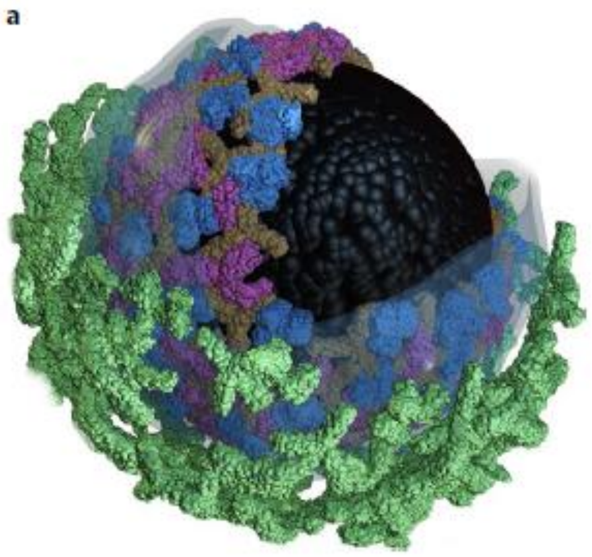
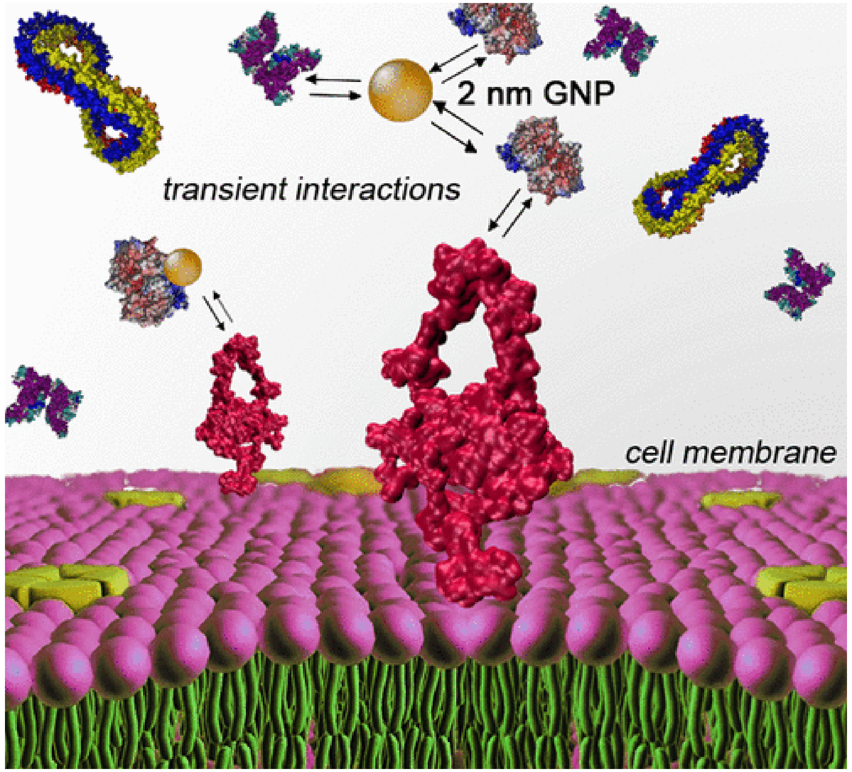
PROTEIN CORONA

In a biological fluid, proteins associate with nanoparticles, and the amount and presentation of the proteins on the surface of the particles leads to an *in vivo* response.
Proteins compete for the nanoparticle ‘‘surface,’’ leading to a protein ‘‘corona’’ that largely defines the biological identity of the particle. Thus, knowledge of rates, affinities, and stoichiometries of protein association with, and dissociation from, nanoparticles is important for understanding the nature of the particle surface seen by the functional machinery of cells.

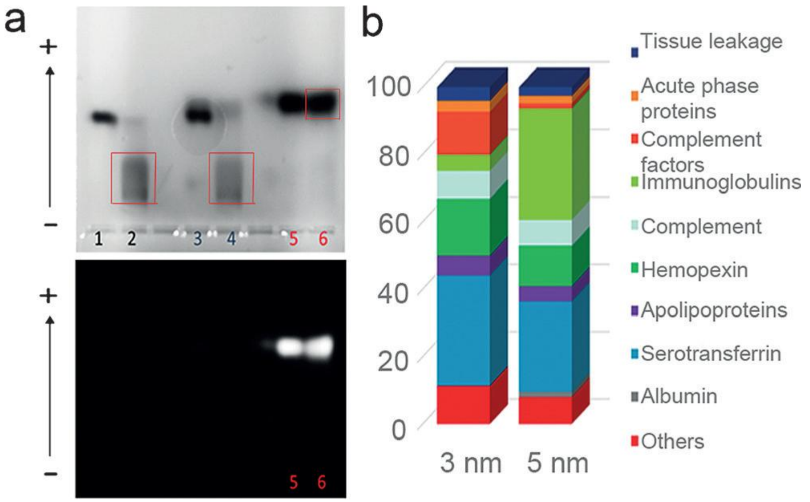
PNAS **2007**, *104*, 2050-2055.
Acc. Chem. Res. **2023**, *56*, 3369-3378





effetto delle dimensioni delle NP

The kinetic and equilibrium binding properties depend on protein identity as well as particle Surface characteristics and size.



ACIE 2017, 56, 4125.

Figure 2. a) 1% Agarose gel-assay in a native buffer. The numbered lanes refer to 5 nm GNP-PEG-COOH in PBS (1) and in HP (2), 3 nm GNP-PEG-COOH in PBS (3) and in HP (4), 2 nm GNP-PEG-COOH in PBS (5) and in HP (6). Below, the image captured by fluorescence detection mode. Note: only 2 nm GNP-PEG-COOH exhibit fluorescence. b) Mass spectrometry analysis of 3 nm and 5 nm GNP-PEGCOOH corona complexes isolated by agarose gel electrophoresis.

decorazione delle NP

Characterization of Protein Corona

- X-ray-Based Techniques to Study the Nano−Bio Interface
- Isothermal TitrationCalorimetry (ITC)
- Surface plasmon resonance technology (SPR)
- Size exclusion chromatography of protein–nanoparticle mixtures / gel filtration
- Protein Identification by Mass Spectrometry upon SDS/PAGE protein separation

J. Am. Chem. Soc. **2007**, *129*, 10747−10753

ITC

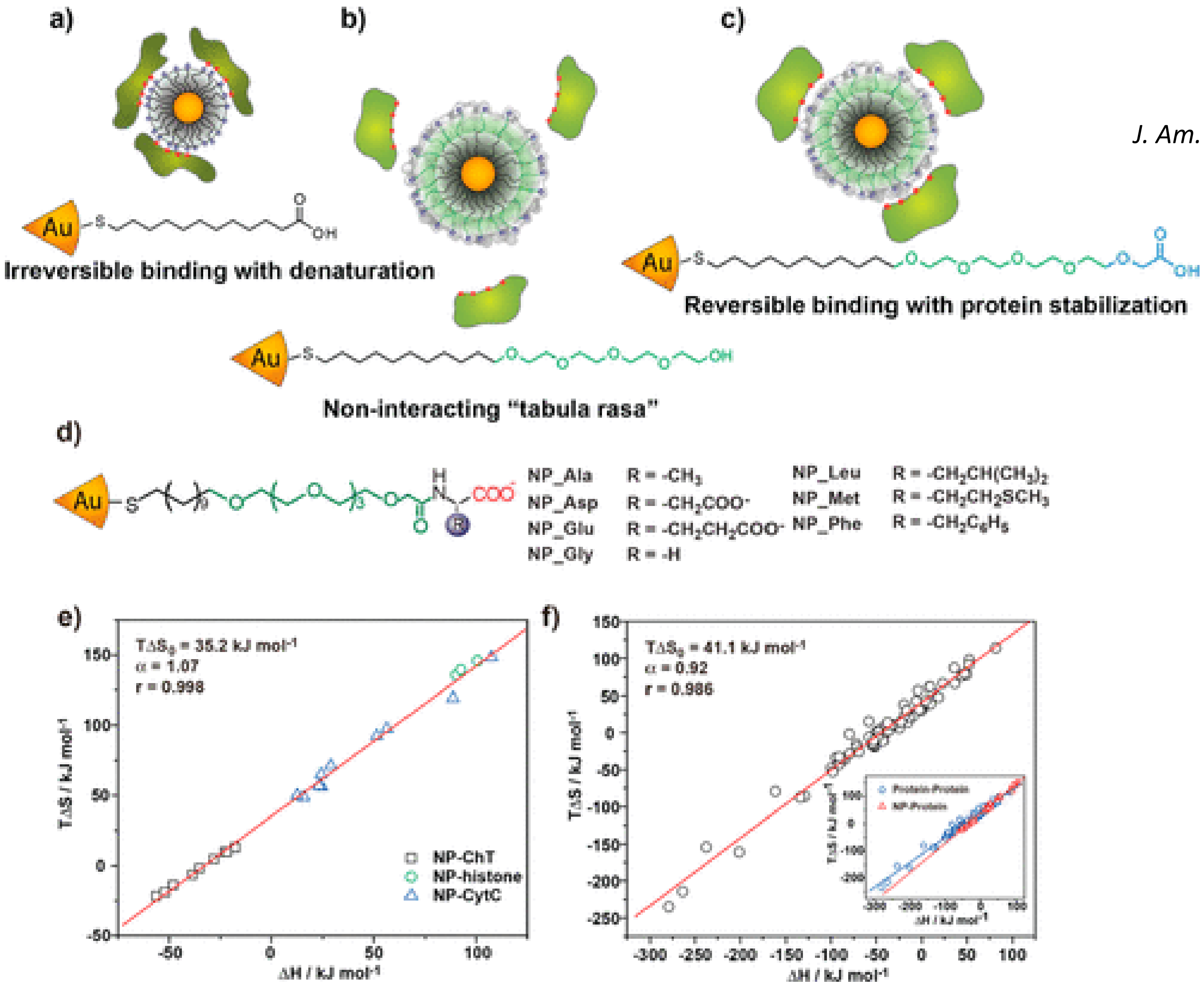
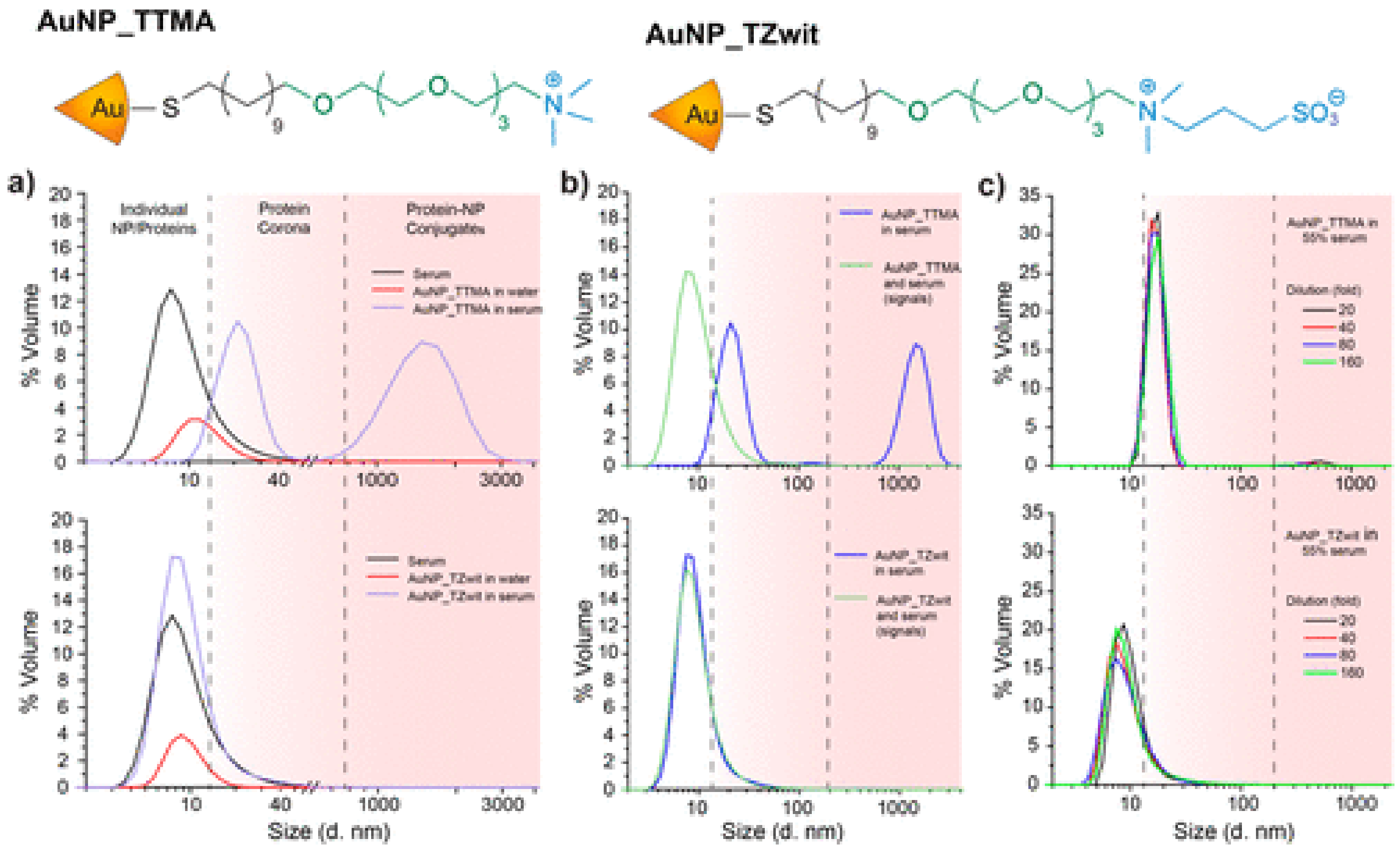


Figure 4. (a) Surfactant-like ligands bind and denature ChT. (b) TEG disrupts protein binding. (c) Appending a carboxylate to the outside of the TEG layer provides ChT binding without denaturation. (d) Gold nanoparticles (2 nm core) with anionic amino acid termini. Quantification of (e) nanoparticle−protein and (f) protein−protein interactions by ITC. Overlap of entropy−enthalpy compensation plots shown in the inset.

DLS



(a) Protein complexation is observed by DLS with AuNP_TTMA but not with AuNP_TZwit. (b) Large aggregates are observed in serum (5%) with AuNP_TTMA but no larger-sized assemblies were observed with AuNP_TZwit. (c) Dilution after incubation in 55% human serum showed no irreversible corona formation with either AuNP_TZwit or AuNP_TTMA, where size increase corresponds to a simple monolayer of protein around the particle.

ACS Nano **2014**, *8*, 6748−6755.