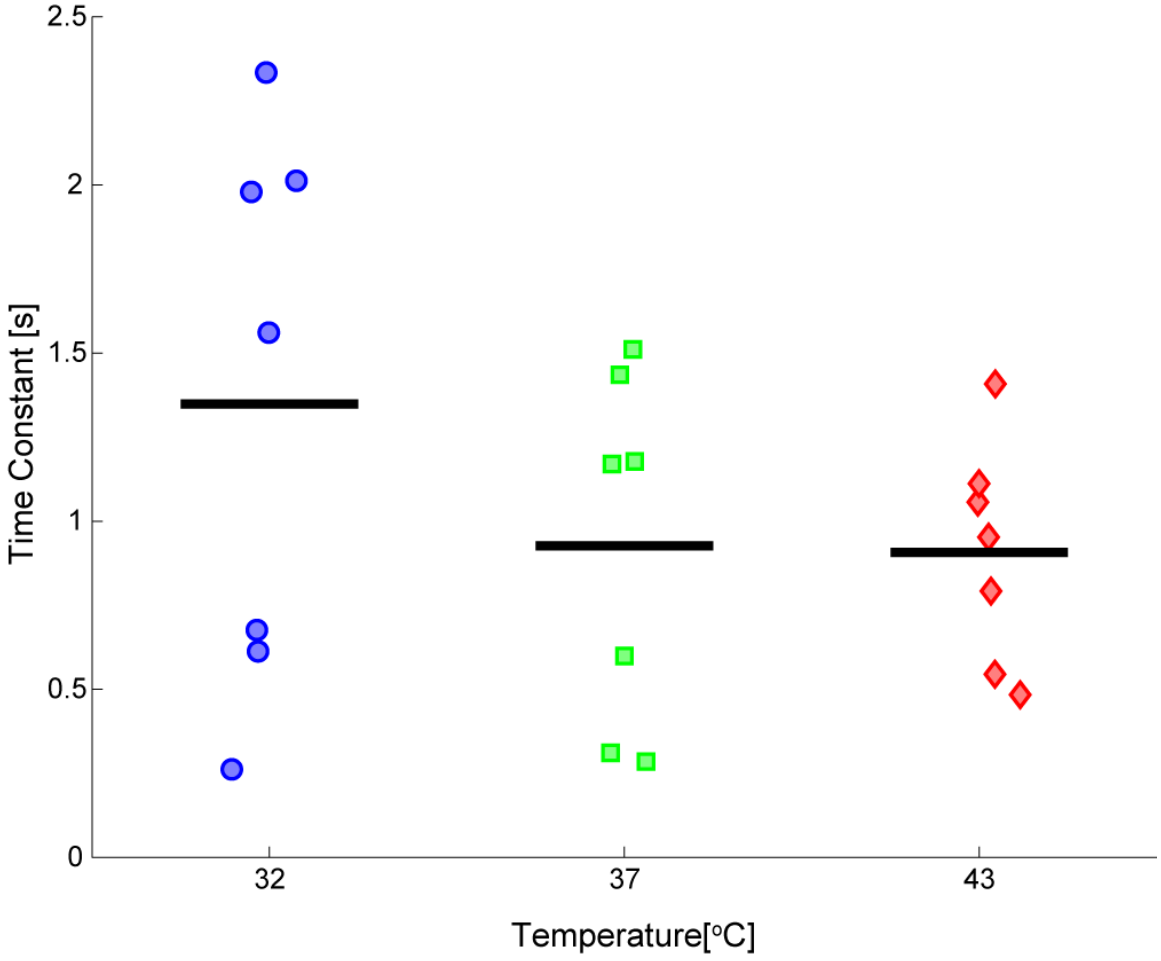
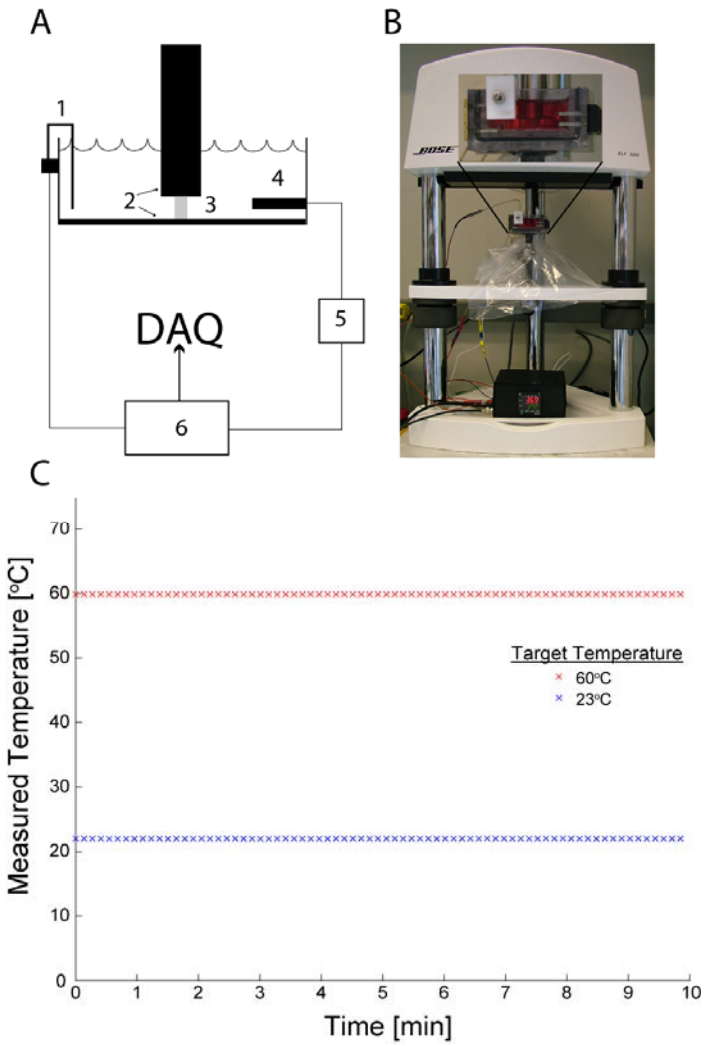
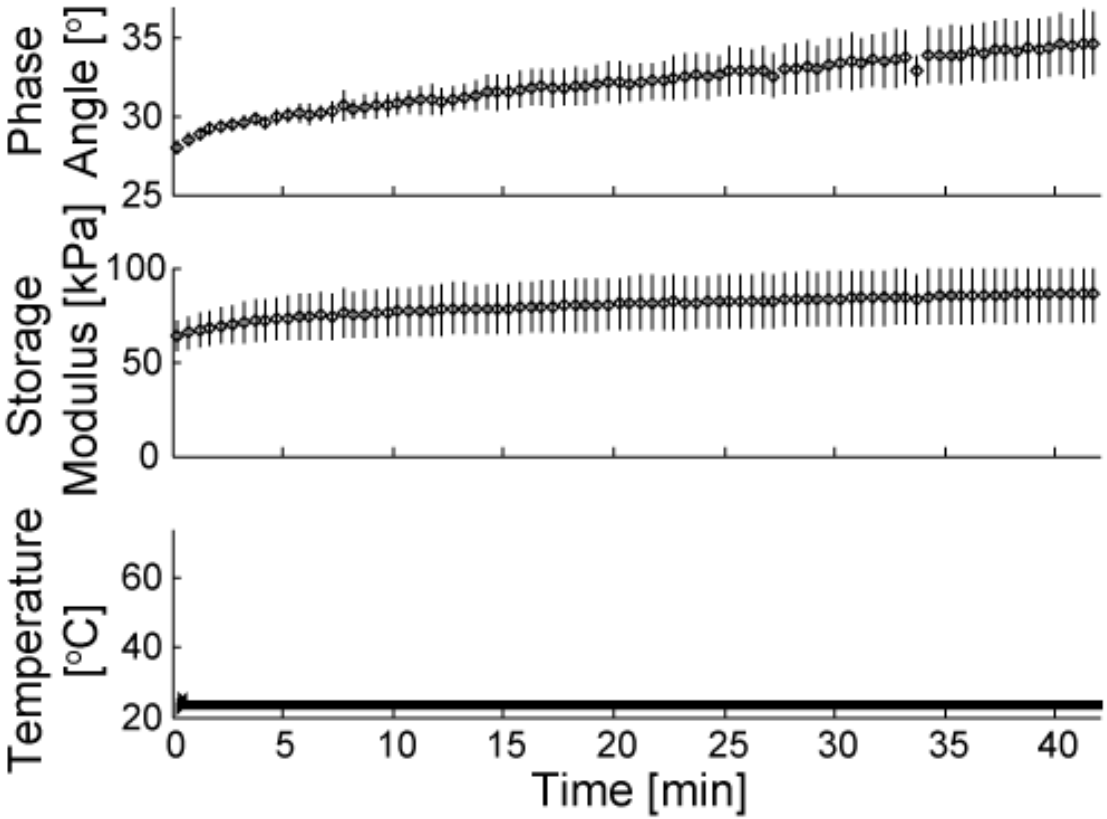

2.5
2
1.5
1
0.5
0
Time Constant [s]
32
37
43
Temperature[°C]

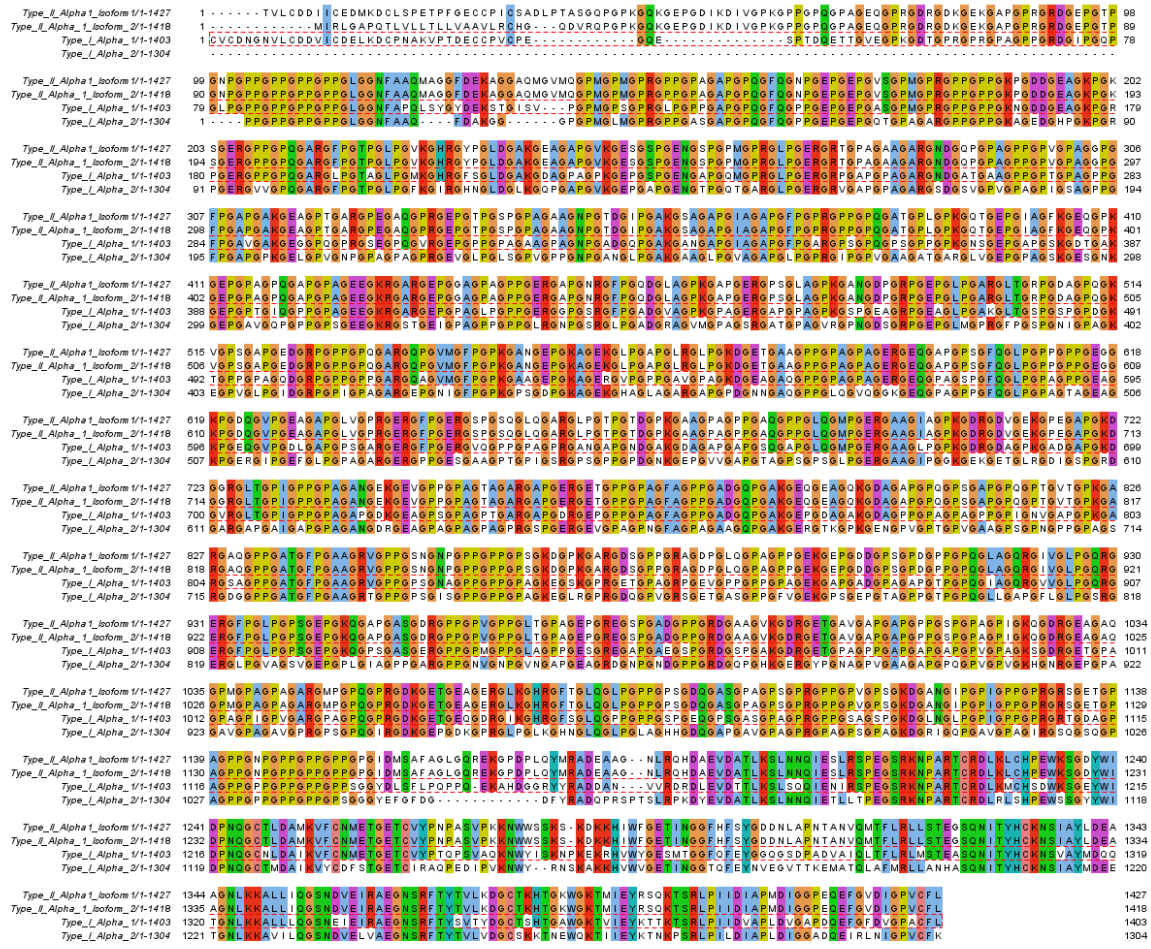
Supplementary Figure 2



Temperature Control System. (A) Schematic of loading system with temperature control. 1. thermocouple 2. polished stainless steel compression platens 3. cartilage sample 4. immersion heater 5. solid state relay 6. temperature controller. (B) Photograph of loading system with temperature control. (C) Validation data. The specimen bath was filled with media, and the temperature was ramped to either 23˚C or 60˚C. Data were collected at steady-state temperature. The standard deviation of the temperature measurements was 0.0070 at 23˚C and 0.0069 at 60˚C. These standard deviations are smaller than the bitwise resolution (0.01˚C) of the temperature controller. At steady state, the thermocouple was manually placed at multiple positions within the bath, and the temperature was found to be spatially-homogeneous (data not shown). During the heating phase between stress-relaxation tests, the temperature reached a peak of 63.1±0.1˚C but dropped to a final steady-state value of 60.1±0.1˚C by the beginning of the second stress-relaxation experiment.


Phase Angle [°]
35
30
25
Storage Modulus [kPa]
100
50
0
Temperature [°C]
60
40
20
0
5
10
15
20
25
30
35
40
Time [min]

Supplemental Figure 4



Substantial protein homology between bovine type I and type II collagen chains. The amino acid sequences of all known bovine type I and II collagen alpha chains (type I: α1 NP_001029211, α2 NP_776945. Type II, α1: Isoform 1 NP_001001135, Isoform 2 NP_001106695) were aligned using ClustalW2[1] and visualized using Jalview.[2] Residues are highlighted when 3 or more are identical in the multiple alignment. Pairwise alignments using BLAST found amino acid identity of 69 and 73% between the α1 chain of type I collagen and isoforms 1 and 2 of the type II chain, respectively. Pairwise alignments using BLAST found amino acid identity of 64% between the α2 chain of type I collagen and both isoforms 1 and 2 of the type II chain, respectively.

[1] MA Larkin *et al*, *Bioinformatics* 2007.
[2] AM Waterhouse *et al*, *Bioinformatics* 2009.