Supporting Information

Ribbon Phase of Dendrimer-Surfactant Complexes

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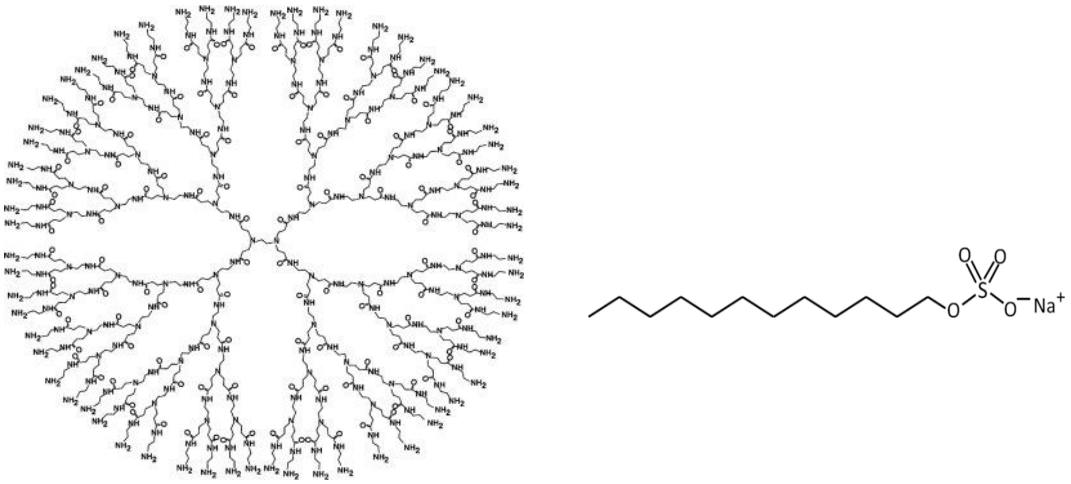


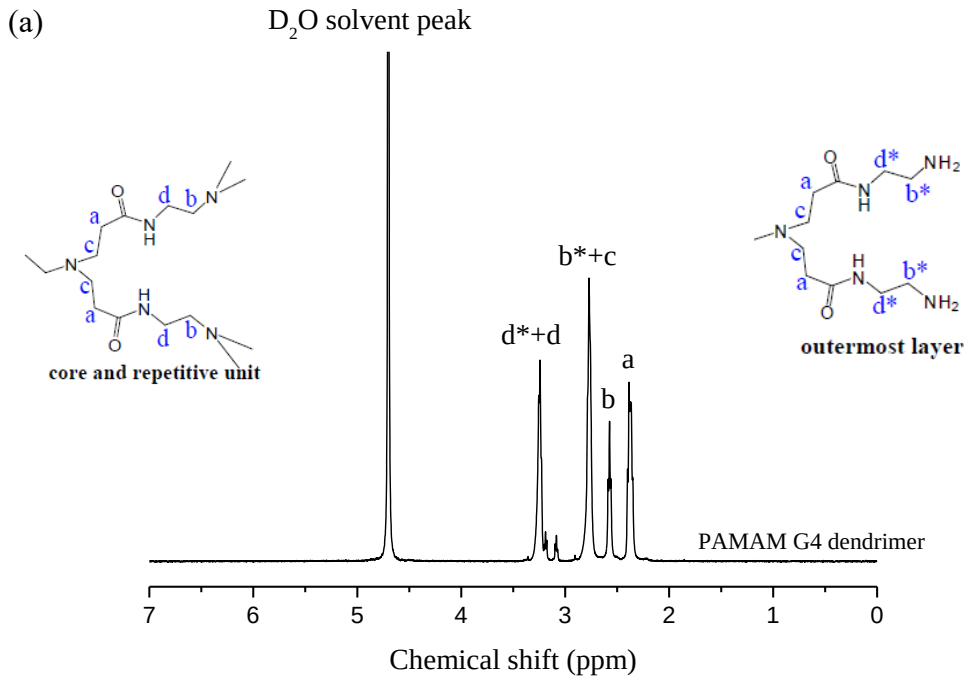
Scheme S1. Chemical structures of PAMAM G4 dendrimer and SDS

^{1}H NMR spectroscopy experiment for determination of actual SDS binding ratio, X_a

^{1}H NMR measurements of PAMAM G4 dendrimer, SDS and their complexes in d4-methanol were performed with a Bruker AVANCE 500 MHz NMR spectrometer at

298.2K. The samples were loaded in 5 mm BBFO smart probe. For the NMR measurement, the complex precipitate in the aqueous solution was collected after centrifugation at 3000 rpm for 5 minutes. The precipitate was then dried followed by dissolving in d_4-methanol for ^{1}H NMR measurement.

Figure S1 (a) and (b) show the ^{1}H NMR spectra and the assignments of the chemical shifts of neat PAMAM G4 dendrimer and SDS, respectively. For the dendrimer, the ^{1}H NMR spectrum shows mainly four peaks associated with the four methylene groups (a~d) of the repetitive unit at the interior and two methylene groups (b* and d*) at the outermost layer of dendrimer[1,2]. In the ^{1}H NMR spectrum of SDS, there are four obvious peaks denoted as 1~4 and their assignments are shown in the left panel of Fig. S1(b). The total area of the methylene peaks is contributed by 992 protons per dendrimer molecule, while one SDS molecule contributes 25 protons to the corresponding proton peaks.



(b)

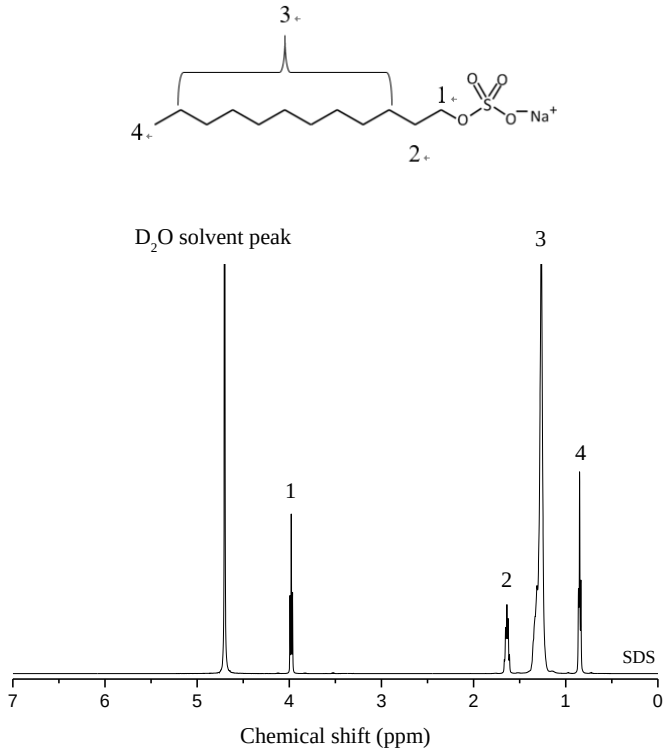


Figure S1. Assignments of the chemical shifts and the corresponding ^{1}H NMR spectra of (a) PAMAM G4 dendrimer and (b) sodium dodecyl sulfate (SDS).

Figure S2 shows the representative ^{1}H NMR spectrum of the x_n/1.0 complex in d_4-methanol. The downfield shifts of the peaks associated with the dendrimer and SDS in the complex relative to those of the pure constituents verified that SDS molecules interacted with PAMAM dendrimer through ionic interaction. The X_a of the complex was calculated as follows. Firstly, we obtained the actual ratio of the number of methylene protons from dendrimer to the protons of SDS from the corresponding integrated peak areas, i.e., $A_{G4}/A_{SDS.}$ This ratio is given by

$$\frac{A_{G4}}{A_{SDS}} = \frac{992}{25n_s} \qquad (1)$$

where n_s is the number of SDS molecules bound with a dendrimer molecule. Then, we used the actual binding number (n_s) of SDS to calculate the actual binding ratio X_a via

$X_a = n_s$ /126. The number 126 denoted the total number of amine groups in a dendrimer molecule. Table S1 lists the X_a of the complex samples prepared.

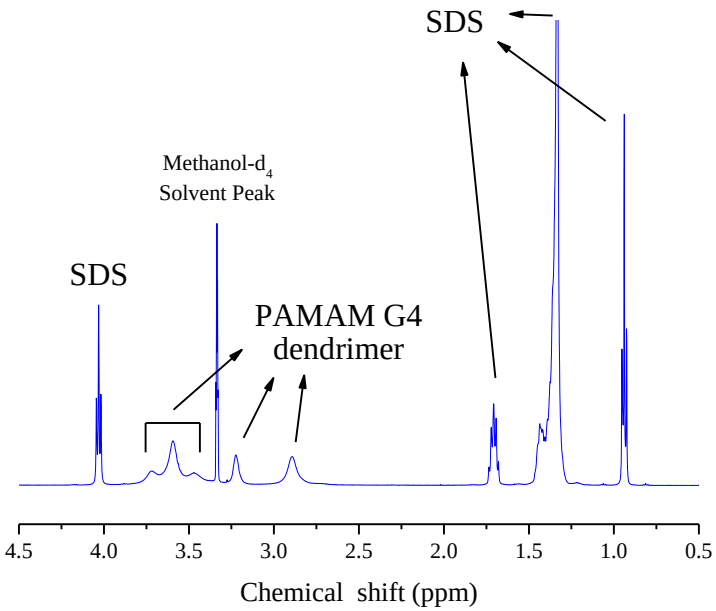


Figure S2. ^{1}H NMR spectrum of the x_n/1.0 complex. The downfield shifts of the peaks associated with the dendrimer and SDS in the complex relative to those of the pure constituents verified that SDS molecules interacted with PAMAM dendrimer through ionic interaction.

Table S1. The actual composition X_a and the lattice parameters of the complex samples prepared

X_n	X_a	Structure	a (Å)	b (Å)	l (Å)	γ (°)
0.1	0.75		48.6	70.6	42.9	55.5
0.3	0.82		48.5	70.76	42.9	55.6
0.4	0.86		48.9	70.88	43	55.3
0.5	0.90	Col_{cr}	48.9	71.04	43	55.3
0.6	0.93		48.7	70.52	42.9	55.4
0.7	0.97		48.6	70.08	43	55.6
0.8	1.01		48.5	70.08	42.9	55.6

0.9	1.04	Col_{ob}	44.8	--	41.2	60
1.0	1.08		44.3	--	41.2	60

The actual compositions of X_n/0.5 and X_n/1.0 complexes as a function of salt concentration

The actual composition of the complex prepared was largely unaffected by the presence of salt, as demonstrated in Figure S3showing that X_a of X_n/0.5 and X_n/1.0 complex samples retained at ca. 0.9 and 1.0, respectively, over the salt concentration range studied.

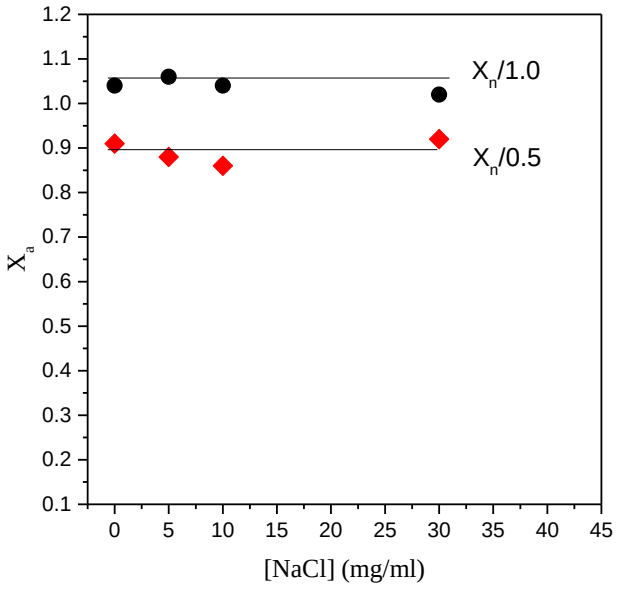


Figure S3. Actual binding ratio, X_a, of X_n/0.5 and X_n/1.0 complexes determined by ^{1}H NMR spectroscopy as a function of NaCl concentration.

References

(1) Hu, J.; Cheng, Y.; Ma, Y.; Wu, Q.; Xu, T., *J. Phys. Chem. B* **2009,** *113* (1), 64-74.

(2) Yang, K.; Cheng, Y.; Feng, X.; Zhang, J.; Wu, Q.; Xu, T., *J. Phys. Chem. B* **2010,** *114* (21), 7265-7273.