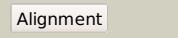
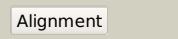
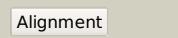
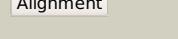
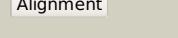
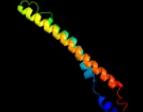
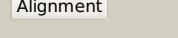
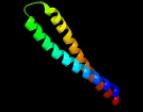
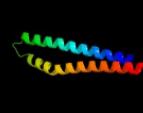
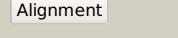
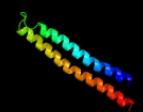
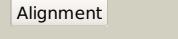
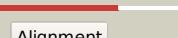
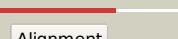


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD3135_(PPE50)_3501331_3501729
Date	Thu Aug 8 16:20:32 BST 2019
Unique Job ID	0118182f01349829

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>			100.0	51	<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 espG5 from m.2 tuberculosis
2	<a href="#">d2g38b1</a>			100.0	32	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
3	<a href="#">c2g38B_</a>			100.0	32	<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>			100.0	17	<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>			98.5	17	<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>			97.8	13	<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>			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 wxx-100 family protein from streptococcus2 agalactiae
8	<a href="#">c4iogD_</a>			97.5	17	<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>			97.4	15	<b>PDB header:</b> unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> esxA; <b>PDBTitle:</b> geobacillus thermonitratificans esxA crystal form I
10	<a href="#">d1wa8a1</a>			96.7	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>			95.2	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>			95.0	18	<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>			94.5	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA</a>			91.7	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>			86.5	19	<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="#">c4i0xI</a>			29.2	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="#">c1bkvA</a>			22.3	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
18	<a href="#">c1bkvB</a>			20.9	50	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
19	<a href="#">c1bkvC</a>			20.9	50	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
20	<a href="#">c5frgA</a>			13.8	63	<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 tocal
21	<a href="#">c2iu1A</a>		not modelled	13.4	14	<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="#">c2y5tG</a>		not modelled	11.7	67	<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 <b>PDB header:</b> immune system
23	<a href="#">c2y5tE</a>		not modelled	11.1	67	<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
24	<a href="#">c4gyxC</a>		not modelled	9.9	45	<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
25	<a href="#">c4gyxB</a>		not modelled	9.8	56	<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
26	<a href="#">c4gyxA</a>		not modelled	9.8	56	<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
27	<a href="#">c2y5tF</a>		not modelled	9.6	67	<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 <b>PDB header:</b> receptor/peptide

28	<a href="#">c2wuhD</a>	Alignment	not modelled	9.3	67	<b>PDB header:</b> D: PDB Molecule:collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
29	<a href="#">c2fulE</a>	Alignment	not modelled	8.9	28	<b>PDB header:</b> translation <b>Chain:</b> E: PDB Molecule:eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of the c-terminal domain of s. cerevisiae eif5
30	<a href="#">c4dmtC</a>	Alignment	not modelled	8.9	45	<b>PDB header:</b> structural protein <b>Chain:</b> C: PDB Molecule:collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
31	<a href="#">c4dmtB</a>	Alignment	not modelled	8.9	45	<b>PDB header:</b> structural protein <b>Chain:</b> B: PDB Molecule:collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
32	<a href="#">c4dmtA</a>	Alignment	not modelled	8.9	45	<b>PDB header:</b> structural protein <b>Chain:</b> A: PDB Molecule:collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
33	<a href="#">c2f6aJ</a>	Alignment	not modelled	8.8	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> J: PDB Molecule:collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
34	<a href="#">c2wuhC</a>	Alignment	not modelled	8.8	67	<b>PDB header:</b> receptor/peptide <b>Chain:</b> C: PDB Molecule:collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
35	<a href="#">c2wuhB</a>	Alignment	not modelled	8.8	67	<b>PDB header:</b> receptor/peptide <b>Chain:</b> B: PDB Molecule:collagen peptide; <b>PDBTitle:</b> crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
36	<a href="#">c4auoE</a>	Alignment	not modelled	8.8	67	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> E: PDB Molecule:triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
37	<a href="#">c4auoH</a>	Alignment	not modelled	8.8	67	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> H: PDB Molecule:triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
38	<a href="#">c2f6aL</a>	Alignment	not modelled	8.2	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> I: PDB Molecule:collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
39	<a href="#">c2f6aE</a>	Alignment	not modelled	8.2	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> E: PDB Molecule:collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
40	<a href="#">c2f6aF</a>	Alignment	not modelled	8.2	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> F: PDB Molecule:collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
41	<a href="#">c2f6aH</a>	Alignment	not modelled	8.2	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> H: PDB Molecule:collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
42	<a href="#">c2f6aG</a>	Alignment	not modelled	8.2	57	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> G: PDB Molecule:collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
43	<a href="#">c6a0aA</a>	Alignment	not modelled	8.2	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: PDB Molecule:collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
44	<a href="#">c3kziE</a>	Alignment	not modelled	8.1	44	<b>PDB header:</b> electron transport <b>Chain:</b> E: PDB Molecule:cytochrome b559 subunit alpha; <b>PDBTitle:</b> crystal structure of monomeric form of cyanobacterial photosystem ii
45	<a href="#">c2drxB</a>	Alignment	not modelled	8.0	67	<b>PDB header:</b> structural protein <b>Chain:</b> B: PDB Molecule:collagen like peptide; <b>PDBTitle:</b> structure analysis of (pog)4-(log)2-(pog)4
46	<a href="#">c2drxA</a>	Alignment	not modelled	7.9	67	<b>PDB header:</b> structural protein <b>Chain:</b> A: PDB Molecule:collagen like peptide; <b>PDBTitle:</b> structure analysis of (pog)4-(log)2-(pog)4
47	<a href="#">c2mqsD</a>	Alignment	not modelled	7.6	67	<b>PDB header:</b> hydrolase <b>Chain:</b> D: PDB Molecule:thp_t chain; <b>PDBTitle:</b> transient collagen triple helix binding to a key metalloproteinase in2 invasion and development: spin labels to structure
48	<a href="#">c6a0cB</a>	Alignment	not modelled	7.6	50	<b>PDB header:</b> structural protein <b>Chain:</b> B: PDB Molecule:collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
49	<a href="#">c2v53B</a>	Alignment	not modelled	7.5	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: PDB Molecule:collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
50	<a href="#">c2v53C</a>	Alignment	not modelled	7.5	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: PDB Molecule:collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
51	<a href="#">c2v53D</a>	Alignment	not modelled	7.5	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: PDB Molecule:collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
52	<a href="#">c2drxC</a>	Alignment	not modelled	7.4	67	<b>PDB header:</b> structural protein <b>Chain:</b> C: PDB Molecule:collagen like peptide; <b>PDBTitle:</b> structure analysis of (pog)4-(log)2-(pog)4
53	<a href="#">c4auoF</a>	Alignment	not modelled	7.4	67	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> F: PDB Molecule:triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
54	<a href="#">c4auoD</a>	Alignment	not modelled	7.4	67	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> D: PDB Molecule:triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide

55	<a href="#">c4auoG_</a>	Alignment	not modelled	7.4	67	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> G: <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
56	<a href="#">c2drtB_</a>	Alignment	not modelled	7.4	67	<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-(pog)5
57	<a href="#">c2drtA_</a>	Alignment	not modelled	7.4	67	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen like peptide; <b>PDBTitle:</b> structure analysis of (pog)4-log-(pog)5
58	<a href="#">c1qsuC_</a>	Alignment	not modelled	7.3	67	<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
59	<a href="#">c2drtC_</a>	Alignment	not modelled	7.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen like peptide; <b>PDBTitle:</b> structure analysis of (pog)4-log-(pog)5
60	<a href="#">c6a0aB_</a>	Alignment	not modelled	7.2	67	<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
61	<a href="#">c6a0aC_</a>	Alignment	not modelled	7.2	67	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
62	<a href="#">c3jcue_</a>	Alignment	not modelled	7.2	33	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b559 subunit alpha; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
63	<a href="#">c1cagC_</a>	Alignment	not modelled	7.2	67	<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
64	<a href="#">c1cagA_</a>	Alignment	not modelled	7.2	67	<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
65	<a href="#">c3ponB_</a>	Alignment	not modelled	7.0	36	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mbl collagen-like peptide; <b>PDBTitle:</b> crystal structure of mbl collagen-like peptide
66	<a href="#">c3pobC_</a>	Alignment	not modelled	7.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> mbl collagen-like peptide; <b>PDBTitle:</b> crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
67	<a href="#">c3pobB_</a>	Alignment	not modelled	7.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mbl collagen-like peptide; <b>PDBTitle:</b> crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
68	<a href="#">c3ponA_</a>	Alignment	not modelled	7.0	36	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mbl collagen-like peptide; <b>PDBTitle:</b> crystal structure of mbl collagen-like peptide
69	<a href="#">c3pobD_</a>	Alignment	not modelled	7.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> mbl collagen-like peptide; <b>PDBTitle:</b> crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
70	<a href="#">d2axte1</a>	Alignment	not modelled	6.9	44	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Cytochrome b559 subunits <b>Family:</b> Cytochrome b559 subunits
71	<a href="#">c6a0cC_</a>	Alignment	not modelled	6.7	67	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
72	<a href="#">c6a0cA_</a>	Alignment	not modelled	6.7	67	<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
73	<a href="#">c1cagB_</a>	Alignment	not modelled	6.7	67	<b>PDB header:</b> collagen <b>Chain:</b> B: <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="#">c1cgdB_</a>	Alignment	not modelled	6.7	67	<b>PDB header:</b> collagen <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> hydration structure of a collagen peptide
75	<a href="#">c1cgdC_</a>	Alignment	not modelled	6.7	67	<b>PDB header:</b> collagen <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> hydration structure of a collagen peptide
76	<a href="#">c1cgdA_</a>	Alignment	not modelled	6.7	67	<b>PDB header:</b> collagen <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> hydration structure of a collagen peptide
77	<a href="#">d1vlfn1</a>	Alignment	not modelled	6.6	40	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Cna protein B-type domain <b>Family:</b> Cna protein B-type domain
78	<a href="#">c1qsuA_</a>	Alignment	not modelled	6.5	67	<b>PDB header:</b> structural protein <b>Chain:</b> A: <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
79	<a href="#">c1qsuB_</a>	Alignment	not modelled	6.5	67	<b>PDB header:</b> structural protein <b>Chain:</b> B: <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
80	<a href="#">c6hg7A_</a>	Alignment	not modelled	6.4	67	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(ii) chain; <b>PDBTitle:</b> crystal structure of a collagen ii fragment containing the binding2 site of pedf and comp, (pog)4-lkg hrg ftg lqg-pog(4)

81	<a href="#">c6hg7C</a>	Alignment	not modelled	6.4	67	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen alpha-1(ii) chain; <b>PDBTitle:</b> crystal structure of a collagen ii fragment containing the binding2 site of pedf and comp, (pog)4-lkg hrg ftg lgg-pog(4)
82	<a href="#">c6hg7B</a>	Alignment	not modelled	6.4	67	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-1(ii) chain; <b>PDBTitle:</b> crystal structure of a collagen ii fragment containing the binding2 site of pedf and comp, (pog)4-lkg hrg ftg lgg-pog(4)
83	<a href="#">c2mq5B</a>	Alignment	not modelled	6.4	67	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> thp_l_and_m_chain; <b>PDBTitle:</b> transient collagen triple helix binding to a key metalloproteinase in2 invasion and development: spin labels to structure
84	<a href="#">c2mq5C</a>	Alignment	not modelled	6.4	67	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> thp_l_and_m_chain; <b>PDBTitle:</b> transient collagen triple helix binding to a key metalloproteinase in2 invasion and development: spin labels to structure
85	<a href="#">c3b2cB</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
86	<a href="#">c1ei8F</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> contractile protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- <b>PDBTitle:</b> structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide
87	<a href="#">c3b2cC</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
88	<a href="#">c3b2cF</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
89	<a href="#">c3b2cl</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> I: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
90	<a href="#">c1ei8B</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- <b>PDBTitle:</b> structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide
91	<a href="#">c1ei8A</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- <b>PDBTitle:</b> structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide
92	<a href="#">c3b2cG</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> G: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
93	<a href="#">c1ei8E</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> contractile protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- <b>PDBTitle:</b> structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide
94	<a href="#">c1ei8D</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> contractile protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide (pro-hyp-gly)4-pg-(pro-hyp- <b>PDBTitle:</b> structural consequences of a discontinuity in the repeating2 tripeptide sequence of a collagen-like triple-helical3 peptide
95	<a href="#">c3b2cE</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
96	<a href="#">c3b2cD</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
97	<a href="#">c3b2cA</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
98	<a href="#">c3b2cH</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [{pro-hyp(r)-2 gly}4-{hyp(s)-pro-gly}2-{pro-hyp(r)-gly}4]3
99	<a href="#">c2klwC</a>	Alignment	not modelled	6.3	67	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> (pog)10; <b>PDBTitle:</b> solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions