Supplementary Information

Tuning of Silica Nanoparticles-Lysozyme Protein Complexes in presence of SDS Surfactant

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1. Contrast matching in SANS

Isotopes of the same element can have significantly different scattering lengths for neutrons. For example, the scattering length of hydrogen is negative (-0.374×10^{-12} cm) and that deuterium is positive ($+0.667 \times 10^{-12}$ cm). Due to the difference in the scattering lengths of H and D, it is possible to have a very good contrast between the hydrogenous particle and the solvent by deuterating either the particle or the solvent. Scattered neutron intensity in a SANS experiment depends on the contrast factor, $(\rho_p - \rho_s)^2$, the square of the difference between the average scattering length densities of the particle and solvent. The values of ρ_p and ρ_s depend on the chemical composition of the particle and the solvent. The contrast between the particle and the solvent can be varied continuously by using mixed hydrogenated and deuterated solvents. Various possibilities of contrast variation by using D_2O and/or H_2O as solvent are shown in Fig. S1. Fig. S1(a) shows a hydrogenous spherical particle suspended in H_2O. Let the scattering length densities be ρ_p of the particle and ρ_H of the solvent. In this case, $\rho_p \sim \rho_H$ and thus the particle is not visible for neutrons. However, the solvent can be replaced with D_2O, so the scattering length density of D_2O is ρ_D which is quite different from ρ_p. Fig. S1(b) shows a two-component system suspended in H_2O or D_2O. Let ρ_1 and ρ_2 be the scattering

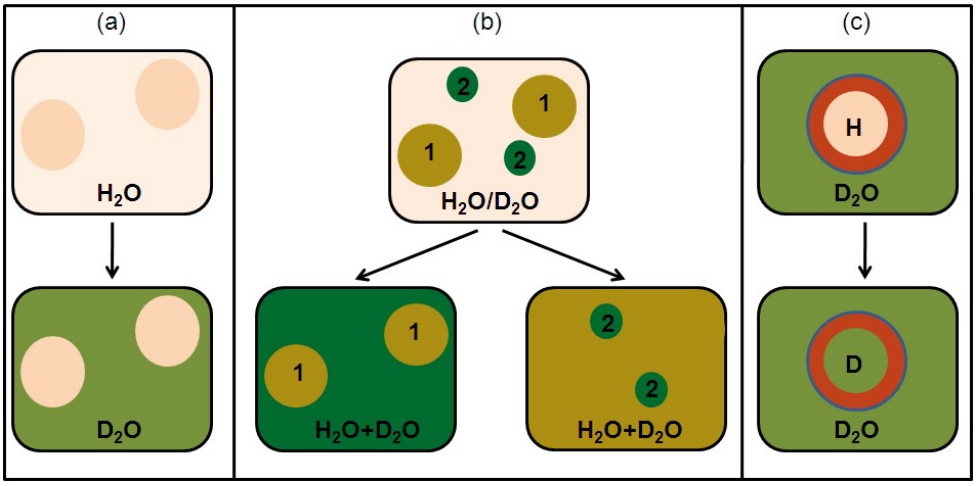

Fig. S1 Various possibilities of contrast variations in SANS experiment (a) solvent replacement, (b) use of combination of H_2O-D_2O as a solvent and (c) isotope labelling where the core is deuterated.

length densities of the components 1 and 2, respectively. The solvent has a scattering length density ρ_s, which can be varied by varying the relative amounts of H_2O and D_2O in the solvent. Thus ρ_s can be either matched with ρ_1 so that the SANS distribution is determined by component 2 alone or ρ_s with ρ_2 so that the SANS intensity is governed by component 1 alone. This method is called "external contrast variation". Deuterium labeling is another way of contrast matching [Fig. S1(c)]. Considering a spherical core-shell particle is placed in D_2O solvent. The constituents of the inner core are different from those of the outer shell of the particle. By deuterating the core of the particle, scattering length densities of the core (ρ_{core}) and D_2O (ρ_D) can be matched, thus only the shell is visible. In a similar way, the scattering signal only from the core can be obtained by deuterating the shell (ρ_{shell}). This method is known as "internal contrast variation". In the present manuscript, we have used the "external contrast variation" or contrasting matching by solvent approach. The materials used for this study are listed in Table S1 along with their scattering length density.

Table S1. The calculated scattering length densities and contrast of different components of silica nanoparticles and surfactants in aqueous solution.

Component	Scattering Length Density (cm^{-2})	Contrast matching point used (% vol D_2O)
Silica Nanoparticles	3.81×10^{10}	62
SDS	0.31×10^{10}	0
Lysozyme	2.62×10^{10}	0
D_2O	6.38×10^{10}	-
H_2O	-0.56×10^{10}	-

The contrast matching point for silica nanoparticles has been experimentally verified while for the lysozyme, it is taken from the literature.[1,2] The scattering intensity of silica nanoparticles obtained at different H_2O/D_2O volume ratios are shown in Fig. S2.

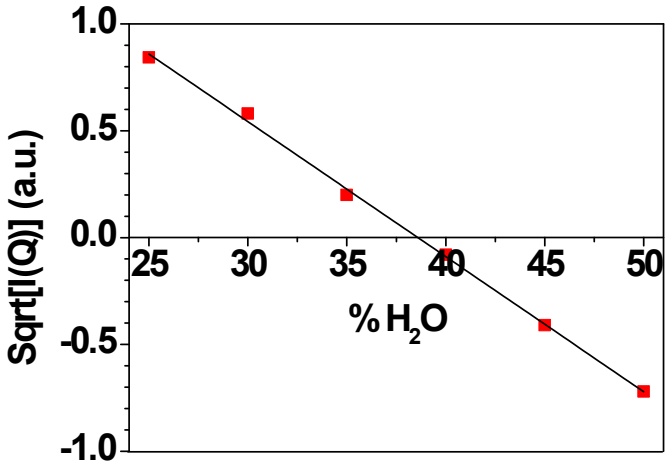

Fig. S2 Square root of the scattering intensity after correcting for incoherent background for 1 wt % silica nanoparticle system as a function of % H_2O in the mixed (H_2O/D_2O) solvent.

2. Physical States of binary complexes of lysozyme-SDS and ternary complexes of HS40-lysozyme-SDS at different SDS concentration (0-35.0 mM)

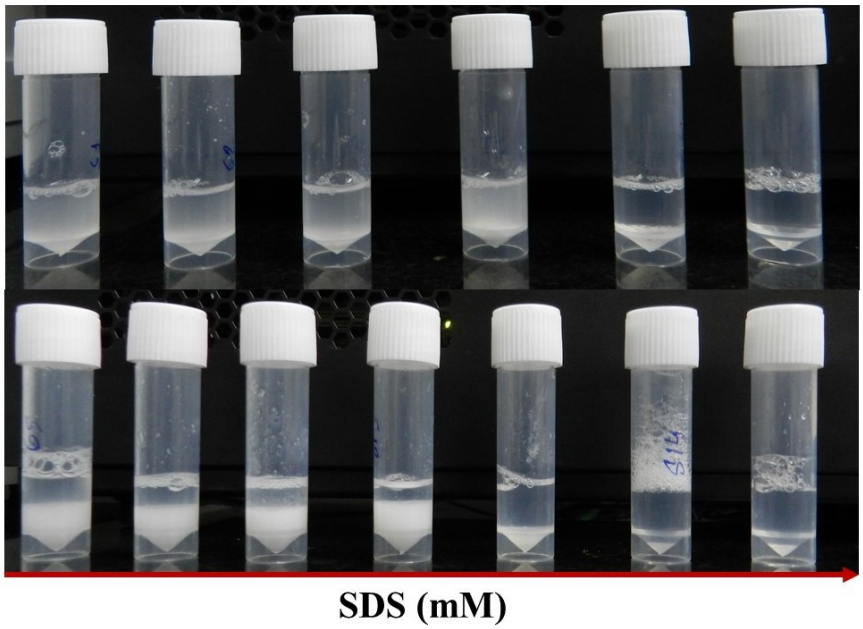

Fig. S3 Physical state of 1wt% lysozyme with 0.7-35.0 mM SDS (top) and 1wt% HS40-1wt% lysozyme with 0-35.0 mM SDS (bottom).

3. SANS of pure components

The scattering profiles of pure 1 wt% HS40 silica nanoparticle, 1 wt% lysozyme protein, and 35.0 mM SDS surfactant obtained from SANS are shown in Fig. S2. They are significantly different from each other due to the different size and contrast of the components. The SANS data of HS40 silica nanoparticles has been fitted by the spherical particle form factor following the log-normal distribution.[3,4,1] The analysis gives the mean radius of 7.9 nm with a polydispersity of 0.16.[4,5] The scattering profile of lysozyme has been fitted by the form factor contribution alone ($P(Q)$) due to the absence of interparticle interaction ($S(Q)\sim1$). The model fitting by a prolate ellipsoid ($\varepsilon > 1$) provides the semimajor axis of 2.5 nm and the semiminor axis of 1.3 nm. SDS surfactants (35 mM) also form prolate ellipsoidal shape micelles with semiminor axis and semimajor axes, as 1.6 and 2.7 nm, respectively.[6] $S(Q)$ for charged micelles has been calculated using the screened Coulomb potential under mean spherical

approximation.[7] It gives an additional fitting parameter, the effective charge on the micelle, which is found to be ~23 e.u. The structural parameters obtained from the fitting of SANS data (Table S1) of all the three components are in agreement with those reported in the literature.[4,8,9]

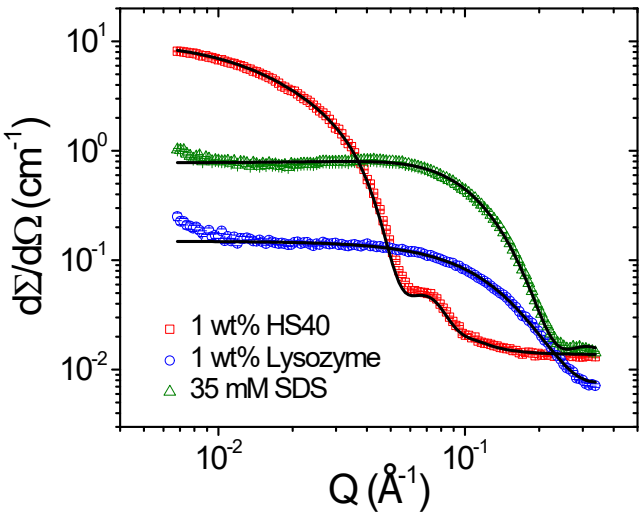

Fig. S4 SANS data of 1 wt% HS40 silica nanoparticles, 1 wt% lysozyme protein, and 35.0 mM SDS surfactant in D_2O. Data have been fitted by polydisperse sphere for silica nanoparticle and prolate ellipsoid for lysozyme protein and SDS micelles.

Table S2 Fitted structural parameters of individual components of 1wt% HS40 silica nanoparticles, 1wt% lysozyme protein, and 35 mM SDS in D_2O.

System	Shape	Polydispersity	Mean radius (nm)	Semimajor axis (nm)	Semiminor axis (nm)	Effective radius (nm)
1wt% HS40	Spherical	0.16±0.02	7.9±0.2	-	-	-
1wt% Lysozyme	Prolate ellipsoidal	-	-	2.5±0.1	1.3±0.1	1.6
35.0 mM SDS	Prolate ellipsoidal	-	-	2.8±0.1	1.6±0.1	1.9

4. DLS results of 1wt% HS40 nanoparticles without and with 1wt% lysozyme

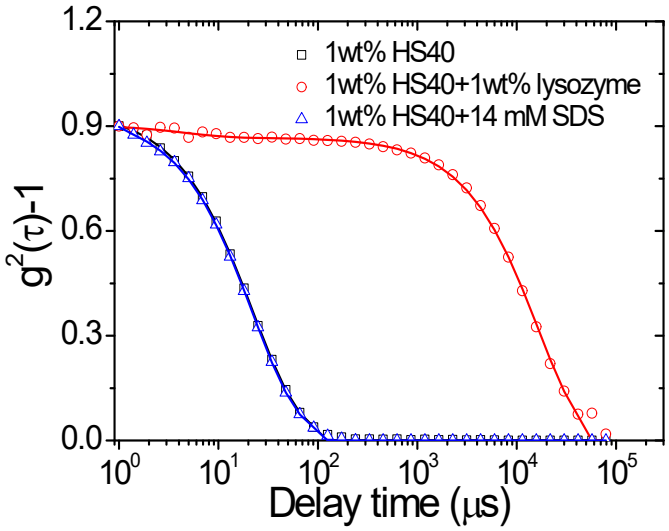

Fig. S5 DLS data of 1wt% HS40, 1wt% HS40+1 wt% lysozyme, and 1wt% HS40+14 mM SDS.

5. Adsorption isotherm of lysozyme

The adsorption of lysozyme protein on HS40 silica nanoparticles has been studied using UV−vis spectroscopy. The concentration of silica nanoparticles has been kept fixed at 1wt% while the concentration of lysozyme varied from 0 to 2 wt% in the mixture. The free protein (if any) has been separated from nanoparticles using centrifuge at 10000 rpm for 10 min. The absorbance spectra at ~280 nm, are used to determine the lysozyme concentration in the supernatant. The difference between the pristine lysozyme solution and supernatant concentrations gives the amount of adsorbed protein. Fig. S4 shows the adsorption isotherm of lysozyme on the HS40 silica nanoparticles. The adsorption for lysozyme protein as a function of its concentration (C) has been calculated using the following equation

$$A = A_0 \left(1 - e^{-KC}\right) \quad \text{(S1)}$$

where A_0 is the saturation value and K is the adsorption coefficient.[1]

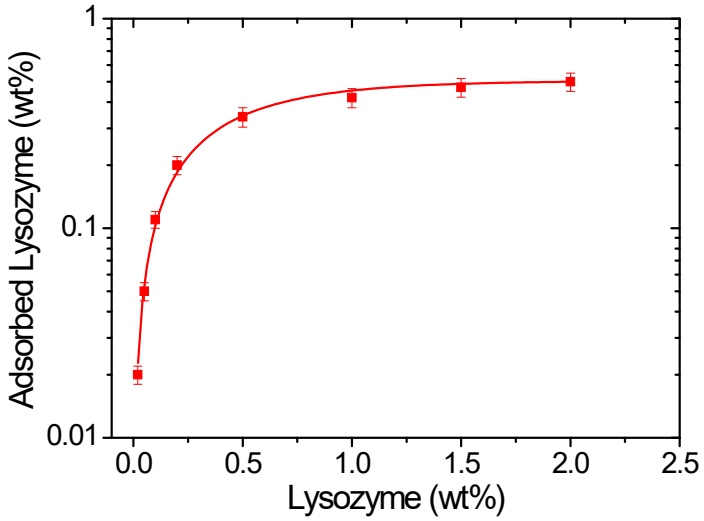

Fig. S6 Adsorption isotherms of lysozyme on 1 wt% HS40 silica nanoparticles at pH 7.0.

6. SANS results of 1wt% HS40 nanoparticles with 35 mM SDS

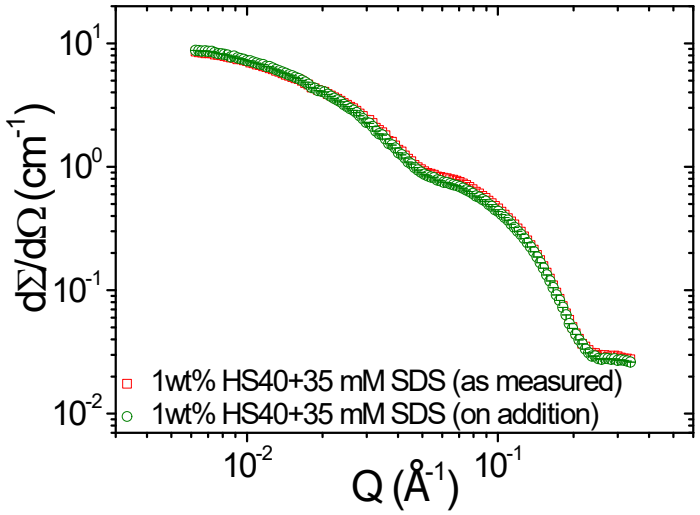

Fig. S7 SANS data from the two-component system of 1 wt% HS40 silica nanoparticles, 35.0 mM SDS surfactant mixed together in D_2O is compared to the sum of scattering from HS40 nanoparticles and SDS micelles.

Table S3 Fitted Parameters of 1wt% HS40 with varying concentrations of SDS (7-35 mM) in D_2O.

System	Structure	Nanoparticle radius (nm)	Micelle Size		Charge (e.u.)	Aggregation number
			Semimajor axis (nm)	Semiminor axis (nm)		
HS40+7 mM SDS	Nanoparticles + Micelles	7.9±0.3	2.9±0.1	1.6±0.1	-	91±4
HS40+14 mM SDS			3.0±0.2	1.6±0.1	-23.4	93±6
HS40+35 mM SDS			3.1±0.2	1.6±0.1	-23.4	94±7

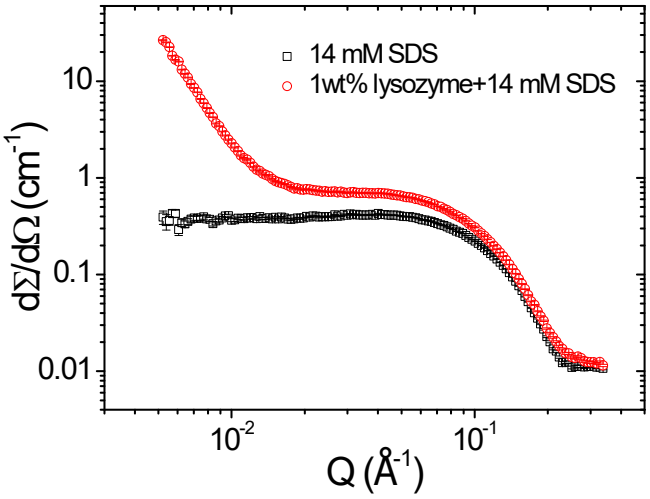

Fig. S8 Comparison of scattering of 14 mM SDS in the absence and presence of oppositely charged lysozyme.

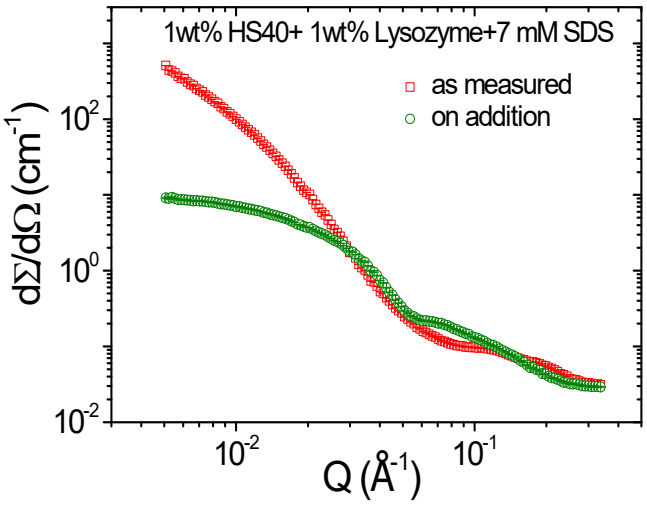

Fig. S9 SANS data from the three-component system of 1 wt% HS40 silica nanoparticles, 1 wt% lysozyme protein, and 7.0 mM SDS surfactant mixed together in D_2O.

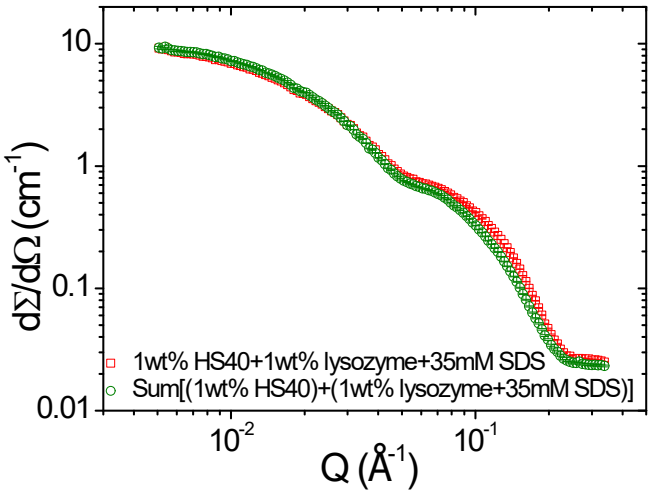

Fig. S10 SANS data from three-component system of 1 wt% HS40+1 wt% lysozyme+35.0 mM SDS surfactant compared with the sum of scattering of 1 wt% HS40 and 1 wt% lysozyme+35 mM SDS.

Table S4. The fitted structural parameters of SANS data of 1 wt% HS40 + 1 wt% lysozyme in the presence of 0-35.0 mM SDS (S/P=0-50) in D_2O.

SDS concentration (mM)	Structure	Core radius R_m(nm)	Shell thickness	Scattering length density of the shell ($\times 10^{10}$ cm^{-2})	Fractal dimension D_m	Building block radius R_b (nm)	Semimajor axis (nm)	Semiminor axis (nm)
0	Fractal Aggregates	7.9±0.2	1.4±0.2	5.71±0.30	1.94±0.25	9.5±0.5	-	-
1.4		7.9±0.2	3.6±0.2	5.40±0.27	2.27±0.21	12.5±0.4	-	-
7.0		12.4±0.5	4.0±0.3	4.42±0.22	2.32±0.20	13.1±0.7	-	-
14.0	Fractal Aggregates+ isotropic complexes of lysozyme-SDS	7.9±0.2	-	-	2.28±0.20	9.3±0.5	1.6±0.1	2.9±0.1
35.0	HS40 nanoparticles + isotropic complexes of lysozyme-SDS	7.9±0.2	-	-	-	-	1.6±0.1	3.6±0.2

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