Understanding Protein-Nanoparticle Interaction: A New Gateway to Disease Therapeutics

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SUPPORTING INFORMATION

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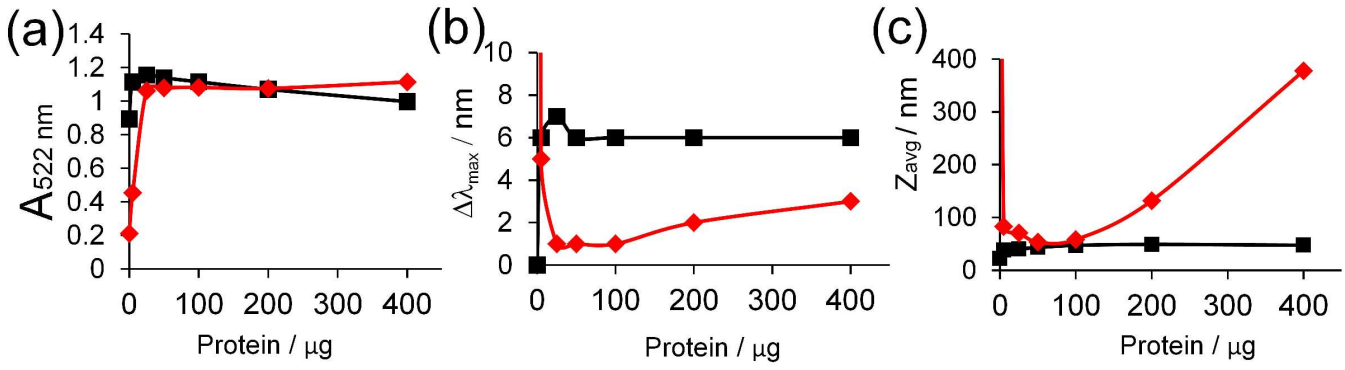

Figure S1. (a) Absorbance of naked 20 nm AuNP with various conc. of A2780 lysate (black line) at 522 nm. Absorbance of the AuNP at respective protein conc. upon addition of 1% NaCl solution (Red line). (c) Shift in wavelength (Δλ) of naked 20 nm AuNP with various conc. of A2780 lysate (black line). Change in wavelength (Δλ) at respective protein conc. upon addition of 1% NaCl solution (Red line). (d) Average size of 20 nm AuNP with increasing conc. of protein (black line). The red line shows the size of the respective particles after addition of 1% NaCl.

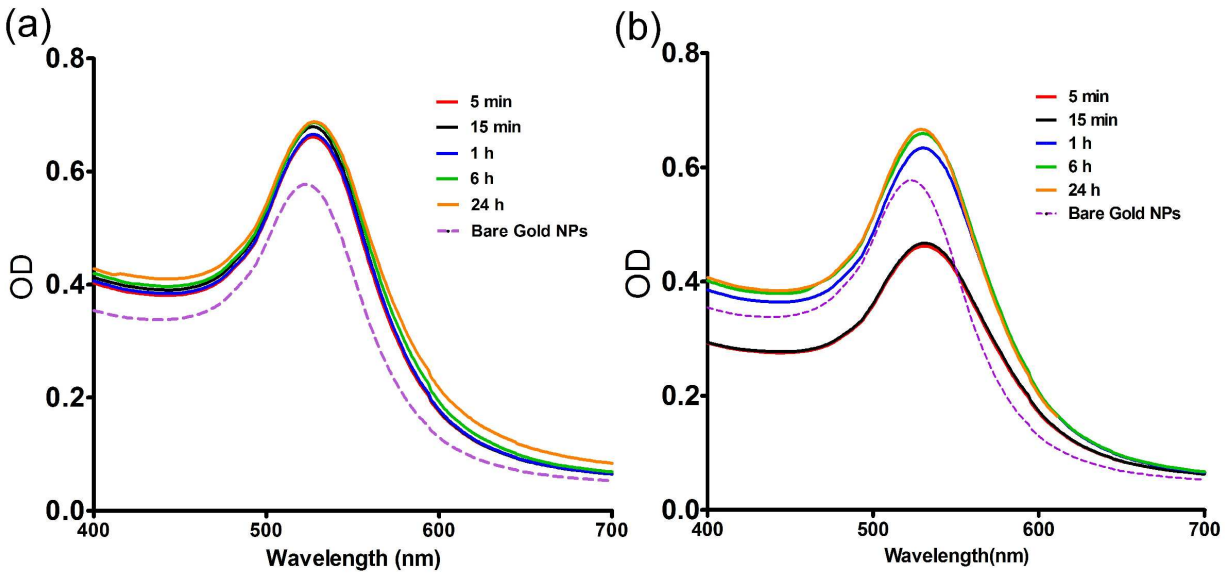

Figure S2. UV-Vis spectroscopic analysis of bare AuNPs (purple dash) and NP-protein complex after incubation of NPs with A2780 lysates at various time points. Measurements were conducted either a) directly after incubation or b) after centrifugation and resuspension in water to remove unbound proteins.

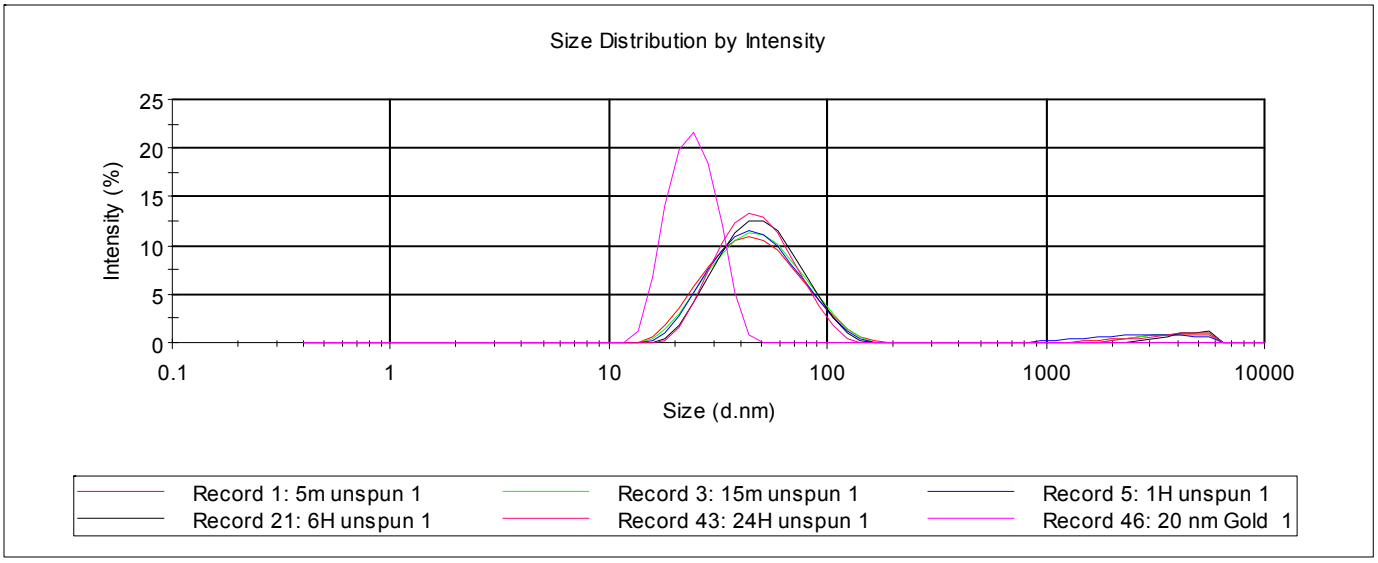

Figure S3. Characterization of AuNPs after incubation with A2780 lysates for different time points using dynamic light scattering. NPs were analyzed directly after incubation period. The distribution of the particle diameters is represented by % intensity. The z-average diameter of at all-time points is 42.90 nm while that of NPs was 22.81.

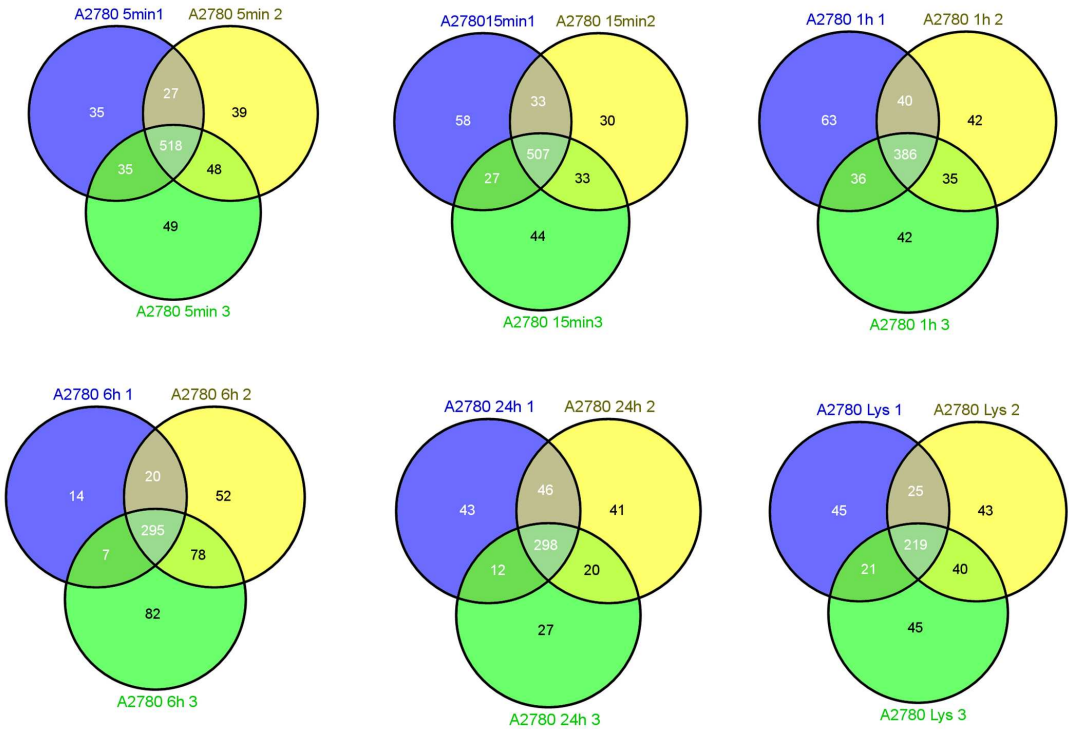

Figure S4. The identification of the proteins in the protein-NP complex derived from A2780 using tandem mass spectrometry (MS/MS). Venn diagram depicts reproducibility of the identification process.

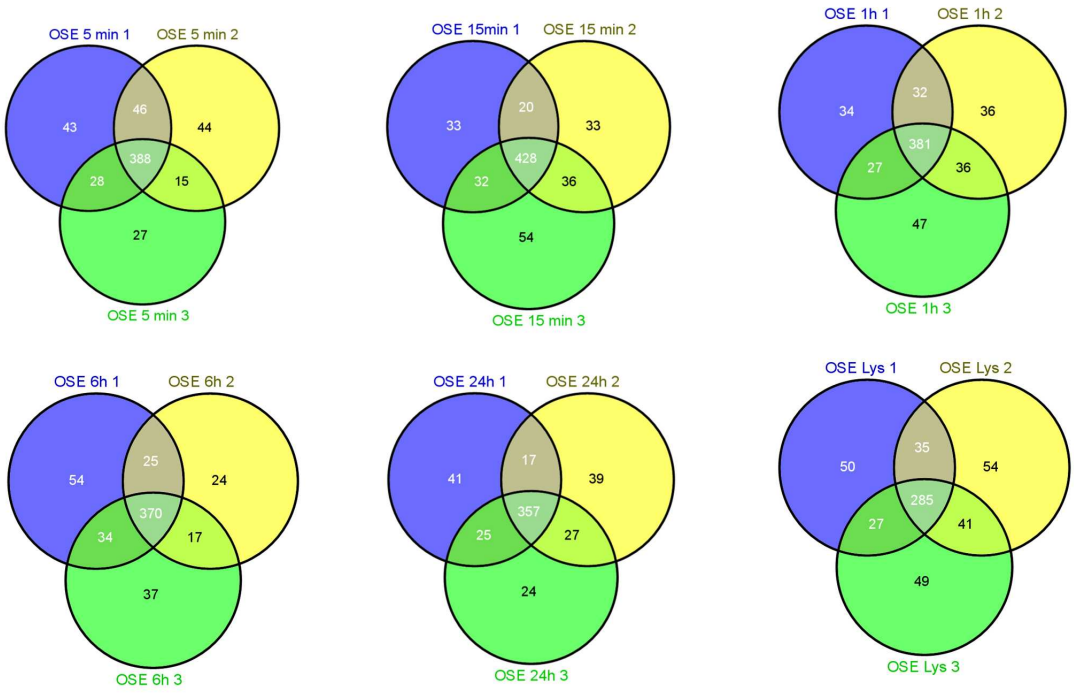

Figure S5. The identification of the proteins in the protein-NP complex derived from OSE using MS/MS analysis. Venn diagram depicts reproducibility of the identification process.

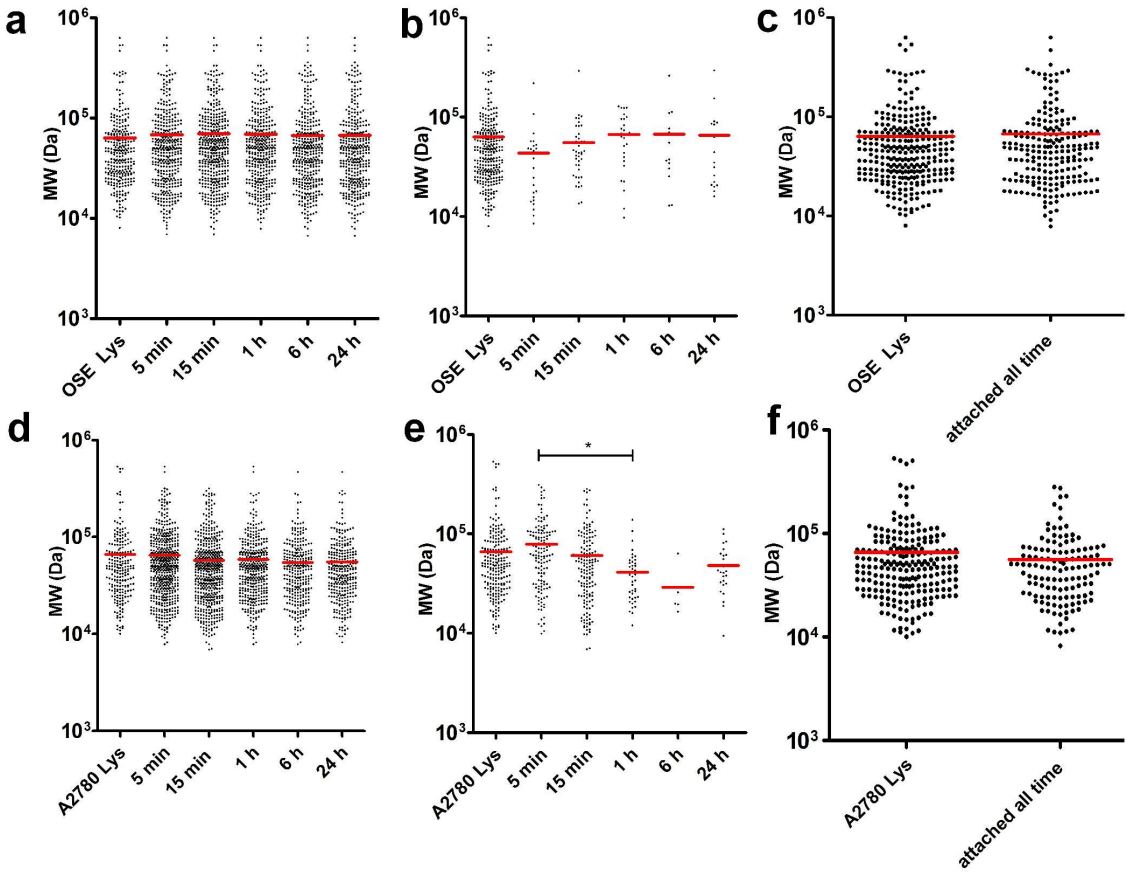

Figure S6. MW of proteins detected in the protein-NP complex derived from OSE and A2780 lysates. Comparisons made of proteins present over time (a,d), proteins exclusive at a given time point (b,e) and proteins found in the complex at all time points (c,f). (Turkey's Multiple Comparison test, *P≤0.05).

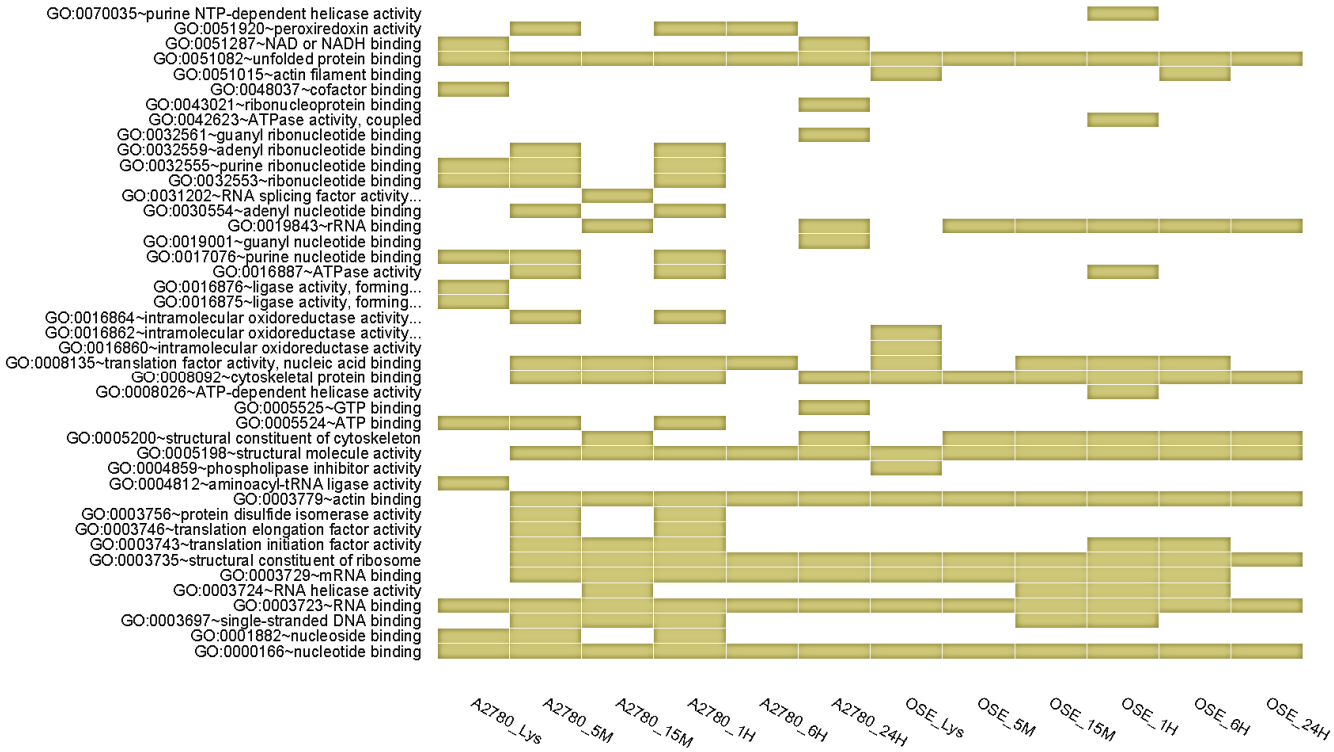

Figure S7. Dynamic view of Gene Ontology (molecular function) terms enriched in proteins detected at different time points. Molecular function terms that are significantly enriched among one or more lists are shown. Color of matrices indicate a given GO term is associated with proteins detected at a given time point (Bonferroni corrected P-values ($P <= 0.05$)). A colored cell indicates that a given GO term is significantly enriched among the proteins detected at the given time point and white color indicates that the GO term is not associated at the time-point. Term enrichment analysis was performed using DAVID v6.1 using default settings. Human proteome was defined as the background.