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Supplementary Information

Self-assembling and cellular distribution of a series of transformable peptides

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‡ Equal contribution.

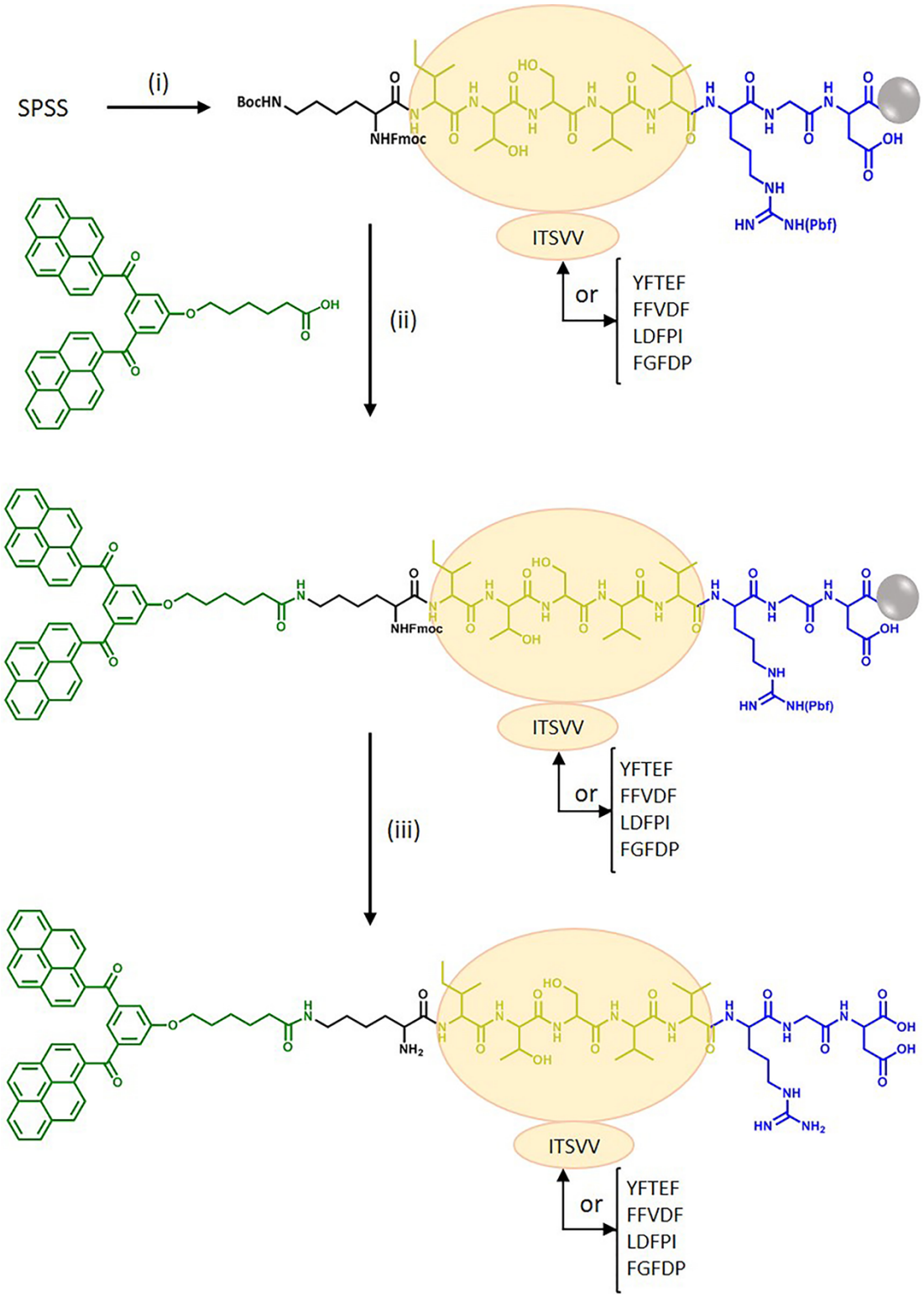

Figure S1. Synthetic route of TP1, 2, 3, 4 and 5 (i) 2% DBU, DMF; Fmoc solid-phase peptide synthesis method: NMM, N-HBTU, DMF ; (ii) BP-COOH, NMM, HBTU, DMF; (iii) TFA/TIS/H_2O (v/v/v = 95:2.5:2.5), 3 h, ice bath.

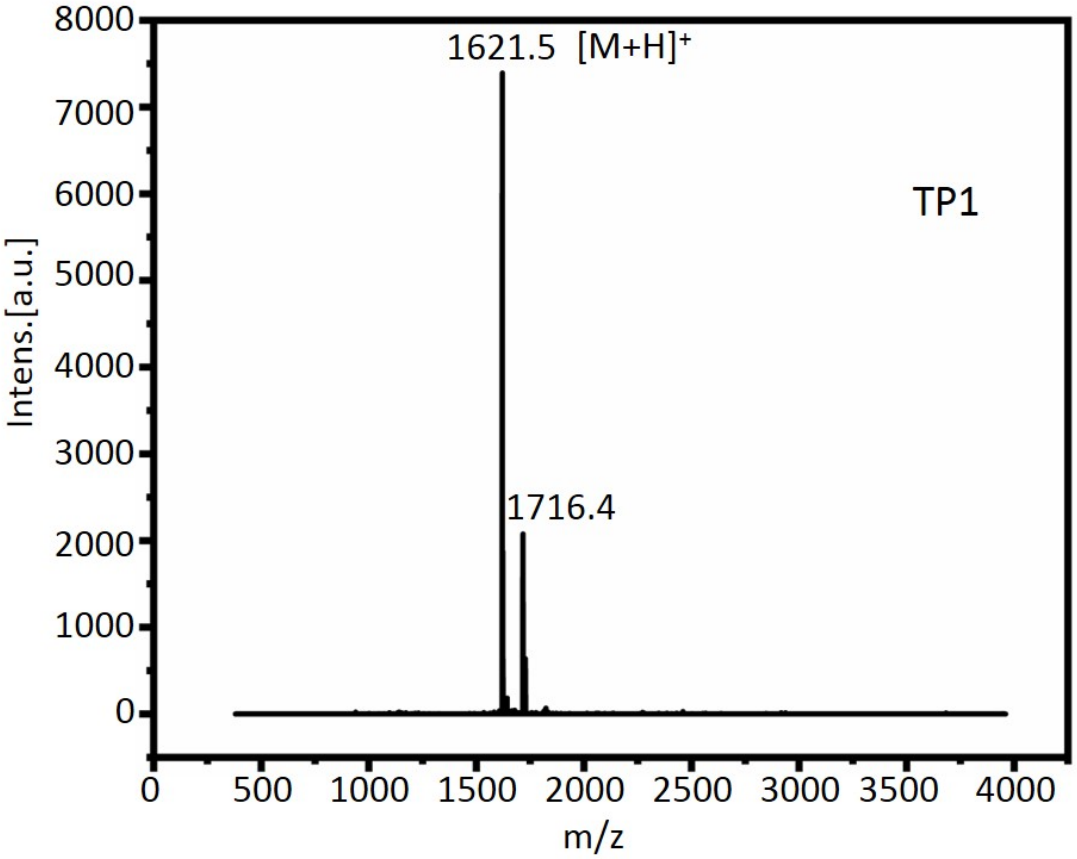

Figure S2. MALDI-TOF mass spectrum of TP1.

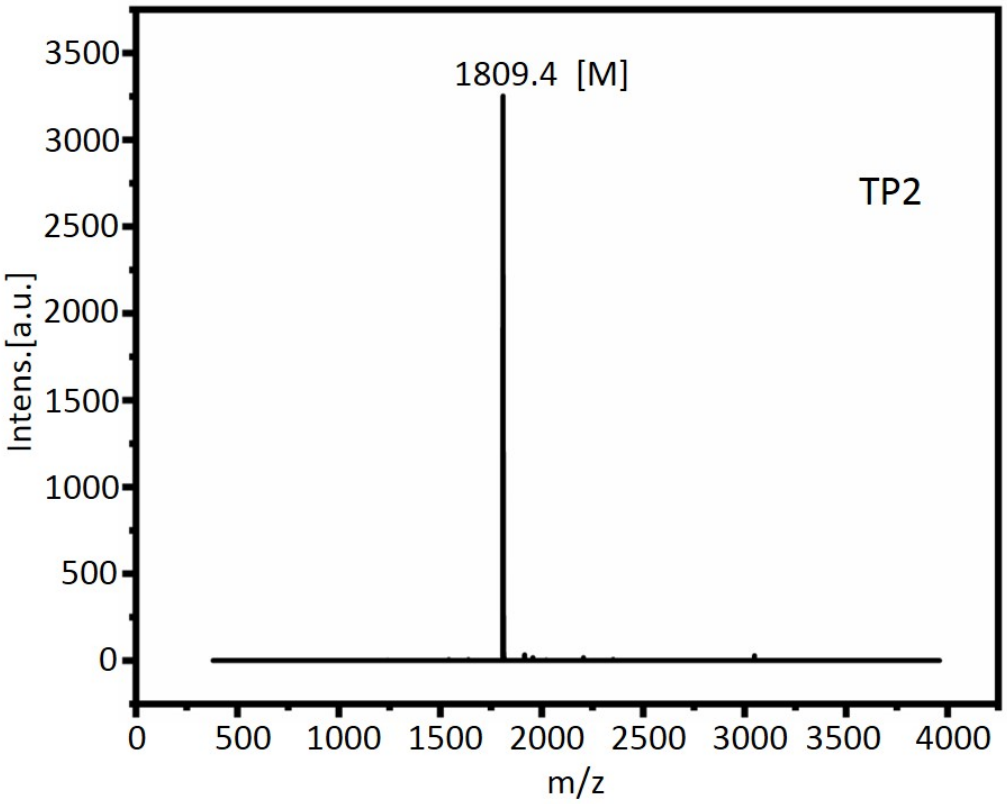

Figure S3. MALDI-TOF mass spectrum of TP2.

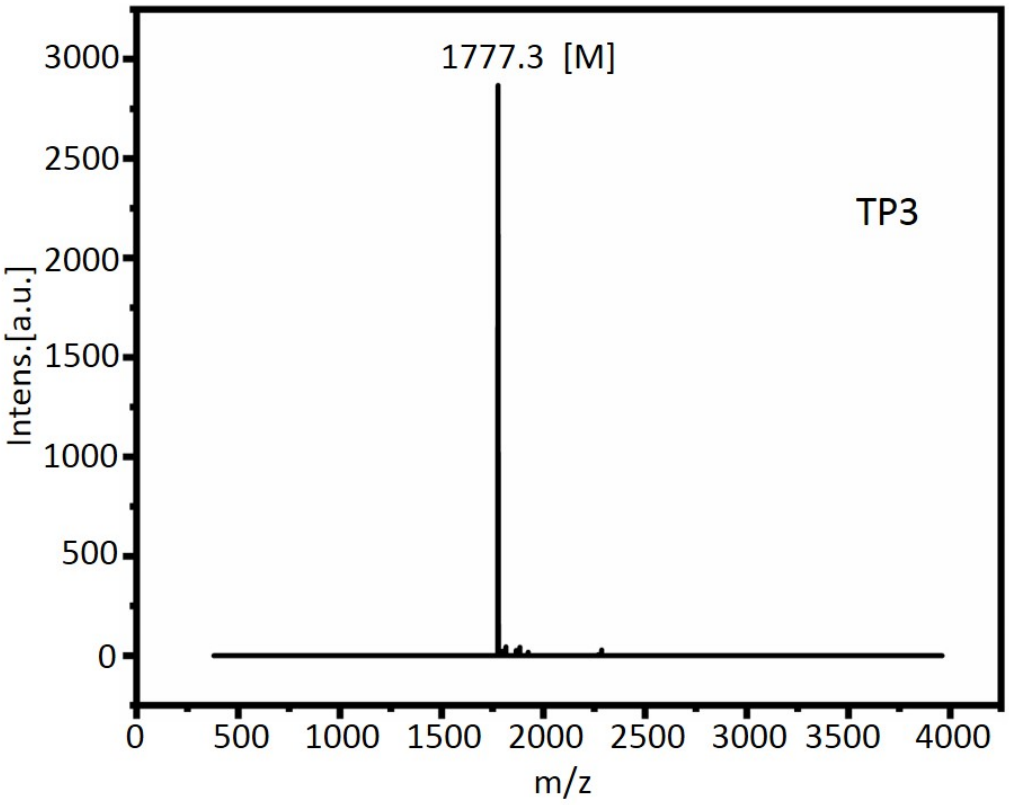

Figure S4. MALDI-TOF mass spectrum of TP3.

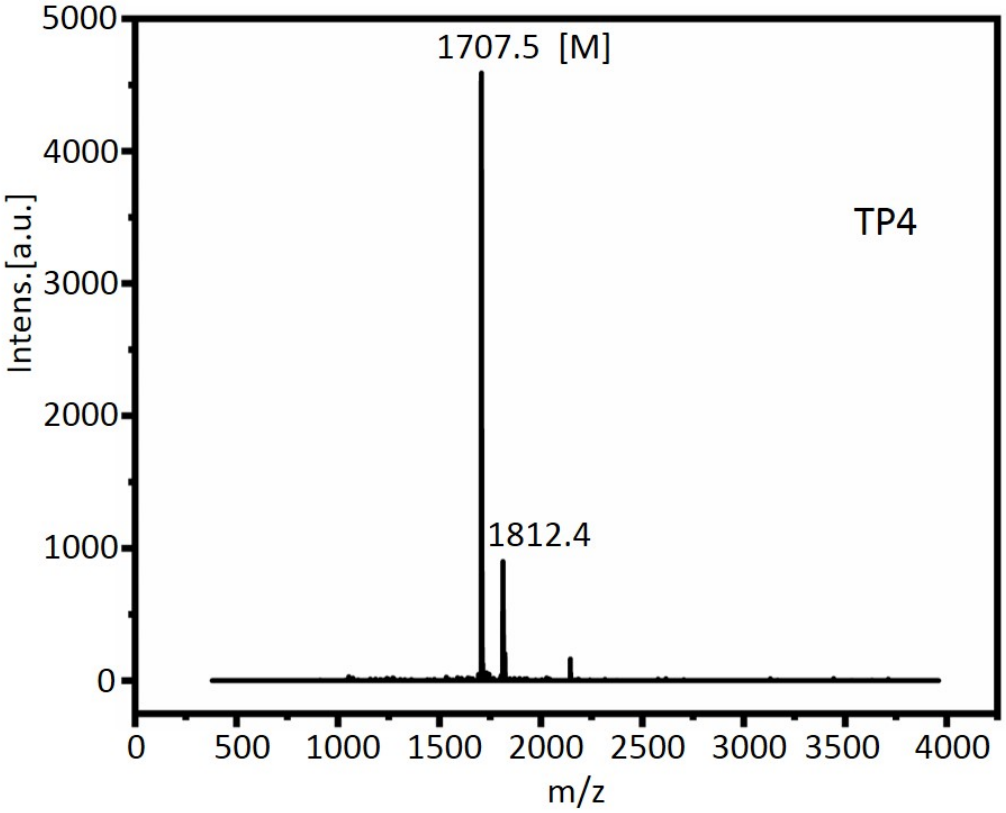

Figure S5. MALDI-TOF mass spectrum of TP4**.**

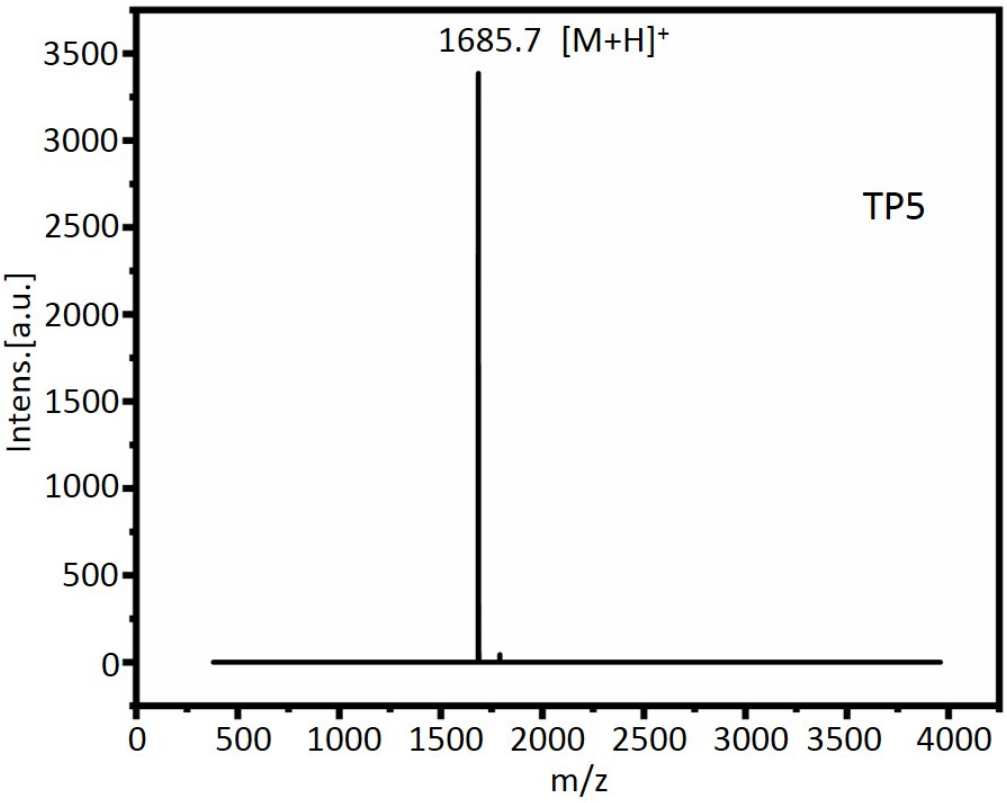

Figure S6. MALDI-TOF mass spectrum of TP5.

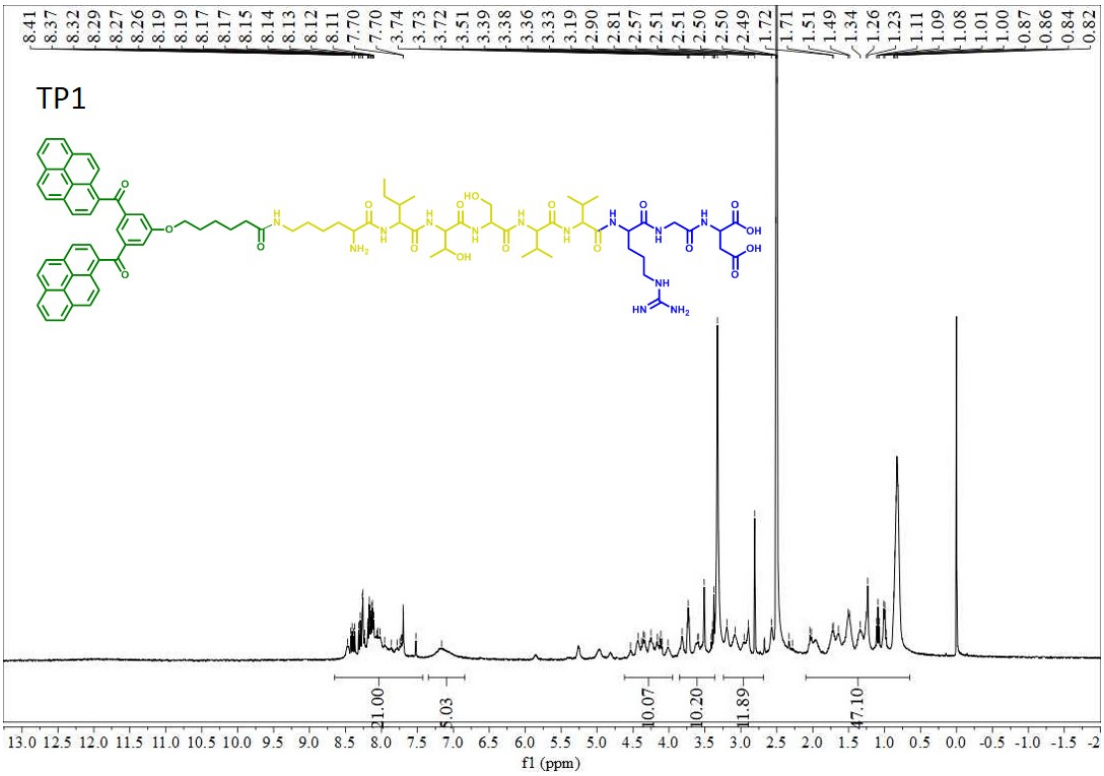

Figure S7. ^{1}H NMR spectrum of TP1.

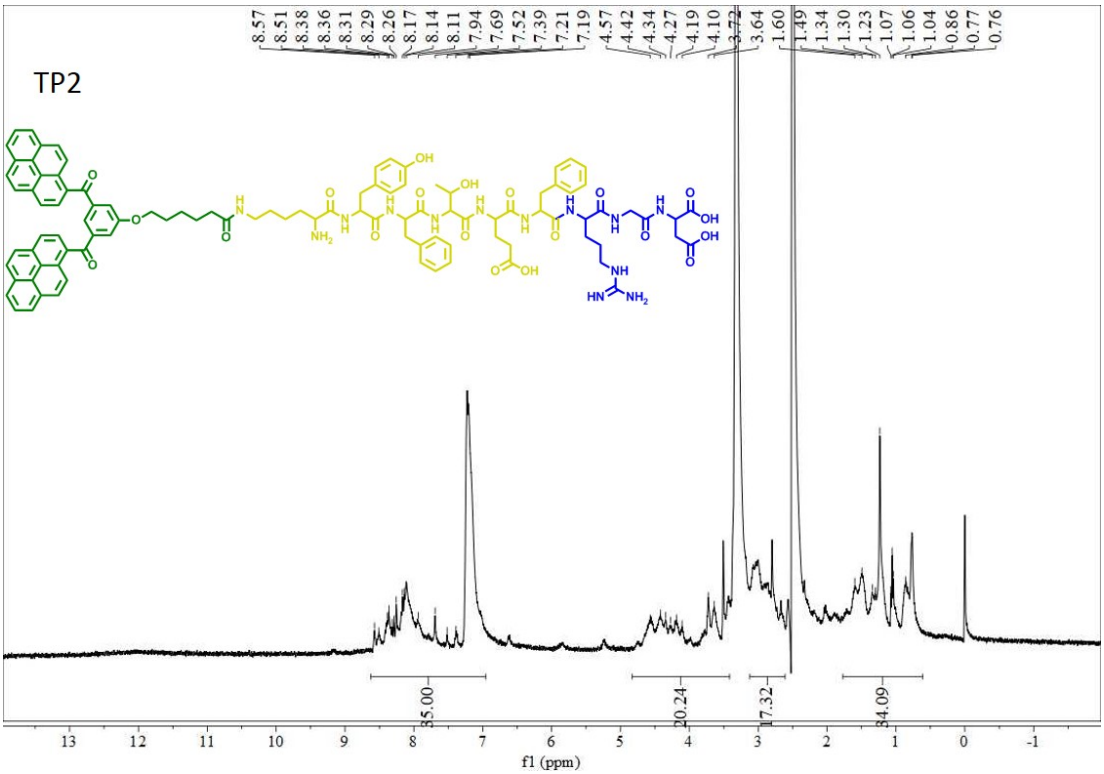

Figure S8. ^{1}H NMR spectrum of TP2.

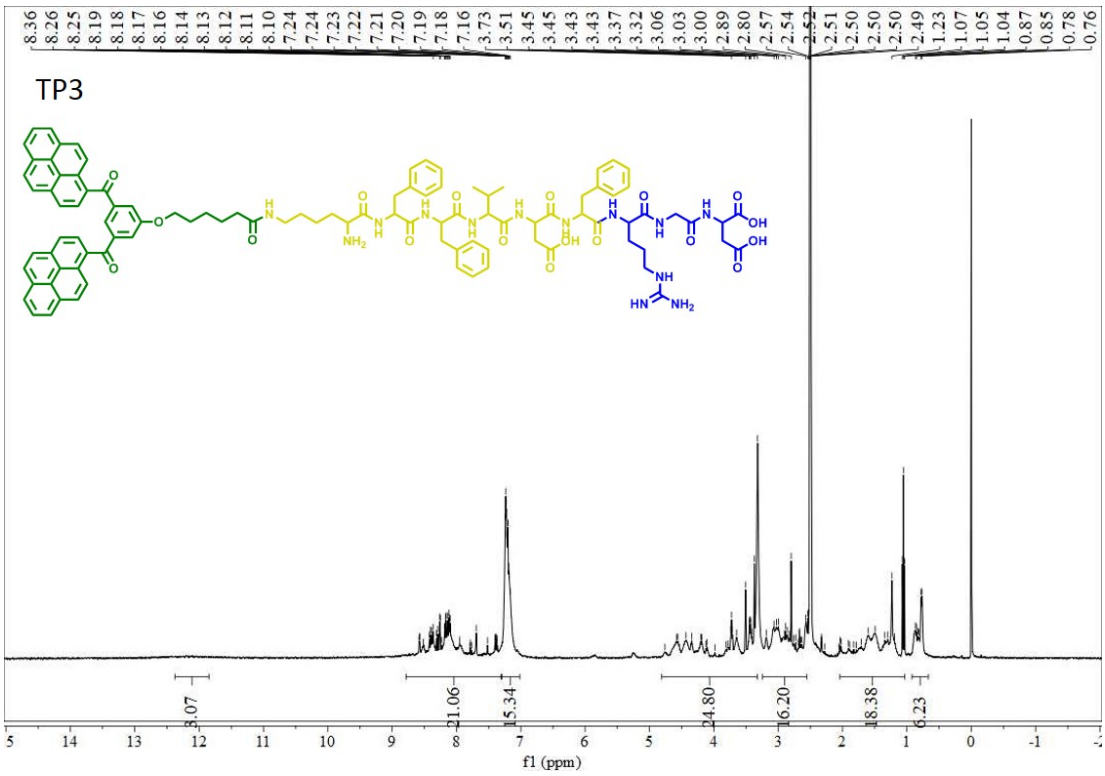

Figure S9. ^{1}H NMR spectrum of TP3.

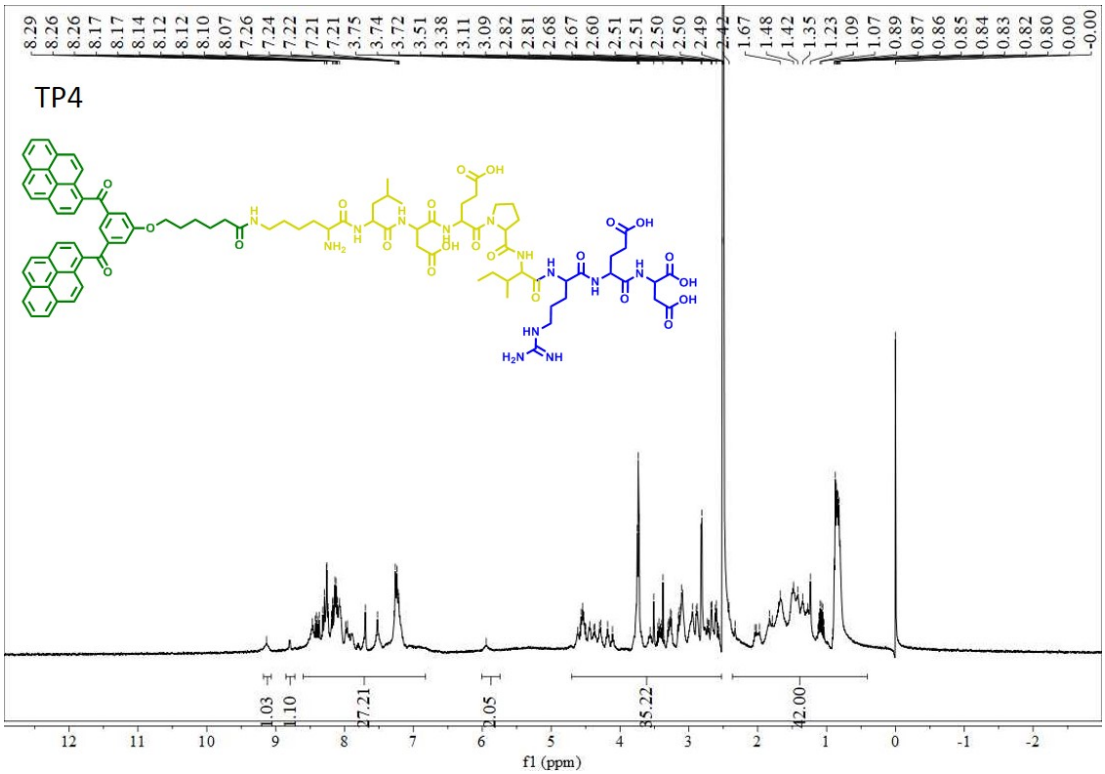

Figure S10. ^{1}H NMR spectrum of TP4.

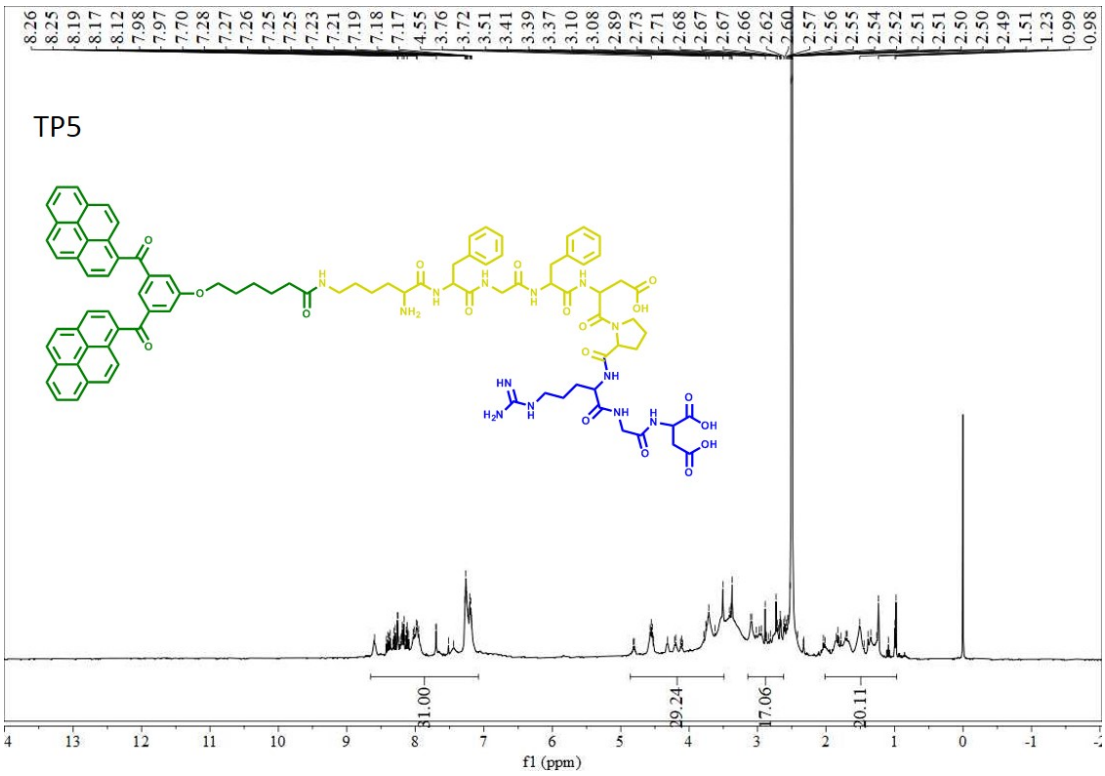

Figure S11. ^{1}H NMR spectrum of TP5.

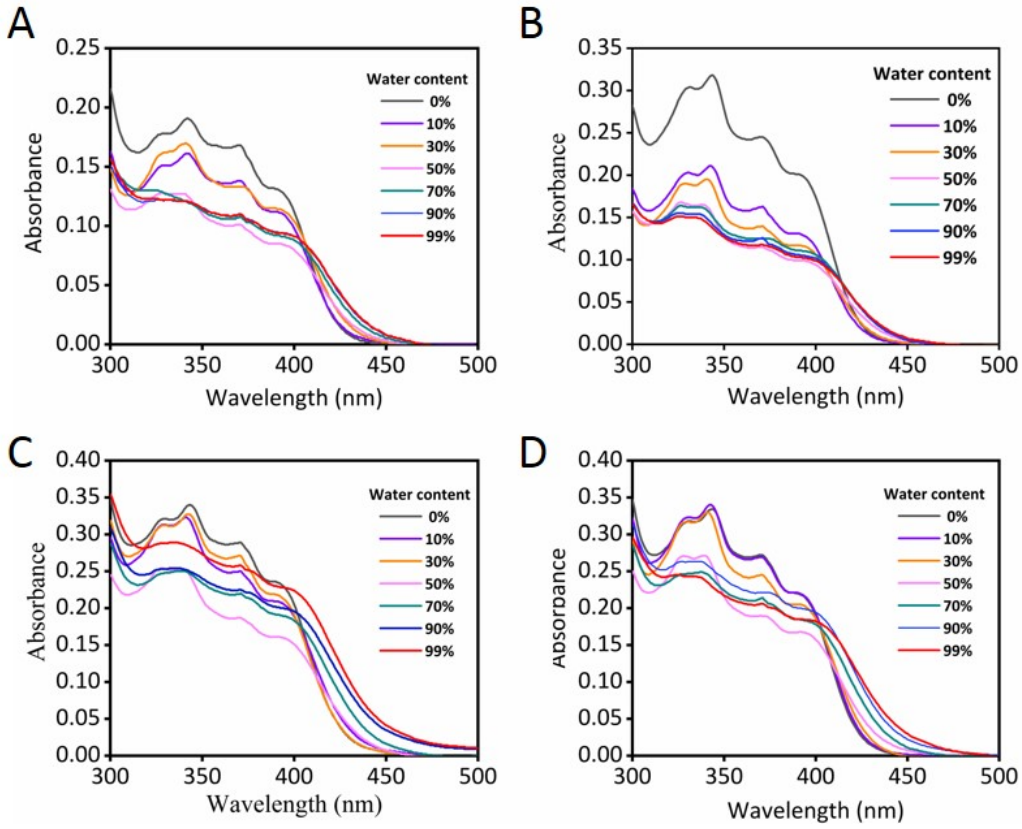

Figure S12. UV-vis characteristics spectra of self-assembly process to form (A) TP2, (B) TP3, (C) TP4 and (D) TP5 nanoparticles or nanosheets in mixed H_2O/DMSO solutions

(c = 3.0 × 10 $^{-5}$ M).

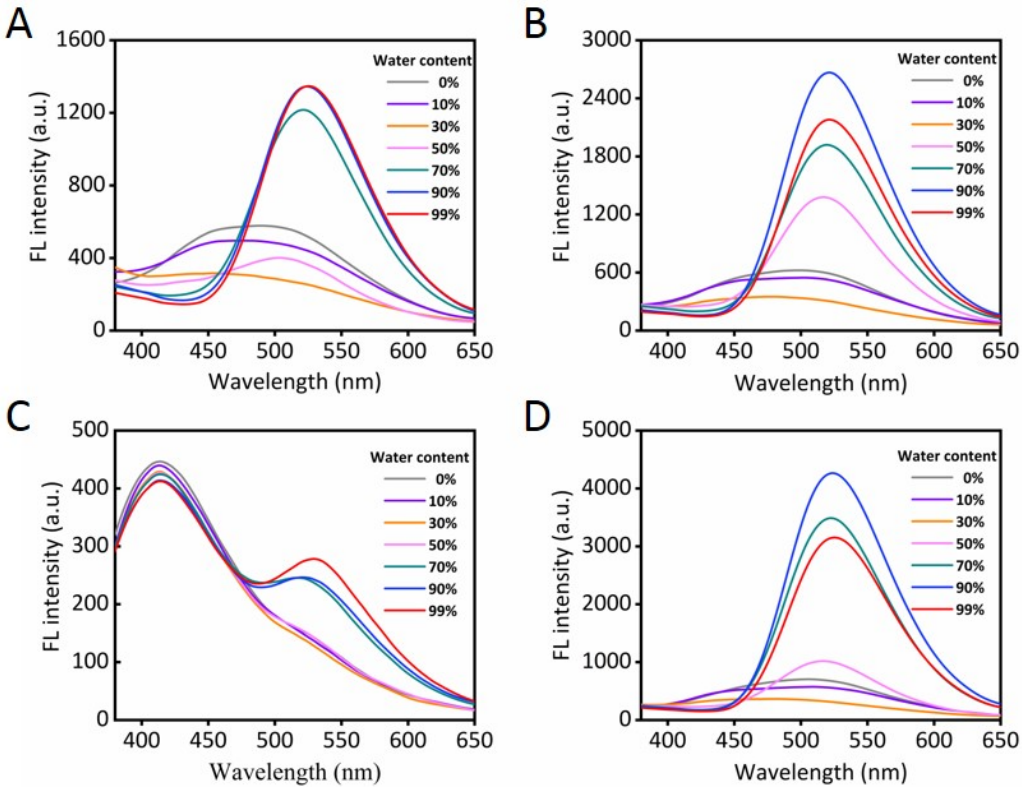

Figure S13. Fluorescence characteristics spectra of self-assembly process to form (A) TP2, (B) TP3, (C) TP4 and (D) TP5 nanoparticles or nanosheets in mixed H_2O/DMSO solutions (c = 3.0 × 10 $^{-5}$ M).

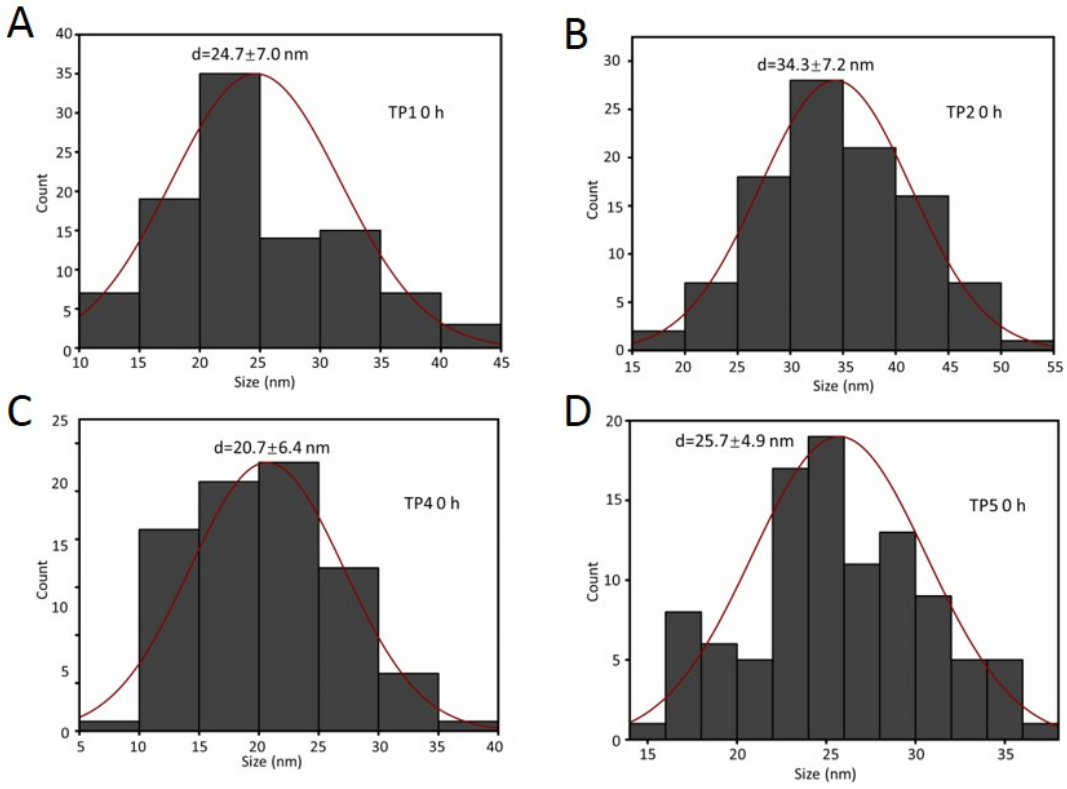

Figure S14. The size distribution of TP1, TP2, TP4 and TP5 nanoparticles at 0 h from TEM images.

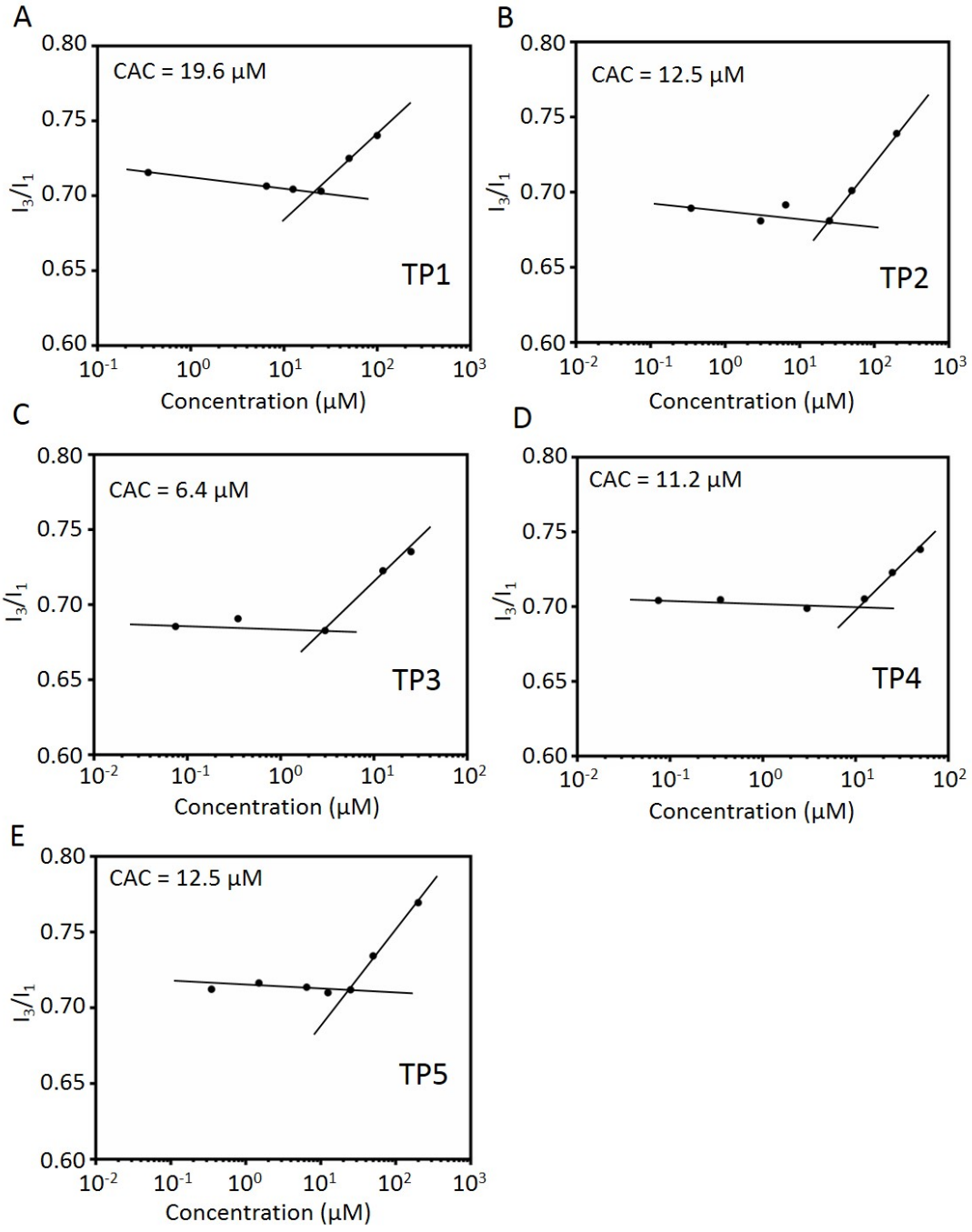

Figure S15. CAC values of TPs that measured by the pyrene fluorescence method.

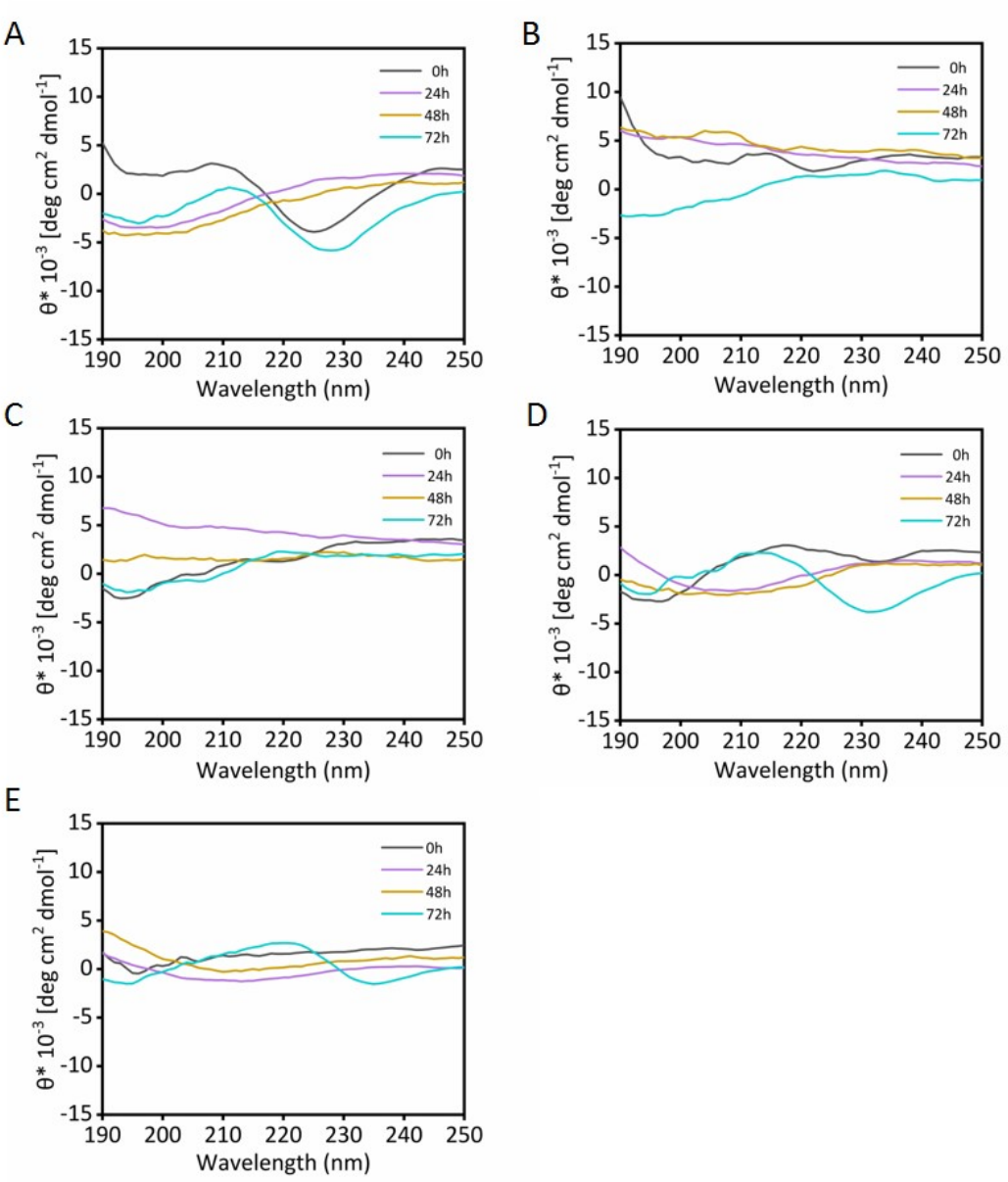

Figure S16. CD of (A) TP1, (B) TP2, (C) TP3, (D) TP4 and (E) TP5 nanoaggregates structural evolution in the presence of Ca^{2+} ions in aqueous solutions ($c = 3.0 \times 10^{-5}$ M) in 72 h.

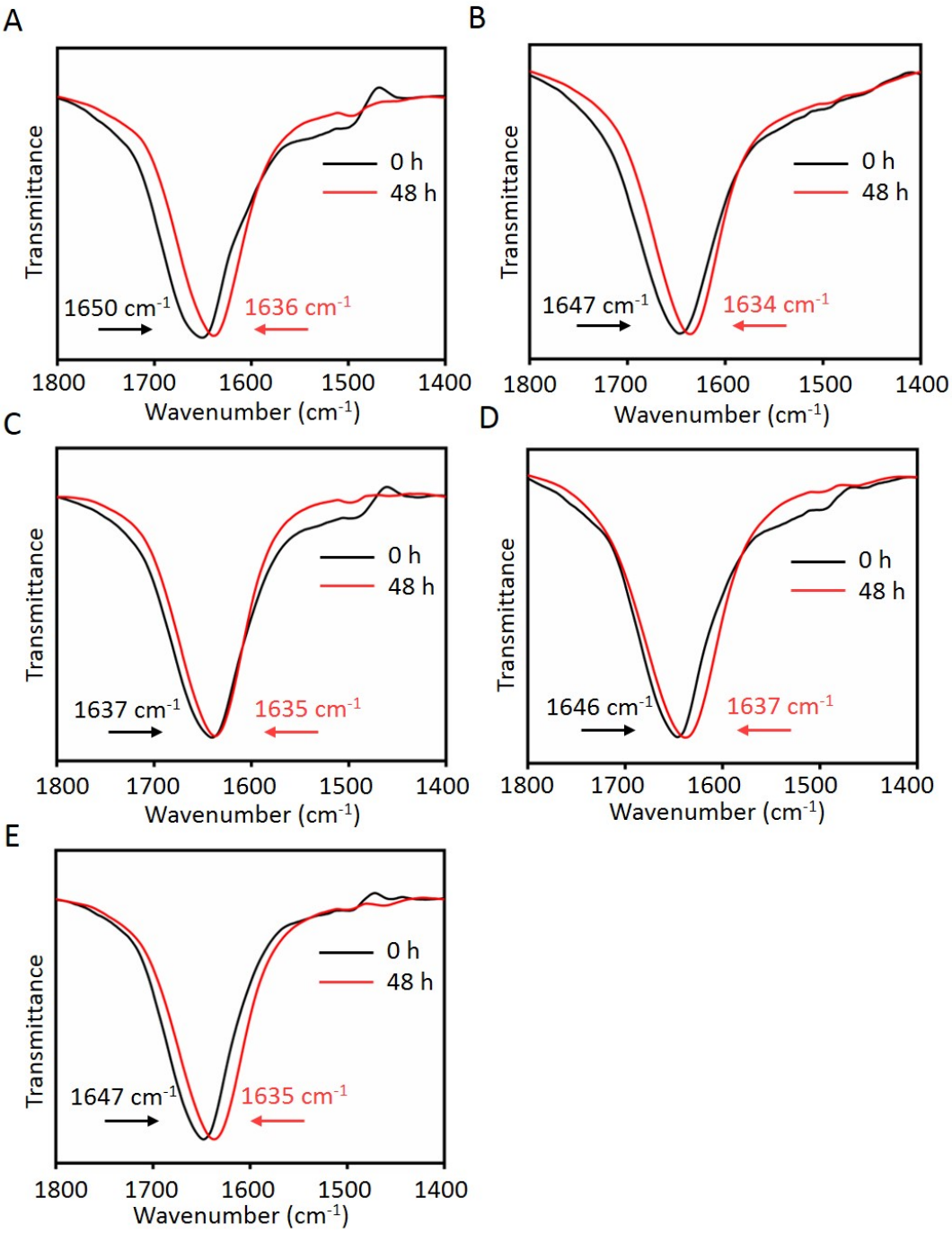

Figure S17. Fourier transform infrared spectra of TPs, (A) TP1, (B) TP2, (C) TP3, (D) TP4 and (E) TP5, at 0 h and 48 h.

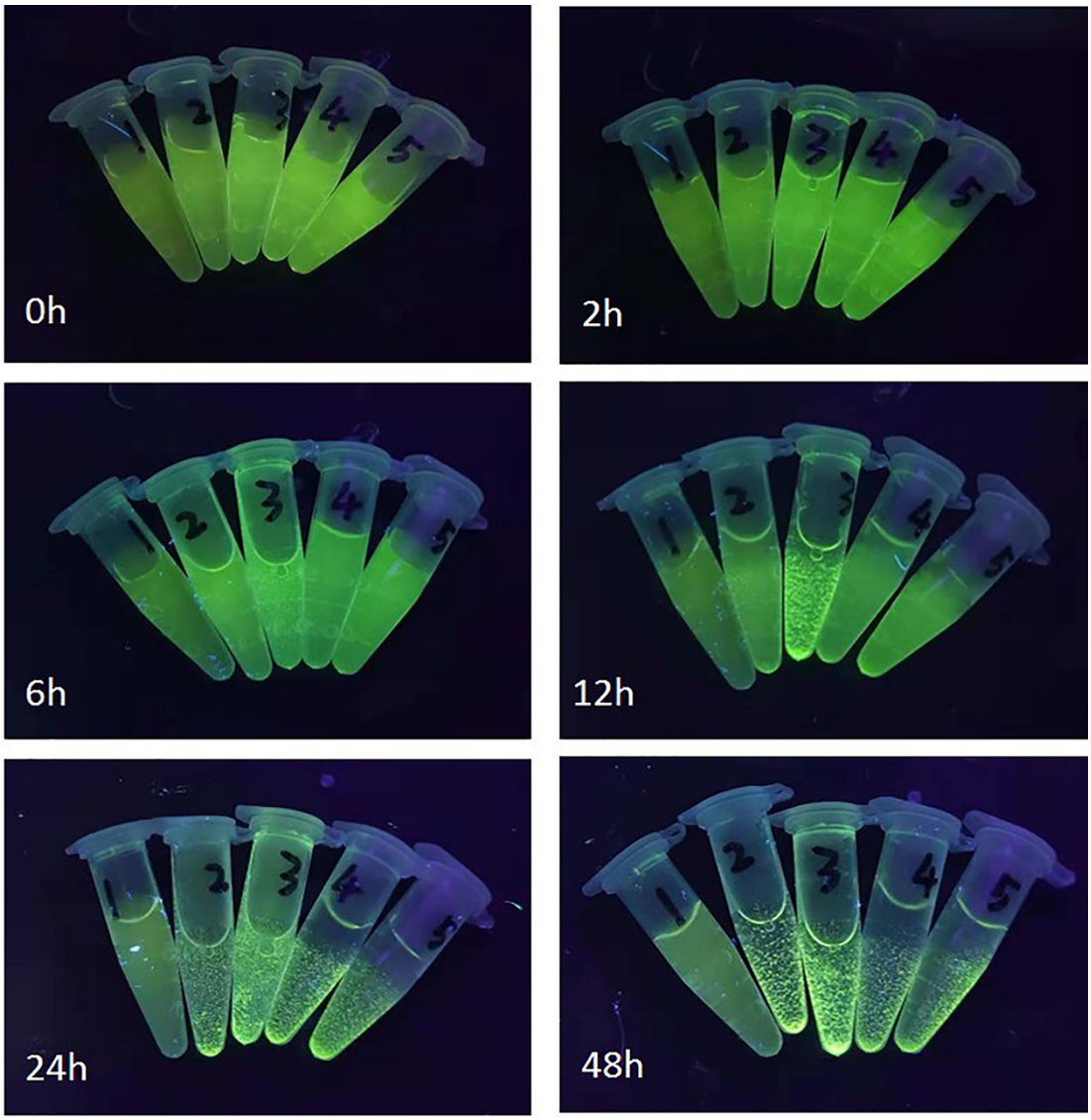

Figure S18. Time-dependent aggregation state of the TP1-5 from left (1) to right (5) in mixed H_2O/DMSO solutions (c = 3.0 × 10^{-5} M) at 0, 2, 6, 12, 24, 48 h observed under the 365 nm UV lamp.

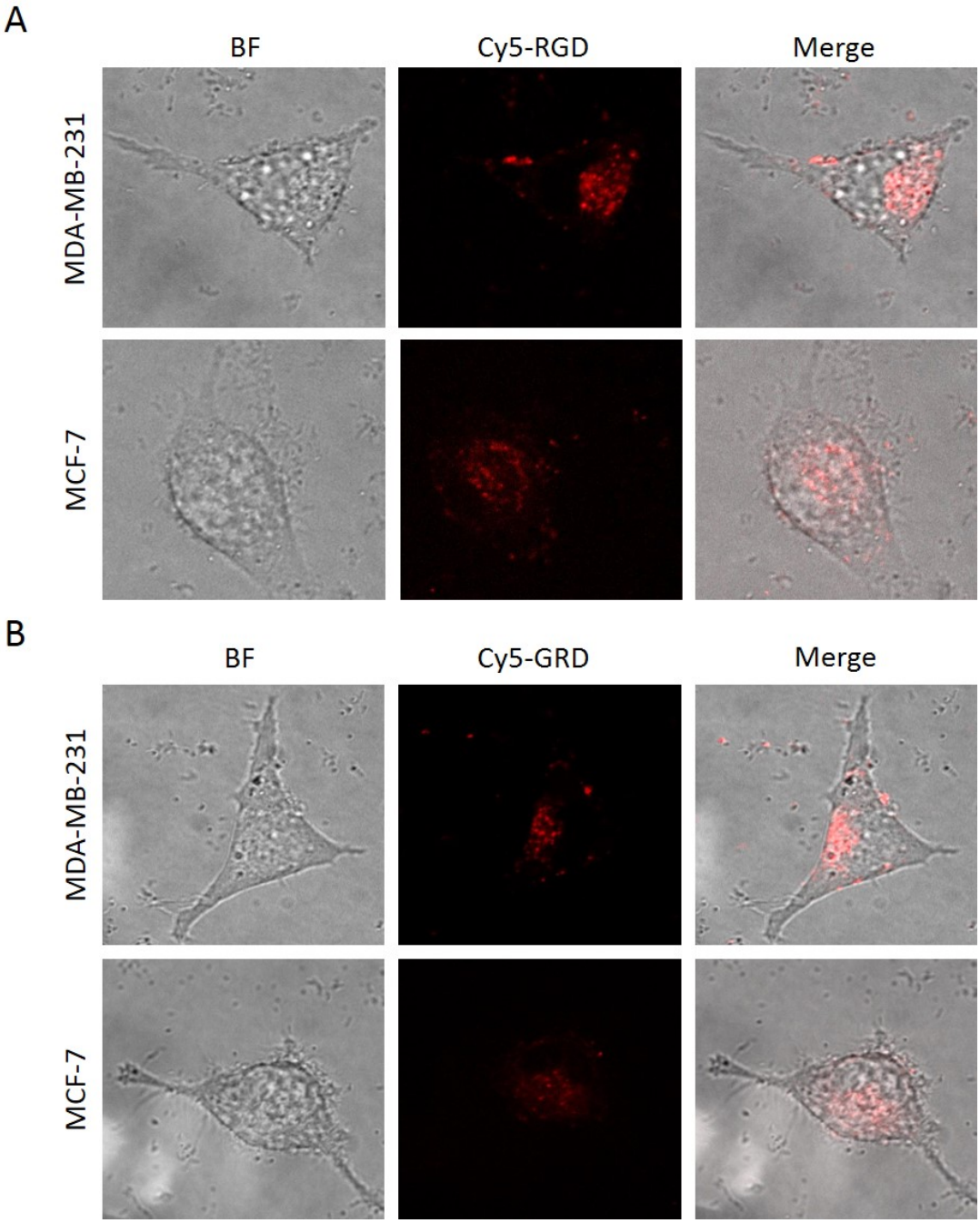

Figure S19. The targeting peptide RGD and the scrambled sequence GRD were prepared with a fluorescent dye Cy5 label. Cy5-RGD and Cy5-GRD cultured with MDA-MB-231 and MCF-7 cells for 1 h, respectively. It was found that the peptides were internalized into cells.

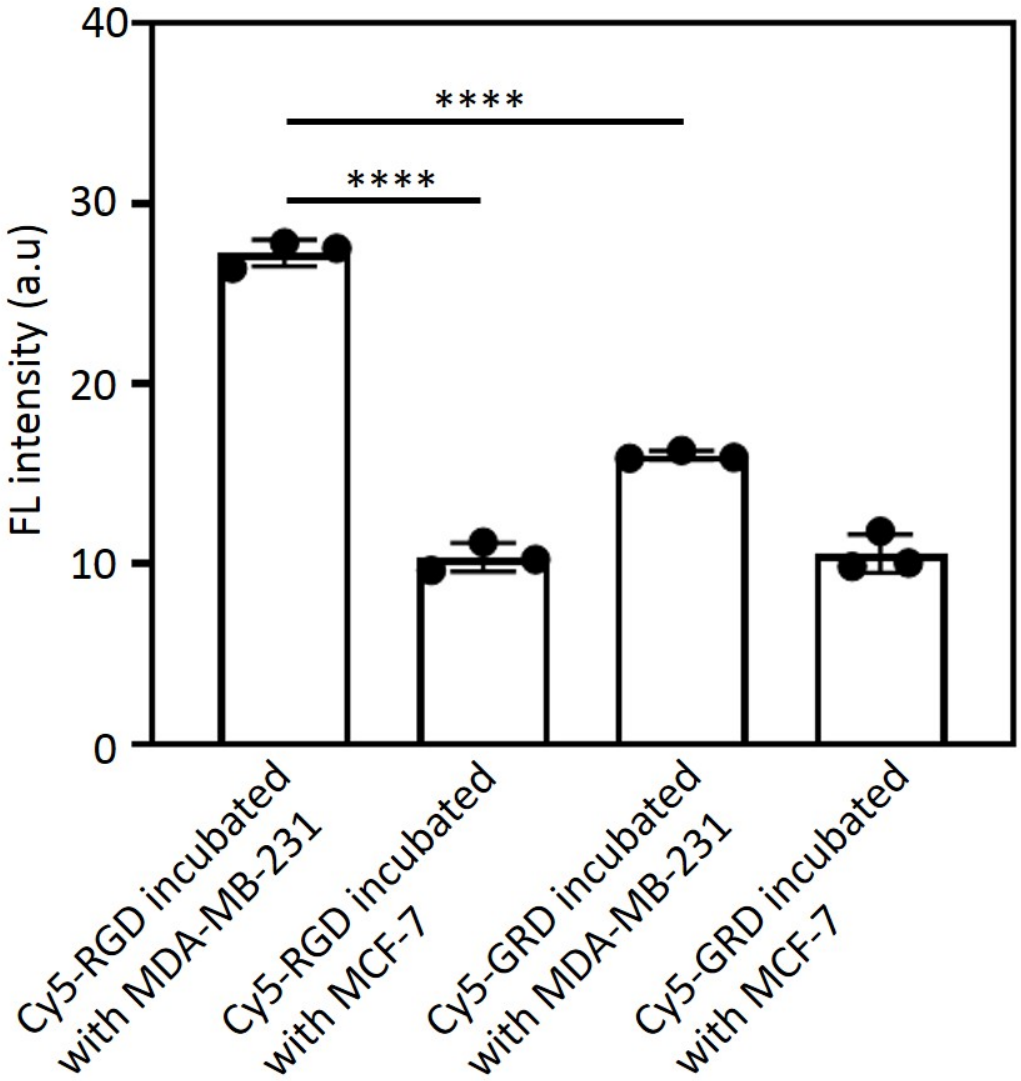

Figure S20. The quantitative analysis of fluorescence intensity of intracellular Cy5-RGD and Cy5-GRD. The results indicated that the uptake of RGD by MDA-MB-231 cells was higher than that by MCF-7 cells, suggesting that the expression of integrin on MDA-MB-231 cells was higher than that on MCF-7 cells. In addition, the Cy5-RGD treated MDA-MB-231 cells with high integrin expression showed higher fluorescence intensity than Cy5-GRD treatment, suggesting that RGD had target selectivity for MDA-MB-231 cells with high integrin expression over MCF-7 cells with low expression of integrin.

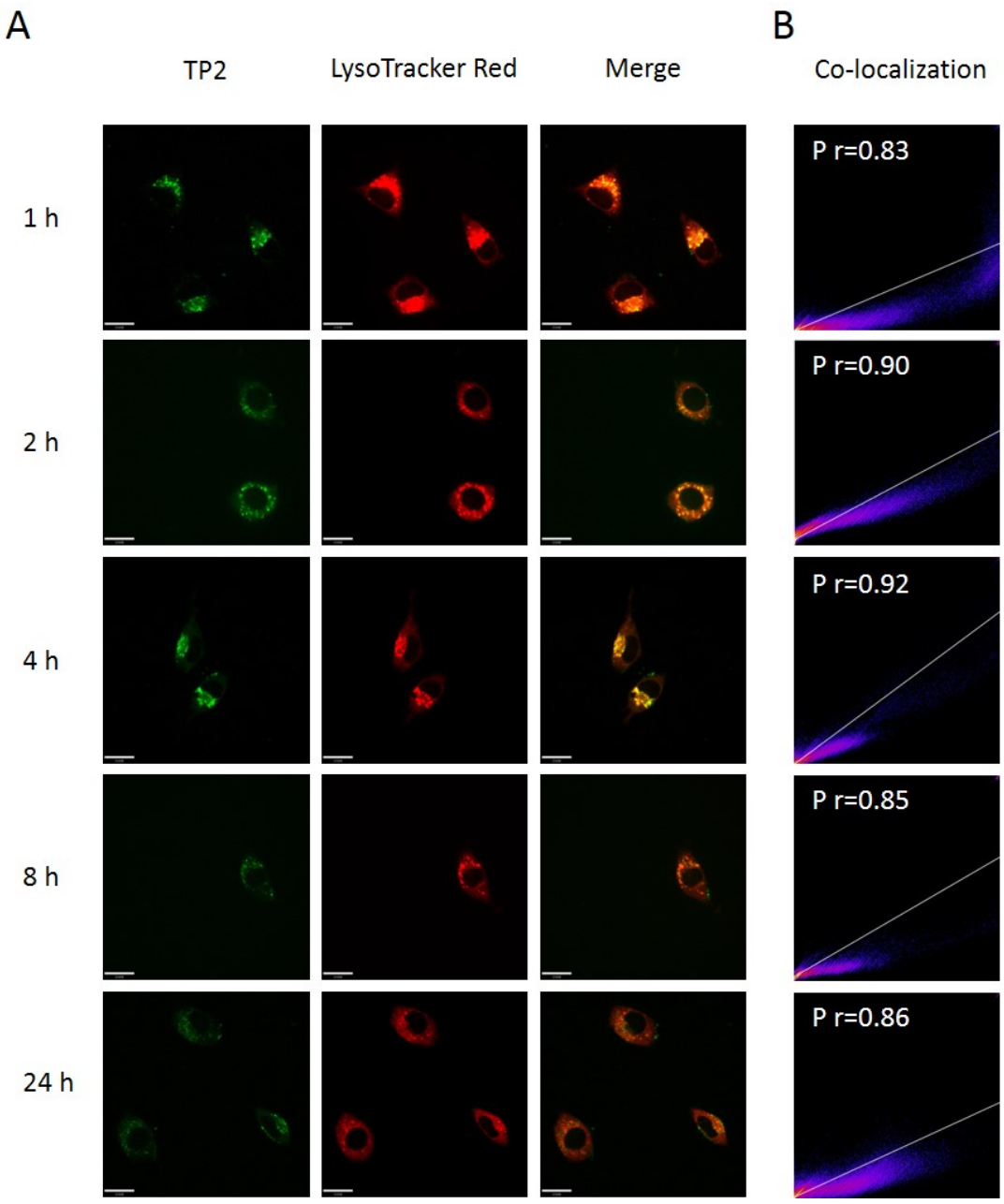

Figure S21. Biodistribution of TP2 in MDA-MB-231 cells. (A) CLSM images of MDA-MB-231 cells incubated with TP2 (40 μM) in a time-dependent (1, 2, 4, 8, 24 h) mode, indicating the lysosomal distribution of TP2. Red (Lyso-Tracker Red) denotes lysosome. Green denotes TP2. The scale bar is 17 μm. (B) Corresponding colocalization analysis of images from 'A'.

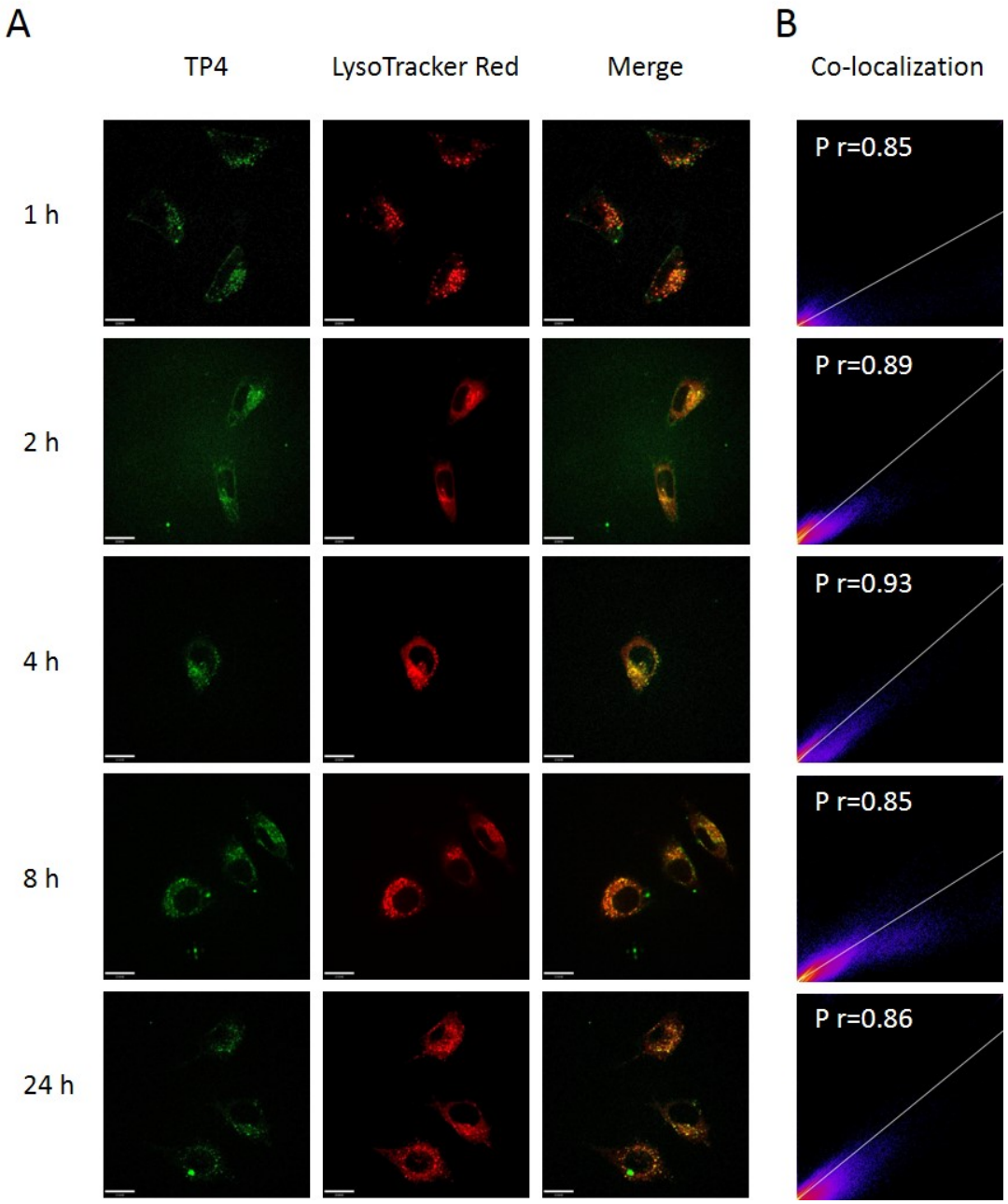

Figure S22. Biodistribution of TP4 in MDA-MB-231 cells. (A) CLSM images of MDA-MB-231 cells incubated with TP4 (40 μM) in a time-dependent (1, 2, 4, 8, 24 h) mode, indicating the lysosomal distribution of TP4. Red (Lyso-Tracker Red) denotes lysosome. Green denotes TP4. The scale bar is 17 μm. (B) Corresponding colocalization analysis of images from 'A'.

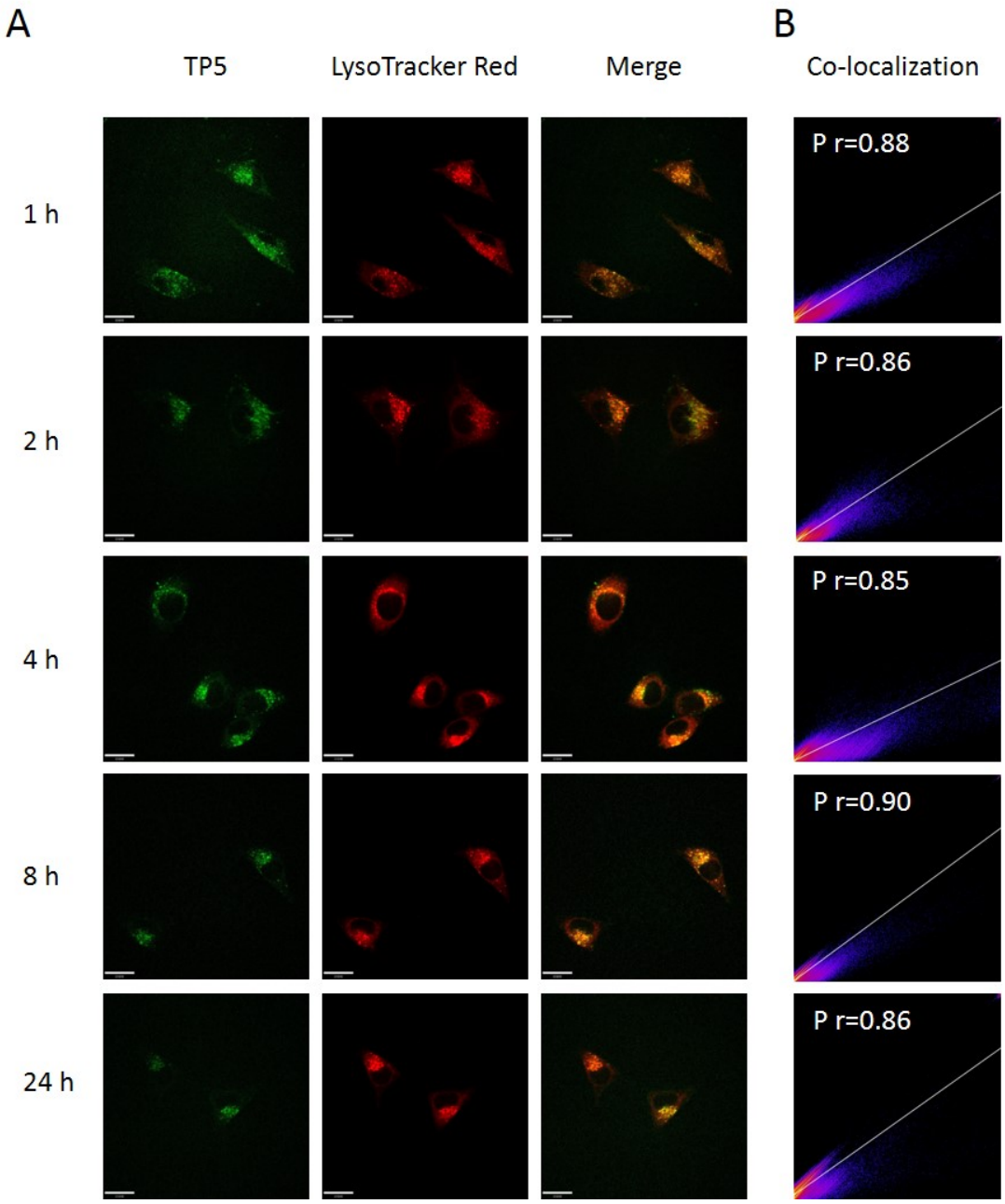

Figure S23. Biodistribution of TP5 in MDA-MB-231 cells. (A) CLSM images of MDA-MB-231 cells incubated with TP5 (40 μM) in a time-dependent (1, 2, 4, 8, 24 h) mode, indicating the lysosomal distribution of TP5. Red (Lyso-Tracker Red) denotes lysosome. Green denotes TP5. The scale bar is 17 μm. (B) Corresponding colocalization analysis of images from 'A'.

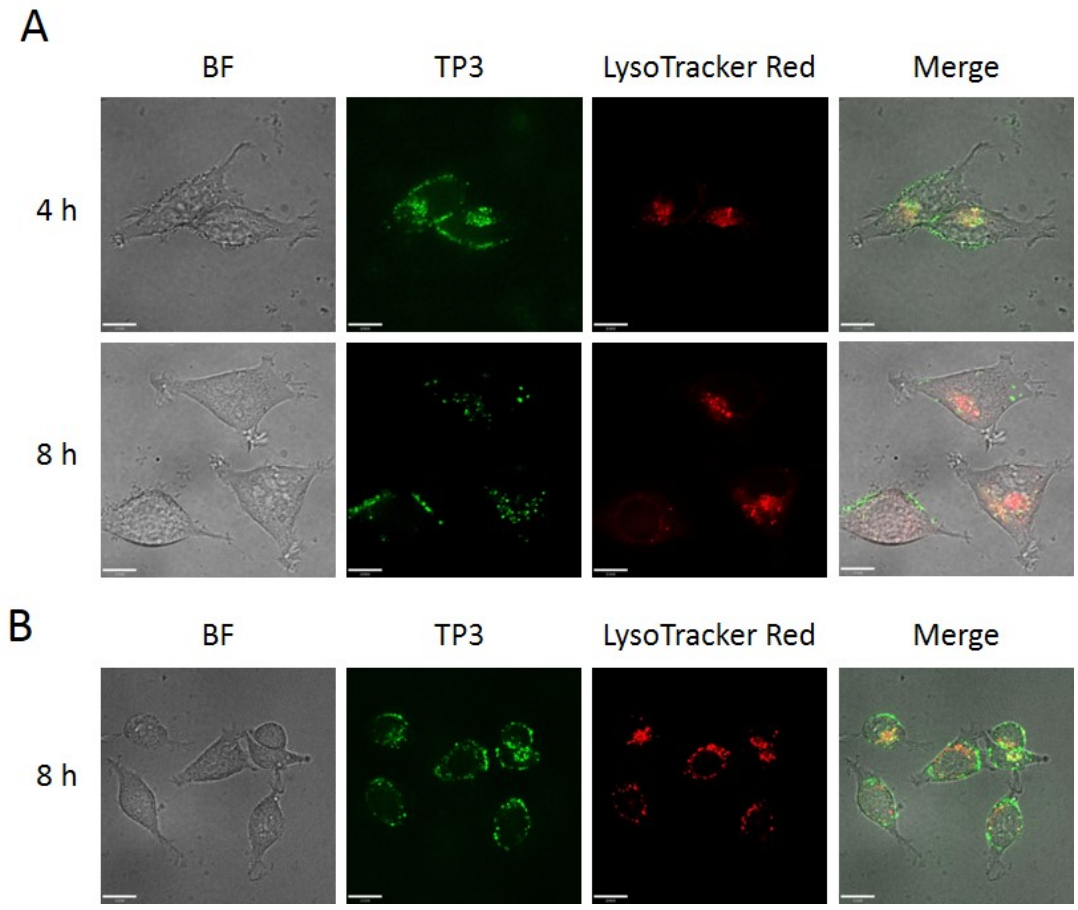

Figure S24. Time-dependent (4, 8 h) CLSM images for analyzing biodistribution of TP3 by MDA-MB-231 cells. (A) TP3 at 80 μM, (B) TP3 at 120 μM. Red (Lyso-Tracker Red) denotes lysosome, green denotes TP3. The scale bar is 17 μm.

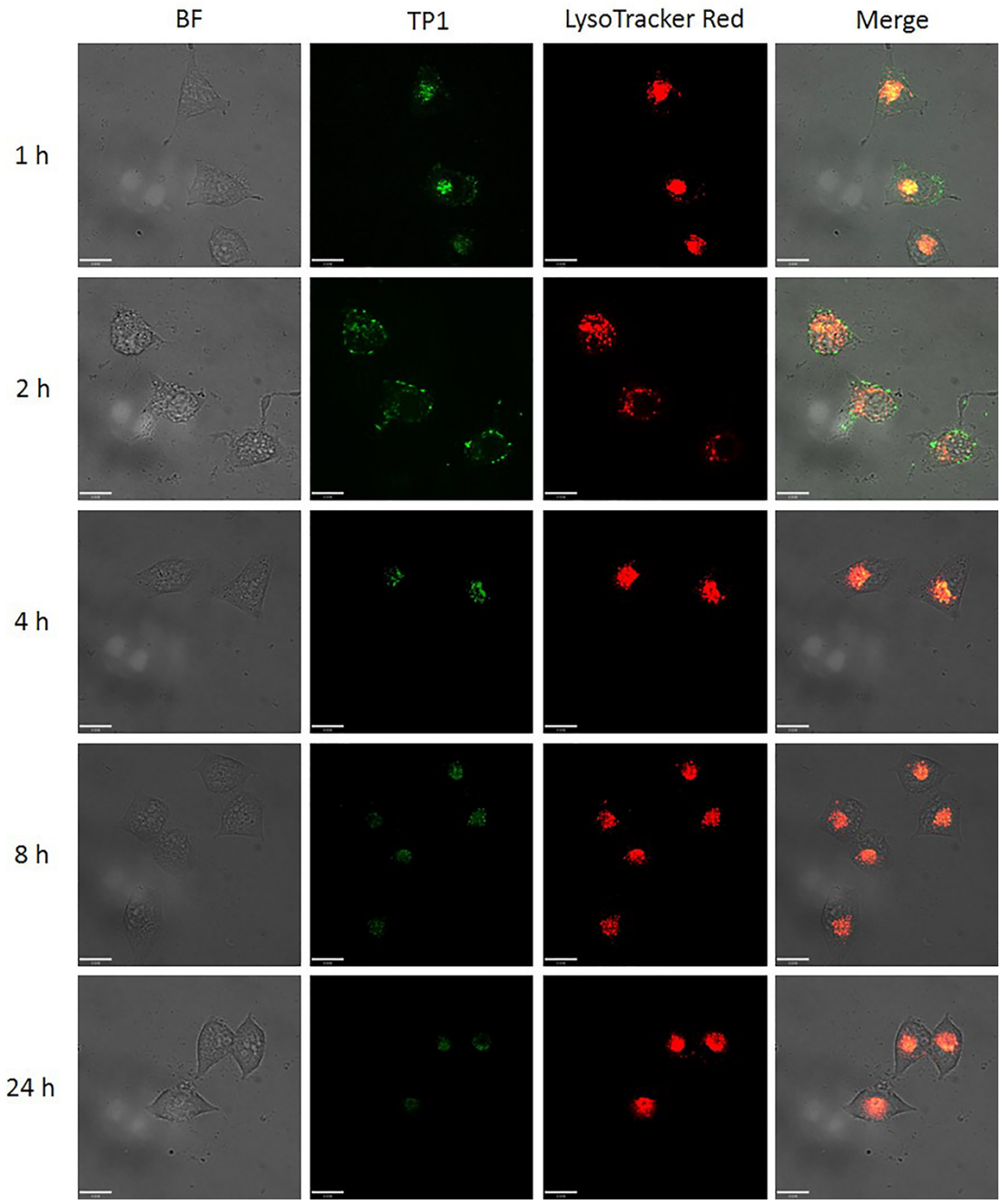

Figure S25. Time-dependent (1, 2, 4, 8, 24 h) CLSM images for analyzing biodistribution of TP1 at 40 μM by MCF-7 cells. Red (Lyso-Tracker Red) denotes lysosome, green denotes TP1. The scale bar is 17 μm.

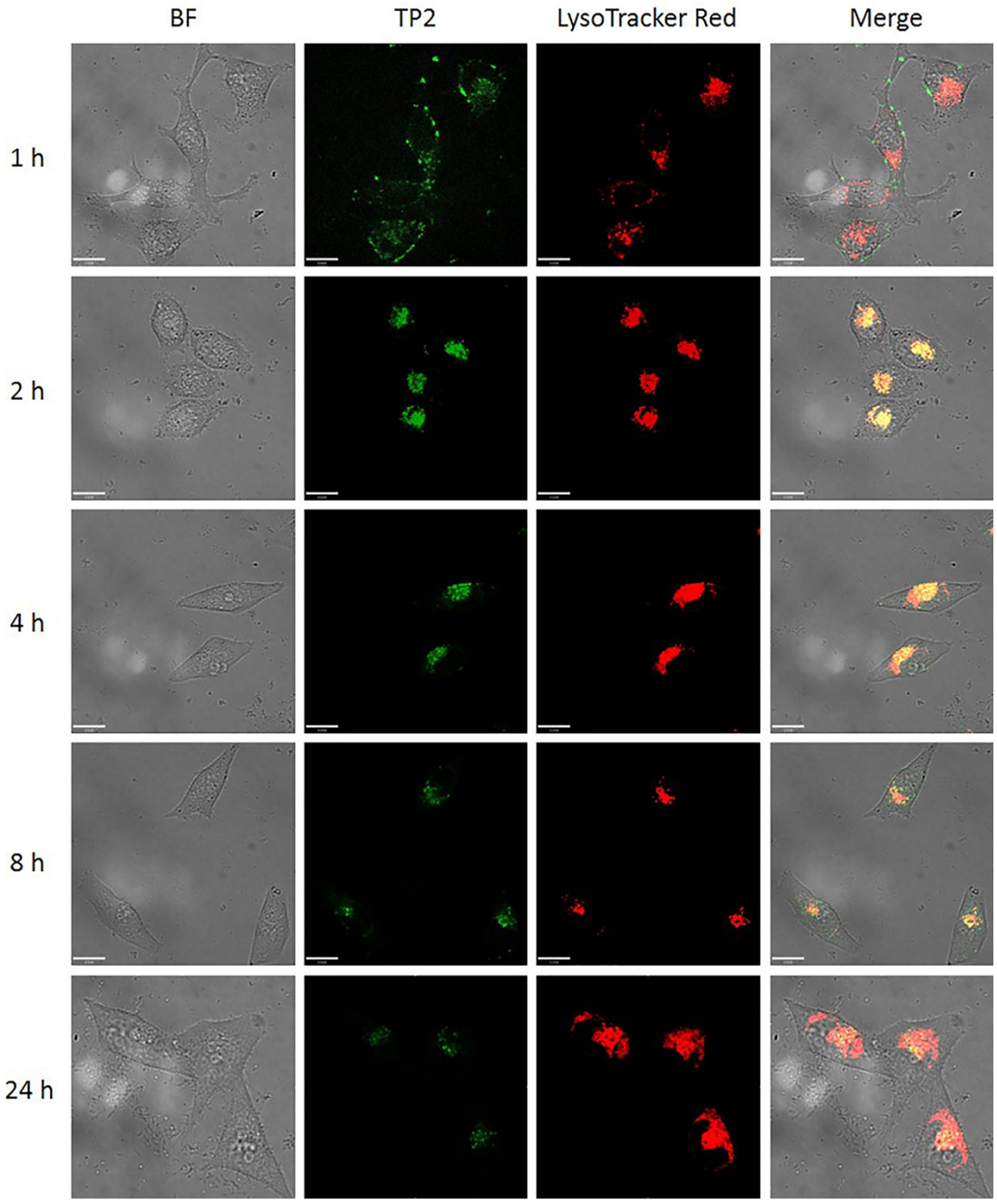

Figure S26. Time-dependent (1, 2, 4, 8, 24 h) CLSM images for analyzing biodistribution of TP2 at 40 μM by MCF-7 cells. Red (Lyso-Tracker Red) denotes lysosome, green denotes TP2. The scale bar is 17 μm.

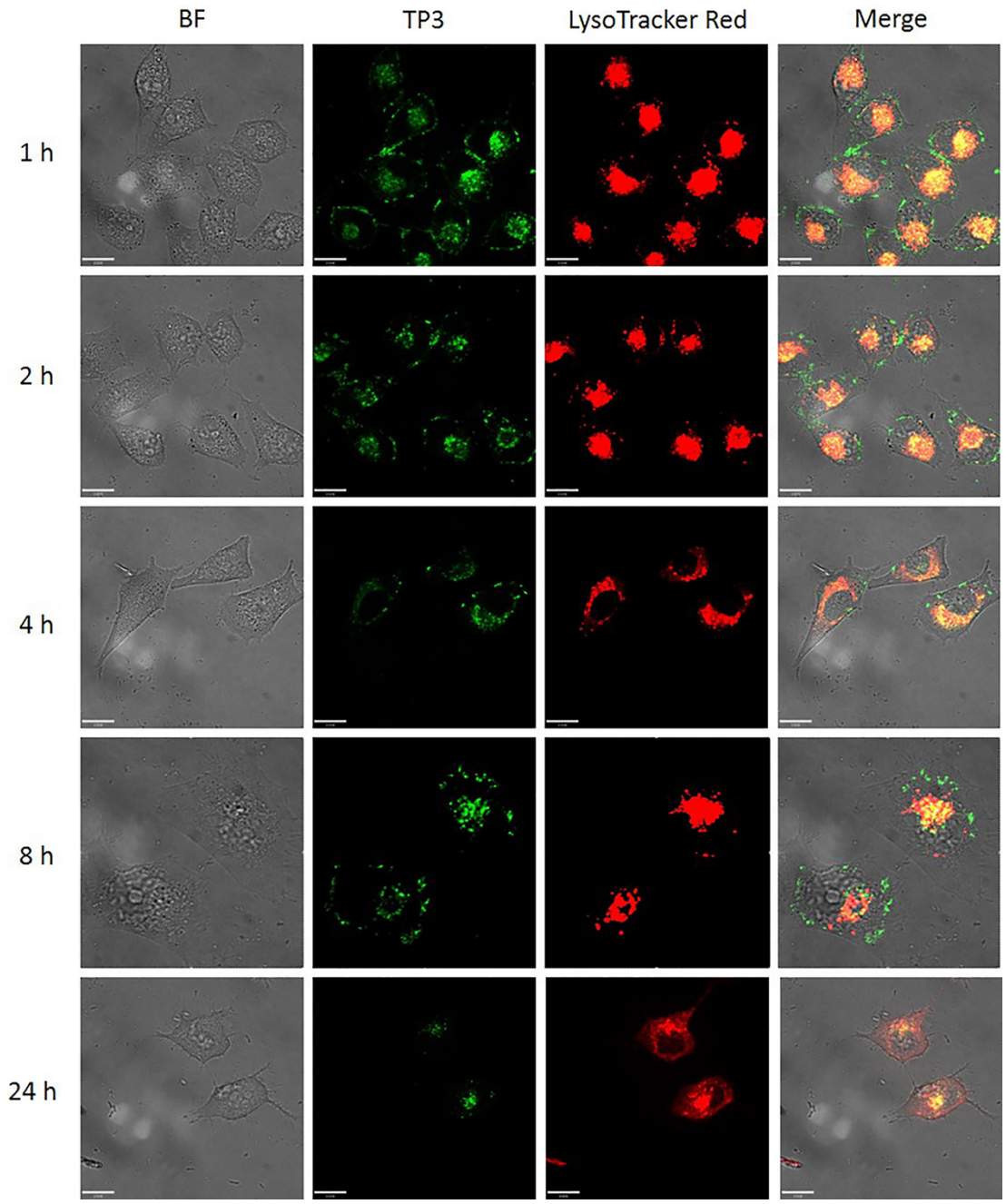

Figure S27. Time-dependent (1, 2, 4, 8h) CLSM images for analyzing biodistribution of TP3 at 40 μM by MCF-7 cells. Red (Lyso-Tracker Red) denotes lysosome, green denotes TP3. The scale bar is 17 μm.

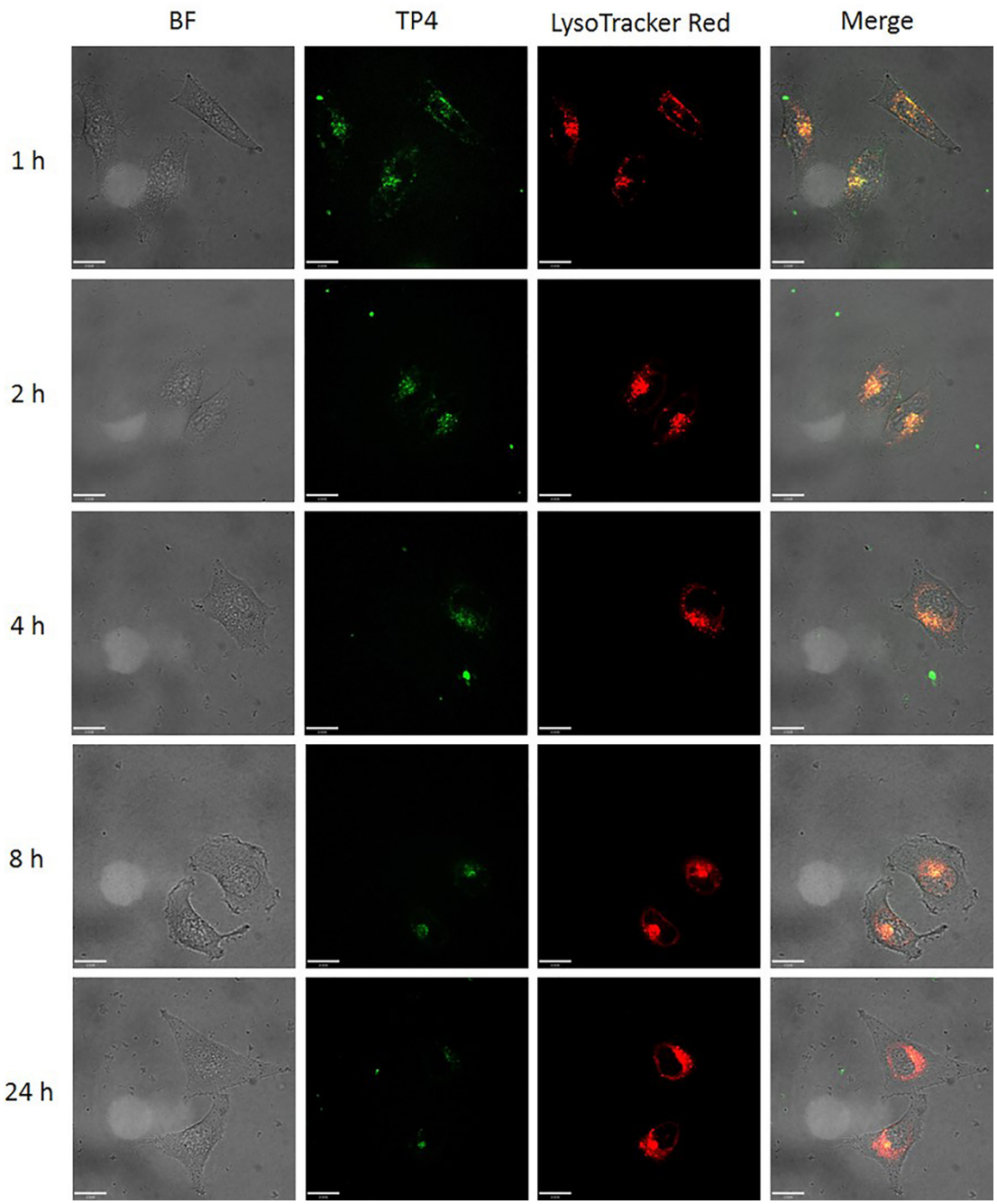

Figure S28. Time-dependent (1, 2, 4, 8, 24 h) CLSM images for analyzing biodistribution of TP4 at 40 μM by MCF-7 cells. Red (Lyso-Tracker Red) denotes lysosome, green denotes TP4. The scale bar is 17 μm.

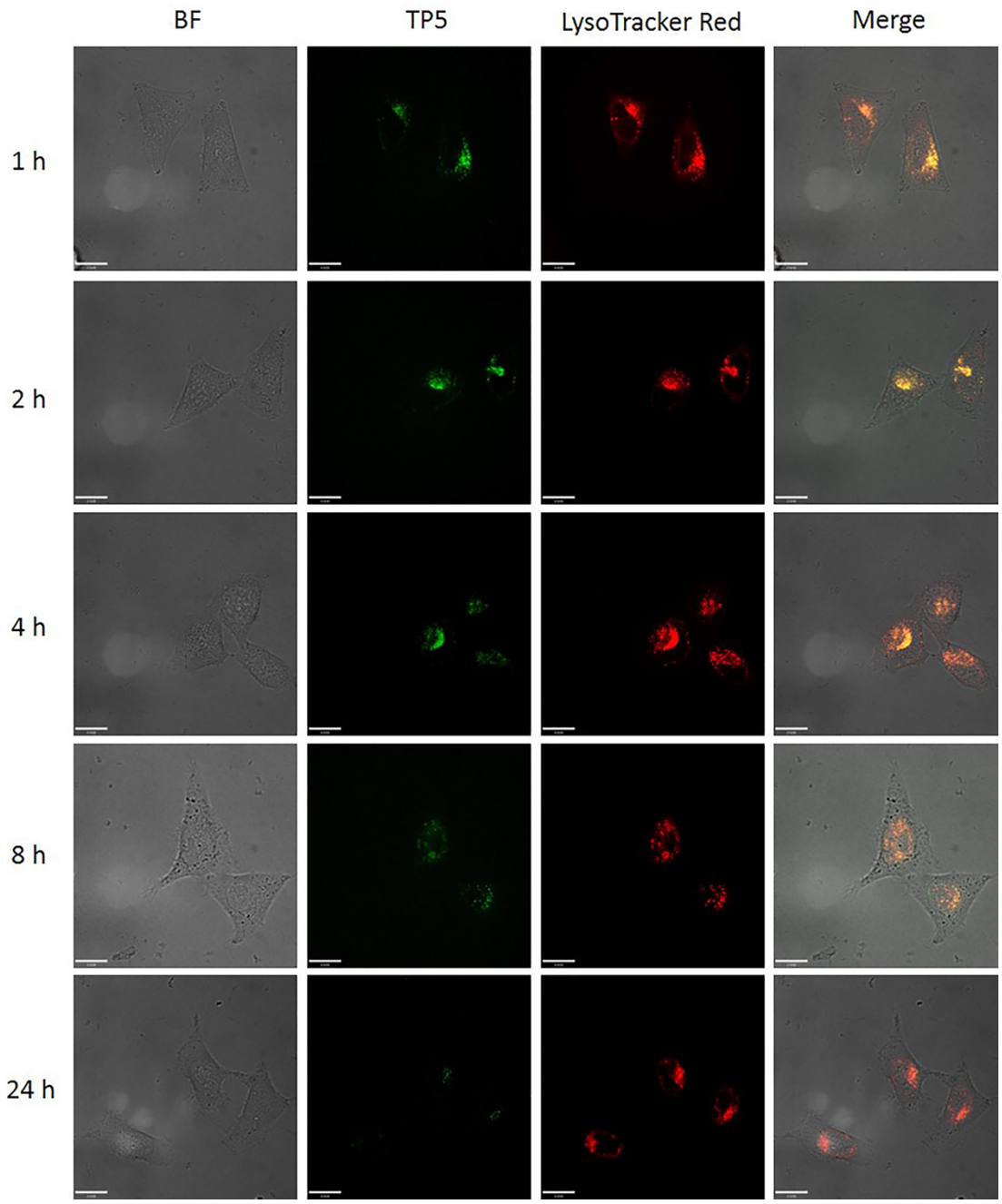

Figure S29. Time-dependent (1, 2, 4, 8, 24 h) CLSM images for analyzing biodistribution of TP5 at 40 μM by MCF-7 cells. Red (Lyso-Tracker Red) denotes lysosome, green denotes TP5. The scale bar is 17 μm.

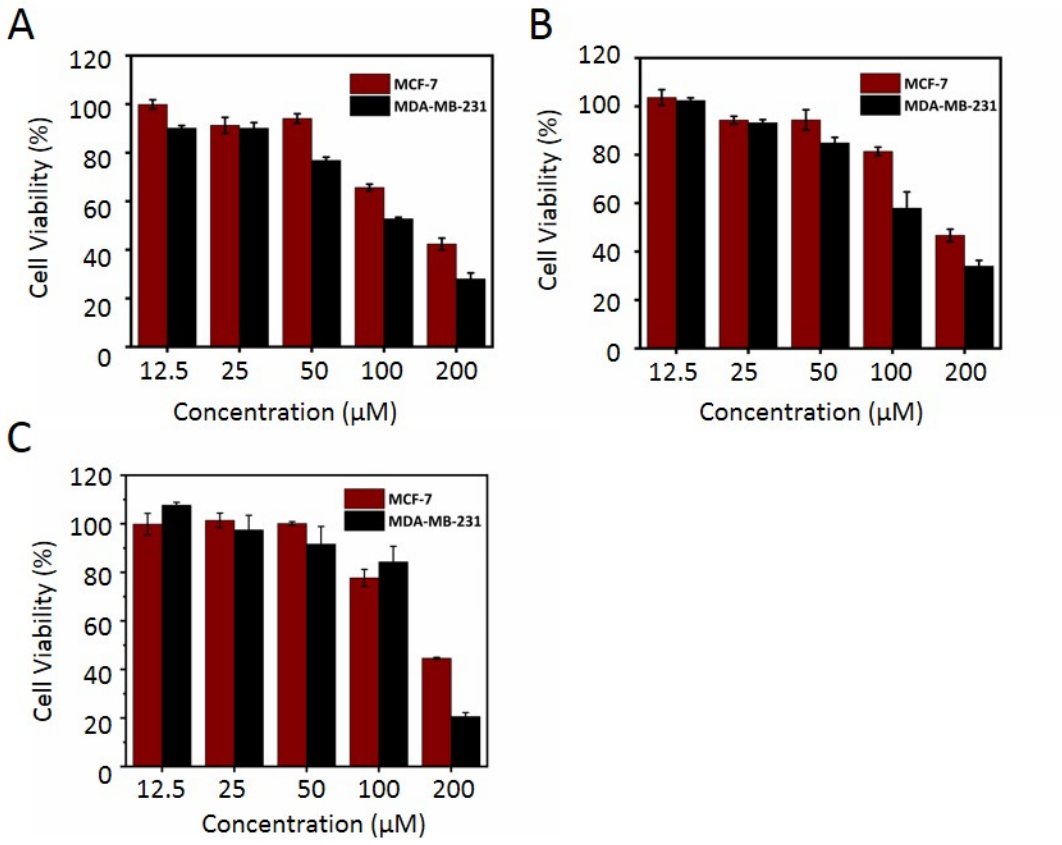

Figure S30. CCK-8 cell viability assay for (A) TP2, (B) TP4 and (C) TP5 after incubation with MDA-MB-231 cells and MCF-7 cells for 24 h.

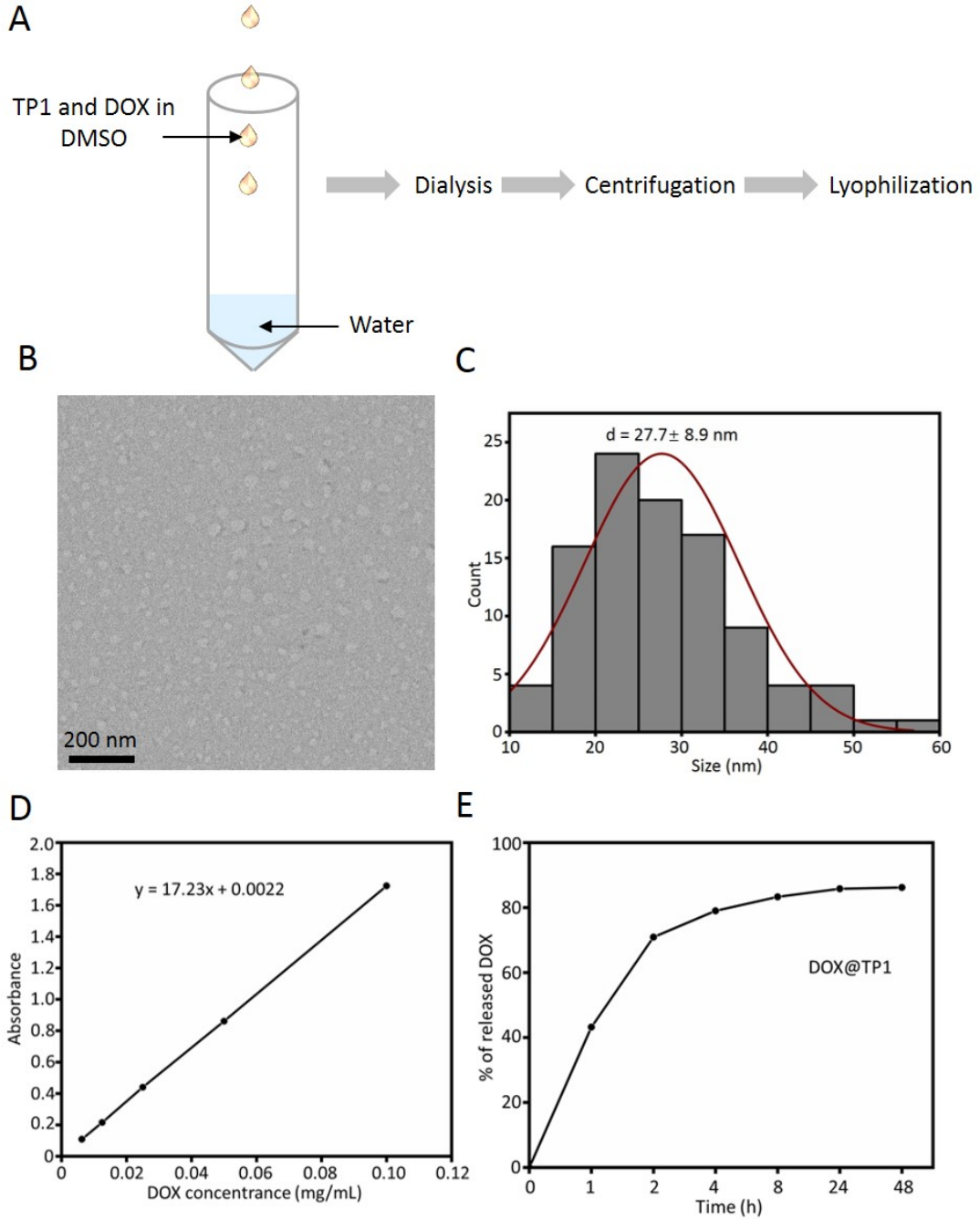

Figure S31. The preparation and characterized of DOX@TP3 NPs. (A) The schematic illustration of DOX@TP1 NPs. (B) TEM image of TP1@DOX NPs. (C) The size distribution of DOX@TP1 NPs from TEM images. (D) The standard curve of DOX concentration at 488 nm by UV spectrometer. (E) The release profile of DOX@TP1 in vitro.

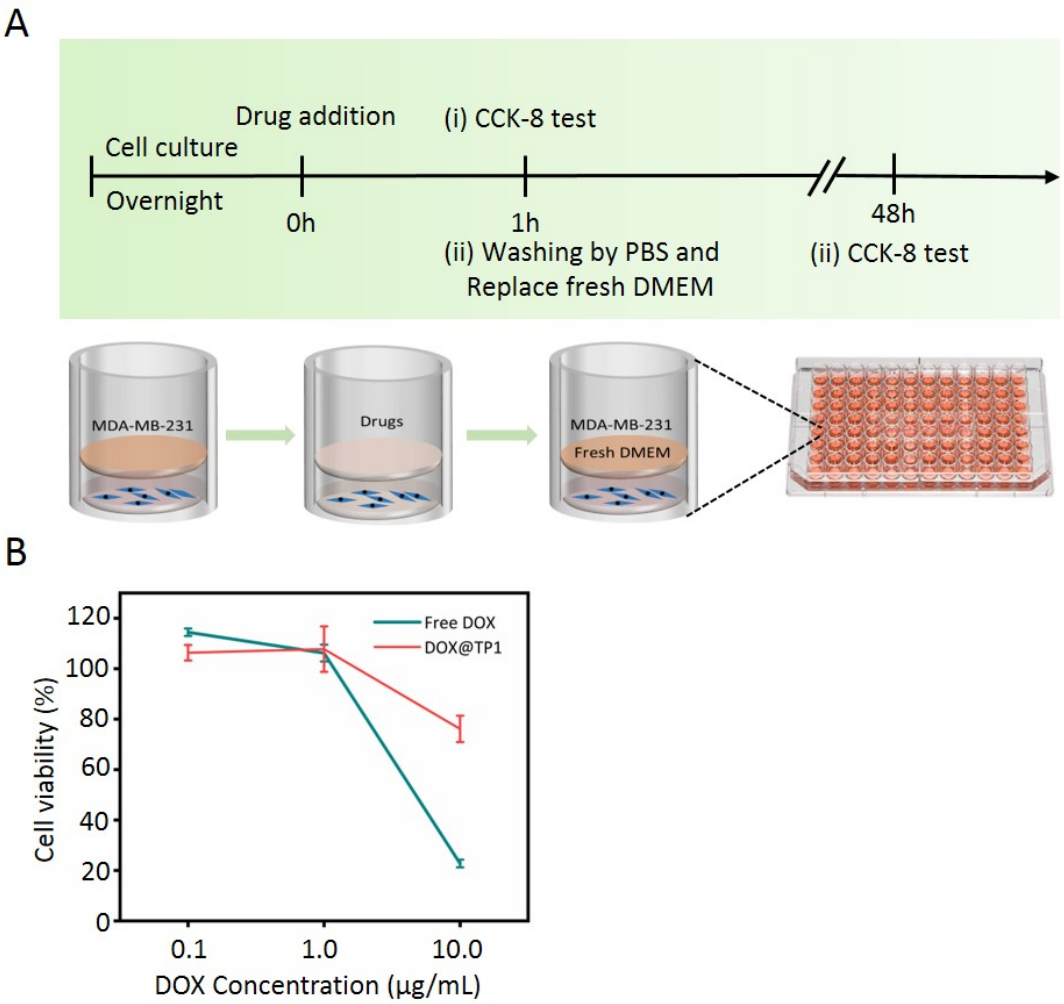

Figure S32. In vitro anti-tumor effect for Free DOX and DOX@TP1 after incubation with MDA-MB-231 cells. (A) The schematic illustration of CCK-8 test. (B) CCK-8 cell viability assay for free DOX and DOX@TP1 after incubation with MDA-MB-231 cells for 48 h.