
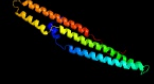







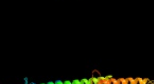







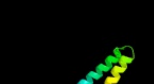






# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1361c\_(PPE19)\_1532449\_1533639  
 Date Wed Jul 31 22:05:46 BST 2019  
 Unique Job ID 51cee06001ed1424

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	53	<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="#">c2g38B_</a>	 Alignment		100.0	36	<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="#">d2g38b1</a>	 Alignment		100.0	36	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	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
5	<a href="#">c4wj2A_</a>	 Alignment		98.8	12	<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		97.9	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
7	<a href="#">c4iogD_</a>	 Alignment		97.8	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		97.8	14	<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		97.6	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
10	<a href="#">d1wa8a1</a>	 Alignment		97.0	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		96.1	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		95.8	15	<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		95.7	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		94.5	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		90.1	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		79.5	17	<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		19.3	19	<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="#">c1bkvA_</a>	Alignment		16.4	50	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
19	<a href="#">c1bkvC_</a>	Alignment		15.5	50	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
20	<a href="#">c1bkvB_</a>	Alignment		15.5	50	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
21	<a href="#">c2iu1A_</a>	Alignment	not modelled	13.3	22	<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
22	<a href="#">c2fulE_</a>	Alignment	not modelled	12.2	22	<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
23	<a href="#">c5frgA_</a>	Alignment	not modelled	11.5	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
24	<a href="#">c5kq1C_</a>	Alignment	not modelled	9.7	42	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> proline-rich nuclear receptor coactivator 2; <b>PDBTitle:</b> crystal structure of s. pombe dcp1/dcp2 in complex with h. sapiens2 pncr2
25	<a href="#">c5kq4F_</a>	Alignment	not modelled	9.7	42	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> proline-rich nuclear receptor coactivator 2; <b>PDBTitle:</b> crystal structure of s. pombe dcp1/dcp2 in complex with h. sapiens2 pncr2 and synthetic cap analog
26	<a href="#">c5kq1F_</a>	Alignment	not modelled	9.5	42	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> proline-rich nuclear receptor coactivator 2; <b>PDBTitle:</b> crystal structure of s. pombe dcp1/dcp2 in complex with h. sapiens2 pncr2
27	<a href="#">d1zeeal</a>	Alignment	not modelled	9.4	29	<b>Fold:</b> Indolic compounds 2,3-dioxygenase-like <b>Superfamily:</b> Indolic compounds 2,3-dioxygenase-like <b>Family:</b> Indoleamine 2,3-dioxygenase-like
28	<a href="#">c5kq4C_</a>	Alignment	not modelled	9.3	42	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> proline-rich nuclear receptor coactivator 2; <b>PDBTitle:</b> crystal structure of s. pombe dcp1/dcp2 in complex with

									n. sapiens2 pncr2 and synthetic cap analog
29	<a href="#">c1vytF_</a>	Alignment	not modelled	7.8	25				<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel beta3 subunit complexed with aid
30	<a href="#">c2lkqA_</a>	Alignment	not modelled	6.3	56				<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin lambda-like polypeptide 1; <b>PDBTitle:</b> nmr structure of the lambda 5 22-45 peptide
31	<a href="#">c4mveB_</a>	Alignment	not modelled	6.1	19				<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of tcur_1030 protein from thermomonospora curvata
32	<a href="#">d1paqa_</a>	Alignment	not modelled	6.1	12				<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
33	<a href="#">c1paqA_</a>	Alignment	not modelled	6.1	12				<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
34	<a href="#">c3h6pB_</a>	Alignment	not modelled	6.0	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
35	<a href="#">c3juiA_</a>	Alignment	not modelled	6.0	8				<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
36	<a href="#">c2ke4A_</a>	Alignment	not modelled	5.9	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 cip4
37	<a href="#">c2kg7A_</a>	Alignment	not modelled	5.9	35				<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
38	<a href="#">c4xb6D_</a>	Alignment	not modelled	5.5	40				<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; <b>PDBTitle:</b> structure of the e. coli c-p lyase core complex
39	<a href="#">c6aokA_</a>	Alignment	not modelled	5.4	22				<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ceg4; <b>PDBTitle:</b> crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
40	<a href="#">c6cgjA_</a>	Alignment	not modelled	5.2	33				<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein lem4 (lpg1101); <b>PDBTitle:</b> structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila