Supporting Information

Peptide chitosan/dextran core/shell vascularized 3D constructs for wound healing

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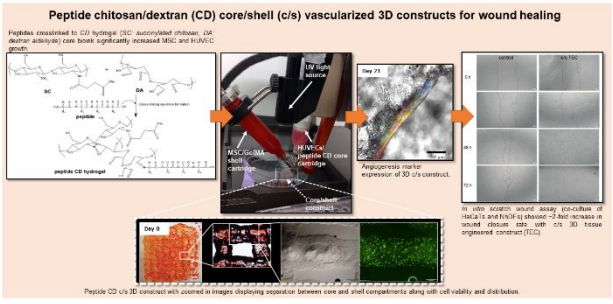


Supplementary Figures

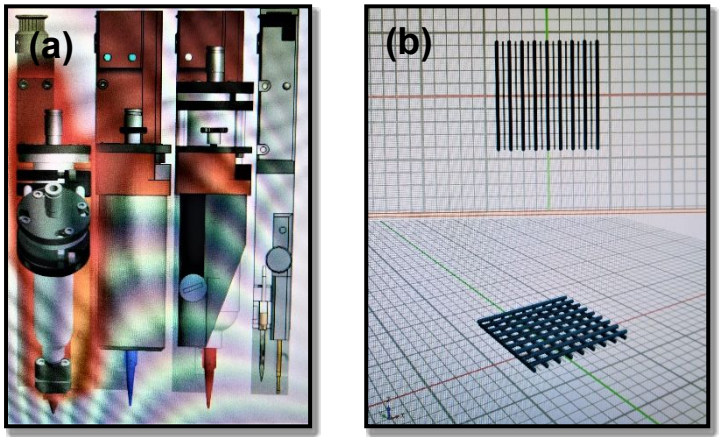
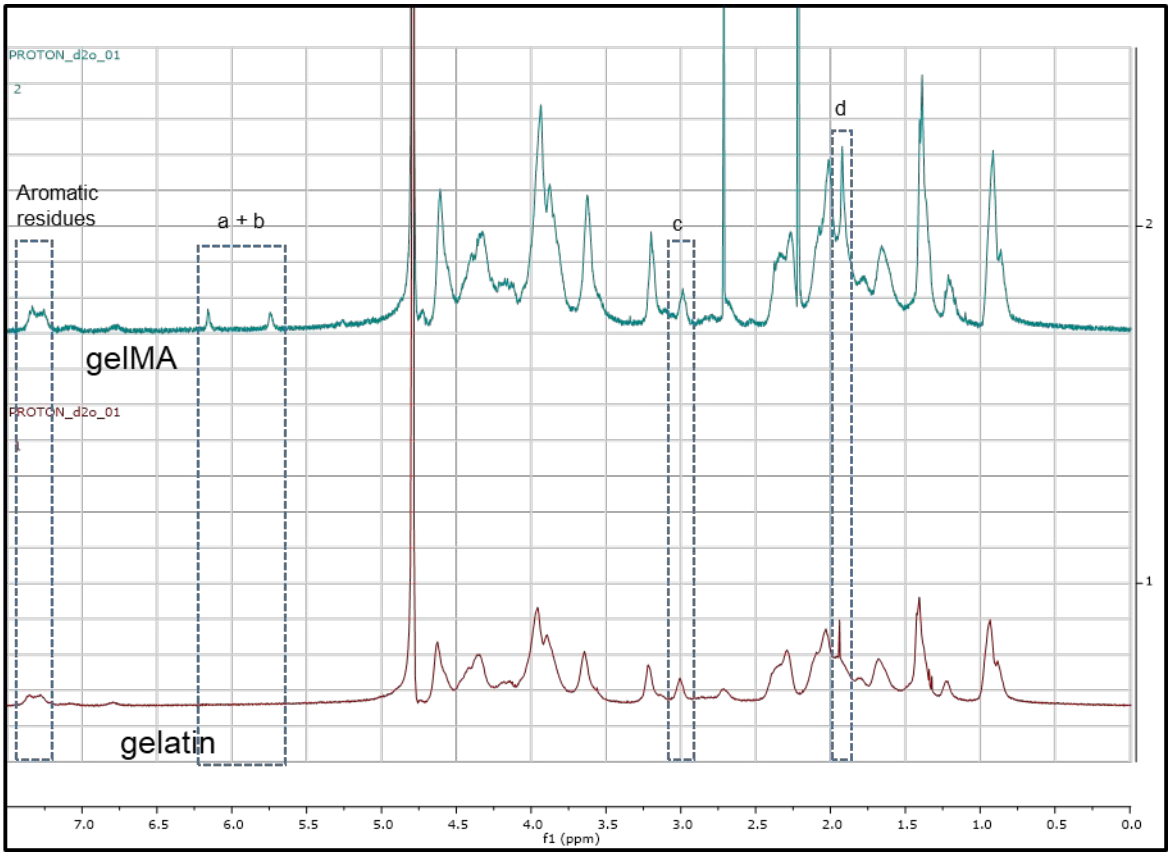


Figure S1. Bioscaffolder generator configuration and software pattern. (a) Configuration of the four axes Bioscaffolder used to biofabricate the print. Note: C/s represented in axis 1 (far left) with UV attachment on axis 3. (b) A representation of the scaffold patterning of 3D architecture as provided by the scaffold generator software.



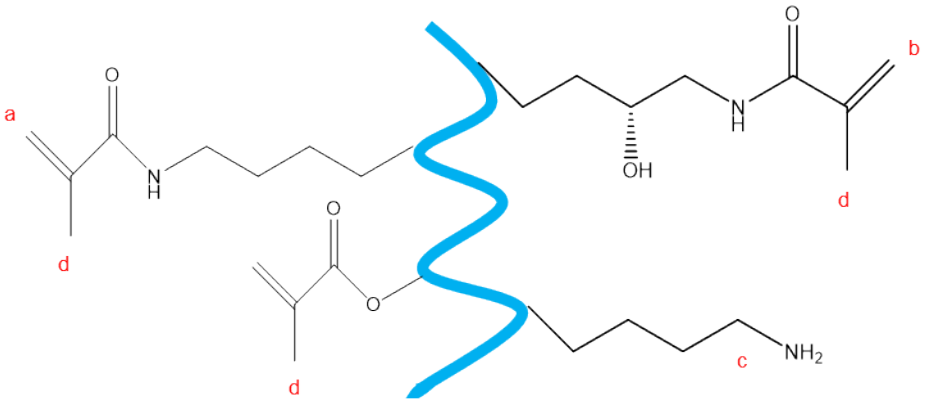
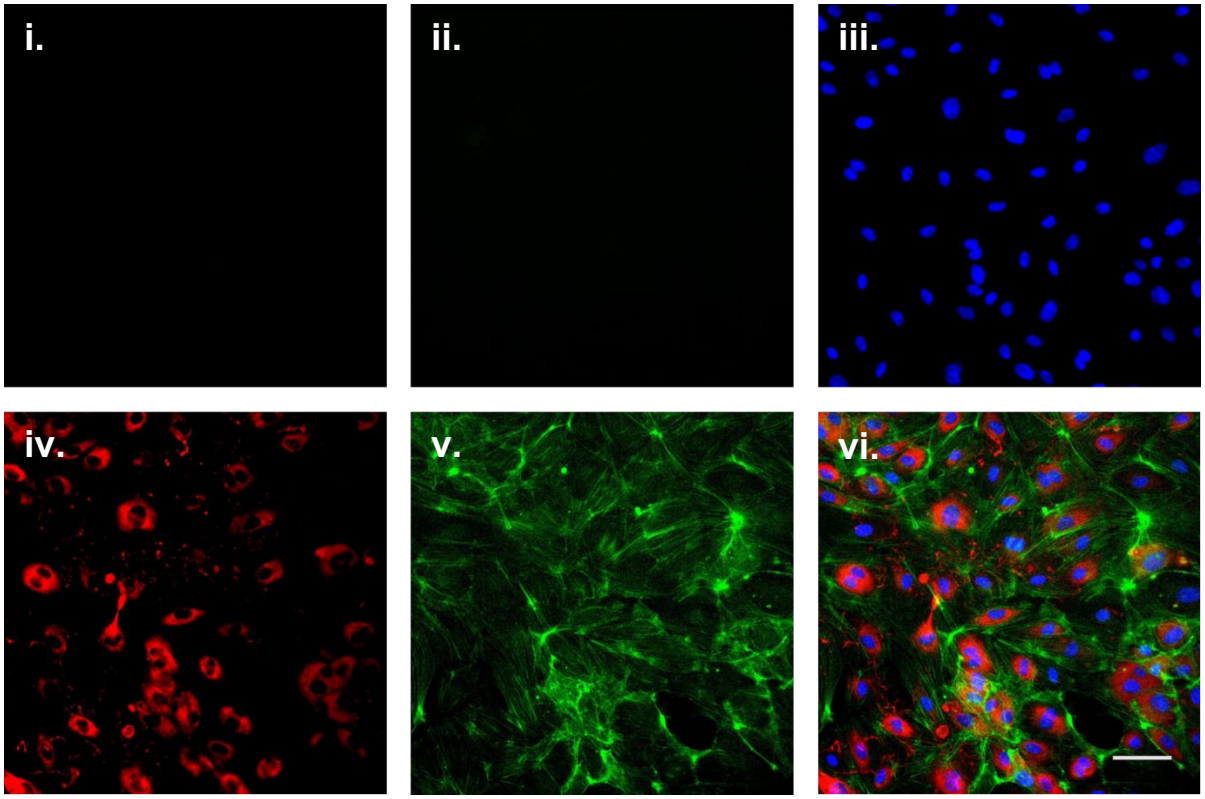


Figure S2. ^{1}H-NMR spectra of gelatin methacryloyl (top) and unmodified gelatin (bottom) in D_2O. a-d: Schematic of specific protons of methacrylamide groups in lysine and hydroxylysine residues, methylene protons of unmodified lysine and methyl protons of methacrylate groups, respectively.

a.



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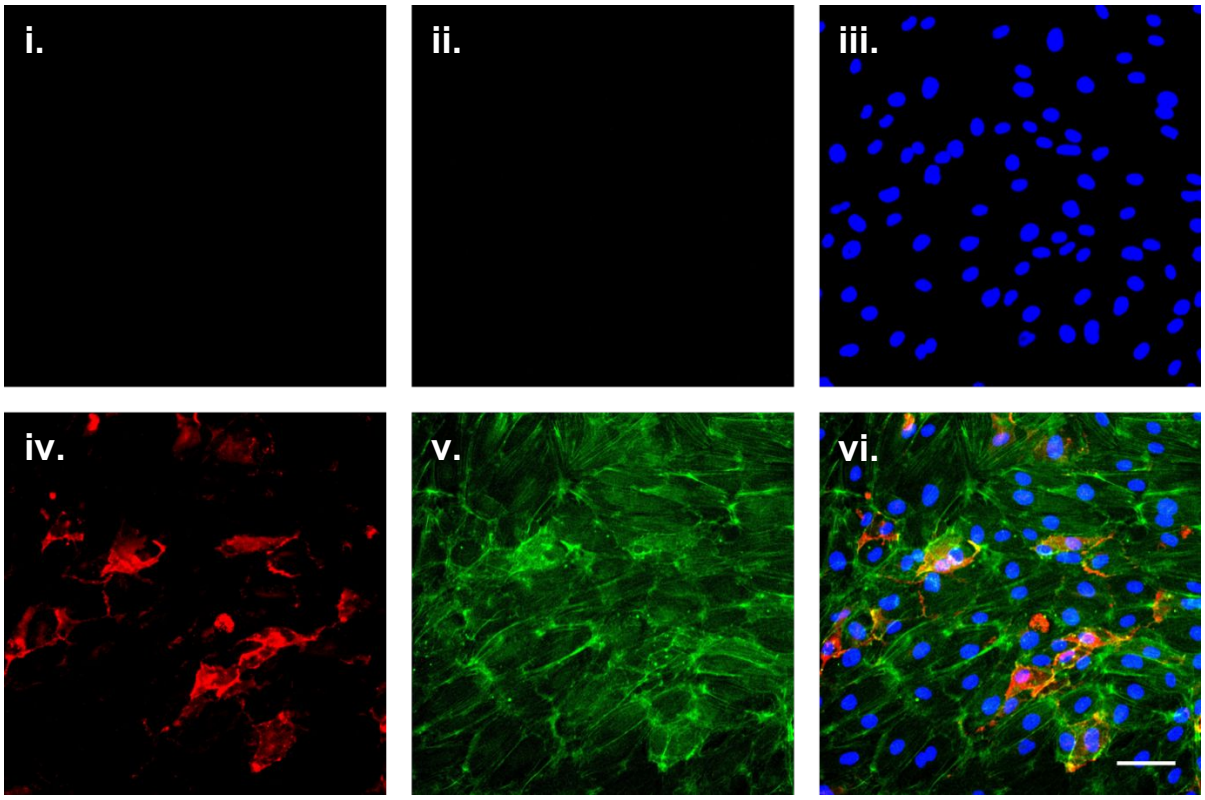
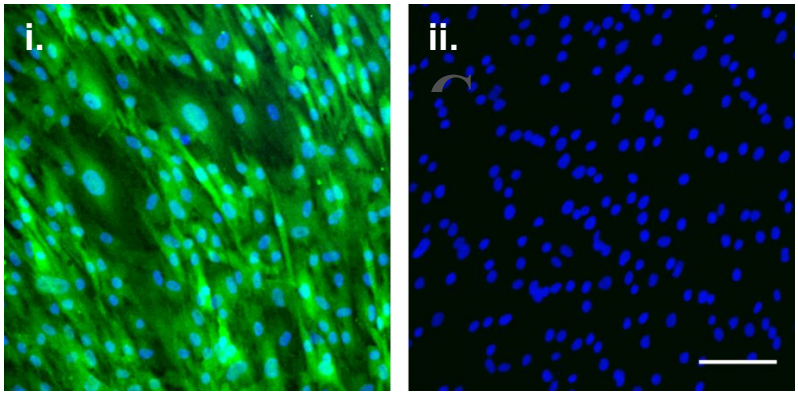


c.



d.

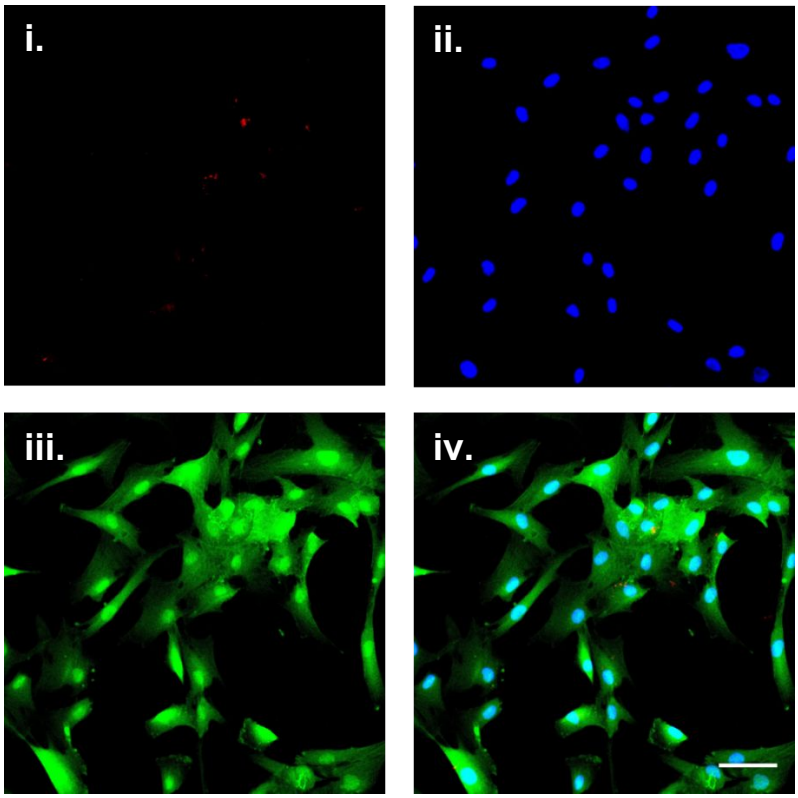


Figure S3. (a) HUVECs are positive for vWF staining. a-i) secondary goat anti-rabbit-alexa 594 only (red channel), a-ii) phalloidin-alexa-488 negative (green channel), a-iii) Hoechst 33342 (blue channel) a-iv) vWF antibody and secondary goat anti-rabbit-alexa-594 (red channel), a-v) phalloidin-alexa-488 (green channel), a-vi) Composite image of a-iii,iv,v.Scale bar = 50µm.
(b) HUVECs are positive for CD31 staining. b-i) secondary goat anti-rabbit-alexa 594 only (red channel), b-ii) phalloidin-alexa-488 negative (green channel), b-iii) Hoechst 33342 (blue channel) b-iv) CD31 antibody and secondary goat anti-rabbit-alexa-594 (red channel), b-v) phalloidin-alexa-488 (green channel), b-vi) Composite image of b-iii,iv,v.Scale bar = 50µm.
(c) T0253 cells express GFP. c-i) T0523 cells stained with Hoechst 33342 (composite of green and blue channels), c-ii) UBET7 MSC cell line (composite of green and blue channels). Scale bar = 100um.
(d) T0253 cells are negative for vWF staining. d-i) vWF antibody and secondary goat anti-rabbit-alexa-594 (red channel), d-ii) Hoechst 33342 (blue channel) d-iii) phalloidin-alexa-488 (green channel), d-iv) Composite image of d-i, ii, & iii. Scale bar = 50µm.

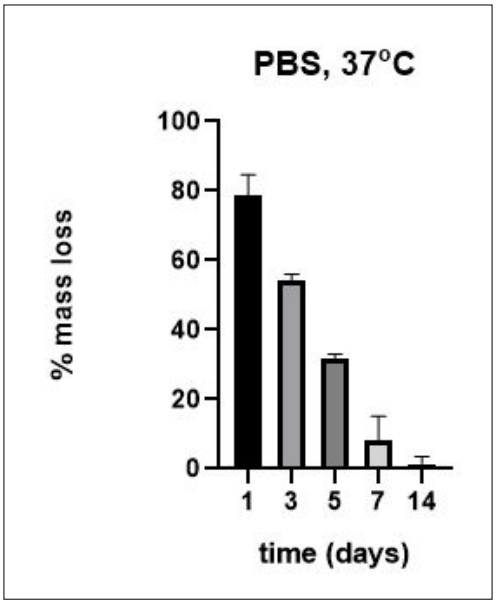


Figure S4. Percent mass loss in PBS at 37° of two-layer acellular core shell peptide-CD/GelMA constructs over 14 days. Error bars represent standard deviation. Acellular degradation rate was assessed by placing two layer cross-linked c/s TECs (n= 3) in pre-weighed, individual dishes, followed by the addition of PBS and storage in an incubator at 37°. The remaining c/s construct mass was obtained after carefully removing all the PBS from the dish, then weighing the construct together with the dish so as not to break the samples. Degradation percentages were calculated using the equation (%) = [1 – (dry mass/wet mass)] 100. Ordinary one-way ANOVA analysis (GraphPad Prism 8.1.1, San Diego, CA, USA) revealed a statistically significant difference between all time points measured with a $p < 0.0001$ and R^2 of 0.9852.