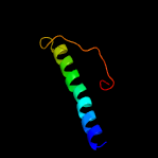
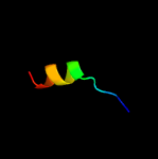

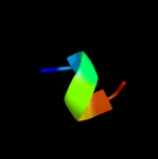

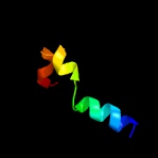

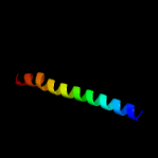


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3865_(-)_4341744_4342055
Date	Sat Aug 10 22:05:04 BST 2019
Unique Job ID	7396fc2c41d273c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1wa8a1</a>	 Alignment		97.7	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
2	<a href="#">c4iogD</a>	 Alignment		97.4	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
3	<a href="#">c3gvmA</a>	 Alignment		97.3	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
4	<a href="#">c3zbcC</a>	 Alignment		96.7	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
5	<a href="#">c2vs0B</a>	 Alignment		96.6	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
6	<a href="#">c4lwsA</a>	 Alignment		95.3	6	<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
7	<a href="#">c4lwsB</a>	 Alignment		95.2	10	<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
8	<a href="#">c4wj2A</a>	 Alignment		91.3	26	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
9	<a href="#">d1wa8b1</a>	 Alignment		90.6	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
10	<a href="#">c2kg7B</a>	 Alignment		77.8	14	<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
11	<a href="#">c4xy3A</a>	 Alignment		70.7	22	<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

12	<a href="#">c4i0xA</a>	Alignment		38.9	13	<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 esxf (mab_3112-2 mab_3113) complex
13	<a href="#">c2kg7A</a>	Alignment		23.8	23	<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
14	<a href="#">c3qm1C</a>	Alignment		10.6	29	<b>PDB header:</b> chaperone/protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> nucleotide exchange factor sil1; <b>PDBTitle:</b> the structural analysis of sil1-bip complex reveals the mechanism for2 sil1 to function as a novel nucleotide exchange factor
15	<a href="#">c4af3D</a>	Alignment		9.3	29	<b>PDB header:</b> transferase/inhibitor <b>Chain:</b> D; <b>PDB Molecule:</b> inner centromere protein; <b>PDBTitle:</b> human aurora b kinase in complex with incenp and vx-680
16	<a href="#">c2vgpD</a>	Alignment		9.2	29	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> inner centromere protein a; <b>PDBTitle:</b> crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor
17	<a href="#">c5jx6C</a>	Alignment		8.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> glucanase; <b>PDBTitle:</b> gh6 orpinomyces sp. y102 enzyme
18	<a href="#">d2c52b1</a>	Alignment		8.6	15	<b>Fold:</b> Nuclear receptor coactivator interlocking domain <b>Superfamily:</b> Nuclear receptor coactivator interlocking domain <b>Family:</b> Nuclear receptor coactivator interlocking domain
19	<a href="#">d1kbha</a>	Alignment		8.2	19	<b>Fold:</b> Nuclear receptor coactivator interlocking domain <b>Superfamily:</b> Nuclear receptor coactivator interlocking domain <b>Family:</b> Nuclear receptor coactivator interlocking domain
20	<a href="#">c1svfC</a>	Alignment		7.1	24	<b>PDB header:</b> viral protein <b>Chain:</b> C; <b>PDB Molecule:</b> protein (fusion glycoprotein); <b>PDBTitle:</b> paramyxovirus sv5 fusion protein core
21	<a href="#">d1zca1</a>	Alignment	not modelled	6.8	45	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
22	<a href="#">c6gr8B</a>	Alignment	not modelled	6.5	29	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> inner centromere protein; <b>PDBTitle:</b> human aurkc incenp complex bound to brd-7880
23	<a href="#">c6nkoA</a>	Alignment	not modelled	6.3	27	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> forh; <b>PDBTitle:</b> crystal structure of forh
24	<a href="#">d1t95a2</a>	Alignment	not modelled	6.0	28	<b>Fold:</b> FYSH domain <b>Superfamily:</b> FYSH domain <b>Family:</b> Hypothetical protein AF0491, N-terminal domain
25	<a href="#">d1pkxa1</a>	Alignment	not modelled	6.0	36	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
26	<a href="#">c3oeiB</a>	Alignment	not modelled	5.9	13	<b>PDB header:</b> toxin, protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> relj (antitoxin rv3357); <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
27	<a href="#">c6chgF</a>	Alignment	not modelled	5.4	29	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> kla0e03521p; <b>PDBTitle:</b> crystal structure of the yeast compass catalytic module
28	<a href="#">d1p9qc2</a>	Alignment	not modelled	5.4	28	<b>Fold:</b> FYSH domain <b>Superfamily:</b> FYSH domain <b>Family:</b> Hypothetical protein AF0491, N-terminal domain