# **Supporting Information**

Backbone Engineered γ-Peptide Amphitropic Gels for Immobilization of Semiconductor Quantum dots and 2D Cell Culture

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1. ORTEP Diagram of Boc-γPhe-γPhe-OEt:



**Figure S1**: ORTEP diagram of peptide Boc-γPhe-γPhe-OEt (CCDC 1532237). H-atoms are omitted for clarity. Ellipsoids are drawn at 50% probability.

2. ORTEP Diagram of NH<sub>2</sub>-γPhe-γPhe-OH:



**Figure S2:** ORTEP diagram of peptide NH<sub>2</sub>-γPhe-γPhe-OH (CCDC 1532238). H-atoms are omitted for clarity. Ellipsoids are drawn at 50% probability.

#### 3. Crystallographic Information of Peptides

**Crystal structure analysis of Boc-γPhe-γPhe-OEt:** Crystals of **Boc-γPhe-γPhe-OEt** were grown by slow evaporation from a solution of ethyl acetate. A single crystal (0.1 × 0.06 × 0.02 mm) was mounted on loop with a small amount of the paraffin oil. The X-ray data were collected at 100K temperature on a Bruker APEX(II) DUO CCD diffractometer using Mo Kα radiation ( $\lambda = 0.71073$  Å), ω-scans (2θ = 56.66), for a total of 12748 independent reflections. Space group P 21, a = 5.172(8), b = 27.15(4), c = 9.752(14), β = 95.20(3), V = 1364(3) Å<sup>3</sup>, monoclinic, Z = 2 for chemical formula C<sub>29</sub> H<sub>38</sub> N<sub>2</sub> O<sub>5</sub>, with one molecule in asymmetric unit; ρcalcd = 1.204 gcm<sup>-3</sup>,  $\mu = 0.082$  mm<sup>-1</sup>, F (000) = 532. The structure was obtained by direct methods using SHELXS-97.<sup>[11]</sup> The final R value was 0.0710 (wR2 = 0.1549) 6480 observed reflections (F0 ≥ 4σ (|F0|)) and 330 variables, S = 0.897. The largest difference peak and hole were 0.316 and -0.274eÅ<sup>3</sup>, respectively.

**Crystal structure analysis of NH**<sub>2</sub>-γ**Phe**-γ**Phe**-OH: Crystals of NH<sub>2</sub>-γ**Phe**- γ**Phe**-OH were grown by slow evaporation from a solution of water. A single crystal (0.4 × 0.1 × 0.18 mm) was mounted on loop with a small amount of the paraffin oil. The X-ray data were collected at 100K temperature on a Bruker APEX(II) DUO CCD diffractometer using Mo Kα radiation ( $\lambda = 0.71073$  Å),  $\omega$ -scans (2 $\theta = 54.9$ ), for a total of 18173 independent reflections. Space group P1, a = 5.0140(10), b = 11.531(2), c = 18.198(4), 95.463(4), V = 1047.3(4) Å<sup>3</sup>, monoclinic, Z = 2 for chemical formula C<sub>22</sub> H<sub>28</sub> N<sub>2</sub> O<sub>4</sub>, with one molecule in asymmetric unit;  $\rho$ calcd = 1.204 gcm<sup>-3</sup>,  $\mu = 0.084$  mm<sup>-1</sup>, F (000) = 330. The structure was obtained by direct methods using SHELXS-97.<sup>[11]</sup> The final R value was 0.0448 (wR2 = 0.1336) 7091 observed reflections (F0 ≥ 4 $\sigma$  ([F0])) and 507 variables, S = 0.787. The largest difference peak and hole were 0.532and -0.268eÅ<sup>3</sup>, respectively.

### 4. General experiment details

# Synthesis of peptide P1-P5:

Synthesis of peptide **P1**, **P2**, **P3**, **P4** and **P5** were carried out by conventional solution phase methods using racemization free fragment condensation strategy. The Boc group was used for the *N*-terminal protection and the C-terminus was protected either with ethyl or methyl esters. The Boc-(*S*)- $\beta$ -Phe was synthesized by Arndt–Eistert homologation of Boc-Phe and Boc-(*S*)- $\gamma$ -Phe was synthesized by Wittig reaction followed by catalytic hydrogenation. Couplings were carried out using *N*-Ethyl-*N'*-(3-dimethylaminopropyl)carbodiimide hydrochloride (EDC) and 1- hydroxybenzotriazole (HOBt). C-terminal methyl or ethyl group was deprotected by using aqueous sodium hydroxide. The final compound was fully characterized by mass spectrometry, <sup>1</sup>H NMR spectroscopy and <sup>13</sup>C NMR spectroscopy.

### 5. Characterization of peptide P1-P5:

## Peptide P1

<sup>1</sup>H NMR (400 MHz, DMSO-*d*<sub>6</sub>)  $\delta$  12.82 (bs, 1H), 8.11 (d, *J* = 7.9 Hz, 1H), 7.41 – 7.07 (m, 10H), 6.87 (d, *J* = 8.8 Hz, 1H), 4.48 (m, , 1H), 4.17 (m, 1H), 3.09 (m, 1H), 2.99 – 2.86 (m, 2H), 2.67 (m, 1H), 1.28 (s, 9H). <sup>13</sup>C NMR (101 MHz, DMSO-*d*<sub>6</sub>)  $\delta$  173.22, 172.10, 155.54, 138.56, 137.79, 129.68, 129.62, 128.64, 128.43, 126.91, 126.60, 78.49, 56.13, 53.78, 37.90, 37.25, 28.58. HR-MS m/z calculated for C<sub>23</sub>H<sub>28</sub>N<sub>2</sub>O<sub>5</sub> is [M+H]<sup>+</sup> 413.2076 and observed 413.2076.



# Peptide P2

<sup>1</sup>H NMR (400 MHz, DMSO- $d_6$ )  $\delta$  7.90 (d, J = 8.2 Hz, 1H), 7.32 – 6.99 (m, 10H), 6.59 (d, J = 8.5 Hz, 1H), 4.31 – 4.12 (m, 1H), 3.82 (m, 1H), 2.67 (m, , 2H), 2.28 (m, 2H), 2.11 (m, 2H), 1.25 (s, 9H). <sup>13</sup>C NMR (101 MHz, DMSO- $d_6$ )  $\delta$  173.27, 169.84, 155.22, 139.47, 139.26, 129.72, 129.64, 128.62, 128.47, 126.57, 126.34 77.95, 49.76, 47.97, 41.11, 28.73. HR-MS m/z calculated for C<sub>25</sub>H<sub>32</sub>N<sub>2</sub>O<sub>5</sub> is [M+H]<sup>+</sup> 441.2389 and observed 441.2382



# Peptide P3

<sup>1</sup>H NMR (400 MHz, DMSO-*d*<sub>6</sub>)  $\delta$  12.13 – 11.76 (m, 1H), 7.59 (d, *J* = 8.5 Hz, 1H), 7.21 (m, 4H), 7.13 (m, 6H), 6.63 (d, *J* = 8.8 Hz, 1H), 4.04 – 3.62 (m, 1H), 3.55 – 3.41 (m, 1H), 2.60 (m,4H), 2.25 – 1.91 (m, 4H), 1.70 – 1.33 (m, 4H), 1.27 (s, 9H). <sup>13</sup>C NMR (101 MHz, DMSO-*d*<sub>6</sub>)  $\delta$  172.06, 155.77, 139.67, 139.43, 129.65, 128.57, 128.55, 77.86, 52.03, 49.81, 41.16, 40.97 33.02, 31.05, 30.86, 29.71, 28.78. HR-MS m/z calculated for C<sub>27</sub>H<sub>36</sub>N<sub>2</sub>O<sub>5</sub> is [M+H]<sup>+</sup> 469.2702 and observed 469.2702



# Peptide P4

<sup>1</sup>H NMR (400 MHz, DMSO- $d_6$ )  $\delta$  11.95 (s, 1H), 7.45 (d, J = 8.9 Hz, 1H), 6.54 (d, J = 9.1 Hz, 1H), 3.78 (m,1H), 3.42 (m, 1H), 2.24 – 2.09 (m, 2H), 2.03 (m, 2H), 1.72 – 1.02 (m, 18H), 0.91 – 0.74 (m, 12H). <sup>13</sup>C NMR (101 MHz, DMSO- $d_6$ )  $\delta$  174.83, 172.05, 155.93, 77.65, 48.38, 46.07, 44.34, 32.99, 32.21, 31.00, 30.87, 28.75, 24.90, 24.88, 23.61, 23.58, 22.39. HR-MS m/z calculated for C<sub>21</sub>H<sub>40</sub>N<sub>2</sub>O<sub>5</sub> is [M+H]<sup>+</sup> 401.3015 and observed 401.3015.



### Peptide P5

<sup>1</sup>H NMR (400 MHz, DMSO- $d_6$ )  $\delta$  12.39 – 11.97 (m, 2H), 8.24 (d, J = 8.2 Hz, 1H), 7.23 (m, , 5H), 7.20 – 7.14 (m, 6H), 7.05 (d, J = 8.8 Hz, 1H), 6.80 – 6.73 (dd, 1H), 6.51 (dd, J = 15.4, 5.6 Hz, 1H), 5.87 (dt, J = 15.0, 4.0 Hz, 1H), 5.66 (dd, J = 15.9, 1.7 Hz, 1H), 4.69 (m, J = 8.5, 1H), 4.24 (m, 1H), 2.91 – 2.82 (m, 1H), 2.78 – 2.64 (m, 3H), 1.26 (s, 9H). <sup>13</sup>C NMR (101 MHz, DMSO- $d_6$ )  $\delta$  167.45, 164.63, 155.44, 148.43, 143.80, 138.51, 129.73, 129.62, 128.73, 128.59, 127.05, 126.85, 126.65, 123.51, 121.57, 78.27, 53.20, 51.53, 28.72. HR-MS m/z calculated value for C<sub>27</sub>H<sub>32</sub>N<sub>2</sub>O<sub>5</sub> is [M+H]<sup>+</sup> 465.2389 and observed 465.2389



#### 6. Gelation study:

Peptide **P3** was placed in a glass vial and heated on a hot air gun after the addition of 1 mL of 100 mM or 50 mM phosphate buffer (pH 7.46) to give a clear solution. The solution was sonicated and upon standing at room temperature for a few minutes (almost 10 minutes) it produced a transparent gel. This was confirmed by vial inversion experiment. The minimum gelation concentration of the formation of hydrogel was found to be 5 mg/mL. For the cell culture experiments, gel was made in PBS buffer. The solution of peptide **P3** (6 mg) in PBS buffer (1 mL) was heated using hot air gun, after some time the clear dissolved solution was pipetted out and sonicated. The solution slowly transformed into gel upon standing at room temperature. For the organogel, similar procedure was followed using different aromatic solvents such as benzene, tolune, mesytelene and xylene.

# 7. Details of gelation study in various solvents of peptide P1 to P5

Solvent	P1	P2	P3	P4	P5
Phosphate					
buffer (100	Sol	Opaque gel <sup>a</sup>	Transparent	Sol	Sol
mM)			σel		
			50		
Benzene	Sol	Unstable gel	Transparent	$\mathrm{Sol}^{\mathrm{b}}$	Crystaline
			gel		fiber <sup>b</sup>
Toluene	Transparent	Unstable gel	Transparent	Sol <sup>b</sup>	Crystaline
	gel		gel		fiber <sup>b</sup>
Xylene	Transparent	Transparent	Transparent	Sol <sup>b</sup>	Crystaline
	gel	gel	gel		fiber <sup>b</sup>
Mesitylene	Transparent	Transparent	Transparent	Sol <sup>b</sup>	Crystaline
	gel	gel	gel		fiber <sup>b</sup>

(In the following gelation experiments, 6 mg of peptide was used in 1mL of solvent)

<sup>a</sup>Difficult to solubilize completely. After prolonged heating, the amount which was dissolved formed an

opaque hydrogel at room temperature. <sup>b</sup>After 24 hours it start aggregating.

### 8. Microscopy:

FE-SEM experiments were performed by drop casting a small amount of gel samples (4  $\mu$ L) on SiO2/Si substrate and dried under room temperature, imaged using Zeiss DSM 950 scanning electron microscope with tungsten filament as electron source operated at 10 kV. Similarly TEM sample were prepared by depositing dilute gel sample (4 $\mu$ L) on copper grid, dried at room temperature and imaged using a FEI Tecnai G2 F20 X-TWIN TEM at an accelerating voltage of 200 kV.

### 9. Rheology:

The rheology experiments were performed on hydrogel as well as organogles (6 mg/mL) using a TAARES rheometer.

#### **10.** Spectroscopy:

Circular dichroism (CD) spectra between 200 and 300 nm were recorded in a JASCO 815 spectrometer at room temperature with different concentration of peptide in 100 mM phosphate buffer. Further the fluorescence of the peptide **P3** organogels were measured using fluorescence spectrometer, pure peptides in DMF were used as control. The samples were excited at 259 nm, and the emission spectra were collected from 269 to 500 nm. Powder XRD data of xerogel samples were collected at 3-40° using a Rigaku D/max-2500 instrument (Cu/KR-1).

# 11. Biocompatibility experiment of the hydrogel P3:

Cell Culture or peptide hydrogels **P3**. Prior to 2D-culture, Thin gel was made after mixing DMEM:Hydrogel (1:1) and coating the culture plate for 3 hours. Subsequently, solution is

aspirated and plate was dried for 5-10 minutes. Cells were collected from a subconfluent monolayer by trypsin-EDTA treatment, and were re-suspended in complete medium containing DMEM, 10% FBS, and 1% Penicillin/Streptomycin solution. Cells suspension in complete medium was pipetted into each well. The 96-well plate was placed in incubator at 37 °C under 5% of CO<sub>2</sub> atmosphere. Cells were evenly distributed on the gel surfaces by gently pipetting the medium, and the medium was changed every other day. The cultured cells were stained by calcein and imaged by fluorescence microscope.

# 12. Gelation test of the compound P1 to P5 in aromatic solvent



Figure S3: Inverted sample vial test to confirm the gel formation for the peptide P1 in A) Benzene failed to gelate B) Toluene, C) Xylene, D) Mesitylene .



Figure S4: Low strength gel formation for the peptide P2 in A) Benzene B) Toluene, C) Xylene, D) Stable gel formed Mesitylene.



Figure S5: Inverted sample vial experiment to confirm the gel formation for the peptide P3 in A) Benzene; B) Chlorobenzene; C) Toluene; D) Xylene; E) Mesitylene; G) Compound P5 failed to gelate after 6 hours in toluene; H) Compound P4 failed to gelate toluene after 6 hours.

13. Florescence spectra of peptide P3 in gel state and in solution.



Figure S6: Florescence emission spectra ( $\lambda$  = excitation 259 nm) of peptide P3 in DMF solution and organogel in toluene at fixed concentration.

14. Step-strain rehology experiment of peptide hydrogel (P3) at 6mg/mL



Figure S7: Step-strain rehology experiment of peptide hydrogel (P3) at 6mg/mL

# 15. Quantification of cell viability in peptide hydrogel system



**Figure S8:** Quantification of cell viability in peptide hydrogel system, data is represented as mean<u>+</u>SD from three independent experiments. Magnification X63.

16. SEM images of peptide P1, P4, at minimum gelation condition(6mg/mL).



Figure S9: High resolution SEM images peptide P1, P4, at minimum gelation condition (6mg/mL).

11. <sup>1</sup>H, <sup>13</sup>C and mass spectra of compounds P1 to P5





7,212 7,222 7,





























# 12. Reference

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- (2) Sheldrick, G. M. SHELXL-97, Universität Göttingen (Germany) 1997