Macromolecule-network electrostatics controlling delivery of the bio-therapeutic cell modulator TIMP-2

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Figure S1. Analytical HPLC and ESI-mass spectra of MAX8 (A), HLT2 (B), AcVES3 (C), and IE1 (D).



Figure S2. TEM images of peptide fibrils, MAX8 (A), HLT2 (B), AcVES3 (C), and IE1 (D). MAX8 and HLT2 images were adapted from doi: 10.1016/j.biomaterials.2012.06.097.



Figure S3. Cumulative release profiles of 2 mg/mL and 4 mg/mL TIMP-2 from AcVES3 gel.



Figure S4. Cumulative release profiles of 4 mg/mL TIMP-2 from AcVES3 gel measured by ELISA vs. absorbance.

A. Control TIMP-2



Figure S5. Deconvoluted mass spectra of control TIMP-2 (A) and released TIMP-2 from AcVES3 gel collected on day 7 (B) and day 28 (C). The average mass of TIMP-2 used in this study is 22565.6.



Figure S6. Dixon plot of MMP-2 Inhibition kinetics by TIMP-2 (red) and Ala+TIMP-2 (blue). The major tick at $1/V_i=310$ indicates the reciprocal of the average of velocity of the control reaction (without TIMP-2). The lack of a negative slope for the Ala+TIMP-2 measurements is indicative of a complete absence of MMP-2 inhibitory activity in this assay. These findings are consistent with previous findings of a significantly decrease in K_{iApp} for this TIMP-2 mutant form, see reference ⁶².

[1] Wingfield, P. T. P., Sax, J. K. J., Stahl, S. J. S., Kaufman, J. J., Palmer, I. I., Chung, V. V., Corcoran, M. L. M., Kleiner, D. E. D., and Stetler-Stevenson, W. G. W. (1999) Biophysical and functional characterization of full-length, recombinant human tissue inhibitor of metalloproteinases-2 (TIMP-2) produced in Escherichia coli. Comparison of wild type and amino-terminal alanine appended variant with implications for the mechanism of TIMP functions., *The Journal of biological chemistry 274*, 21362-21368.