Supplementary Information

Short peptide-directed synthesis of one-dimensional platinum nanostructures with controllable morphologies

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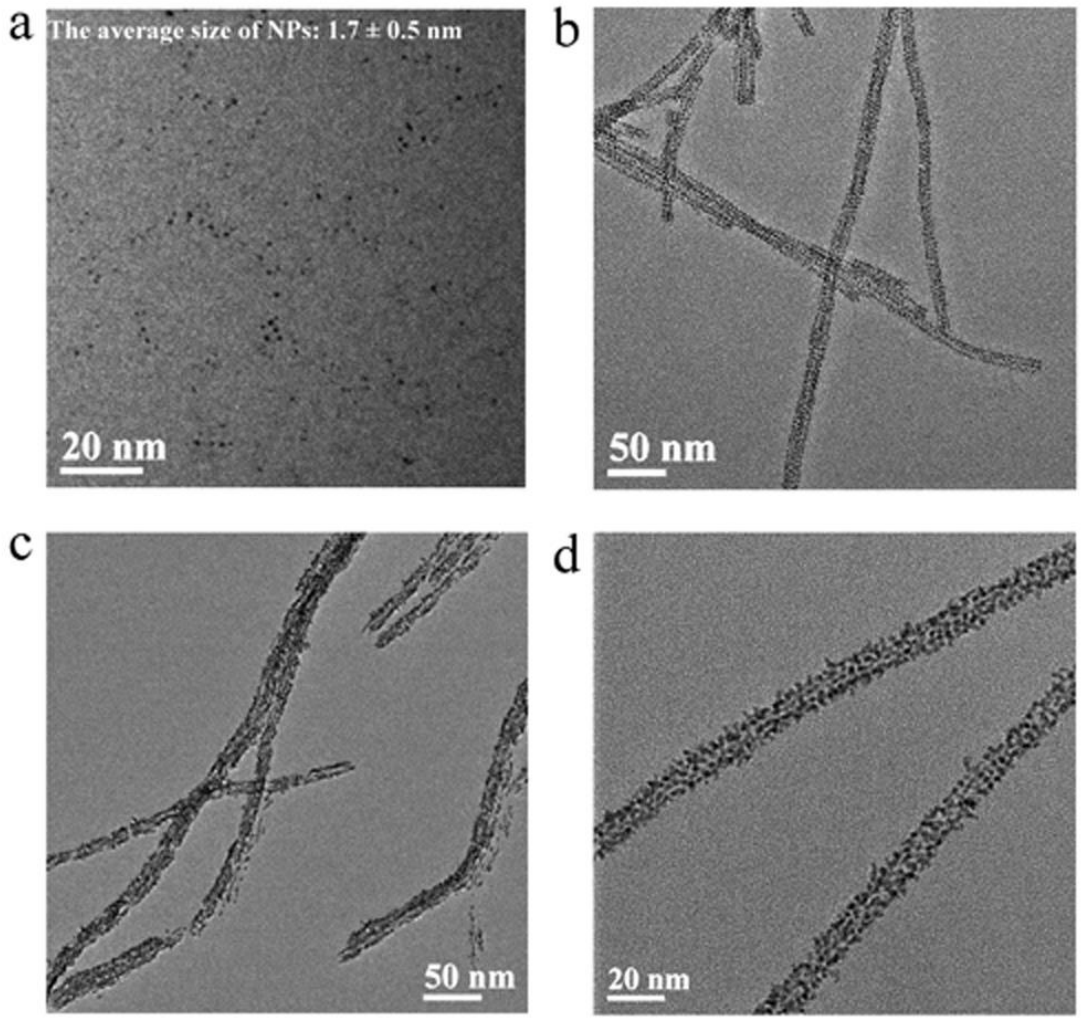
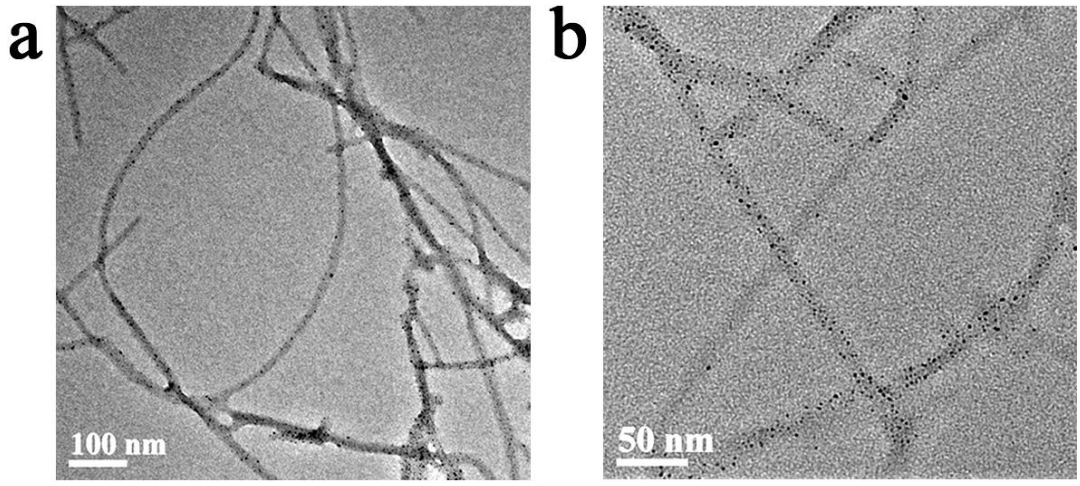
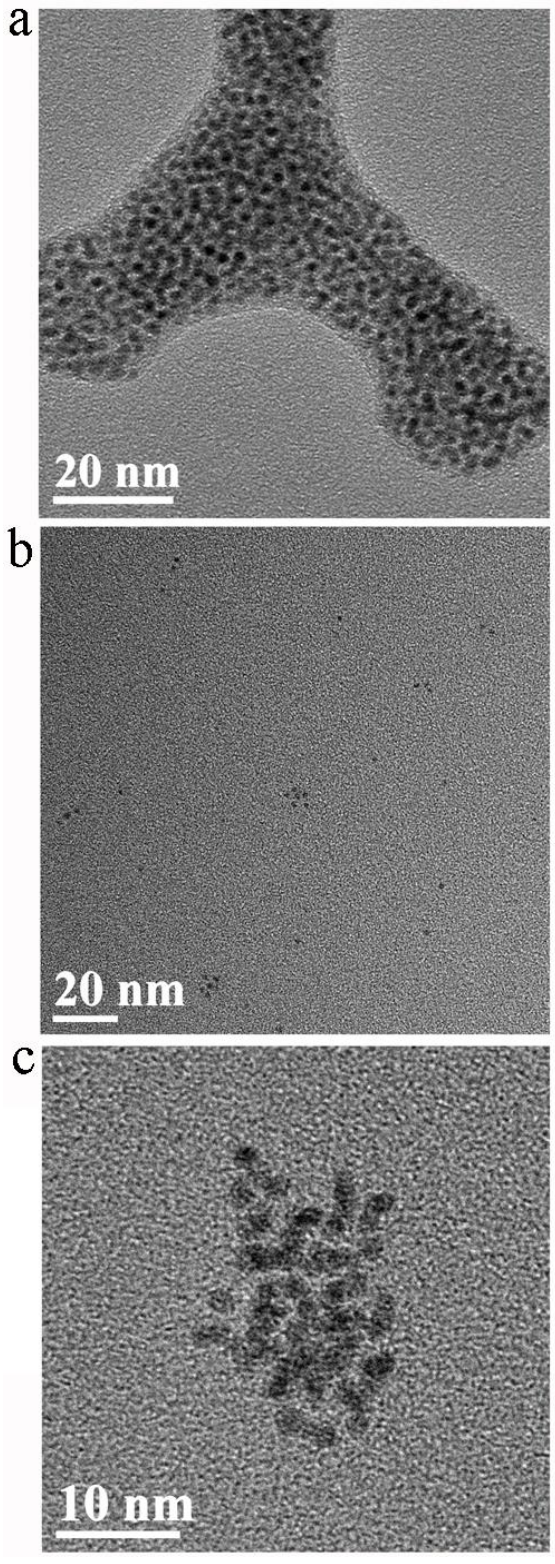


Supplementary Figure S1 TEM micrographs of Pt nanostructures. (**a**) Pt NPs taken after 24 h reaction in the presenc of 0.12 mM P7A. (**b**) 1D discrete Pt NP assemblies produced by reducing K_2PtCl_4 in the presence of 2 mM I_3K and 1 mM P7A after 24 hr reaction. (**c**) 1D continuous Pt NP assemblies produced by reducing K_2PtCl_4 in the presence of 2 mM I_3K but without P7A after 24 hr reaction. (**d**) 1D Pt NP assemblies produced by reducing K_2PtCl_4 in the presence of 2 mM I_3K and 0.24 mM P7A after 24 hr reaction.

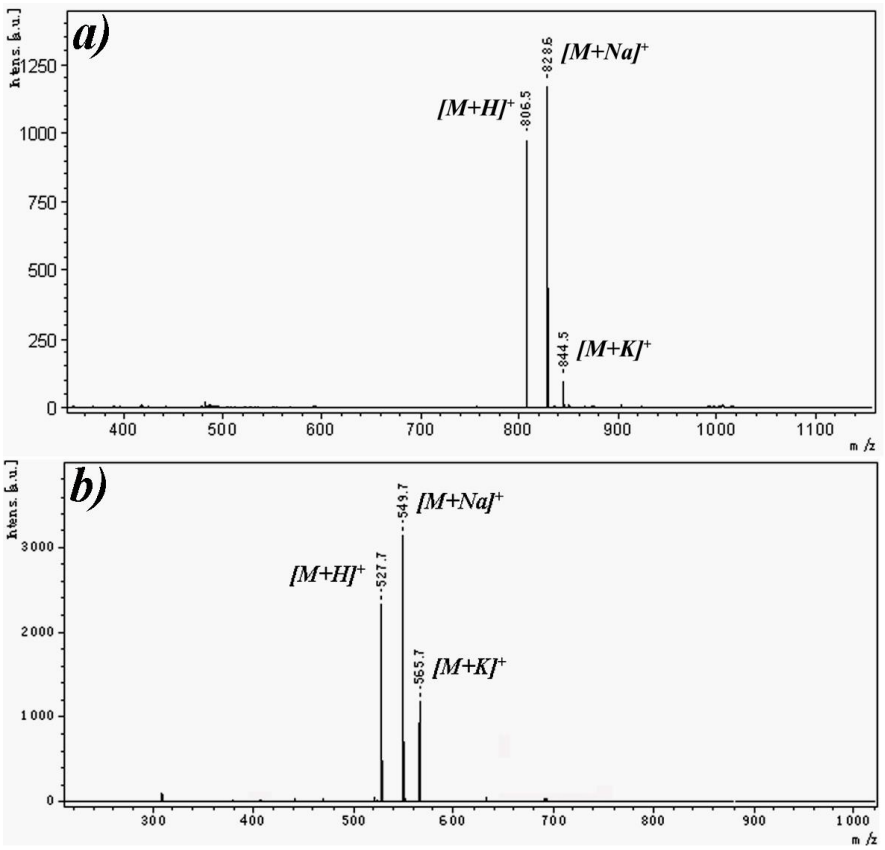


Supplementary Figure S2 1D Pt NP assemblies prepared through adding P7A stabilized Pt NPs into 2 mM I_3K solution. Note that the P7A stabilized Pt NPs were prepared in advance in the presence of 0.12 mM P7A.



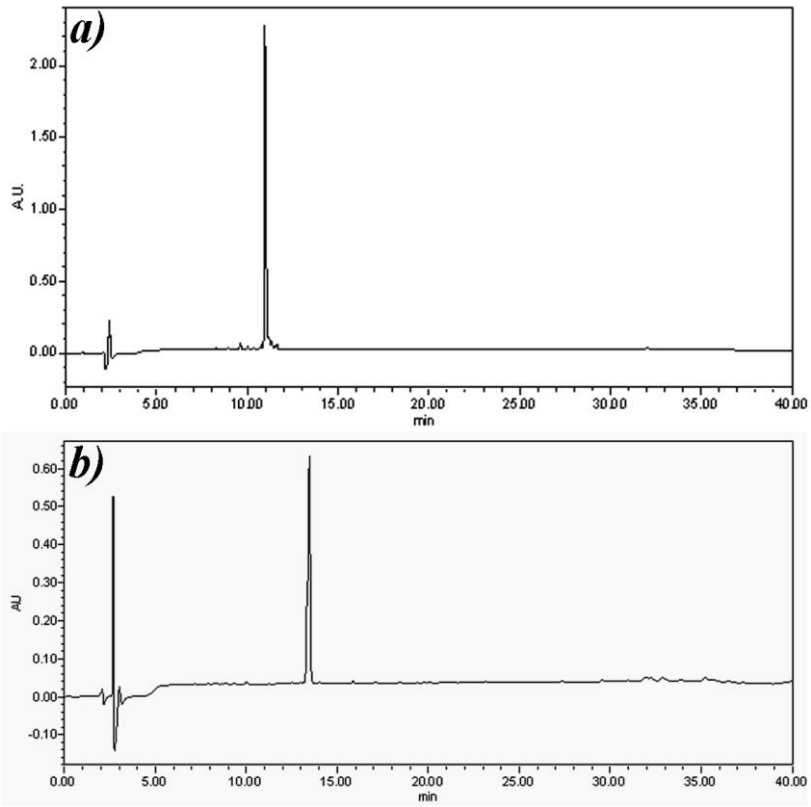
Supplementary Figure S3. TEM characterization of isolated Pt nanostructures at varying pH values. (**a**) P7A-stabilized Pt NPs (obtained after 24 hr) after the solution pH was adjusted from around 7 to 2. (**b**) The above P7A-stabilized Pt NPs after the

solution pH was reversed to 7. (**c**) Pt NPs produced with C-terminal capped P7A instead of P7A (obtained after 30 min).



Supplementary Figure S4 MALDI-ToF MS spectra of peptides. (**a**) P7A and (**b**) I_3K. Mass measurements were carried out on a Bruker Biflex III MALDI-ToF mass spectrometer equipped with a 337 nm nitrogen laser and 4-hydroxy-α-cyanocinnamic acid was used as the matrix. Peptides were dissolved with the matrix in the mixture of acetonitrile and water (1:1, v/v) which contained 1% TFA. About 0.5 μL of the sample solution was placed on a metal sample plate and then allowed to air-dry at ambient temperature. Mass spectra were acquired in positive linear mode with an acceleration voltage of 19 kV. External mass calibration was performed using a standard peptide mixture. Spectra were obtained by setting the laser power close to the threshold of ionization and generally 100 pulses were acquired and averaged. The calculated molecular masses for P7A and I_3K are all well consistent with the observed as follows:

P7A: expected masses $[M + H]^+$=806.9, $[M + Na]^+$=828.9, $[M + K]^+$=844.9; observed masses $[M + H]^+$=806.5, $[M + Na]^+$=828.6, $[M + K]^+$=844.5. I_3K: expected masses $[M + H]^+$=527.7, $[M + Na]^+$=549.7, $[M + K]^+$=565.7; observed masses $[M + H]^+$=527.7, $[M + Na]^+$=549.7, $[M + K]^+$=565.7.



Supplementary Figure S5 Reverse phase HPLC profiles of peptides. (**a**) P7A and (**b**) I_3K. Reversed phase HPLC analyses were performed on a Waters 2695 Alliance HPLC system at a temperature of 25 ^{o}C. Peptides were dissolved in acetonitrile/water (1:1, v/v) and filtered through a 0.22 μm filter, followed by injection into a C18 reversed phase column (4.6 mm × 150 mm). A gradient elution mode was employed: eluent A, 0.1% (v/v) TFA in water, 0→1 min, 95% A, 1→40 min, 95%→5% A, 40→45 min, 5%→95% A; eluent B, 0.1%(v/v) TFA in acetonitrile, 0→1 min, 5%, 1→40 min, 5%→95%, 40→45 min, 95%→5%. Other analytical conditions were as follows: monitoring wavelength at 214 nm; flowing rate of 1.0 ml/min.