Supporting Information

Protein Refolding Assisted by Periodic Mesoporous Organosilicas

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1. Solid-State NMR Characterization

Magic-angle-spinning (MAS) solid-state NMR spectra of E-PMO-A were acquired on a Bruker DSX 400 Spectrometer (400.42 MHz 1H; 100.70 MHz ^{13}C; 79.55 MHz ^{29}Si) using a double resonance 4 mm MAS probe (sample volume ~ 80 L). The MAS rate for both ^{13}C and ^{29}Si samples was 8 kHz. 13C spectra were acquired using tangent ramped cross-polarization from 1H followed by high power proton decoupling (83 kHz TPPM). 2048 complex time points were sampled with a spectral width of 50 kHz and averaged over 2048 scans with a relaxation delay of 4 s. ^{29}Si spectra were acquired using a 90-degree Si pulse (50 kHz) followed by high power proton decoupling (83 kHz TPPM). 2048 complex time points were sampled with a spectral width of 50 kHz and averaged over 16384 scans with a relaxation delay of 4 s.

2. Adsorption of native lysozyme on E-PMO-A and SBA-15 in the presence of PEG

30 mg of mesoporous materials was dispersed in 15 ml of native lysozyme (0.6 mg/ml) solution in 100 mM Tris-HCl buffer containing 2 M urea, 1 mM EDTA, and PEG (M. W. 2000, 10 mg/ml). Control experiments were also carried out in the absence of PEG. At different time intervals, 1 ml of mixture was taken out followed by quick centrifugation. Amount adsorbed was calculated by subtracting the UV absorbance at 280 nm of the supernatant after centrifugation from that of native lysozyme before adsorption.

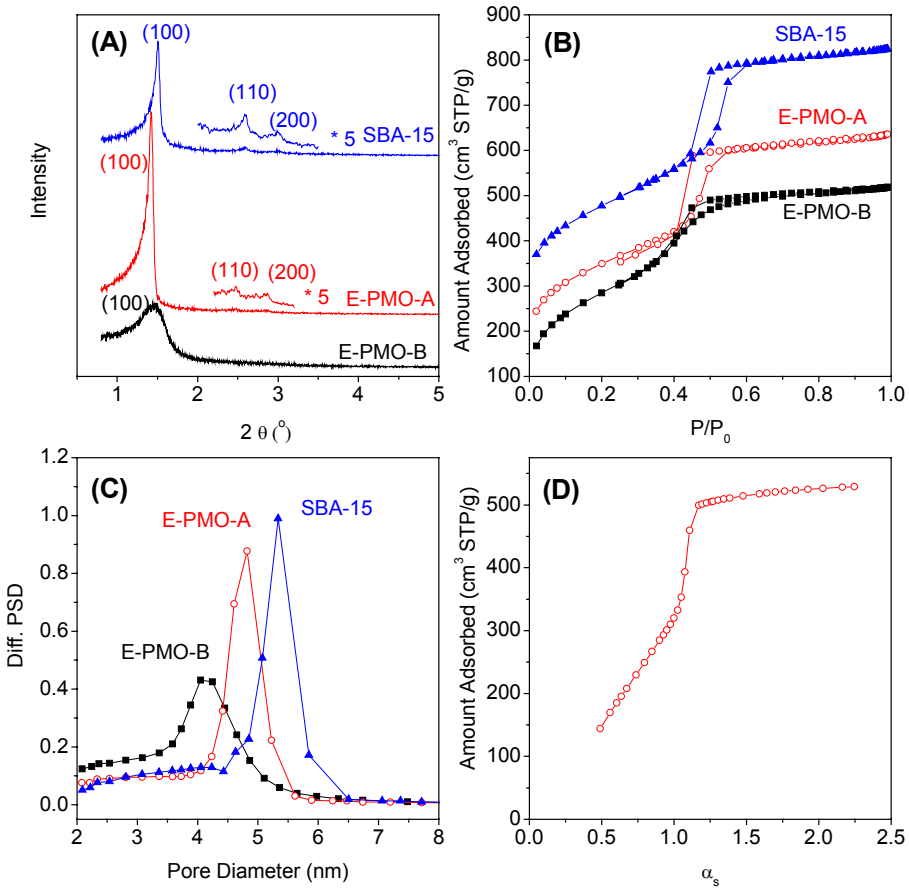

Figure S1. XRD patterns (A), N_2 sorption isotherms at 77 K (B), and KJS pore size distribution plots (C) of mesoporous materials. α_s plot (D) of E-PMO-A. The isotherms (B) of E-PMO-A and SBA-15 are offset vertically by 100 and 200 cm^3/g STP, respectively.

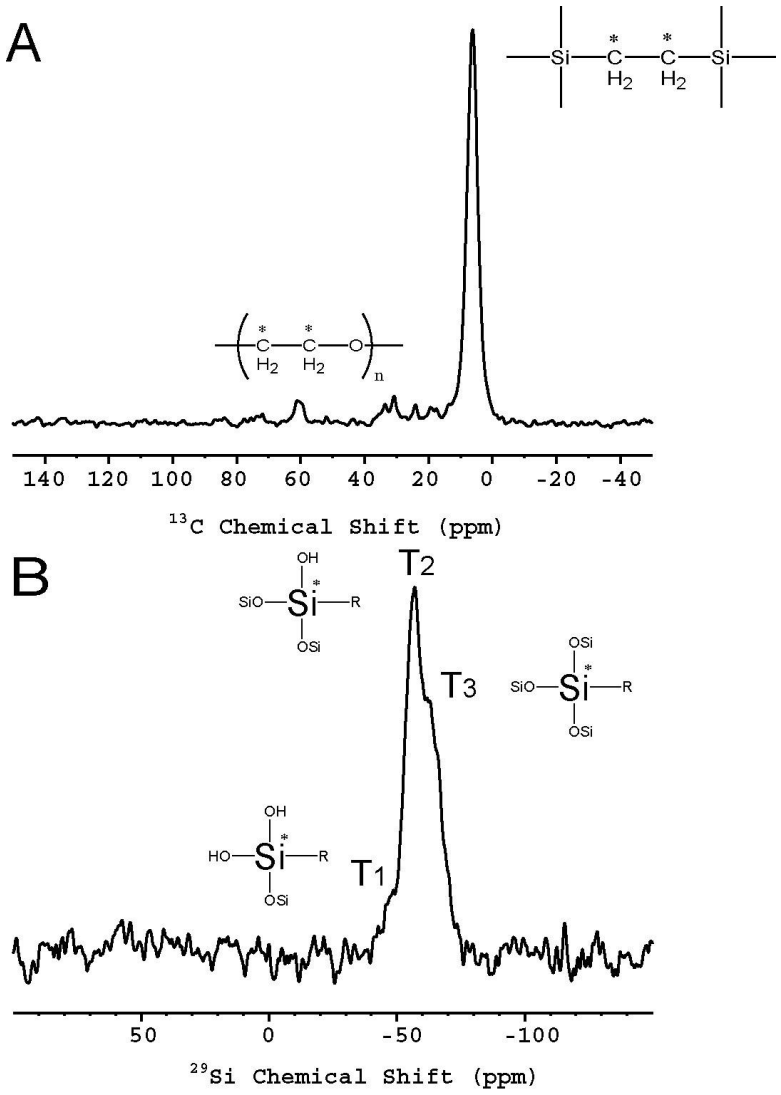

Figure S2. ^{13}C CP/MAS (A) and ^{29}Si MAS (B) spectra of E-PMO-A. The signals were assigned to specific C/Si atoms with different environments, as marked with asterisks. The results indicated the successful removal of the template and a hybrid structure of E-PMO-A.

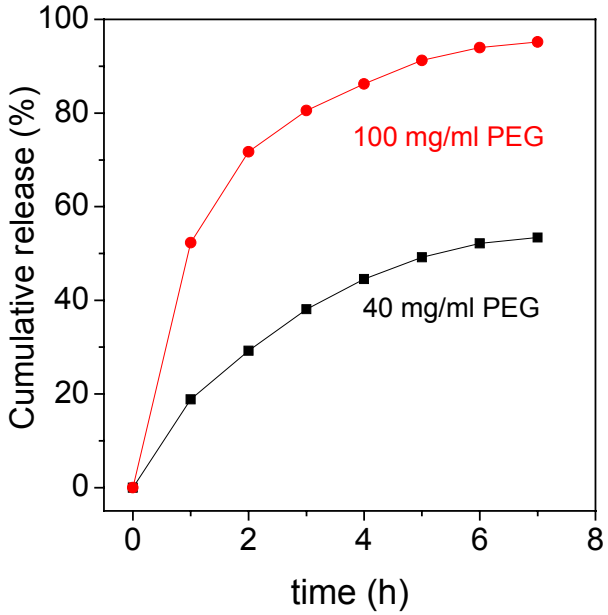

Figure S3. A cumulative release of D-LYS from E-PMO-A in the presence of PEG. At every hour, eluted D-LYS in solutions was removed by centrifugation and same volume of fresh elution solution was added.

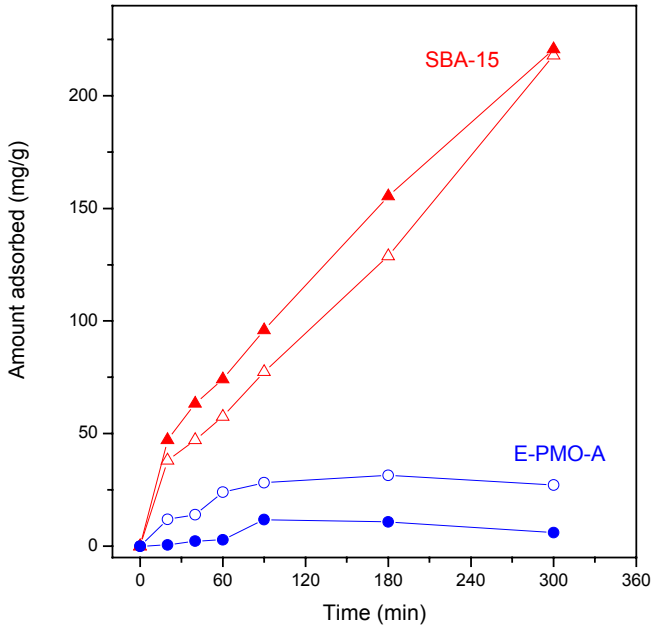

Figure S4. Adsorption of native lysozyme on E-PMO-A and SBA-15 in the absence (open symbols) and presence (open symbols) of PEG (10 mg/ml).