
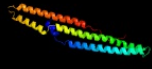
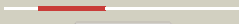
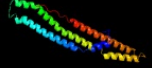



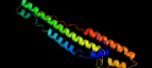



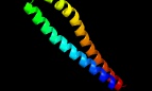



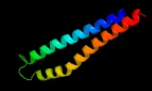



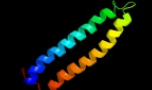




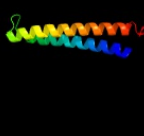

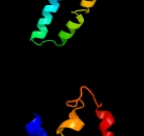

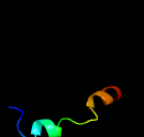

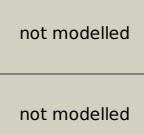


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1387\_(PPE20)\_1561775\_1563394  
 Date Wed Jul 31 22:05:49 BST 2019  
 Unique Job ID 13036ecc3a34c4c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	36	<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	27	<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	27	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	18	<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		97.7	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		97.7	18	<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		97.5	8	<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		97.4	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		97.2	16	<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		96.6	19	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		94.0	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="#">d1wa8b1</a>	Alignment		93.6	14	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
13	<a href="#">c4lwsA</a>	Alignment		92.6	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
14	<a href="#">c4i0xA</a>	Alignment		89.8	12	<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		86.8	13	<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		43.0	18	<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		37.9	28	<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		25.2	21	<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="#">d1zeeA1</a>	Alignment		20.7	46	<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
20	<a href="#">c6et5a</a>	Alignment		17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
21	<a href="#">c6et55</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> 5: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
22	<a href="#">c6et52</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
23	<a href="#">c6et5U</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> U: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
24	<a href="#">c6et5X</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
25	<a href="#">c6et5p</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> P: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
26	<a href="#">c6et5g</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> light-harvesting protein b-1015 beta chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
27	<a href="#">c6et5v</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> V: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
28	<a href="#">c6et5d</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
						<b>PDB header:</b> photosynthesis

29	<a href="#">c6et5R_</a>	Alignment	not modelled	17.4	44	<b>Chain:</b> R: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
30	<a href="#">c6et5y_</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> Y: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
31	<a href="#">c6et5m_</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> reaction center protein m chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
32	<a href="#">c6et5s_</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> S: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
33	<a href="#">c6et5O_</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> O: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
34	<a href="#">c6et5I_</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> I: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
35	<a href="#">c6et5j_</a>	Alignment	not modelled	17.4	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> J: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
36	<a href="#">c4xb6D_</a>	Alignment	not modelled	16.2	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
37	<a href="#">c2nviA_</a>	Alignment	not modelled	15.0	30	<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
38	<a href="#">c6aokA_</a>	Alignment	not modelled	13.0	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
39	<a href="#">c3sjrB_</a>	Alignment	not modelled	12.5	7	<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 unown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
40	<a href="#">c6cgiA_</a>	Alignment	not modelled	11.8	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
41	<a href="#">d1vfn1</a>	Alignment	not modelled	10.8	100	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Cna protein B-type domain <b>Family:</b> Cna protein B-type domain
42	<a href="#">c5I85B_</a>	Alignment	not modelled	10.7	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
43	<a href="#">c1bkvA_</a>	Alignment	not modelled	10.6	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
44	<a href="#">c1bkvB_</a>	Alignment	not modelled	10.2	38	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
45	<a href="#">c1bkvC_</a>	Alignment	not modelled	10.2	38	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
46	<a href="#">c4u39Q_</a>	Alignment	not modelled	9.3	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
47	<a href="#">d2pwwa1</a>	Alignment	not modelled	8.5	29	<b>Fold:</b> TBP-like <b>Superfamily:</b> YugN-like <b>Family:</b> YugN-like
48	<a href="#">c1bzgA_</a>	Alignment	not modelled	8.2	0	<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
49	<a href="#">c2kg7A_</a>	Alignment	not modelled	7.8	47	<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
50	<a href="#">c4mveB_</a>	Alignment	not modelled	7.6	14	<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
51	<a href="#">c1vytF_</a>	Alignment	not modelled	7.4	50	<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
52	<a href="#">c4f3fC_</a>	Alignment	not modelled	7.1	44	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> mesothelin; <b>PDBTitle:</b> crystal structure of msln7-64 morab-009 fab complex
53	<a href="#">c2r5xA_</a>	Alignment	not modelled	6.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein yugn from2 geobacillus kaustophilus hta426
54	<a href="#">c6nbiP_</a>	Alignment	not modelled	6.7	40	<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
55	<a href="#">d1nktA4</a>	Alignment	not modelled	6.6	67	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
56	<a href="#">c3qi7A_</a>	Alignment	not modelled	6.4	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
57	<a href="#">c5dn4A_</a>	Alignment	not modelled	6.2	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan hydrolase flgj; <b>PDBTitle:</b> structure of the glycoside hydrolase domain from salmonella2 typhimurium flgj
58	<a href="#">c1vytE_</a>	Alignment	not modelled	6.1	50	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
59	<a href="#">c2jtwA_</a>	Alignment	not modelled	6.1	38	<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
60	<a href="#">c4dexB_</a>	Alignment	not modelled	5.5	38	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent n-type calcium channel subunit alpha-1b; <b>PDBTitle:</b> crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav2.2 i-ii linker.
61	<a href="#">c4gyxC_</a>	Alignment	not modelled	5.5	31	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
62	<a href="#">c2wseE_</a>	Alignment	not modelled	5.5	35	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> photosystem i reaction center subunit iv a, chloroplastic; <b>PDBTitle:</b> improved model of plant photosystem i
63	<a href="#">c6fxoA_</a>	Alignment	not modelled	5.4	67	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional autolysin; <b>PDBTitle:</b> crystal structure of major bifunctional autolysin
64	<a href="#">d1zs4a1</a>	Alignment	not modelled	5.4	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Bacteriophage CII protein
65	<a href="#">d1fcda3</a>	Alignment	not modelled	5.3	23	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like domain <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
66	<a href="#">c2lkqA_</a>	Alignment	not modelled	5.3	22	<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
67	<a href="#">c2iunD_</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> avian adenovirus celo long fibre; <b>PDBTitle:</b> structure of the c-terminal head domain of the avian adenovirus celo2 long fibre (p21 crystal form)
68	<a href="#">d1ev7a_</a>	Alignment	not modelled	5.2	38	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease NaeI
69	<a href="#">c4dmtA_</a>	Alignment	not modelled	5.1	36	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
70	<a href="#">c4dmtC_</a>	Alignment	not modelled	5.1	36	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
71	<a href="#">c4dmtB_</a>	Alignment	not modelled	5.1	36	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide