
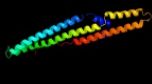

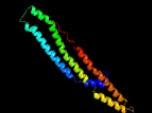

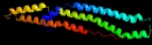

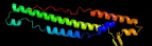

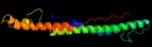



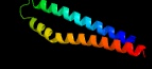









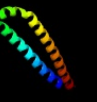

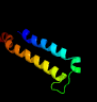
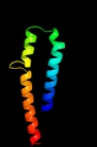






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1807_(PPE31)_2048393_2049604
Date	Fri Aug 2 13:30:41 BST 2019
Unique Job ID	8d2eb1d36d9e8ea2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	65	<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	16	<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		98.7	16	<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	14	<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="#">c3gvmA_</a>	 Alignment		97.6	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
8	<a href="#">c4iogD_</a>	 Alignment		97.5	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
9	<a href="#">c3zbhC_</a>	 Alignment		97.4	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
10	<a href="#">d1wa8a1</a>	 Alignment		96.5	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		94.7	14	<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		94.4	19	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
13	<a href="#">c4lwsA</a>	Alignment		94.3	19	<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		92.9	16	<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		86.3	16	<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		57.7	25	<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		20.3	22	<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		17.9	44	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
19	<a href="#">c1bkvB</a>	Alignment		17.0	44	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
20	<a href="#">c1bkvC</a>	Alignment		17.0	44	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
21	<a href="#">c5frgA</a>	Alignment	not modelled	14.4	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
22	<a href="#">c4xb6D</a>	Alignment	not modelled	9.6	22	<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
23	<a href="#">c2nviA</a>	Alignment	not modelled	9.5	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
24	<a href="#">c5lc5a</a>	Alignment	not modelled	8.9	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nahd-ubiquinone oxidoreductase chain 3; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
25	<a href="#">c2lkqA</a>	Alignment	not modelled	8.8	44	<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
26	<a href="#">c2iu1A</a>	Alignment	not modelled	8.4	17	<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
27	<a href="#">c4gyxC</a>	Alignment	not modelled	8.0	36	<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
28	<a href="#">c6aokA</a>	Alignment	not modelled	7.9	33	<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
29	<a href="#">c1bzigA</a>	Alignment	not modelled	7.9	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
30	<a href="#">c4dmtB</a>	Alignment	not modelled	7.9	31	<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
31	<a href="#">c4dmtA</a>	Alignment	not modelled	7.9	31	<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
32	<a href="#">c4dmtC</a>	Alignment	not modelled	7.9	31	<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
33	<a href="#">c2ke4A</a>	Alignment	not modelled	7.8	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 cjp4
34	<a href="#">c4gyxB</a>	Alignment	not modelled	7.7	36	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> B: <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
35	<a href="#">c4gyxA</a>	Alignment	not modelled	7.7	36	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> A: <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
36	<a href="#">c6nblP</a>	Alignment	not modelled	7.5	80	<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
37	<a href="#">c6cglA</a>	Alignment	not modelled	7.4	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
38	<a href="#">c5l85B</a>	Alignment	not modelled	7.4	18	<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
39	<a href="#">c2fulE</a>	Alignment	not modelled	7.3	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
40	<a href="#">c3sjrB</a>	Alignment	not modelled	7.2	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 unknwn function protein cv_1783 from2 chromobacterium violaceum atcc 12472
41	<a href="#">c5ucOB</a>	Alignment	not modelled	6.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein cog5400; <b>PDBTitle:</b> crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
42	<a href="#">c2y5tG</a>	Alignment	not modelled	6.8	50	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
43	<a href="#">d1zeeA1</a>	Alignment	not modelled	6.7	32	<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
44	<a href="#">c4lzxB</a>	Alignment	not modelled	6.7	35	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> iq domain-containing protein g; <b>PDBTitle:</b> complex of iqcg and ca2+-free cam
45	<a href="#">c5lzkB</a>	Alignment	not modelled	6.6	4	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> protein fam83b; <b>PDBTitle:</b> structure of the domain of unknown function duf1669 from human fam83b
46	<a href="#">c2y5tE</a>	Alignment	not modelled	6.5	50	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
47	<a href="#">c1vytF</a>	Alignment	not modelled	6.3	25	<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
48	<a href="#">c3trhI</a>	Alignment	not modelled	6.3	19	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase <b>PDBTitle:</b> structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
49	<a href="#">d1vfn1</a>	Alignment	not modelled	6.2	60	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Cna protein B-type domain <b>Family:</b> Cna protein B-type domain
50	<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
51	<a href="#">c4m1lB</a>	Alignment	not modelled	5.8	36	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> iq domain-containing protein g; <b>PDBTitle:</b> complex of iqcg and ca2+-bound cam
52	<a href="#">c5hl8B</a>	Alignment	not modelled	5.8	33	<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 <b>PDB header:</b> receptor/peptide

53	<a href="#">c2wuhD_</a>	Alignment	not modelled	5.7	50	<b>Chain:</b> D: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
54	<a href="#">c2i94B_</a>	Alignment	not modelled	5.7	50	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rhodopsin kinase; <b>PDBTitle:</b> nmr structure of recoverin bound to rhodopsin kinase
55	<a href="#">c2y5tF_</a>	Alignment	not modelled	5.7	50	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
56	<a href="#">c6a0aA_</a>	Alignment	not modelled	5.6	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
57	<a href="#">d1khba2</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
58	<a href="#">c3juiA_</a>	Alignment	not modelled	5.4	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
59	<a href="#">c2wuhB_</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> receptor/peptide <b>Chain:</b> B: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
60	<a href="#">c2wuhC_</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> receptor/peptide <b>Chain:</b> C: <b>PDB Molecule:</b> collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
61	<a href="#">c2f6aJ_</a>	Alignment	not modelled	5.4	43	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> J: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
62	<a href="#">c4e18A_</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 48; <b>PDBTitle:</b> the unliganded structure of c.bescii cela gh48 module
63	<a href="#">c6a0cB_</a>	Alignment	not modelled	5.2	38	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
64	<a href="#">c4auoE_</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> E: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
65	<a href="#">c4auoH_</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> H: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
66	<a href="#">c1qsuC_</a>	Alignment	not modelled	5.1	38	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein ((pro-hyp-gly)4- glu-lys-gly(pro-hyp-gly)5); <b>PDBTitle:</b> crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly(pro-hyp-gly)5
67	<a href="#">c2f6aE_</a>	Alignment	not modelled	5.1	43	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
68	<a href="#">c2f6aG_</a>	Alignment	not modelled	5.1	43	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> G: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
69	<a href="#">c2f6aI_</a>	Alignment	not modelled	5.1	43	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> I: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
70	<a href="#">c2f6aH_</a>	Alignment	not modelled	5.1	43	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
71	<a href="#">c2f6aF_</a>	Alignment	not modelled	5.1	43	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
72	<a href="#">c2drxB_</a>	Alignment	not modelled	5.1	50	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen like peptide; <b>PDBTitle:</b> structure analysis of (pog)4-(log)2-(pog)4
73	<a href="#">c1cagA_</a>	Alignment	not modelled	5.0	38	<b>PDB header:</b> collagen <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
74	<a href="#">c1cagC_</a>	Alignment	not modelled	5.0	38	<b>PDB header:</b> collagen <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution