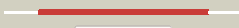




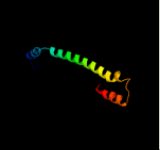

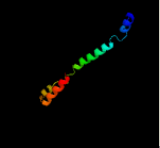

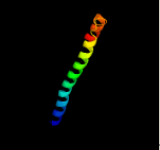
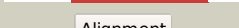

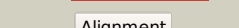

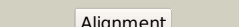
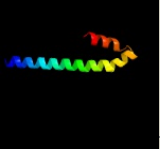
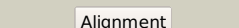
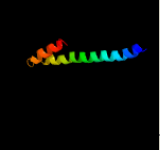
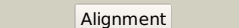





# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
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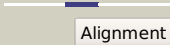

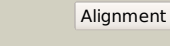
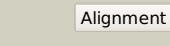



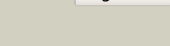
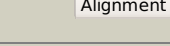
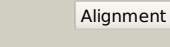
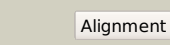
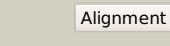
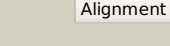
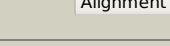
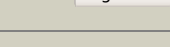
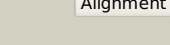
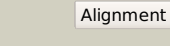
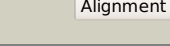
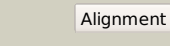
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	40	<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		99.9	39	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
3	<a href="#">c2g38B_</a>	 Alignment		99.9	39	<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		99.7	21	<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="#">c4iogD_</a>	 Alignment		95.6	19	<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
6	<a href="#">c2vs0B_</a>	 Alignment		95.6	16	<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="#">c3zbhC_</a>	 Alignment		94.8	25	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
8	<a href="#">c3gvmA_</a>	 Alignment		94.6	22	<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="#">d1wa8a1</a>	 Alignment		94.4	22	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
10	<a href="#">c4i0xA_</a>	 Alignment		93.3	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 esxf (mab_3112-2 mab_3113) complex
11	<a href="#">c4lwsB_</a>	 Alignment		88.3	18	<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		87.6	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>	Alignment		87.4	26	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4wjzA_</a>	Alignment		84.0	19	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
15	<a href="#">c2kg7B_</a>	Alignment		54.1	25	<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="#">c1bkvA_</a>	Alignment		25.2	44	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
17	<a href="#">c1bkvC_</a>	Alignment		23.7	44	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
18	<a href="#">c1bkvB_</a>	Alignment		23.7	44	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
19	<a href="#">c4i0xl_</a>	Alignment		23.6	20	<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
20	<a href="#">c3h6pB_</a>	Alignment		15.4	41	<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
21	<a href="#">c4bz4D_</a>	Alignment	not modelled	14.8	33	<b>PDB header:</b> copper-binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> copper-repressible polypeptide; <b>PDBTitle:</b> cora is a surface-associated copper-binding protein2 important in methylomicrobium album bg8 copper acquisition
22	<a href="#">c4gyxC_</a>	Alignment	not modelled	12.6	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
23	<a href="#">c4gyxA_</a>	Alignment	not modelled	11.6	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
24	<a href="#">c4gyxB_</a>	Alignment	not modelled	11.6	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
25	<a href="#">c2y5tG_</a>	Alignment	not modelled	11.1	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
26	<a href="#">c2kg7A_</a>	Alignment	not modelled	11.0	41	<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
27	<a href="#">d1dipa1</a>	Alignment	not modelled	10.9	29	<b>Fold:</b> beta-Prism II <b>Superfamily:</b> alpha-D-mannose-specific plant lectins <b>Family:</b> alpha-D-mannose-specific plant lectins <b>PDB header:</b> immune system

28	<a href="#">c2y5tE</a>	Alignment	not modelled	10.5	67	<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
29	<a href="#">c4dmtC</a>	Alignment	not modelled	10.1	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
30	<a href="#">c4dmtA</a>	Alignment	not modelled	10.1	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
31	<a href="#">c4dmtB</a>	Alignment	not modelled	10.1	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
32	<a href="#">c2y5tF</a>	Alignment	not modelled	9.0	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
33	<a href="#">c2wuhD</a>	Alignment	not modelled	8.8	67	<b>PDB header:</b> receptor/peptide <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
34	<a href="#">c2lkqA</a>	Alignment	not modelled	8.4	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
35	<a href="#">c2wuhB</a>	Alignment	not modelled	8.3	67	<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
36	<a href="#">c2wuhC</a>	Alignment	not modelled	8.3	67	<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
37	<a href="#">c4auoH</a>	Alignment	not modelled	8.2	67	<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
38	<a href="#">c4auoE</a>	Alignment	not modelled	8.2	67	<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
39	<a href="#">c2drxB</a>	Alignment	not modelled	7.6	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)2-(pog)4
40	<a href="#">c2drxA</a>	Alignment	not modelled	7.5	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)2-(pog)4
41	<a href="#">c2f6aJ</a>	Alignment	not modelled	7.4	57	<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
42	<a href="#">c6a0aA</a>	Alignment	not modelled	7.4	50	<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
43	<a href="#">c2mqSD</a>	Alignment	not modelled	7.1	67	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> thp_t_chain; <b>PDBTitle:</b> transient collagen triple helix binding to a key metalloproteinase in2 invasion and development: spin labels to structure
44	<a href="#">c2v53B</a>	Alignment	not modelled	7.0	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
45	<a href="#">c2v53C</a>	Alignment	not modelled	7.0	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> C; <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
46	<a href="#">c2v53D</a>	Alignment	not modelled	7.0	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> D; <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
47	<a href="#">c2drxC</a>	Alignment	not modelled	7.0	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)2-(pog)4
48	<a href="#">c6dzsD</a>	Alignment	not modelled	7.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> mycobacterial homoserine dehydrogenase thra in complex with nadp
49	<a href="#">c5vmoB</a>	Alignment	not modelled	7.0	50	<b>PDB header:</b> viral protein/apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2 interacting mediator of cell death; <b>PDBTitle:</b> crystal structure of grouper iridovirus giv66:bim complex
50	<a href="#">c2f6aE</a>	Alignment	not modelled	6.9	57	<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
51	<a href="#">c2f6aH</a>	Alignment	not modelled	6.9	57	<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
52	<a href="#">c2f6aI</a>	Alignment	not modelled	6.9	57	<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
53	<a href="#">c2f6aG</a>	Alignment	not modelled	6.9	57	<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
54	<a href="#">c2f6aF</a>	Alignment	not modelled	6.9	57	<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

55	<a href="#">c2drtA</a>	Alignment	not modelled	6.9	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
56	<a href="#">c2drtB</a>	Alignment	not modelled	6.9	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="#">c1qsuC</a>	Alignment	not modelled	6.9	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
58	<a href="#">c2drtC</a>	Alignment	not modelled	6.9	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
59	<a href="#">c4auoF</a>	Alignment	not modelled	6.9	67	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> F: <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
60	<a href="#">c4auoG</a>	Alignment	not modelled	6.9	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
61	<a href="#">c4auoD</a>	Alignment	not modelled	6.9	67	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> D: <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
62	<a href="#">c6a0cB</a>	Alignment	not modelled	6.8	50	<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
63	<a href="#">c1cagA</a>	Alignment	not modelled	6.8	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
64	<a href="#">c1cagC</a>	Alignment	not modelled	6.8	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
65	<a href="#">c6a0aC</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
66	<a href="#">c6a0aB</a>	Alignment	not modelled	6.7	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
67	<a href="#">d1ev7a</a>	Alignment	not modelled	6.4	36	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease NaeI
68	<a href="#">c1cgdA</a>	Alignment	not modelled	6.3	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
69	<a href="#">c1cagB</a>	Alignment	not modelled	6.3	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
70	<a href="#">c1cgdB</a>	Alignment	not modelled	6.3	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
71	<a href="#">c1cgdC</a>	Alignment	not modelled	6.3	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
72	<a href="#">c3pobD</a>	Alignment	not modelled	6.3	45	<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
73	<a href="#">c3ponA</a>	Alignment	not modelled	6.3	45	<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
74	<a href="#">c3ponB</a>	Alignment	not modelled	6.3	45	<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
75	<a href="#">c3pobC</a>	Alignment	not modelled	6.3	45	<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
76	<a href="#">c3pobB</a>	Alignment	not modelled	6.3	45	<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
77	<a href="#">c6a0cC</a>	Alignment	not modelled	6.3	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
78	<a href="#">c6a0cA</a>	Alignment	not modelled	6.3	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
79	<a href="#">c1qsuB</a>	Alignment	not modelled	6.1	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="#">c1qsuA</a>	Alignment	not modelled	6.1	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

81	<a href="#">c6hg7A_</a>	 Alignment	not modelled	6.0	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 lgg-pog(4)
82	<a href="#">c6hg7C_</a>	 Alignment	not modelled	6.0	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)
83	<a href="#">c6hg7B_</a>	 Alignment	not modelled	6.0	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)
84	<a href="#">c2mqsB_</a>	 Alignment	not modelled	5.9	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
85	<a href="#">c2mqsC_</a>	 Alignment	not modelled	5.9	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
86	<a href="#">c1ei8E_</a>	 Alignment	not modelled	5.9	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
87	<a href="#">c1ei8A_</a>	 Alignment	not modelled	5.9	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
88	<a href="#">c3b2cH_</a>	 Alignment	not modelled	5.9	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
89	<a href="#">c1ei8F_</a>	 Alignment	not modelled	5.9	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
90	<a href="#">c3b2cF_</a>	 Alignment	not modelled	5.9	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
91	<a href="#">c3b2cC_</a>	 Alignment	not modelled	5.9	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
92	<a href="#">c3b2cE_</a>	 Alignment	not modelled	5.9	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
93	<a href="#">c3b2cI_</a>	 Alignment	not modelled	5.9	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
94	<a href="#">c3b2cD_</a>	 Alignment	not modelled	5.9	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
95	<a href="#">c1ei8B_</a>	 Alignment	not modelled	5.9	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
96	<a href="#">c3b2cG_</a>	 Alignment	not modelled	5.9	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
97	<a href="#">c3b2cB_</a>	 Alignment	not modelled	5.9	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
98	<a href="#">c1ei8D_</a>	 Alignment	not modelled	5.9	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
99	<a href="#">c2klwC_</a>	 Alignment	not modelled	5.9	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