

Supplemental data

Collagen I (Alpha-1)

CO1A1_HUMAN GPAGAPGTPGPQGIAGQRGVVGLPGQR
CO1A1_RAT GPAGSPGTPGPQGIAGQRGVVGLPGQR
CO1A1_MOUSE GPAGSPGTPGPQGIAGQRGVVGLPGQR
CO1A1_BOVIN GPAGAPGTPGPQGIAGQRGVVGLPGQR
CO1A1_CHICK GPIGAPGTPGPQGIAGQRGVVGLPGQR
CO1A1_Canis GPAGAPGTPGPQGIAGQRGVVGLPGQR
CO1A1_CYNPY GPAGAPGTPGPQGIAGQRGVVGLPGQR

Collagen I (Alpha-2)

CO1A2_HUMAN GTAGPPGTPGPQGLLGAPGILGLPGSR
CO1A2_RAT GTTGPPGTAGPQGLLGAPGILGLPGSR
CO1A2_MOUSE GTAGAPGTAGPQGLLGAPGILGLPGSR
CO1A2_BOVIN GTAGPPGTPGPQGLLGAPGFLGLPGSR
CO1A2_CHICK GAAGPPGTPGPQGILGAPGILGLPGSR
CO1A2_CANFA GTAGPPGTPGPQGLLGAPGILGLPGSR
CO1A2_RANCA GPAGPPGAAGPSGVLGARGILGLPGTR
CO1A2_ONCMY GPPGAPGTAGPQGVLPSPGFVGLPGSR

Collagen II (Alpha-1)

CO2A1_HUMAN GPSGAEPPGPQGLAGQRGIVGLPGQR
CO2A1_RAT GPSGSDGPPGPQGLAGQRGIVGLPGQR
CO2A1_MOUSE GPSGLDGPPGPQGLAGQRGIVGLPGQR
CO2A1_XENTR GPSGPDGPPGPQGLSGQRGIVGLPGQR
CO2A1_XENLA GPSGPDGPPGPQGLSGQRGIVGLPGQR

Collagen III (Alpha-1)

CO3A1_HUMAN GAQGGPPGAPGPLGIAGITGARGLAGPP
CO3A1_RAT GAQGGPPGSPGPLGIAGLTGARGLAGPP
CO3A1_MOUSE GAQGGPPGSPGPLGIAGLTGARGLAGPP
CO3A1_BOVIN GPQGGPPGAPGPLGIAGLTGARGLAGPP

Figure S1. Alignment of the sequences at the collagenase cleavage sites in types I-III collagens across different species. Cleavage triplet is colored in red. Non-conserved residues are colored in blue.

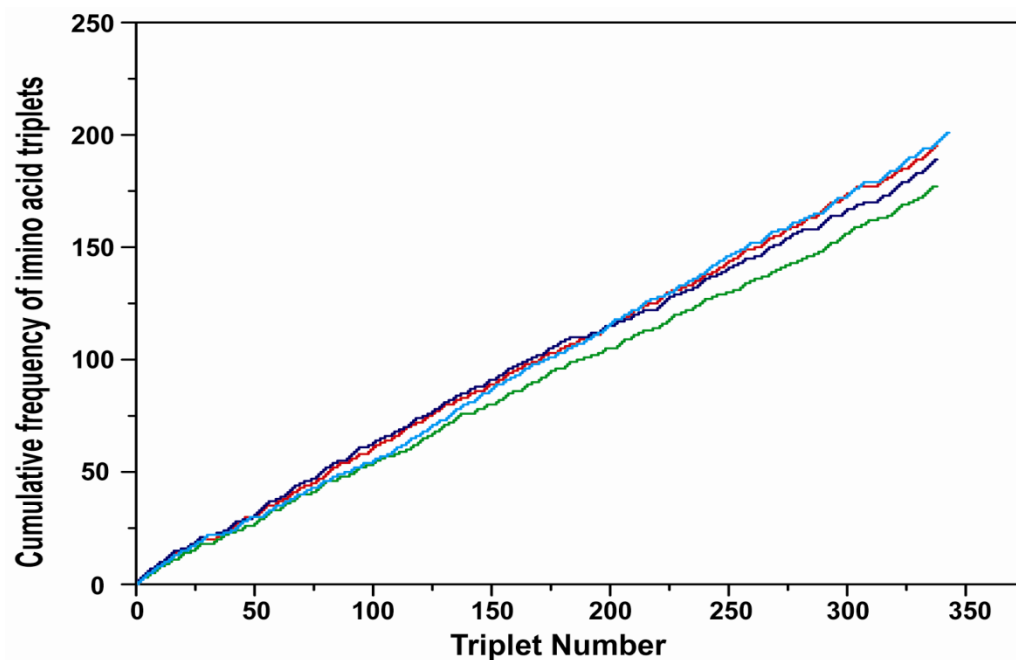


Figure S2. Cumulative frequency of imino acid triplets in CO1A1(red), CO1A2(green), CO2A1(blue) and CO3A1(cyan). CO1A1, CO1A2, CO2A1 and CO3A1 have totally 195, 177, 189 and 201 imino acid triplets, respectively.

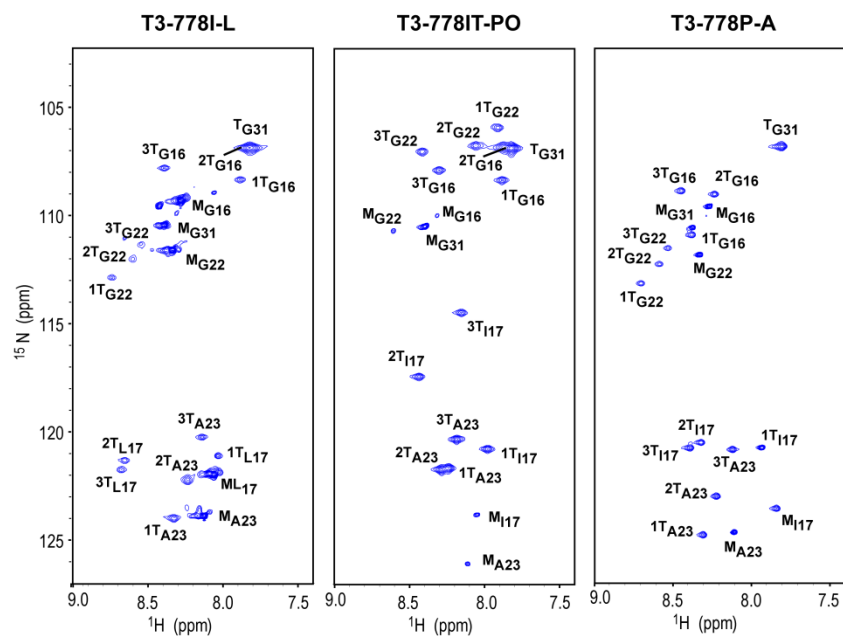


Figure S3. ^1H - ^{15}N HSQC spectra of peptides T3-778[I-L], T3-778[IT-PO] and T3-778[P-A]. All the spectra were obtained at pH 3.1 at 20 °C. The peaks corresponding to the monomer and trimer state are denoted with a superscript M or T. The superscripted number 1, 2 and 3 corresponds to the leading, middle and lagging chains, respectively.

Table S1. Protection factors of model peptides.

Residues	T3-778	T3-778[I-L]	T3-778[IT-PO]	T3-778[P-A]	Residues	T3-785
1G16	1598+/-824	2254+/-345	2709+/-750	584+/-70.1	1G15	525.2+/-39.6
3G16	753+/-144	563+/-36.5	857+/-110	647+/-88.7	3G15	541+/-56.2
1H17	1.7+/-0.2	1.2+/-0.5	1.1+/-0.2	3.2+/-0.2	1L16	98.3+/-5.9
2H17	10.9+/-0.9	5+/-0.5	10.5+/-1.2	6.1+/-0.4	2L16	213.4+/-13.9
3H17	6.2+/-0.6	3.2+/-0.3	1.5+/-0.3	3.8+/-0.2	3L16	236.5+/-15.9
1G22	658+/-161	1170+/-137	388+/-27.9	2072+/-1631	1A17	27+/-2
2G22	N/A	4079+/-2962	847+/-109	856+/-425	2A17	14+/-1.4
3G22	622+/-293	N/A	1026+/-204	636+/-236	3A17	14.7+/-1.7
1A23	9.5+/-1	12.8+/-1.4	17.9+/-2.5*	8.9+/-0.7	1G18	649+/-65.1
2A23	10+/-1.3	7.8+/-0.7	17.9+/-2.5*	11.8+/-1.0	2G18	868+/-100.3
3A23	18.2+/-2.7	9+/-0.9	14.1+/-2.1	9.7+/-0.6	3G18	612+/-41.8
G31	651+/-57.7	1068+/-67	1185+/-80	303+/-17.7	G24	325+/-16.2

* Hydrogen exchange experiments were performed at 10°C and pD 2.3-2.8 for the peptide set. Trimer resonances for 1A23 and 2A23 are overlapped.