Supporting Information

Figure S1. DLS measurement of bAgNP-lysozyme heated from room temperature to 71.4°C and cooled back down to room temperature. (A) Hydrodynamic radius of lysozyme. (B, C) Hydrodynamic radius of bAgNP-lysozyme versus temperature during heating for increasing NP:protein ratios. Lysozyme of 0.9 mg/mL (A-D). bAgNPs of 0.044 mg/mL (B) and 0.088 mg/mL (C, D). (D) Hydrodynamic radius of bAgNP-lysozyme versus temperature during cooling. The diamond, triangles, squares and stars represent data points obtained from different sample wells of the same conditions.
Figure S2. DLS measurement of bAgNP-ALact heated from room temperature to 71.4°C and cooled back down to room temperature. (A, B) Hydrodynamic radius of ALact during heating and cooling. (C, D) Hydrodynamic radius of bAgNP-ALact versus temperature during heating and cooling. ALact: 0.9 mg/mL (A-D). bAgNPs: 0.088 mg/mL (C-D). The diamond, triangles, squares and stars represent data points obtained from different sample wells of the same conditions.

Figure S3. The CD spectra of protein secondary structures in exposure to bAgNPs.
**Figure S4.** The binding of capping molecules to an AgNP. (A) Two commonly-used capping molecules, citrate and PEI, were studied in DMD simulations. The probability of forming contacts with the NP surface in the simulations was calculated as a function of temperature. PEI displays a stronger binding to NP than citrate because PEI requires a higher temperature to dissociate from the NP surface. The snapshot structures of PEI (B) and citrate (C) bound to NP surface suggest that the strong binding of PEI is due to the electrostatic interactions between the charged amines and their “image” charges.
Figure S5. The binding of multiple PEI molecules with an AgNP surface. The counter ions (green spheres) are able to screen the electrostatic repulsion between highly charged PEI molecules (in stick representation), so that multiple PEI molecules can cover the surface of the AgNP to prevent NP-NP aggregation. In our simulations, eight generation-3 PEI dendrimers are able to cover an AgNP surface area of $8.1 \times 8.2$ nm$^2$. Both the top (A) and side (B) views of a PEI-capped NP structure in DMD simulations are shown.
Figure S6. (A) The representative structure of the folding intermediate of lysozyme obtained from DMD simulations. Compared to the native structure (B), the intermediate corresponds to a loss in beta-sheets.