Supporting Information

Materials and reagents

Cetyltrimethylammonium bromide (CTAB), triethanolamine (TEA), tetraethyl orthosilicate (TEOS, 98%), 1,2-bis(triethoxysilyl)ethane (BTEE), sodium salicylate (NaSal), bovine serum albumin (BSA), human serum albumin (HSA), lysozyme, sodium phosphate dibasic (Na_2HPO_4), sodium phosphate monobasic (NaH_2PO_4) and doxorubicin (Dox) were purchased from Sigma-Aldrich. Hydrochloric acid (HCl) and ethanol were purchased from ChemSupply Pty Ltd. All chemicals were used as received without purification.

Characterizations

Transmission electron microscopy (TEM) images were obtained using J HT7700-EXALENS with an accelerated voltage of 50~80 kV. The samples for TEM were washed through ethanol several times and dispersed in ethanol. Then, DMONs were dried on carbon film on a Cu grid. Nitrogen adsorption-desorption was conducted using a Micromeritics ASAP Tristar II 3020 system to measure isotherms at 77 K. The samples were degassed at 120 °C for 12 hours on a vacuum line. The pore size distribution curve was calculated based on the adsorption branch of the isotherms using Barrett-Joyner-Halanda isotherm (BJH) method. Specific surface areas were measured through the Brunauer–Emmett–Teller (BET) method, while the total pore volume was measured through the amount adsorbed at a maximum relative pressure (P/P_0) of 0.99. Zeta potential was measured at room temperature through Zetasizer Nano-ZS from Malvern Instrument. Before measurement, samples were dispersed in PBS (0. 01M pH 3, 5, 7.4, 9, 11). Solid state ^{29}Si nuclear magnetic resonance (NMR) spectra were measured by Bruker Advance III spectrometer with 7T magnet, Zirconia rotor, 4 mm, rotated at 7 k. Fourier transform infrared spectroscopy (ATR-FTIR) characterization was conducted on a ThermoNicolet Nexus 6700 FTIR spectrometer equipped with Diamond ATR Crystal. Thermo gravimetric analysis (TGA) was tested on METTLER

TOLEDO TGA/DSC1STARe System under air flow (25–800°C, 10°C/min). X-ray photo-electron spectroscopy (XPS) profiles were acquired using a Kratos Axis ULTRA.

Synthesis of DMONs

Na_2HPO_4/NaH_2PO_4 buffer solutions with pH 5.7 and 6.2 were prepared firstly for the following use. CTAB and NaSal were used as structure-directing agents. To fabricate DMONs-6.2, 3.125 mL of pH 6.2 buffer was mixed with 9.375 mL of Milli Q water. Then 190 mg of CTAB and 84 mg of NaSal were added into the above solution at 80 °C in an oil bath under continuous stirring for 1 hour. Afterwards, a mixture of 0.8 mL of BTEE and 1 mL of TEOS was added for another 12 hour stirring under 80 °C. DMONs-5.7 were fabricated following a similar procedure by using pH 5.7 buffer. The products were washed thoroughly by ethanol and centrifuged (20000 rpm, 5mins) for three times. Then, the samples were extracted through ethanol/HCI solution under 60 °C. Finally, DMONs were collected and dried for further use. DMONs-6.2 were sterilized in 70% ethanol for 4 hours, and collected as DMONs-6.2 (sterilized).

Protein and drug loading/release

For protein loading, BSA, HSA and Lysozyme were dispersed in PBS (0.01M pH 7.4) to prepare stock solution (1 mg/mL), respectively. Similarly, DMONs-6.2, DMONs-6.2(sterilized) and DMONs-9.4 were dispersed in PBS (0.1 M, pH 7.4) to prepare a stock solution (2 mg/mL). Then, 0.5 mL of nanoparticle and 0.5 mL of protein stock solutions were mixed at 10 °C for 12 hours under stirring. Afterwards, the samples were centrifuged and the supernatant was collected for UV-Vis measurement at 280 nm to determine the protein concertation. Moreover, DMONs after protein loading were collected for TEM characterization. For Dox loading, Dox was dispersed in PBS (0.01 M, pH 7.4) to prepare a stock solution (1 mg/mL). 0.5 mL of Dox and 0.5 mL of DMONs-6.2 stock solutions were mixed at 4°C for 12 hours stirring. Samples were centrifuged, and supernatant was collected for UV-Vis measurement at 480 nm to determine the Dox concertation. The amount of protein/Dox adsorbed was calculated by the concentration difference between before and after adsorption. For drug release,

2mg of DMONs-6.2/Dox and DMONs-6.2(sterilized)/Dox were dispered in 1.5 ml PBS (0.01M pH 5 and pH 7.4), respectively. Solutions were incubated at 37°C in 200 rpm for 12 hours. At different time points, supernatant was collected for UV-Vis measurement at 480 nm to determine the release Dox concertation.

Cell viability test

MTT ((3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay was used to determine the drug delivery efficiency of DMONs-6.2. 4T1 cancer cells were seeded in 96 well plates with a density of 8000 cells per well for 24 hours. Dox loaded DMONs-6.2 were added to incubate with the cells at Dox concentration of 2, 4, 8 and 12 μg/mL, using pure Dox as positive control. After 24 hours incubation, each well was added 20 μL of 5 mg/mL MTT solution and was incubated for 4 hours. Then, 100 μL of DMSO was used to replace the medium in each well. After that, 96 well plates were analyzed through microplate reader at 540 nm. For the cytotoxicity of DMONs-6.2, DMONs-6.2 in various concentrations of 3.125, 6.25, 12.5, 25, 50, 100 μg/mL were used to treat the cells following similar procedures.

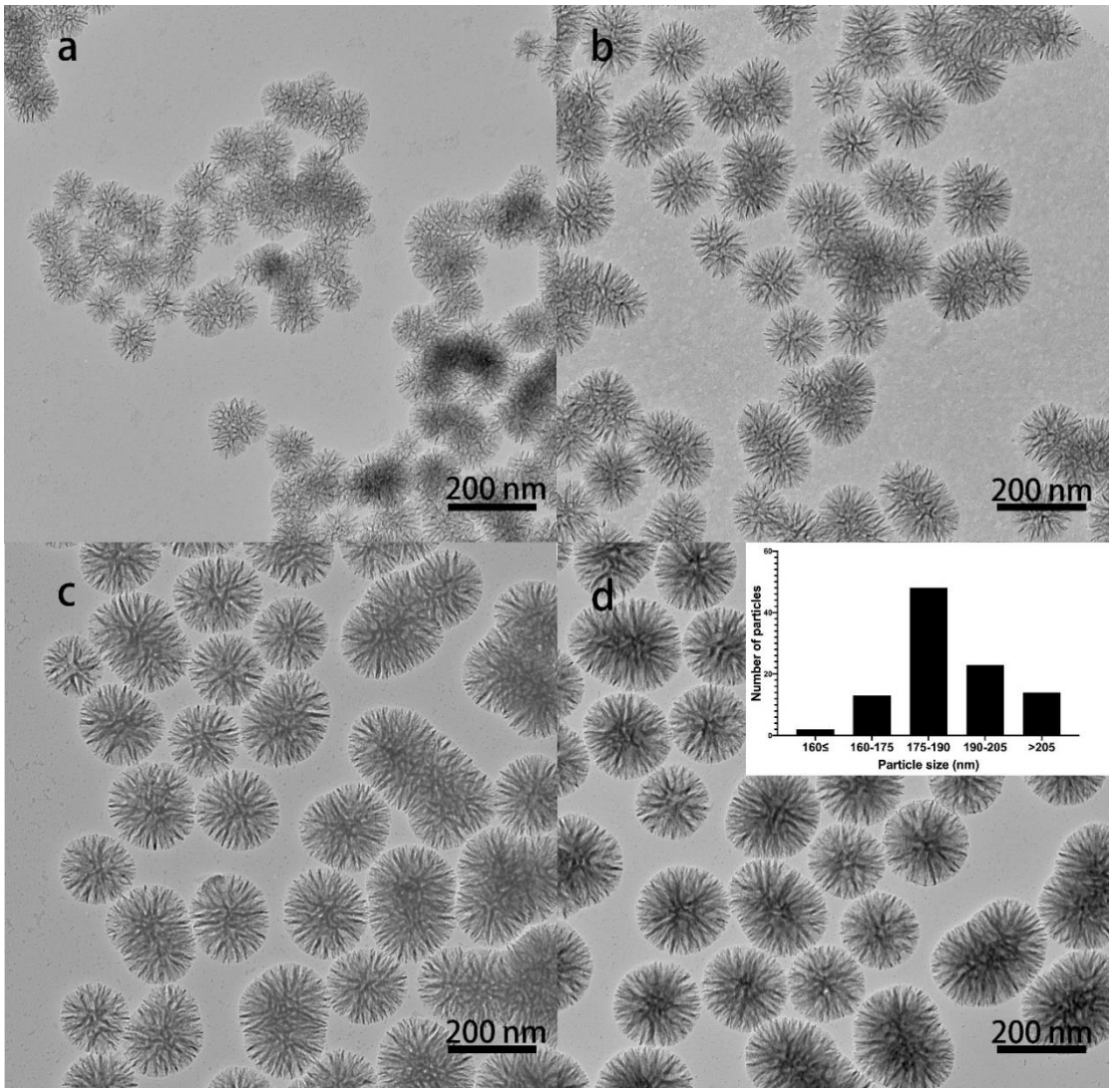

Figure S1. TEM images of DMONs-6.2 collected at reaction time of 2 h, 4 h, 8 h and 12 h. Inset is particle size distribution histogram counted from 100 particles.

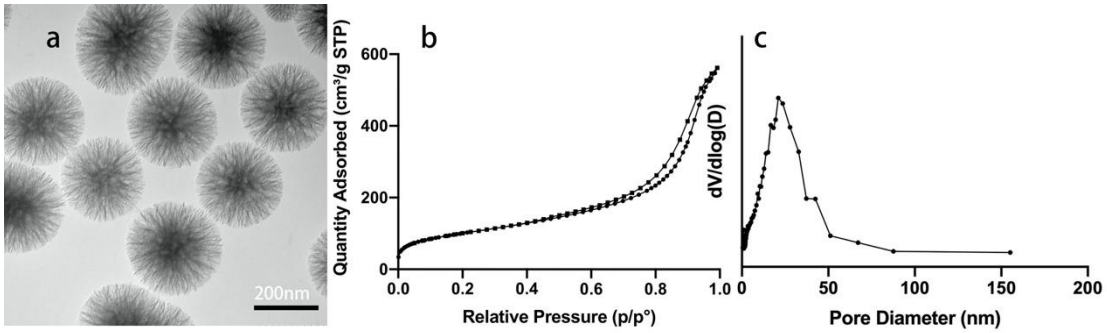

Figure S2. TEM images of DMONs-9.4 (a); N_2 adsorption−desorption isotherm for DMONs-9.4 (b) and pore size distribution for DMONs-9.4(c).

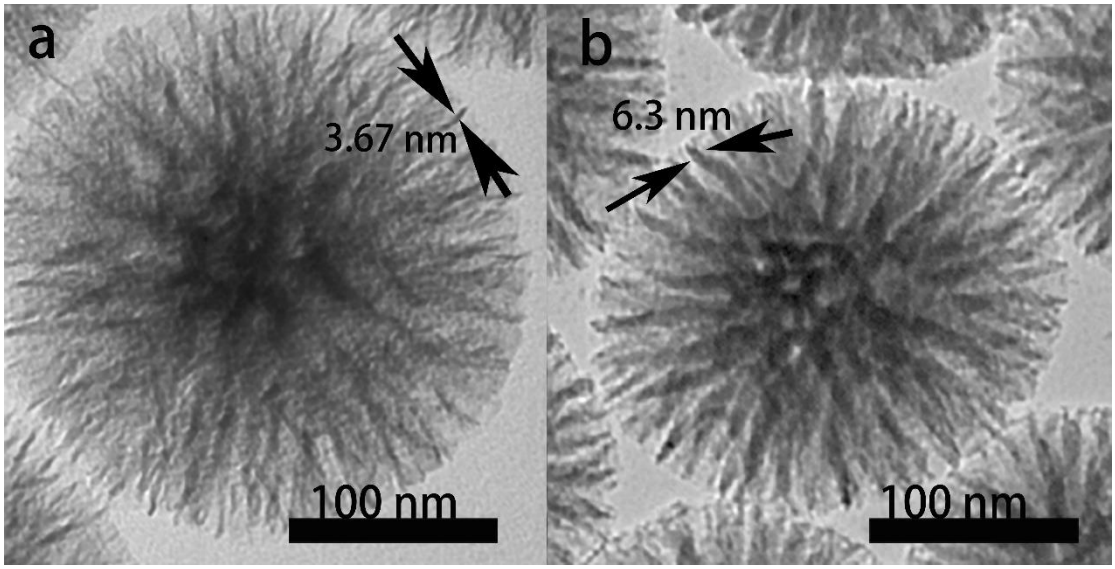

Figure S3. TEM images of DMONs-9.4 (a) and DMONs-6.2 (b).

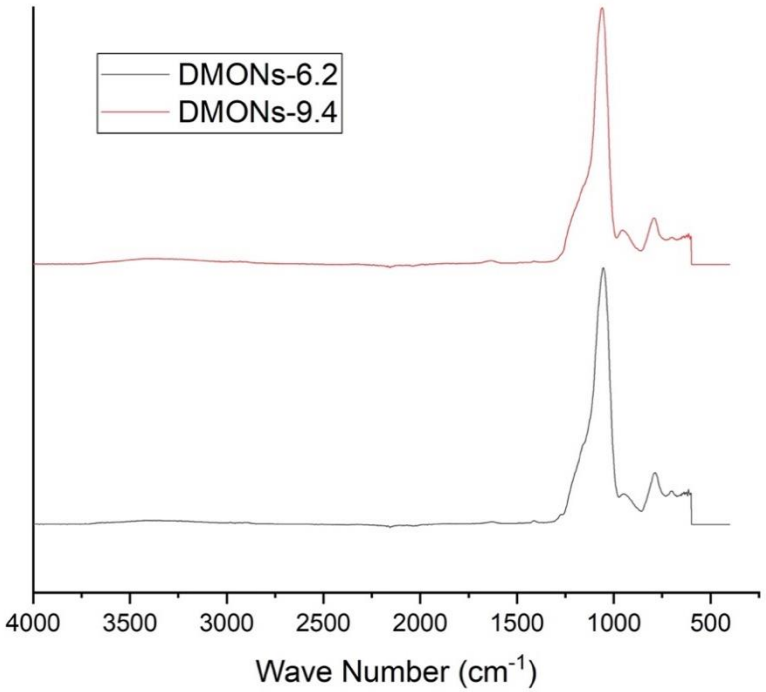

Figure S4. Full FTIR spectra for DMONs-6.2 and DMONs-9.4.

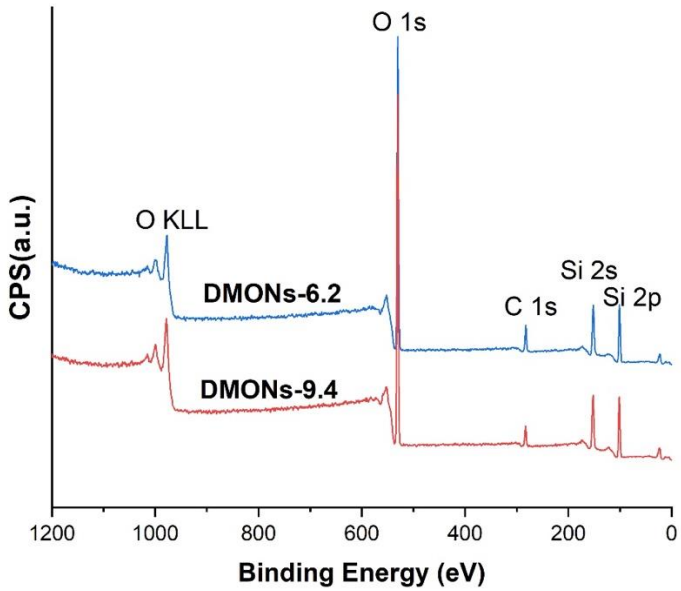

Figure S5. XPS spectra of DMONs-6.2/9.4.

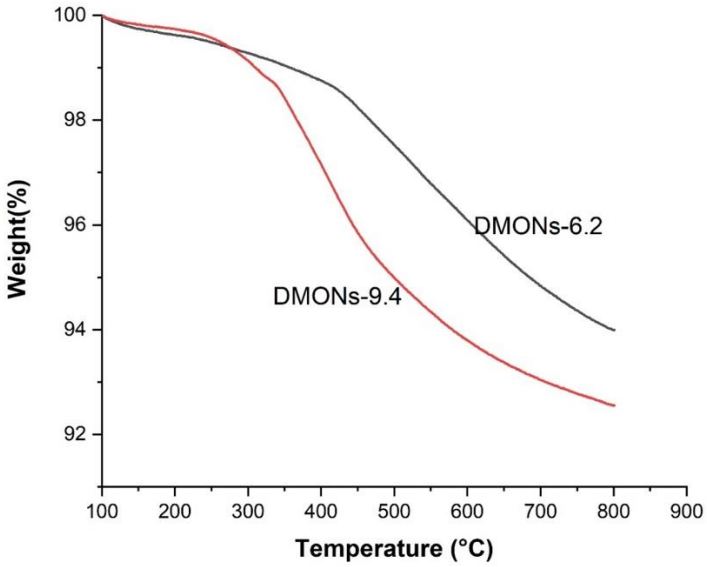

Figure S6. TGA profiles of DMONs-6.2 and DMONs-9.4.

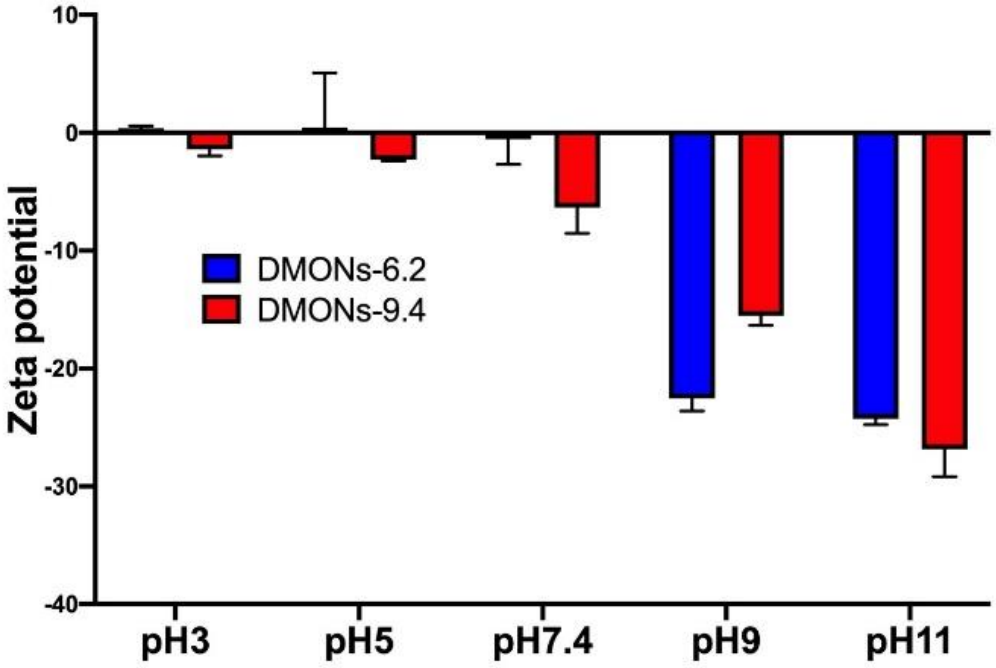

Figure S7. Zeta potential in the full pH range for DMONs-6.2 and DMONs-9.4.

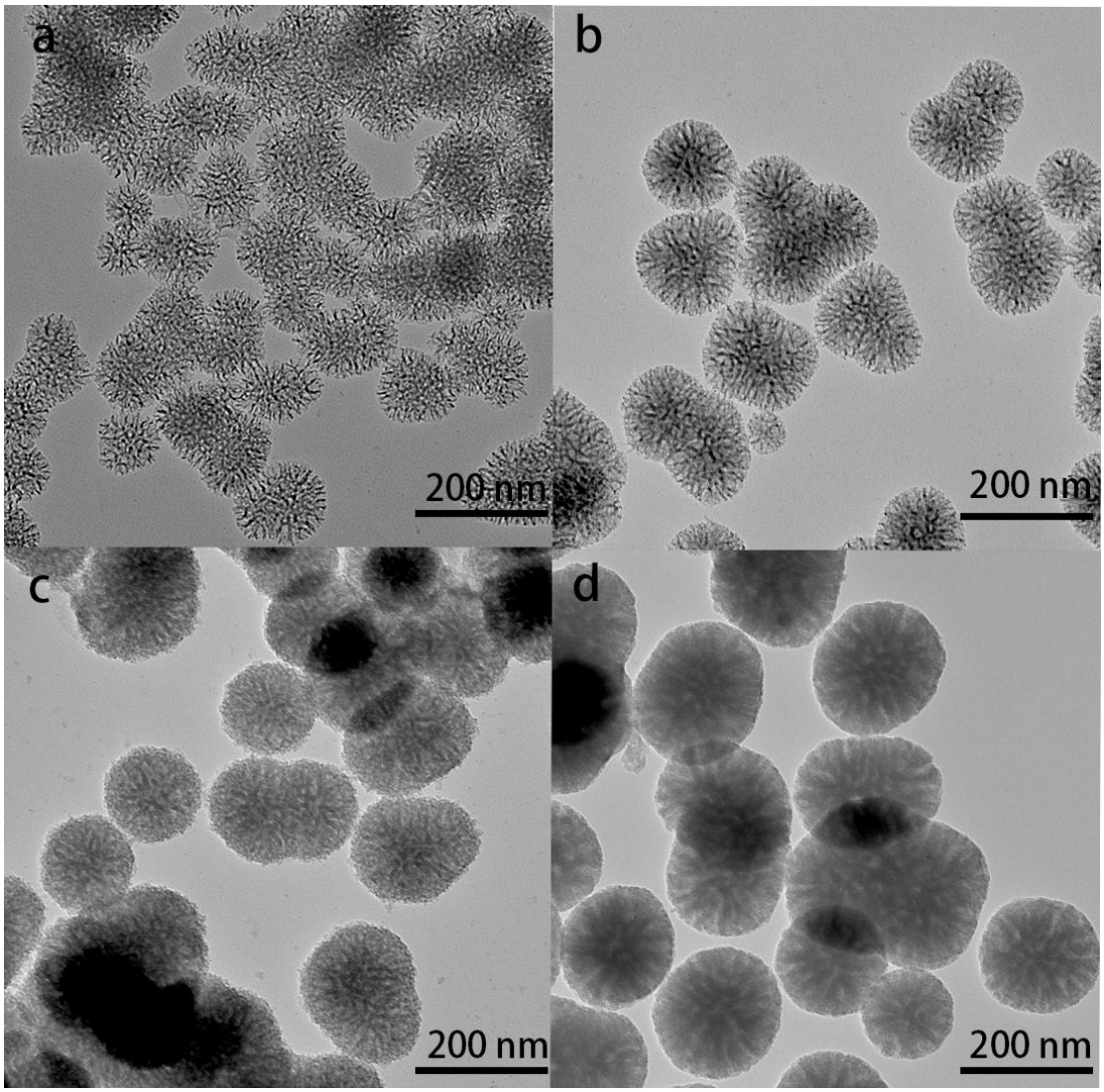

Figure S8. TEM image of DMONs-5.7 collected at reaction time of 2 h (a), 4 h (b), 8 h (c) and 12 h (d).

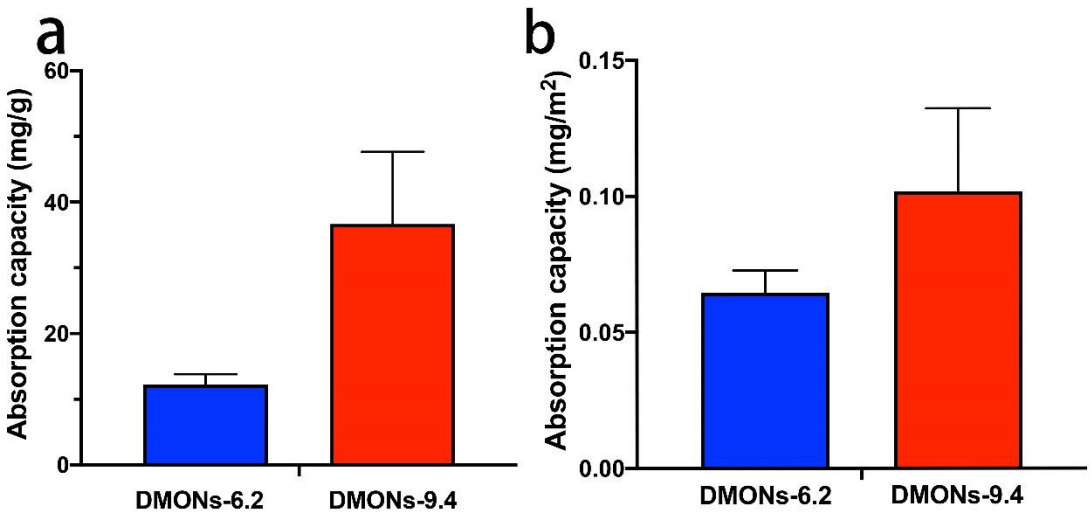

Figure S9. Summary of the HSA adsorption capacity for DMONs-6.2 and DMONs-9.4 per mass (a) and surface area (b).

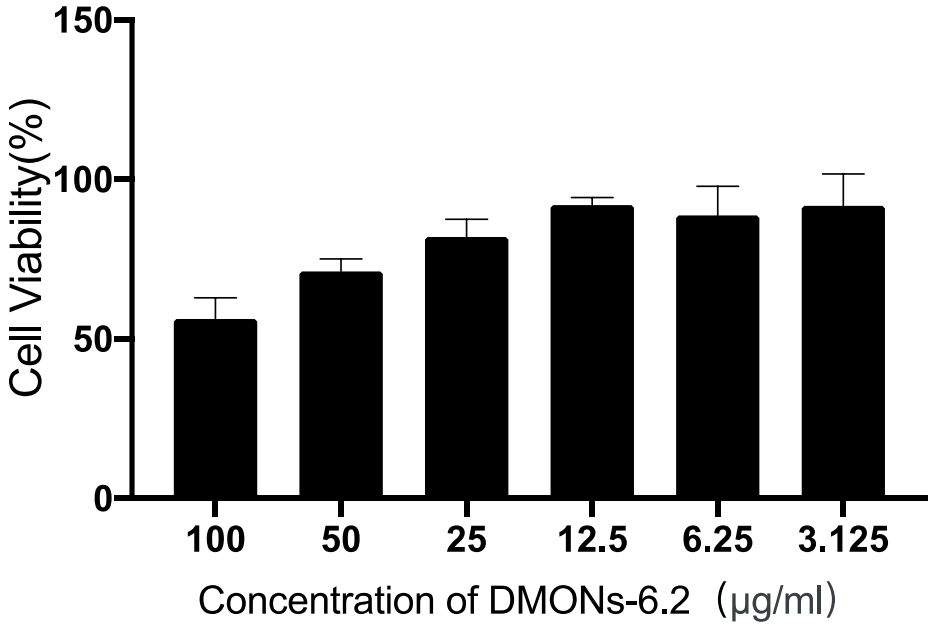

Figure S10. Cell viability of 4T1 cancer cells after treatment at different concentrations of DMONs-6.2.

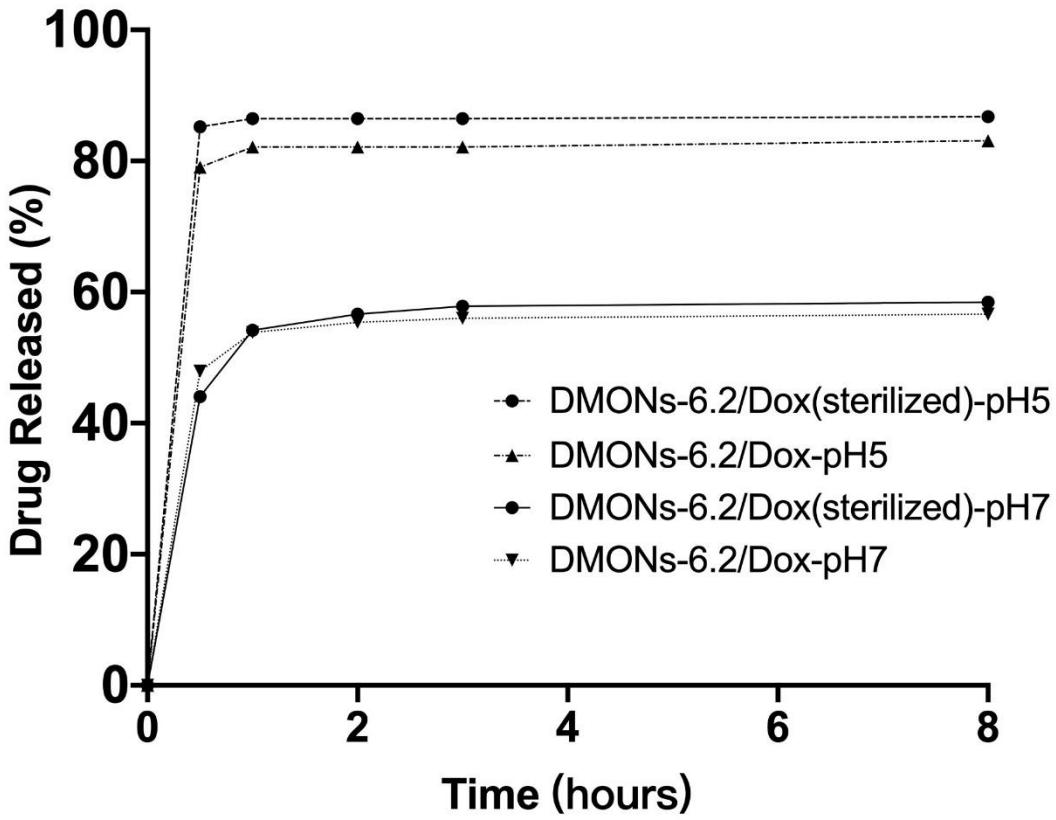

Figure S11. The drug release profiles for DMONs-6.2/Dox and DMONs-6.2 (sterilized)/Dox in pH 5 and pH 7, respectively.

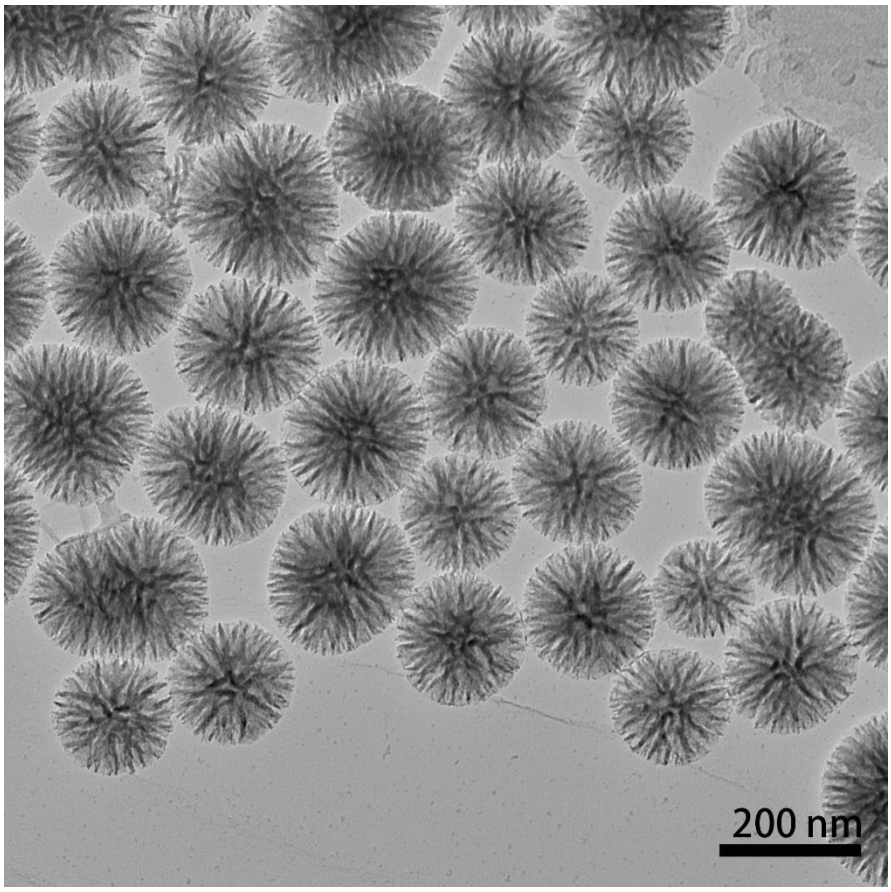

Figure S12. TEM image of DMONs-6.2 (sterilized).

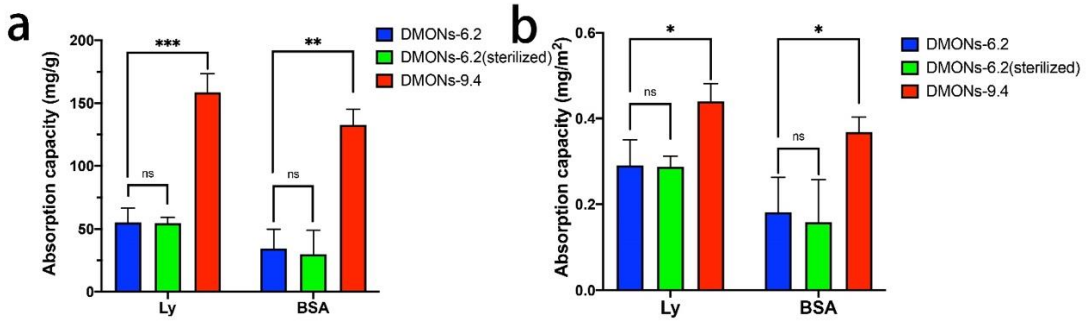

Figure S13. Protein adsorption capacity of DMONs-6.2, DMSNs-6.2 (sterilized) and DMONs-9.4 in per g of mass (a) and per m^2 of surface area (b).

Table S1. Textural properties of DMONs/DMSNs.

Samples	S_{BET}[a] ($m^2 \cdot g^{-1}$)	V_{Total}[b] ($cm^3 \cdot g^{-1}$)	Pore Size (nm)
DMONs-9.4	360.2	0.87	21.0
DMONs-6.2	189.6	0.51	28.2

[a]S_{BET}: Specific surface area.
[b]V_{Total}: Total pore volume.

Table S2. Carbon contents of DMONs-6.2 and DMONs-6.2 quantified by EA and XPS.

Samples	Carbon (wt %, EA)	Carbon (At %, XPS)
DMONs-9.4	6.71	10.58
DMONs-6.2	5.77	14.26