Supplementary Information

Design, characterization and evaluation of β-hairpin peptide hydrogels as support for osteoblast cell growth and bovine lactoferrin delivery

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Table of Contents

Figure S1. LCMS profile of purified peptide H4LMAX.

Figure S2. LCMS profile of purified peptide H4LMAX-RGDS.

Figure S3. LCMS profile of purified peptide H2LRDMAX.

Figure S4. Loss modulus (*G′′*) of 1 wt % peptide hydrogels.

Figure S5. Frequency sweep (0.2 % strain) of 1 wt % hydrogel of H4LMAX-RGDS and H2LRDMAX.

Figure S6. Strain sweep (6 rad.s^{-1}) of 1 wt % hydrogel of H4LMAX-RGDS and H2LRDMAX.

Figure S7. ATR-FTIR spectra of a hydrogels.

Figure S8. Storage (*G′*) and loss modulus (*G′′*) of 1 wt % H4LMAX-RGDS hydrogel containing LF.

Figure S9. Cumulative LF release profiles from 1 wt % H4LMAX and H4LRDMAX.

Figure S10. Transmission electron micrographs of a 50-fold water diluted sample 1 wt % H4LMAX-RGDS containing LF.

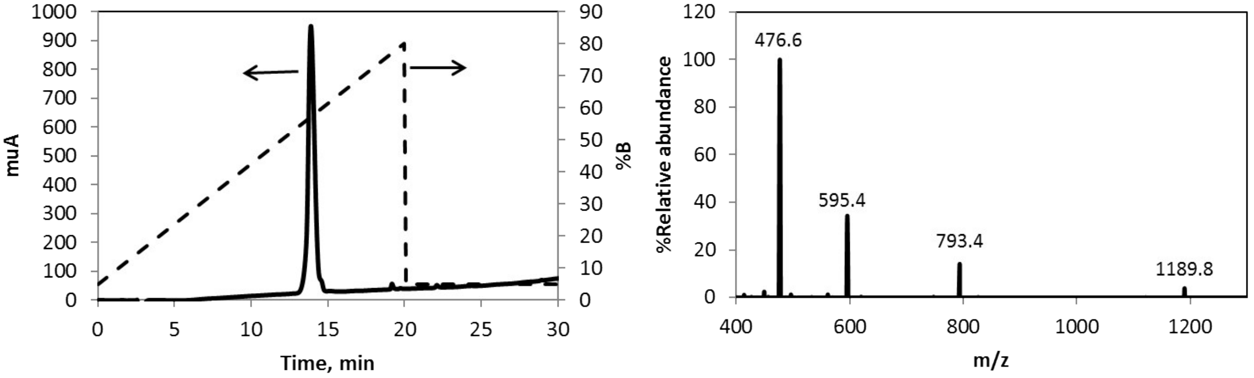

Figure S1. LCMS profile of purified peptide H4LMAX (t_R = 13.9 min, ca 98 % as analysed by peak area of RP-HPLC at 214 nm). ESI-MS spectrum of H4LMAX, mass spectra depict m/z ions found at the signal. Peak assignment: $[M + 2H]^{2+}$ obs. 1189.8 (calc. 1190.0); $[M +3H]^{3+}$obs. 793.4 (calc. 793.7); $[M +4H]^{4+}$obs. 595.4 (calc. 595.5); $[M +5H]^{5+}$obs. 476.6 (calc. 476.6).

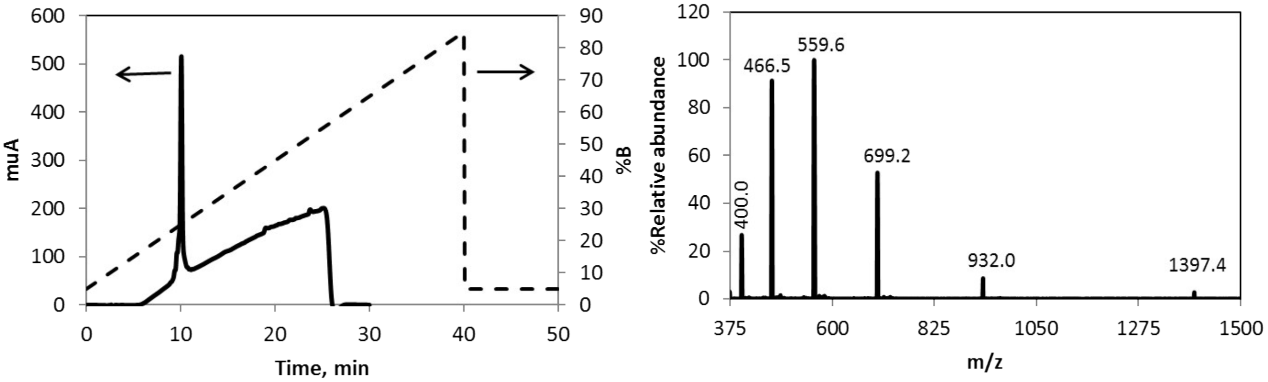

Figure S2. LCMS profile of purified peptide H4LMAX-RGDS (t_R = 10.1 min, ca 99% as analysed by peak area of RP-HPLC at 214 nm). ESI-MS spectrum of H4LMAX-RGDS, mass spectra depict m/z ions found at the signal. Peak assignment: $[M + 2H]^{2+}$ obs. 1397.4 (calc. 1397.7); $[M +3H]^{3+}$obs. 932.0 (calc. 932.2); $[M +4H]^{4+}$obs. 699.2 (calc. 699.4); $[M +5H]^{5+}$obs. 559.6 (calc. 559.7); $[M +6H]^{6+}$obs. 466.5 (calc. 466.6); $[M +7H]^{7+}$obs. 400.0 (calc. 400.1).

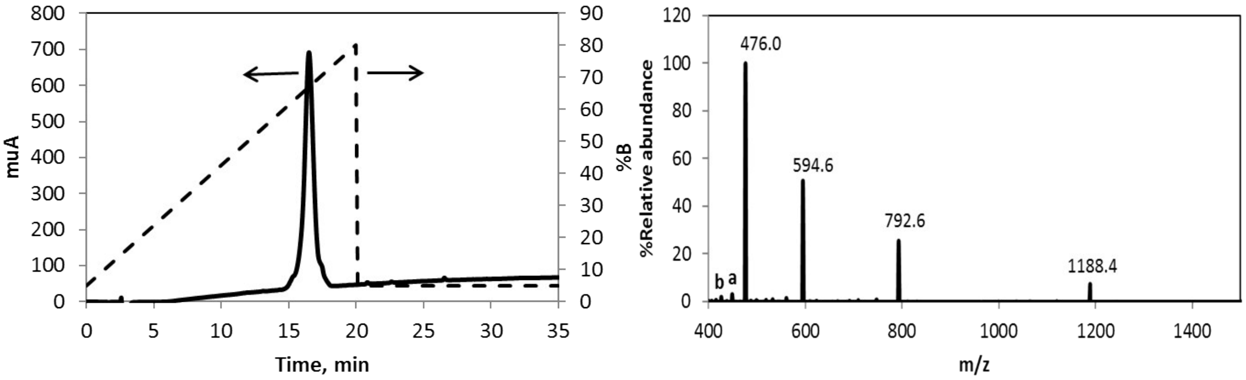

Figure S3. LCMS profile of purified peptide H2LRDMAX (t_R = 16.5 min, ca 94 % as analysed by peak area of RP-HPLC at 214 nm). ESI-MS spectrum of H2LRDMAX, mass spectra depict m/z ions found at the signal. Peak assignment: $[M + 2H]^{2+}$ obs. 1188.4 (calc. 1188.5); $[M + 3H]^{3+}$obs. 792.6 (calc. 792.7); $[M + 4H]^{4+}$obs. 595.5 (calc. 594.8); $[M + 5H]^{5+}$obs. 476.0 (calc. 476.0). The signal labeled as (**a**) corresponds to the His N-terminus truncated peptide $[M + 5H]^{5+}$obs. 448.5 (calc. 448.6). The signal labeled as (**b**) corresponds to the His-Leu N-terminally truncated peptide $[M + 5H]^{5+}$obs. 425.9 (calc. 425.9).

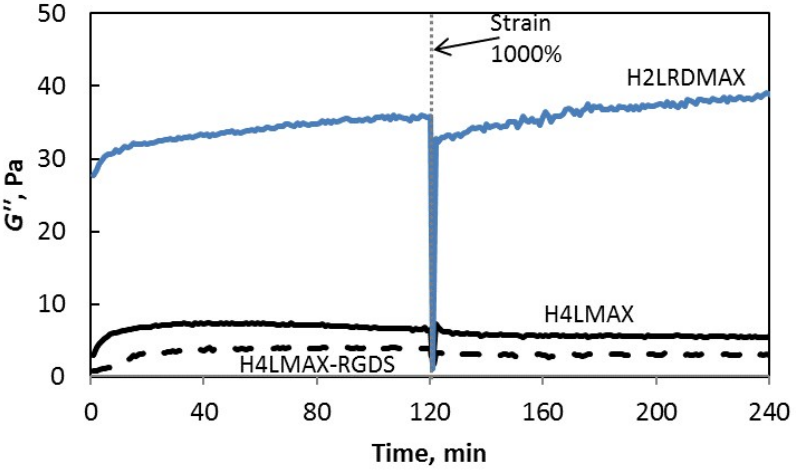

Figure S4. Loss modulus (*G''*) of 1 wt % peptide hydrogels in 50 mM Tris buffer pH 7.4 with 30 mM NaCl at 37 °C as a function of time (6 rad.s^{-1}, 0.2% strain).

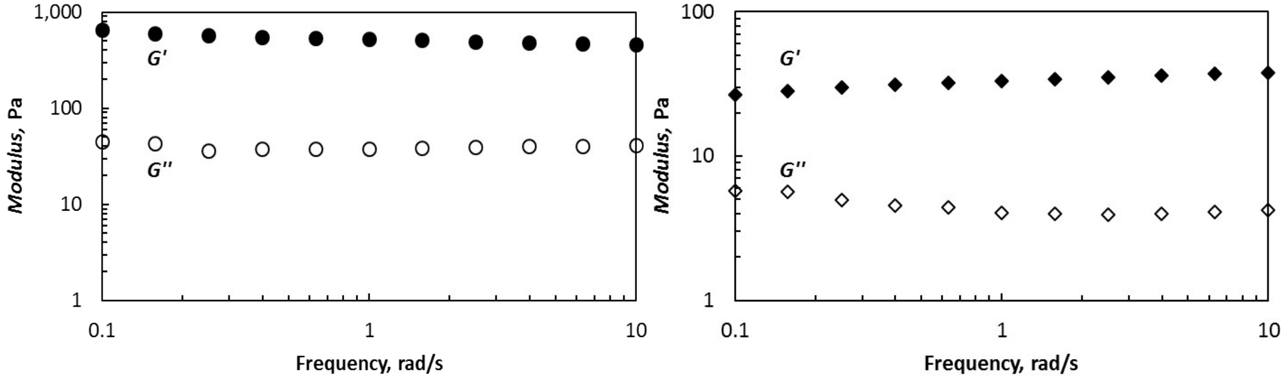

Figure S5. Frequency sweep (0.2 % strain) of 1 wt % hydrogel of H4LMAX-RGDS (left) and H2LRDMAX (right) in 50 mM Tris buffer pH 7.4 with 30 mM NaCl at 37 °C after first dynamic time sweep measurement in Fig S4. *G′* values are represented by filled symbols and *G′′* by open symbols.

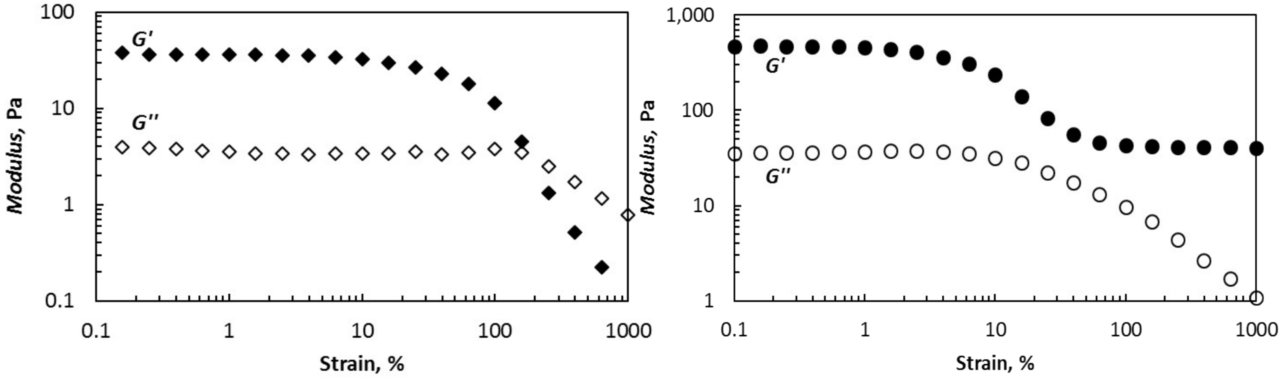

Figure S6. Strain sweep (6 rad.s^{-1}) of 1 wt % hydrogel of H4LMAX-RGDS (left) and H2LRDMAX (right) in 50 mM Tris buffer pH 7.4 with 30 mM NaCl at 37 °C after first dynamic time sweep measurement in Fig S4. *G′* values are represented by filled symbols and *G′′* by open symbols.

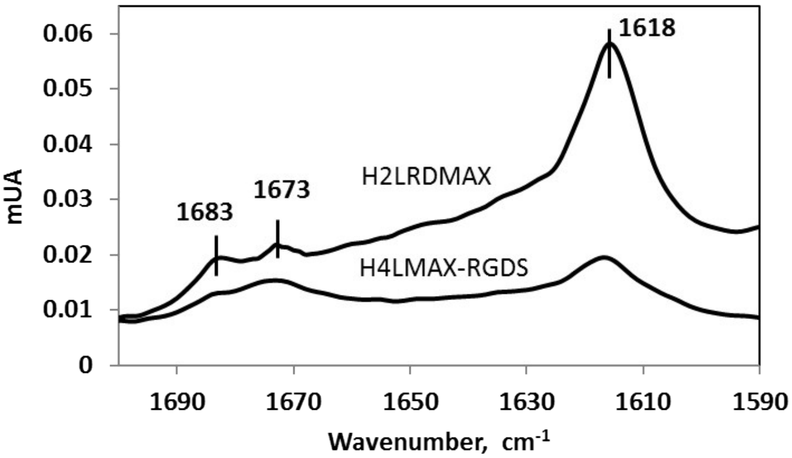

Figure S7. ATR-FTIR spectra of hydrogels at 1 wt % in D_2O with 50 mM Tris buffer pH 7.4 with 30 mM NaCl.

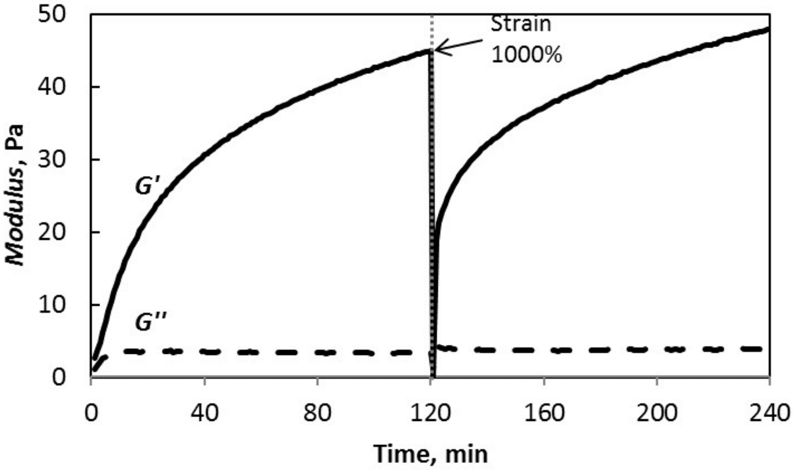

Figure S8. Storage (*G′*) and loss modulus (*G′′*) of 1 wt % H4LMAX-RGDS hydrogel containing 80 μg of LF in 50 mM Tris buffer pH 7.4 with 30 mM NaCl at 37 °C as a function of time (6 rad.s^{-1}, 0.2% strain).

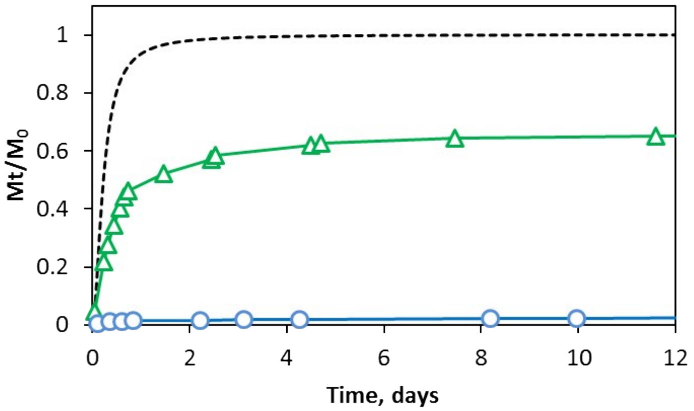

Figure S9. Cumulative LF release profiles from 1 wt % H4LMAX (blue open circles) and H4LRDMAX (green open triangles) hydrogels in 50 mM Tris buffer pH 7.4 with 150 mM NaCl at room temperature. The data points are connected with a solid line to guide the eye of the reader. Error bars are smaller than the symbol where not evident. The black dashed line represents a theoretical LF release scenario driven by the mass action law. Dissolution of the hydrogels was not observed during the experiments.

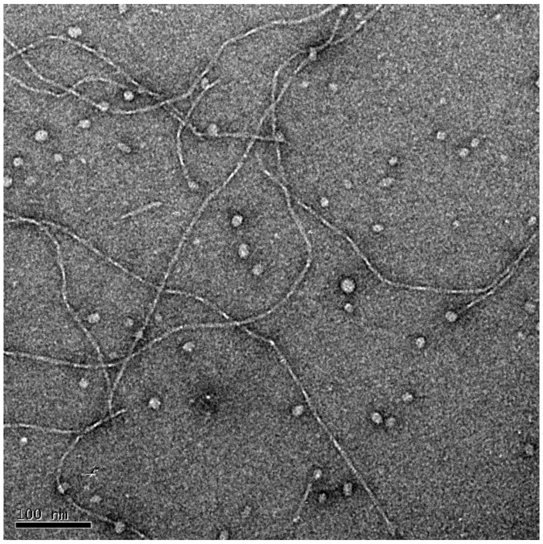

Figure S10. Transmission electron micrographs of a sample of H4LMAX-RGDS with LF 50-fold water diluted from a 1 wt % hydrogel in 50 mM Tris buffer pH 7.4 with 30 mM NaCl and 80 μg of LF. The black scale bar corresponds to 100 nm.