

## Supporting Information for:

### Understanding the Adsorption of Peptides and Proteins onto PEGylated Gold Nanoparticles

Y. Randika Perera,<sup>1,†</sup> Joanna Xiuzhu Xu,<sup>1,†</sup> Dhanush L. Amarasekara,<sup>1</sup> Alex C. Hughes,<sup>1</sup>  
Ibraheem Abbood,<sup>2</sup> and Nicholas C. Fitzkee<sup>1,\*</sup>

<sup>1</sup>Department of Chemistry, Mississippi State University, Mississippi State, Mississippi 39762,  
United States

<sup>2</sup>Department of Chemistry, University of Arkansas at Little Rock, Little Rock, Arkansas 72204,  
United States

<sup>†</sup> These authors contributed equally to this work.

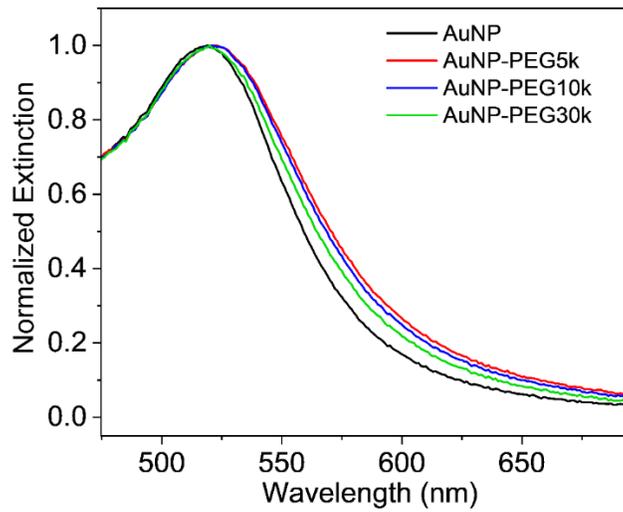
\* To whom correspondence should be addressed:

Email: [nfitzkee@chemistry.msstate.edu](mailto:nfitzkee@chemistry.msstate.edu)

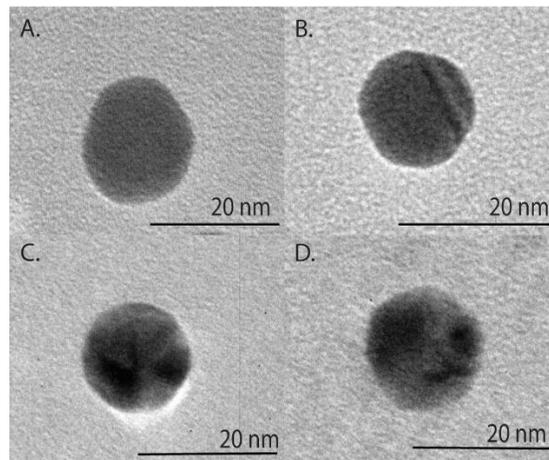
ORCID: 0000-0002-8993-2140

Phone: (662) 325-1288

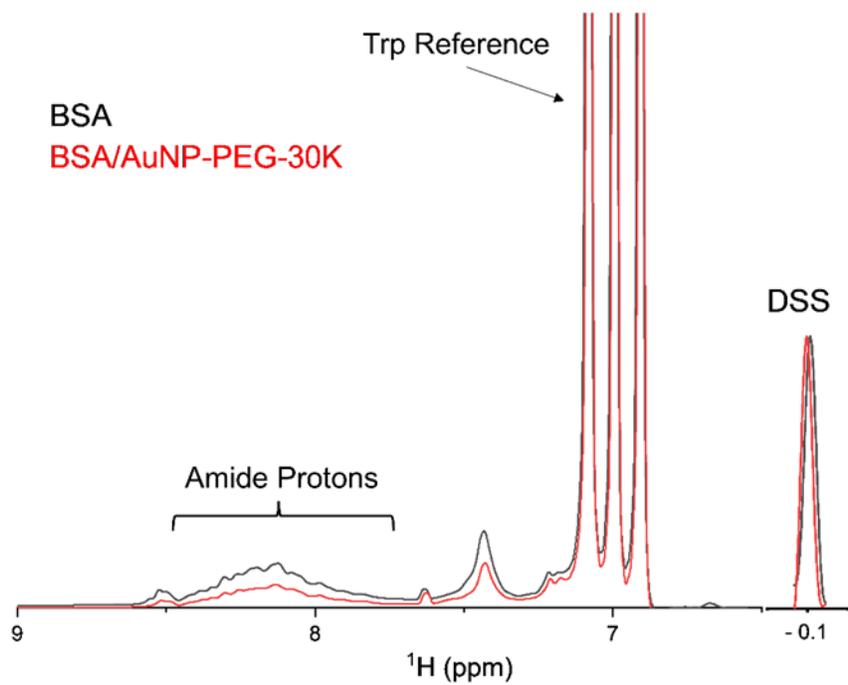
Fax: (662) 325-1618



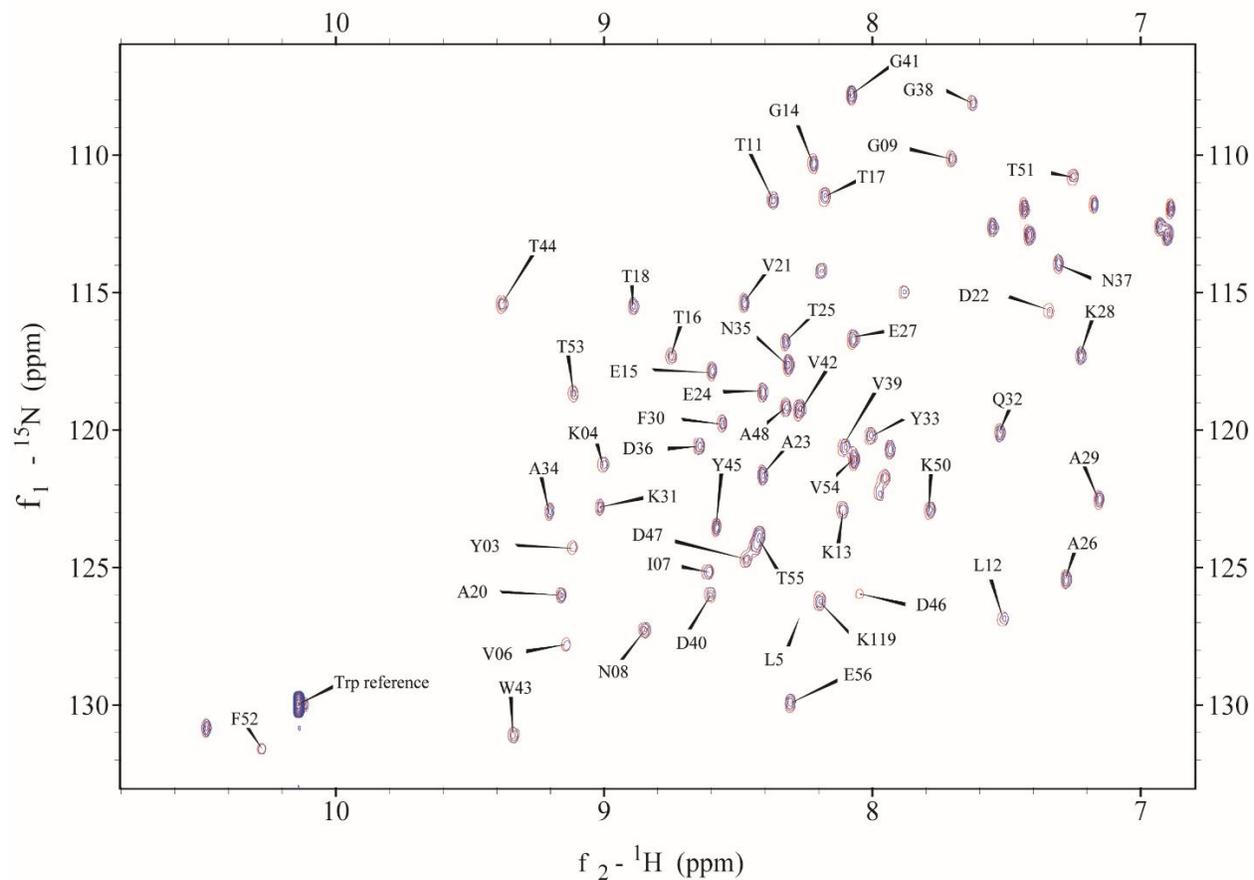
**Figure S1.** UV-vis spectra of (black) bare AuNP, (red) 5K-PEG-SH coated AuNP, (blue) 10K-PEG-SH coated AuNP, (green) 30K-PEG-SH coated AuNP. All spectra are normalized with the maximum extinction to be 1.



**Figure S2.** Transmission electron microscopy (TEM) characterization of PEG-grafted gold nanoparticles. Representative TEM images of (A) AuNP-PEG-5K, (B) AuNP-PEG-10K, (C) AuNP-PEG-30K and (D) bare 15 nm-AuNP.



**Figure S3.** Example of quantifying protein unbound concentrations using 1D NMR for BSA. The black and red spectra are 20  $\mu\text{M}$  BSA control sample and 20  $\mu\text{M}$  BSA mixed with 120 nM AuNP-PEG-30K, respectively. Protein signals are reduced due to NP binding. TopSpin software is used to scale the amide proton region to calculate the amount of signal lost as a function of time.



**Figure S4.** Example of quantifying protein bound concentrations using 2D NMR for K19C GB3. The red and blue spectra are 20  $\mu\text{M}$   $^{15}\text{N}$  labeled K19C GB3 control sample and 20  $\mu\text{M}$  K19C GB3 mixed with 120 nM AuNP-PEG-30K for 1 hr, respectively. Protein signals are reduced due to NP binding. The peak intensities of K19C GB3 control sample and NP-containing sample are first normalized by the external reference  $^{15}\text{N}$ -Trp before determination of the fraction of unbound protein by dividing the latter by the former sample intensities.

**Table S1.** Summary of bound concentration ([bound]) of ligand when mixing 20  $\mu\text{M}$  ligand with 120 nM 15-nm AuNPs and observed rate constants ( $k_{obs}$ ) of 20  $\mu\text{M}$  different ligands onto 120 nM PEGylated AuNPs used in this work

	AuNP-PEG-5K		AuNP-PEG-10K		AuNP-PEG-30K	
	[bound] ( $\mu\text{M}$ )	$k_{obs} \times 10^{-5}$ ( $\text{s}^{-1}$ )	[bound] ( $\mu\text{M}$ )	$k_{obs} \times 10^{-5}$ ( $\text{s}^{-1}$ )	[bound] ( $\mu\text{M}$ )	$k_{obs} \times 10^{-5}$ ( $\text{s}^{-1}$ )
<b>H1.5</b>	$6.8 \pm 0.5$	$1.3 \pm 0.2$	$9.7 \pm 0.2$	$3.0 \pm 0.5$	$12.8 \pm 0.3$	$4.3 \pm 0.2$
<b>H1.5-Cys*</b>	$17.7 \pm 0.2$	$460 \pm 80$	$18.4 \pm 0.2$	$690 \pm 120$	$18.0 \pm 0.2$	$1390 \pm 70$
<b>GSH</b>	$9.6 \pm 0.4$	$2.9 \pm 0.1$	$11.7 \pm 0.1$	$4.0 \pm 0.2$	$14.8 \pm 0.2$	$6.1 \pm 0.2$
<b>wt GB3</b>	$0.4 \pm 0.5$	N/A	$2.4 \pm 0.4$	$1.0 \pm 0.5$	$4.9 \pm 0.5$	$1.9 \pm 0.8$
<b>K19C GB3</b>	$2.0 \pm 0.5$	$5.4 \pm 0.5$	$4.7 \pm 0.4$	$9.0 \pm 1.4$	$7.0 \pm 0.4$	$44 \pm 7$
<b>BSA</b>	$2.0 \pm 0.4$	$7.6 \pm 1.8$	$2.2 \pm 0.4$	$15.0 \pm 1.9$	$3.2 \pm 0.2$	$14 \pm 2$

\* The fastest rate observable in our experiments is approximately  $900 \text{ s}^{-1}$  based on a 15-minute dead time. The rates for H1.5-Cys are therefore approximate.

**Table S2.** Comparison of AuNP-PEG concentrations determined by atomic absorption spectroscopy (AAS) and concentrations determined using the extinction coefficient at 520 nm ( $3.9 \times 10^8 \text{ M}^{-1} \text{ cm}^{-1}$ ), as described in the text.

	[AuNP] by AAS (nM)	[AuNP] by UV-vis (nM)	Difference (%)
<b>AuNP</b>	1.638	1.60	2.5
<b>AuNP-PEG-5K</b>	1.638	1.69	-3.2
<b>AuNP-PEG-10K</b>	1.637	1.73	-5.8
<b>AuNP-PEG-30K</b>	1.637	1.67	-1.8