

Supplemental Information

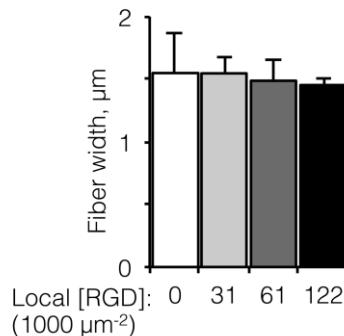
Use of protein-engineered fabrics to identify design rules for integrin ligand clustering in biomaterials

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RGD-elastin in elastin blend of fibers with ligands	Local [RGD], 1000 μm^{-2}	Nearest RGD spacing, nm	Fibers with ligands in mixed fabric	Global [RGD], 1000 μm^{-2}
0%	0	n/a	0%	0
3%	8	14.4	100%	4
6%	15	11.6	100%	9
13%	31	9.1	25%	4
13%	31	9.1	50%	9
13%	31	9.1	100%	18
25%	61	7.2	25%	9
25%	61	7.2	50%	18
25%	61	7.2	100%	35
50%	122	5.7	25%	18
50%	122	5.7	50%	35
50%	122	5.7	100%	71

Supplemental Table 1. Summary of fabrication parameters and resulting local and global ligand densities.



Supplemental Figure 1: Fiber width was unchanged for fibers produced from various RGD-/RDG-elastin blends (n = 3 fabrications per condition).

Supplemental Information S1: Example global ligand density calculation

Measure bulk mass swell ratio:

$$12.0 \pm 0.3 \frac{g \text{ wet}}{g \text{ dry}}$$

Convert to elastin volume fraction (bulk):

$$\frac{1 \text{ g} * \frac{1 \text{ mL elastin}}{1.35 \text{ g elastin}}}{11 \text{ g water} * \frac{1 \text{ mL water}}{1 \text{ g water}} + 1 \text{ g elastin} * \frac{1 \text{ mL elastin}}{1.35 \text{ g elastin}}} = 6.3\% \frac{\text{mL elastin}}{\text{mL bulk}}$$

Measure fiber volume fraction:

$$58 \pm 4\% \frac{\text{mL fibers}}{\text{mL bulk}}$$

Calculate fiber volume swell ratio

$$\frac{6.3\% \frac{\text{mL elastin}}{\text{mL bulk}}}{58\% \frac{\text{mL fibers}}{\text{mL bulk}}} = 11\% \frac{\text{mL elastin}}{\text{mL fiber}}$$

Convert to elastin density (fiber):

$$0.11 \frac{\text{mL elastin}}{\text{mL fiber}} * 1.35 \frac{\text{g elastin}}{\text{mL elastin}} = 0.15 \frac{\text{g elastin}}{\text{mL fiber}} * 10^{12} \frac{\text{pg}}{\text{g}} * 10^{-12} \frac{\text{mL}}{\mu\text{m}^3} = 0.15 \frac{\text{pg elastin}}{\mu\text{m}^3 \text{ fiber}}$$

Convert to [RGD], assuming fiber is 13% RGD-containing elastin (0.52 fmol RGD/fmol elastin):

$$0.15 \frac{\text{pg elastin}}{\mu\text{m}^3 \text{ fiber}} * \frac{\text{fmol elastin}}{33.3 \text{ pg elastin}} * \frac{0.52 \text{ fmol RGD}}{\text{fmol elastin}} * \frac{\text{mol}}{10^{15} \text{ fmol}} * \frac{6.02 * 10^{26}}{\text{mol}} = \frac{2.9 * 10^6}{\mu\text{m}^3 \text{ fiber}}$$

Calculate accessible [RGD] (surface concentration):

$$\frac{2.9 * 10^6}{\mu\text{m}^3 \text{ fiber}} * 0.023 \mu\text{m} = \frac{65 * 10^3}{\mu\text{m}^2 \text{ fiber}}$$

Calculate global [RGD]:

$$\frac{65 * 10^3}{\mu\text{m}^2 \text{ fiber}} * 58\% \frac{\mu\text{m}^2 \text{ fiber}}{\mu\text{m}^2 \text{ matrix}} * 50\% (\text{undersides of fibers are inaccessible}) = \frac{18 * 10^3}{\mu\text{m}^2 \text{ matrix}}$$

Supplemental Information S2: MATLAB script used to generate images of segmented vinculin puncta

```
%% Vinculin Puncta Segmentation
% This script segments confocal max projections of HUVECs stained for
% vinculin and outputs a binary image of individual puncta.

clear
clc
close all

% Read in confocal max projection image and adjust contrast
filename = 'vincetest.tif';
img = imread(filename);
imshow(img);
img = imadjust(img,[0.4 1],[]);
bw = im2bw(img);

% Segment vinculin puncta from peripheral structures (fibers, etc.). Note:
% strel structuring element radii are set to 0 here but should be optimized
% for the input image.
seD = strel('diamond',0);
bw = imerode(bw,seD);
bw = imerode(bw,seD);
se90 = strel('disk',0);
se0 = strel('disk',0);
bw = imdilate(bw,[se90 se0]);
bw = imfill(bw,'holes');

% Binarize image and detect object areas, perimeter, and centroid locations
IL = bwlabel(bw);
stats = regionprops(bw,'Area','Perimeter','Centroid');
% Circularity = 4*pi*area/(perimeter^2)
objareas = [stats.Area];
objperim = [stats.Perimeter];
objcirc = 4*pi*objareas./ (objperim.^2);

% Remove objects outside of defined circularity and area ranges
ind = find(objcirc >= 0 & objareas < 80 & objareas > 3);
Iout = ismember(IL,ind);
figure
imshow(Iout)

% Optional: Draw object outlines and overlay onto input image
perim = bwperim(Iout);
img_perim = img;
img_perim(perim) = 0;
figure
imshow(img_perim)
```