Electronic Supplementary Material (ESI) for RSC Advances
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Supporting Information

Synthesis and characterization of the peptide:

The peptide was prepared by solid-phase peptide synthesis (SPPS) using 2-chlorotrityl chloride resin and the corresponding N-Fmoc protected amino acids with side chains properly protected by a tert-butyl group or Pbf group or Boc group. After the first amino acid was loaded on the resin by its C-terminal, 20% piperidine in anhydrous N,N'-dimethylformamide (DMF) was used to deprotection of Fmoc group. Then the next Fmoc protected amino acid was coupled to the free amino group using O-(benzotriazol-1-yl)-N,N,N',N'-tetramethyluroniumhexafluorophosphate (HBTU) as the coupling reagent and diisopropylethylamine (DIEA) as catalysis reagent. The growth of the peptide chain was according to the established Fmoc SPPS protocol. After the last amino acid was coupled, excessive reagents were removed by a single DMF wash for 5 min (5 mL per gram of resin), followed by 5 times DCM wash for 2 min (5 mL per gram of resin). The peptide was cleaved using 95 % of trifluoroacetic acid (TFA) with 2.5 % of trimethylsilane (TMS) and 2.5 % of H_2O for 30 min. TFA was removed by rotary-evaporate process, then 20 mL per gram of resin of ice-cold diethylether was added. The resulting precipitate was centrifuged for 10 min at 4 ℃ at 10000 rpm. After the supernatant was decanted, the resulting solid was dissolved in DMSO for HPLC separation with MeOH containing 0.05 % of TFA and H_2O containing 5 % MeOH as eluents.

The synthesized compound was characterized by ^{1}H NMR (Bruker ARX-300) using DMSO-d_6 as the solvent. HR-MS was conducted at the Agilent 6520 Q-TOF LC/MS using ESI-L low-concentration tuning mix (lot no. LB60116 from the Agilent Tech).

FEFKFEFKGRGD: ^{1}H NMR (400 MHz, DMSO-d6) δ 8.56 (d, J = 7.7 Hz, 1H), 8.40 (s, 1H), 8.26-7.90 (m, 11H), 7.28-7.09 (m, 20H), 4.54 (dd, J = 11.3, 6.7 Hz, 3H), 4.40-4.18 (m, 6H), 4.10-3.98 (m, 1H), 3.83 -3.59 (m, 5H), 3.16-2.92 (m, 7H), 2.90-2.58 (m, 9H), 2.30-2.11 (m, 4H), 1.89-1.12 (m, 22H). MS: calc. M^+ = 1505.7, obsvd. $(M+1)^+$ = 1506.7, HR-MS: $(M+1)^+$ = 1506.7368.

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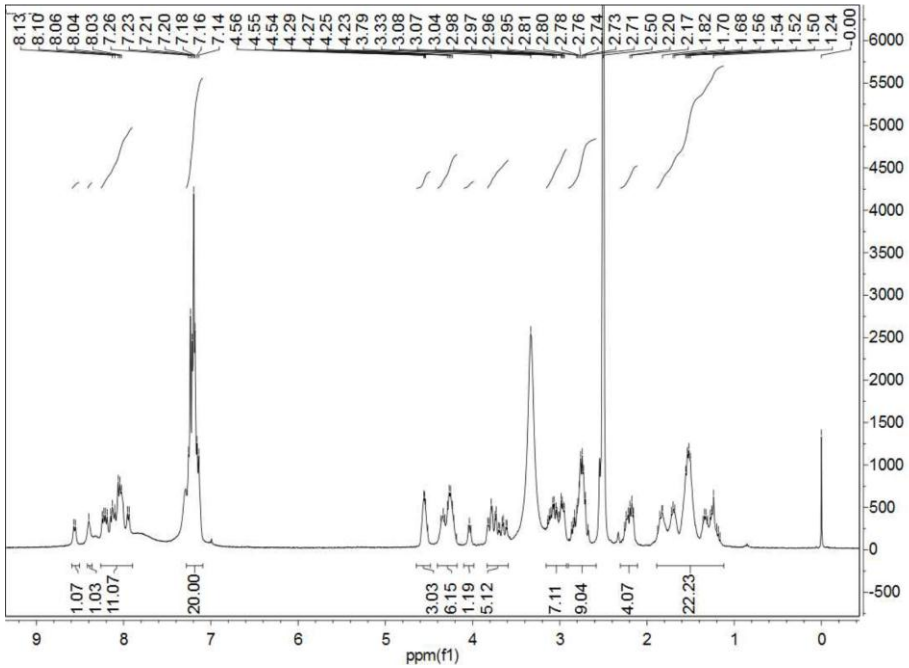

Figure S-1. ^{1}H NMR of FEFKFEFKGRGD

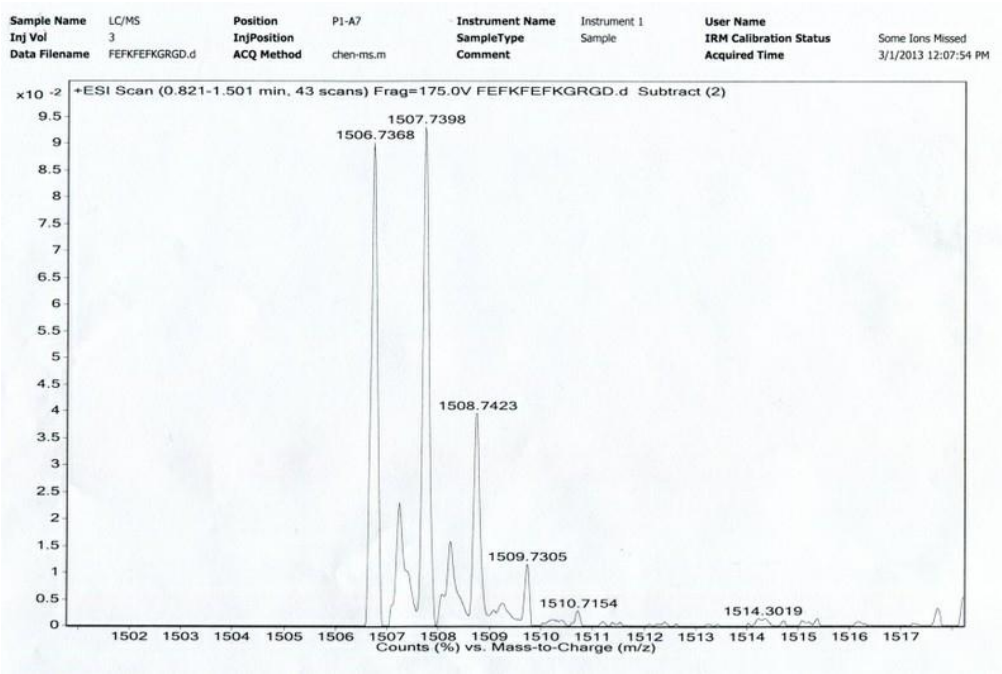

Figure S-2. HR-MS of FEFKFEFKGRGD

Rheology: Rheology test was carried out on an AR 2000ex (TA instrument) system, 40 mm parallel plate was used during the experiment at the gap of 500 μm. For the dynamic time sweep, the sample after mixing two solutions was directly transferred to the rheometer and it was performed at the frequency of 1 rad/s and the strain of 1 %. The gel was characterized for the dynamic frequency

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sweep in the frequency region of 0.1-100 rad/s at the strain of 1 %. For the dynamic strain sweep, it was characterized in the strain region of 0.1-10 % at the frequency of 1 rad/s.

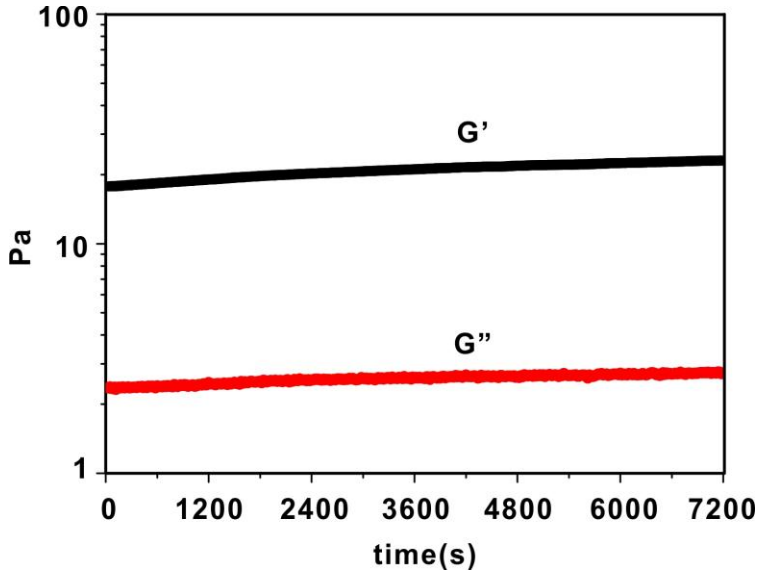

Figure S-3. Rheological measurement with the mode of dynamic time sweep at the frequency of 1 rad/s and strain of 1% for the gel of FEFKFEFKGRGD.

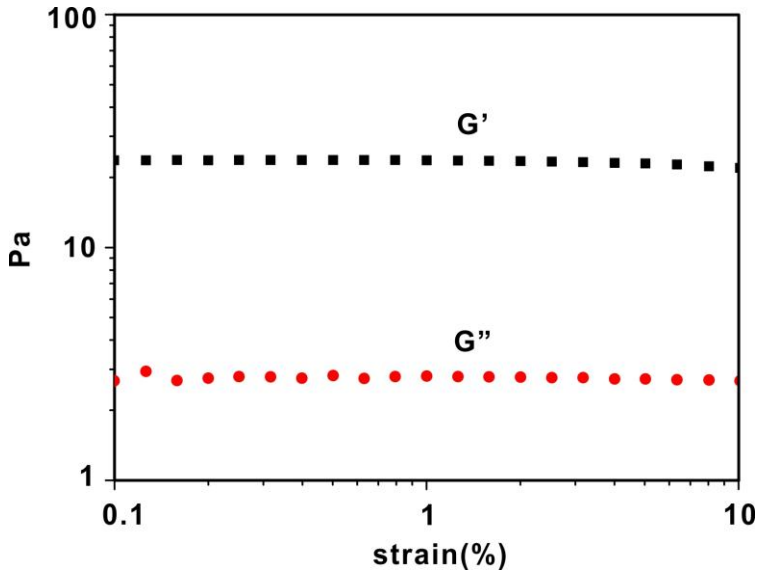

Figure S-4. Rheological measurements with the mode of dynamic strain sweep at the frequency of 1 rad/s for the gel of FEFKFEFKGRGD.

TEM and CD: Transmission electron microscopy (TEM) was manipulated to observe the micromorphology of the gel. The gel was fixed onto the copper grids, and then washed with distilled water 3 times. After being stained by uranyl acetate and dried overnight, gel morphology was observed in Jeol (JEM100CXII) electron microscope at 100 kV. Circular dichroism was measured on Bio-Logic MM450 system under a nitrogen atmosphere. Peptide solution (PBS buffer containing a little peptide) or

hydrogel was added to 0.1 mm quartz cuvette separately using PBS buffer as blank. CD data was collected with the wavelength ranged from 190 nm to 260 nm.

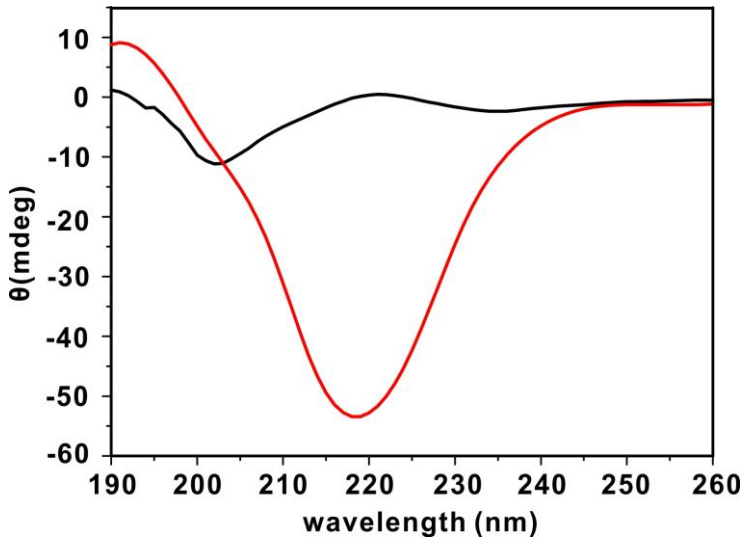

Figure S-5. Circular dichroism spectra of solution and gel condition of FEFKFEFKGRGD. (Black line: solution, red line: hydrogel)

Select: All None Selected:0

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Max ident	Accession
Delftia sp. JDC-3 16S ribosomal RNA gene, partial sequence	2439	2439	99%	0.0	99%	FJ378038.1
Delftia tsuruhatensis strain ARI_5 16S ribosomal RNA gene, partial sequence	2439	2439	99%	0.0	99%	AY684785.1
Delftia tsuruhatensis strain CI-23 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	KC178597.1
Uncultured Comamonadaceae bacterium clone EK_An354 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	JN038272.1
Uncultured Delftia sp. clone B210 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	JF833617.1
Delftia sp. MTQ3 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	HQ327477.1
Delftia sp. BN-HKY4 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	HQ731451.1
Uncultured Delftia sp. clone CHINA39 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	GU563748.1
Uncultured Delftia sp. gene for 16S rRNA, partial sequence, clone: DHUP23	2437	2437	99%	0.0	99%	AB451538.1
Delftia sp. KZ-OAIF2 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	FJ688376.1
Uncultured bacterium clone A5 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	FJ356016.1
Uncultured Delftia sp. clone GI5-002-F11 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	FJ193019.1
Uncultured Delftia sp. clone GI5-004-D05 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	FJ192633.1
Delftia lacustris strain 332 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	EU888308.1
Delftia sp. PRE5 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	EU880508.1
Delftia tsuruhatensis strain BM90 16S ribosomal RNA gene, partial sequence	2437	2437	99%	0.0	99%	EU779949.1

Figure S-6. Bacterium blast from NCBI according to the sequencing result.

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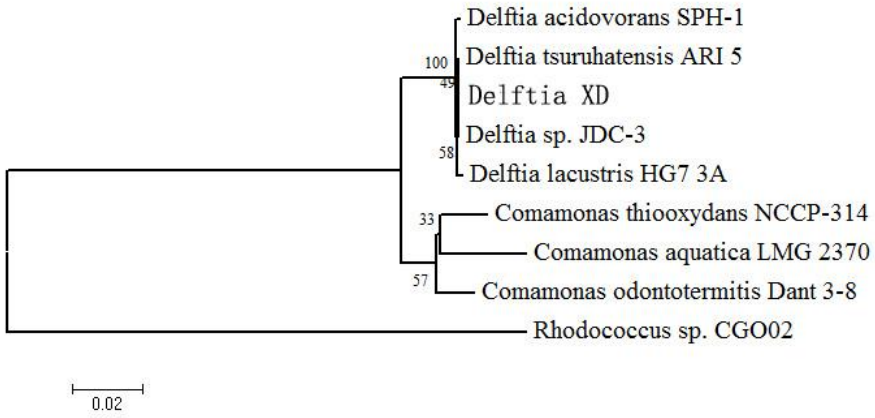

Fig. S-7. Evolutionary tree for the bacterium grew in the hydrogel. The target bacterium was named as *Delftia XD*. (Number means confidence and the length of horizontal line represents similar degree.)

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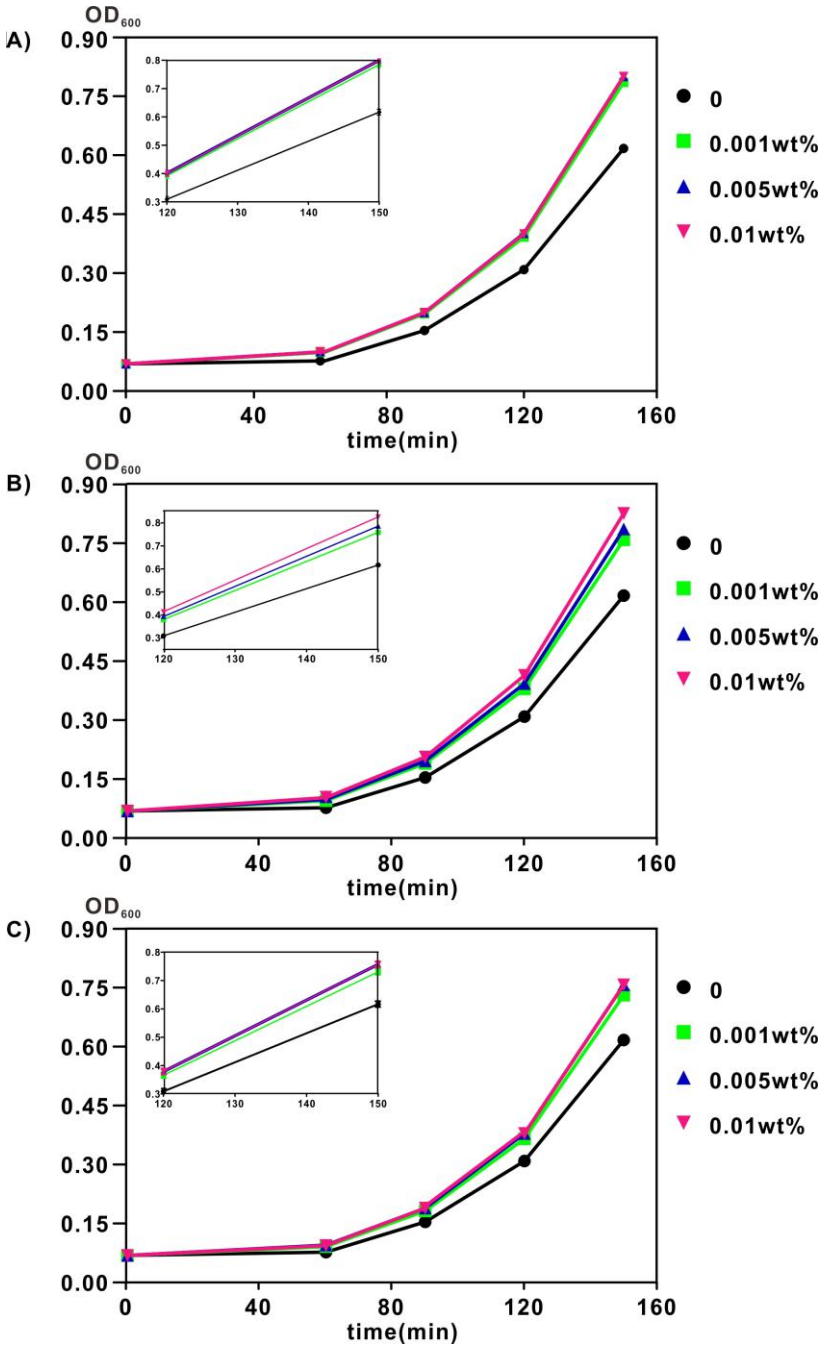

Figure S-8. Growth curve of the target bacterium cultured in LB medium with different concentrations of hydrogels or amino acid. (A: the hydrogel of FEFKFEFKGRGD, B: the hydrogel of FEFKFEFK, C: the amino acid phenylalanine. The illustration in each figure means magnification of time ranged from 120 min to 150 min.)

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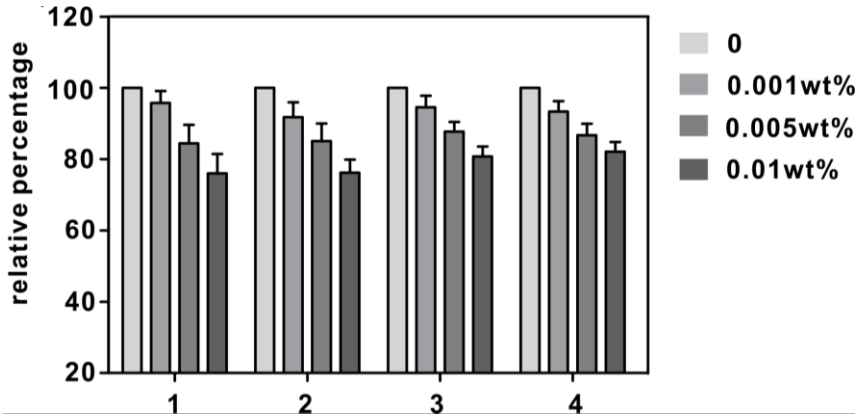

Fig. S-9 Effects of the hydrogel and amino acids on growth effect of *Escherichia coli* (1: FEFKFEFKGRGD, 2: FEFKFEFK, 3: F, 4: K. relative percentage was expressed as the mean ±standard deviation (SD, N = 3)).

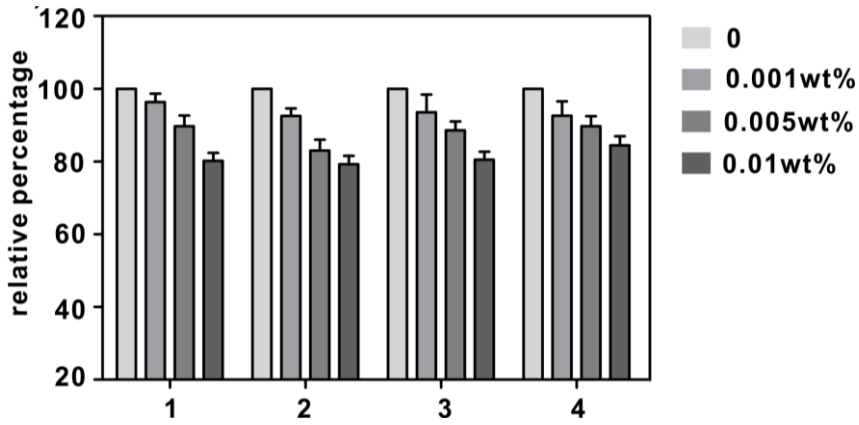

Fig. S-10 Effects of the hydrogel and amino acids on growth effect of *Bacillus subtilis* (1: FEFKFEFKGRGD, 2: FEFKFEFK, 3: F, 4: K. relative percentage was expressed as the mean ±standard deviation (SD, N = 3)).