


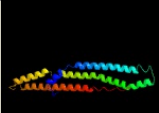

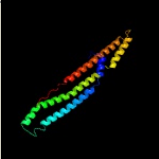

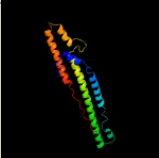

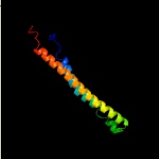

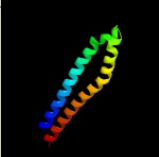

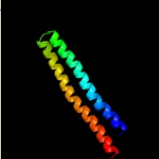

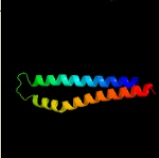

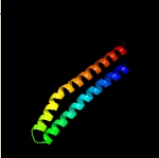

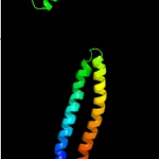

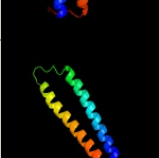


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0453\_(PPE11)\_543177\_544733  
 Date Tue Jul 23 14:50:53 BST 2019  
 Unique Job ID f54f3f14a94e9ecf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	37	<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	30	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
3	<a href="#">c2g38B_</a>	 Alignment		100.0	30	<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	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		98.0	22	<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		97.8	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		97.6	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		97.6	16	<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		97.3	13	<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		96.9	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		95.2	13	<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		94.6	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		94.6	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		93.6	22	<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		89.2	20	<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		67.6	16	<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		58.9	20	<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="#">c3zfsA_</a>	Alignment		27.6	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> f420-reducing hydrogenase, subunit alpha; <b>PDBTitle:</b> cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
19	<a href="#">d1dlpa1</a>	Alignment		17.2	18	<b>Fold:</b> beta-Prism II <b>Superfamily:</b> alpha-D-mannose-specific plant lectins <b>Family:</b> alpha-D-mannose-specific plant lectins
20	<a href="#">d1zeeA1</a>	Alignment		16.4	42	<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
21	<a href="#">c4xb6D_</a>	Alignment	not modelled	12.4	17	<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
22	<a href="#">c1bkvA_</a>	Alignment	not modelled	12.1	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
23	<a href="#">c2kg7A_</a>	Alignment	not modelled	11.7	28	<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
24	<a href="#">c1bkvC_</a>	Alignment	not modelled	11.6	50	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
25	<a href="#">c1bkvB_</a>	Alignment	not modelled	11.6	50	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
26	<a href="#">c2nvjA_</a>	Alignment	not modelled	10.9	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 25mer peptide from vacuolar atp synthase subunit <b>PDBTitle:</b> nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
27	<a href="#">d1vlfn1</a>	Alignment	not modelled	9.7	100	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Cna protein B-type domain <b>Family:</b> Cna protein B-type domain
28	<a href="#">c5abvF_</a>	Alignment	not modelled	8.9	45	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> gh11071p; <b>PDBTitle:</b> complex of d. melanogaster eif4e with the 4e-binding2 protein mextli

29	<a href="#">c5l85B_</a>	Alignment	not modelled	8.1	36	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear fragile x mental retardation-interacting protein 1; <b>PDBTitle:</b> solution structure of the complex between human znhit3 and nufip12 proteins
30	<a href="#">c6aokA_</a>	Alignment	not modelled	7.9	25	<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
31	<a href="#">c6nbiP_</a>	Alignment	not modelled	7.9	60	<b>PDB header:</b> signaling protein <b>Chain:</b> P: <b>PDB Molecule:</b> long-acting parathyroid hormone analog; <b>PDBTitle:</b> cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
32	<a href="#">c1bzgA_</a>	Alignment	not modelled	7.7	29	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> parathyroid hormone-related protein; <b>PDBTitle:</b> the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
33	<a href="#">c2iu1A_</a>	Alignment	not modelled	7.3	28	<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
34	<a href="#">c6cglA_</a>	Alignment	not modelled	7.2	38	<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
35	<a href="#">c3sjrB_</a>	Alignment	not modelled	7.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved unknown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
36	<a href="#">c2fulE_</a>	Alignment	not modelled	6.6	28	<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
37	<a href="#">c1vytF_</a>	Alignment	not modelled	6.3	75	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
38	<a href="#">d1fcdA3</a>	Alignment	not modelled	5.9	23	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
39	<a href="#">c2jtwA_</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane helix 7 of yeast vatpase; <b>PDBTitle:</b> solution structure of tm7 bound to dpc micelles
40	<a href="#">c4u39Q_</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> cell cycle <b>Chain:</b> Q: <b>PDB Molecule:</b> cell division factor; <b>PDBTitle:</b> crystal structure of ftsz:mciz complex from bacillus subtilis
41	<a href="#">c5hl8B_</a>	Alignment	not modelled	5.3	20	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> type ii secretion system protein I; <b>PDBTitle:</b> 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
42	<a href="#">c2lkqA_</a>	Alignment	not modelled	5.3	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
43	<a href="#">c4yv4D_</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> spindle assembly abnormal protein 5; <b>PDBTitle:</b> structure of the c. elegans sas-5 coiled coil domain
44	<a href="#">c5bv9A_</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose 1,4-beta-cellobiosidase; <b>PDBTitle:</b> the structure of bacillus pumilus gh48 in complex with cellobiose