Supporting Information

Evaluation of nonspecific interaction between quantum dots and proteins

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1. Stability of COOH-QDs in buffers with different *I* and pHs

To ensure that the measurements of the interaction are reproducible and believable, the COOH-QD stability in buffers was evaluated. Five buffers with pH from 6~9 in the same ionic strengths (150 mM) were selected. As shown in Figure S1a, in the wide pH range, the intensity of fluorescence and the shape of the emission peak did not change significantly, indicating that COOH-QDs were very stable in the conditions. In pH 5, the intensity of fluorescence was decreased by 30%. This may be caused by the going through of the excessive H^+ in part of the COOH-QDs outer-shell.[1] If the pH was re-adjusted back to 6~9, the intensity of the fluorescence would recover, indicating that the outermost layers of COOH-QDs directly interacting with proteins were not destroyed and remained their characteristic in proper condition.

Four ionic strengths (I = 50 mM, 150 mM, 300 mM and 500 mM) with the same pH (7.2) and five different pHs (5.57, 6.30, 7.32, 8.49 and 9.21) with the same ionic strength (I = 150 mM) were used to evaluate the stability of COOH-QDs. As is shown in Figure S1b, the fluorescence intensity of COOH-QDs decreased slightly with the rising of ionic strengths, which is the same as in the previous reports. The decrease in

fluorescence may be caused by the reducing thickness of the diffuse layers on the COOH-QDs with the increasing of ionic strengths. In high ionic strength buffers, charged particles approach each other close enough during thermal collisions. In this case, the long-range repulsive electrostatic forces were overcome by the short-range attractive van der Waals force.[1] The fluorescence decrease is within 20% in the experimental condition, indicating that COOH-QDs were rather stable in that range of ionic strengths.

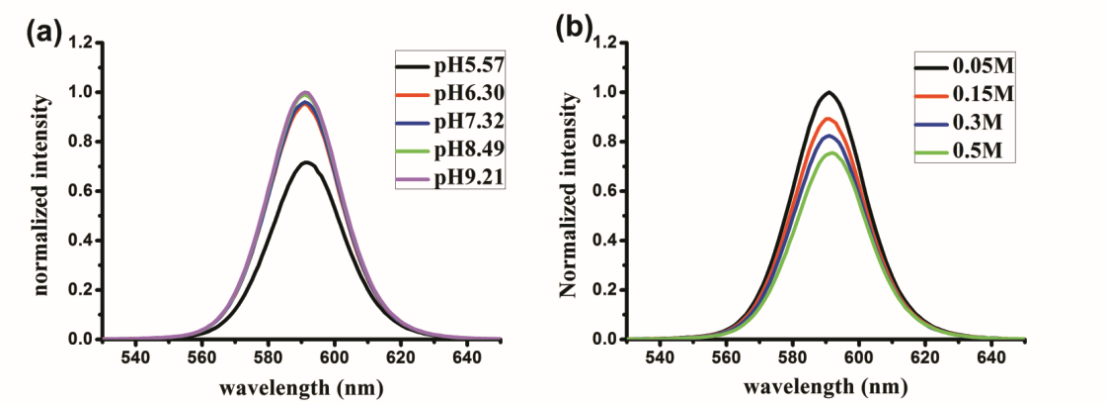

Figure S1. Fluorescence spectra of COOH-QDs in buffers of different ionic strengths (pH 7.2) (a) or pHs (I =150 mM) (b).

2. Force curves obtained in the measurements of nonspecific interaction

As is shown in Figure S2, an obvious negative peak was observed on the retrace curves obtained from the interaction between proteins and COOH-QDs. In different buffers, the depth and shape of the negative peaks varied, indicating that the nonspecific interaction varied. Results were calculated and listed in Table S1 and Table S2.

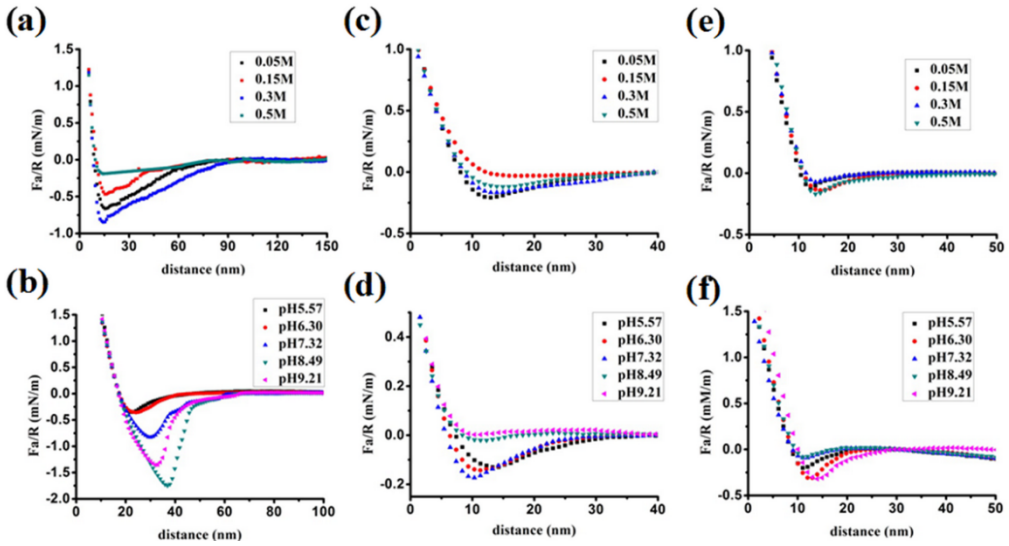

Figure S2. Force curves obtained between proteins (BAS, IgG and WGA) and COOH-QDs in buffers with different ionic strengths and pHs. BSA, ionic strengths (a), pH (b); IgG, ionic strengths (c), pH (d); WGA, ionic strengths (e), pH (f). Forces were normalized by the radius of the colloid probes.

3. The pull-off distance (L_p) and separating energy (E_s) of nonspecific interaction

Accordingly, L_p is the minimum separation at which all of the bonds between the surfaces are broken. The E_s is the work needed to separate the surfaces that is calculated by the area between the retraction curve and the baseline. In the measurements, these two parameters were also calculated as shown in Table S1 and Table S2.

Generally, L_p was affected by the size of proteins, and related with thickness of the charge diffusion layer. E_s were affected by both the F_a and L_p. For BSA, Results showed that the measured L_p for COOH-QDs and BSA were all about 50 nm. Considering that the size of COOH-QDs was about 25 nm and the long axis

of BSA was about 14 nm, the values may be broadened a little by the thickness of hydration layers but still remained in a reasonable range. The negligible changes indicated that both BSA and COOH-QDs were quite stable in their structures during the whole experiment. During the process, E_s was significantly affected by F_a, which meant that due to the increase of electrostatic repulsion, work needed for the separation reduced. For IgG, a sharp decrease of L_p with the increase of ionic strengths were observed, further suggesting that IgG were tightly compressed with the increasing ionic strengths, which may cause IgG conformation to be too compact for the adhesion. The variety of E_s showed the same trend as F_a.

Table S1. The L_p and E_s of the nonspecific interaction between COOH-QDs and three proteins (BSA, IgG and WGA) in buffers with different pHs.

pH	**L_p (nm)**			**E_s (10^{-12}J/m)**		
	BSA	IgG	WGA	BSA	IgG	WGA
5.57	30~55	53~90	13~35	-19±5.8	-1.9±0.6	-2.8±0.9
6.30	21~53	32~50	23~29	-26±12	-1.7±0.4	-4.0±1.5
7.32	27~47	36~51	20~41	-22±17	-2.8±1.4	-3.7±2.3
8.49	20~53	27~63	17~27	-4.4±3.6	-3.1±1.1	-3.0±1.5
9.21	21~47	15~41	25~48	-4.1±1.9	-2.1±1.5	-7.2±4.2

Table S2. The L_p and E_s of the nonspecific interaction between COOH-QDs and three proteins (BSA, IgG and WGA) in buffers with different ionic strengths.

Ionic Stength (mM)	**L_p (nm)**			**E_s (10^{-12}J/m)**		
	BSA	IgG	WGA	BSA	IgG	WGA
50	40~60	33~64	16~33	-1.4±0.8	-4.1±1.3	-1.3±1.2
150	32~57	33~58	11~50	-1.4±0.8	-3.4±0.8	-3.7±2.3
300	41~51	26~58	13~46	-0.8±0.5	-1.2±0.6	-2.2±1.1
500	44~62	13~34	13~30	-1.6±0.7	-0.21±0.13	-2.9±2.2

1. D. Yu, Z. Wang, Y. Liu, L. Jin, Y. Cheng, J. Zhou and S. Cao, *Enzyme and Microbial Technology*, 2007, **41**, 127-132.