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EXAMINING SOLVATOCHROMIC REICHARDT'S DYE IN CATIONIC MICELLES OF DIFFERENT SIZE VIA MOLECULAR DYNAMICS

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Properties of the standard solvatochromic Reichardt's dye 4-(2,4,6-triphenylpyridinium-1-yl)-2,6-diphenylphenolate in micelles of *n*-dodecyltrimethylammonium bromide were investigated by means of molecular dynamics simulations. The characteristics of the location and orientation of the dye molecule as well as the nature of its microenvironment were obtained. These characteristics were compared with those in micelles of cetyltrimethylammonium bromide (CTAB). Deeper immersion of the triphenylpyridium moiety in DTAB micelle was revealed, in accordance with the experimental data. Also, the characteristics of the dye in CTAB micelles of two sizes were compared. They were found slightly different: in bigger micelles, the dye is immersed deeper into the micelle, and is hydrated weaker. The $E_T(30)$ polarity parameter of the studied micellar solutions changes in the same order as the hydration of the oxygen atom of dye molecule in corresponding micelles.

Keywords: *n*-dodecyltrimethylammonium bromide, cetyltrimethylammonium bromide, adsorption, localization, hydration, polarity parameter.

Introduction

Indicator method is a well-established technique widely used for examining various polyelectrolytes and supramolecular aggregates, particularly, proteins, micelles, mono- and bilayers. Generally speaking, it consists in measuring the properties of a particle (molecular probe) that is adsorbed by the object of interest and consequent comparing them with the properties of this probe in pure water. Usually, the UV/vis absorbance or fluorescence spectrum is measured. Consequently, as a molecular probe, solvatochromic, acid-base, and fluorescent indicators are used. This method provided the possibility to estimate such important quantities as surface electric potential, hydrogen-bond donating and accepting abilities, hydration level, and polarity, which are hard or impossible to obtain with other methods [1–3].

However, when probing micelles, the character of the indicator molecule localization and its local medium (or microenvironment) should be revealed in order to understand the meaning of the measured properties. This is because the surface layer (also called Stern layer) is thin (~0.5 nm) and inhomogeneous, thus it is needed to know the particular micelle region the indicator molecule probes. It is already known that in general outline most indicators are situated in the interface between micelle and water, however, a deeper knowledge is still desirable. In particular, it is interesting to reveal the trends in the dependency of state of a dye molecule, solubilized by a micelle, on the characteristics of the surfactant (its charge, head group structure, and length of hydrocarbon tail) [2,3].

In this paper, we investigate the most employed specimen among solvatochromic indicators, namely, 4-(2,4,6-triphenylpyridinium-1-yl)-2,6-diphenylphenolate or the standard Reichardt's dye (RD, Fig. 1). Such indicators provide information about the polarity of micelle surface layer. Actually, polarity is the effective result of two other properties of the medium: relative permittivity and hydrogen bond donating ability, and both of them are simultaneously sensed by solvatochromic indicators [2,3].

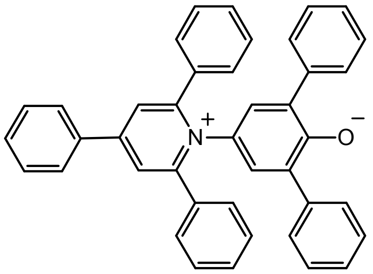

Fig. 1. Molecular structure of the standard Reichardt's dye

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Now we continue our investigation of RD solubilized by micelles of various surfactants. By present, we have studied it in micelles of *n*-hexadecyl-(cetyl-) trimethylammonium bromide (CTAB), sodium *n*-dodecyl sulfate (SDS), and sodium cetyl sulfate (SCS) [4,5]. No significant difference has been found between dye localization and orientation in two last micelles, which are dissimilar in the length of the tail group only [5]. Here we study RD in *n*-dodecyltrimethylammonium bromide (DTAB) micelles in order to compare the dye characteristics with those in CTAB: its homologue with longer tail group. This problem receives extra interest because for RD dissolved in solutions of DTAB and CTAB, experimental data on the molecule location in micelles is available, that is not the case of its SDS and SCS solutions. Another important aspect is the sensitivity of the dye state to the micelle size. Micellar solutions usually contain micelles of a range of sizes, and this distribution changes with surfactant concentration or addition of electrolytes. At the same time, it is computationally demanding to perform simulations of a probe of interest in micelles of several sizes. If this sensitivity is negligible, then simulating RD in micelles of some single aggregation number is sufficient to obtain results, which are representative for micelles of other sizes, as well, and, consequently, for a micellar solution as a whole. Otherwise, it becomes necessary to know the average aggregation number at given conditions of experiment and perform simulations of the probe in such micelles (or even in micelles of several most populated aggregation numbers and then average results).

Basic theory part

MD simulations were performed at standard conditions (temperature of 298 K and pressure of 1 bar). For this, Berendsen couplings were used with the thermostat time constant of 1 ps and the barostat time constant of 1.5 ps. Time step equaled 2 fs, the 3D periodic boundary conditions were imposed. Electrostatic interactions were computed by means of the PME method, while van der Waals interactions were cut off at 1 nm. All covalent bonds were constrained. GROMACS 5 software package was used for simulations.

The potential model for RD was taken from our previous works [4]. It was developed in the framework of the widely used and well-validated OPLS-AA force field. For DTAB, the model was built using the same principle as used for CTAB [6]: all parameters were taken from the force field, except the ones for H–C–C–H and C–C–C–C dihedral angles, which were adopted from [7]. The reason is that the corresponding standard OPLS-AA parameters are not suitable for long hydrocarbon chains and lead to artifacts in properties of higher hydrocarbons and lipids. At the same time, micelle hydrocarbon core resembles a hydrocarbon droplet, thus using improved parameters from [7] is actual for surfactants, too.

The initial configuration was a water box of size 8 nm containing a DTAB micelle with solubilized dye molecule. The number of monomers was chosen 50, in accordance with the experimental data [1]. There were about 16 thousands water molecules in the box. For simulation of RD in CTAB micelle, the aggregation number was chosen to be 95, because in our previous simulations it equaled 80, and the box size was 9.7 nm.

Three 50 ns simulations starting from different initial configurations were performed, and their results were averaged. The first 10 ns of MD trajectories were discarded in analysis as the equilibration.

Results and discussion

The average localization of the RD molecule can be understood from the distribution functions of distance between micelle center of mass (COM) and chosen atoms of the molecule. We selected the O atom that carries large negative charge, and the N atom, which is situated near center of mass of the whole molecule. In order to show the location of the micelle surface layer, the distribution functions of distance micelle COM–N atom in surfactant head groups were calculated, too. The graphs are presented in Fig. 2,a together with the ones for CTAB (95 monomers micelle). Also, the distribution functions in SDS and SCS micelles are presented for comparison (Fig. 2,b) [5]. Because the absolute values of micelle – dye distance in short-tail surfactants (SDS, DTAB) and in long-tail ones (CTAB and SCS) differ due to the larger size of the latter micelles, the graphs in CTAB and SCS are shifted towards origin to make micelle COM–head groups peaks visually coinciding in long- and short-tail surfactants. This makes the picture clearer because the position of the dye relative to the surface layer, not to the micelle center, is of the main interest.

It is also of interest to reveal the orientation of the RD molecule on the interface. For this sake, the pitch angle of the RD molecule, θ, was defined as shown in Fig. 3,a, and its distribution functions were computed (Fig. 3,b).

In DTAB micelles, the indicator is localized notably deeper, than in SDS micelles with equal hydrocarbon tail. Moreover, in comparison with CTAB micelles, in the DTAB ones the localization of RD molecule differs moderately, but its orientation evidently alters. Namely, the ledge with $\theta > 130^0$

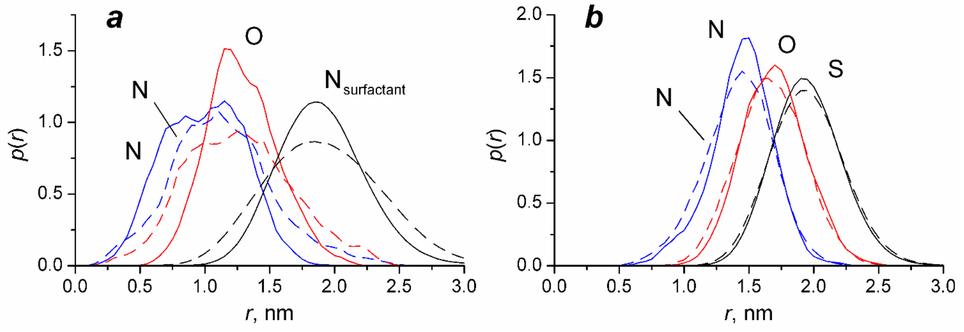

Fig. 2. Distribution functions of distances between micelle COM and N, O atoms of RD and N or S atoms of surfactants. a: DTAB and CTAB, b: SDS and SCS. The curves, corresponding to CTAB and SCS, are shifted left by 0.6 nm and 0.4 nm, respectively, and are dashed for clarity

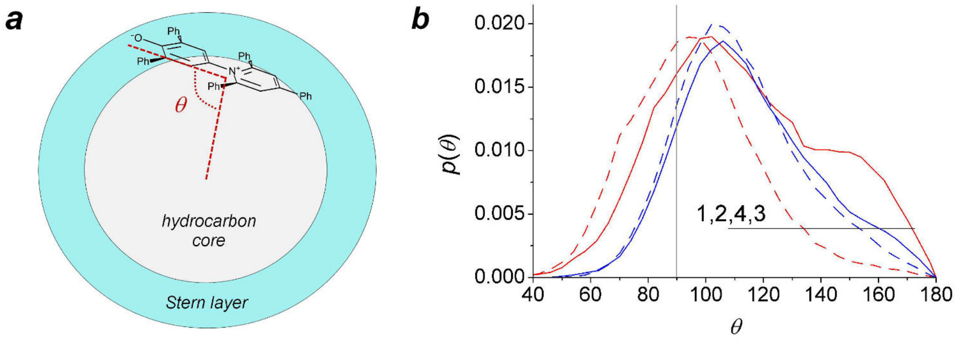

Fig. 3. a: Definition of the pitch angle of RD molecule, θ. b: Distribution functions of θ in micellar solutions of CTAB (1), SCS (2), DTAB (3), SDS (4). Curves for long-tail surfactants are dashed

indicates that the alignment, when the molecule is roughly parallel to the micelle radius and the triphenylpyridinium fragment of RD is completely hidden from water in the micelle core, becomes observed more often. This is somewhat unexpected in the light of identical locus of the molecule in SDS and SCS micelles, which also differ by the tail length only.

Importantly, the obtained results are confirmed by experimental measurements made using ^{1}H NMR spectroscopy. In such studies, the conclusion about the average probe molecule locus in micelle is made on the basis of the change in chemical shifts of surfactant hydrogen atoms when micelles solubilize dye molecules. It is assumed that the larger the change in the chemical shift of given hydrogen atoms is, the closer they are to the probe molecule (in average). Zachariasse et al. [8] showed that in CTAB solution RD exerts the main effect on the α-CH_2, β-CH_2 and $N(CH_3)_3^+$ groups (effect weakens in this order) that corresponds to location of the molecule on the micelle–water interface without deep immersion. Almost the same picture was found by Novaki and El Seoud [9] in DTAB micelles, but with a small difference: δ-CH_2 and $N(CH_3)_3^+$ hydrogen atoms are affected to the same extent, while in CTAB ones δ-CH_2 are affected ~25% weaker. The results of simulations explain this on the atomistic level: in both micelles, the dye is located on the surface, but in DTAB micelles it also readily samples the micelle interior by the triphenylpyridinium moiety.

Apart from localization, the composition of local medium (or microenvironment) of the dye molecule was inspected (Fig. 4). The atoms, surrounding the molecule, were classified on three categories: water atoms, surfactant head group atoms and the atoms of micelle hydrocarbon core (i.e. the atoms of surfactant tail groups). The first CH_2 bead has positive charge in both cationic alkylammonium and anionic sulfate surfactants. Therefore, in the former it was classified as belonging to the head group, while in the latter it was attributed to the tail group.

It can be seen that the microenvironments in micelles with identical head groups differ a little. However, the content of hydrocarbon around the dye and its O atom in DTAB micelles is 7–10% higher than in CTAB ones. This confirms the conclusion made during analysis of DFDs about

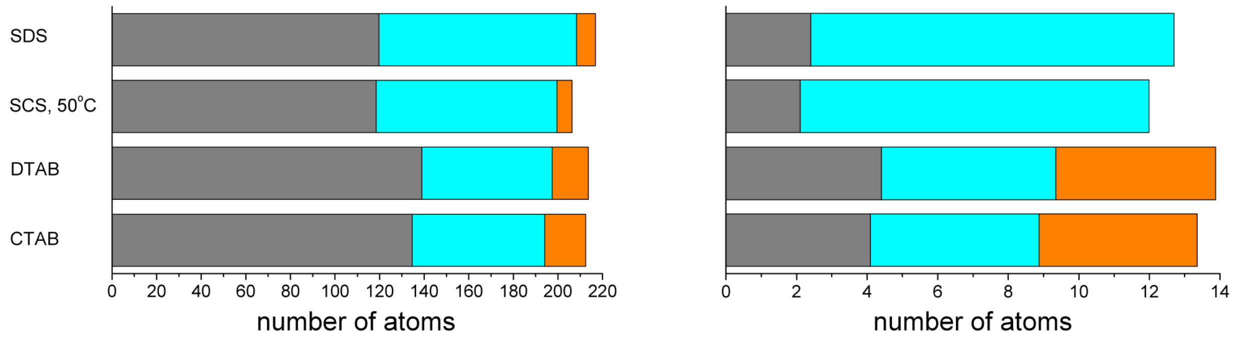

Fig. 4. Compositions of microenvironment of RD molecule (left) and its O atom (right) in various micelles. The first section (gray) shows the number of hydrocarbon atoms, the second section (light blue) shows the number of water atoms, and the last section (orange) shows the number of head group atoms

deeper immersion of the dye into micelle and accords with the NMR data.

As a closely related problem, the effect of micelle size on the state of adsorbed dye molecule has been inspected. For this sake, a simulation of RD in CTAB micelle, composed from 95 monomers instead of 80, was carried out.

Predictably, the obtained micelle has a more elongated shape than the one of 80 monomers, which can be readily seen on a snapshot from MD simulations (Fig. 5). Particularly, the average eccentricity parameter equals 0.15 for the bigger micelle and 0.09 for the smaller one, while the ratio between the maximal and the minimal moments of inertia is 3.5 and 1.2, respectively. Nevertheless, this change has not affected significantly the locus of the RD molecule: the average localization and orientation are similar to those in micelle of 80 monomers (Fig. 6). The widening of peaks on DFDs can be explained by increased non-sphericity of micelles: when for spherical micelles, the distance from center to surface is the same for all surface points, for elongated micelles, a range of values is observed.

The distribution functions of θ are of the same character (in contrast to the case of DTAB when a distinct ledge on distribution function of θ appears), and the small difference can again be attributed to the geometrical reasons.

However, at a closer look, somewhat deeper immersion of the dye into the bigger micelles can be distinguished. For this, the average distances between dye atoms and the micelle center of mass were computed using the DFDs (Table). For clarity, the distances between dye atoms and head groups were computed as well.

Considering the O atom, it resides in average 0.13 nm farther from water in CTAB micelles of 95 monomers, than in the ones of 80 monomers. This shift is quite big and thus is unlikely caused just by the non-sphericity of micelles, i.e. is significant. The N atom is located farther from water, too (by 0.08 nm).

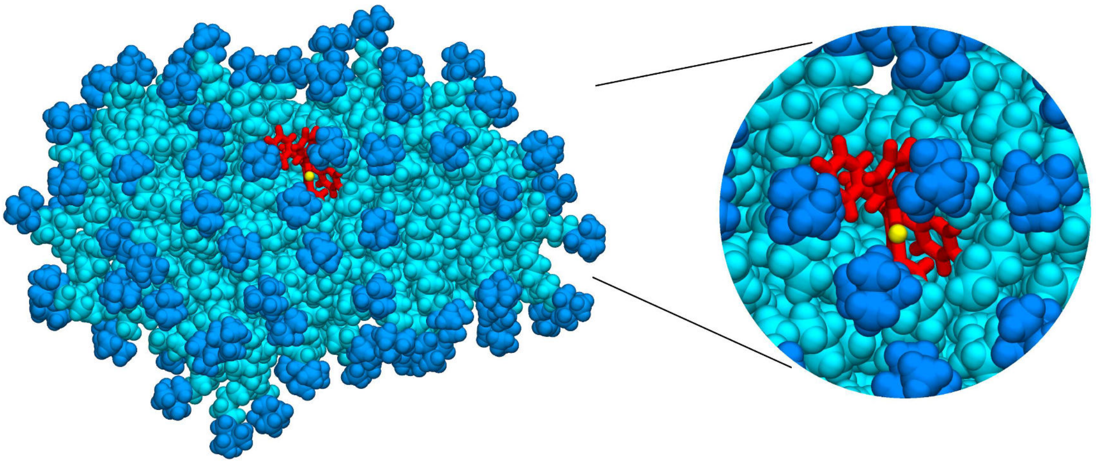

Fig. 5. Instantaneous snapshot from MD simulation of RD in CTAB micelle of 95 monomers. Head groups are colored blue, hydrocarbon core — light blue, RD — red, its O atom — yellow. Counter-ions and water are omitted for clarity. At inset the neighborhood of dye is shown

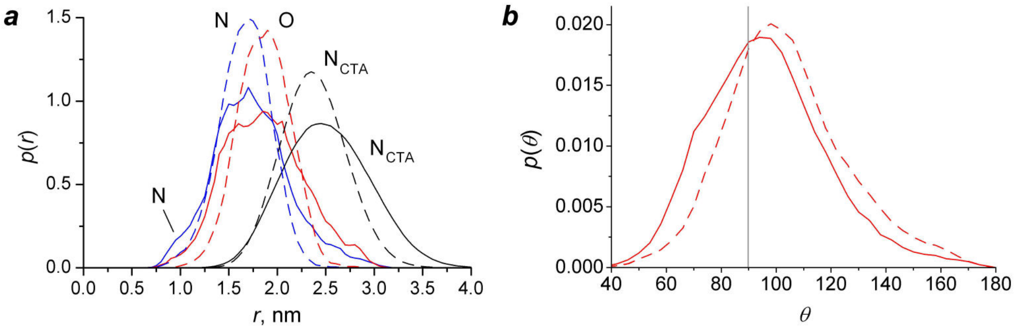

Fig. 6. a: Distribution functions of distances between micelle COM and N, O atoms of RD and N atoms of CTAB. b: Distribution functions of θ. The curves for 95 monomers micelle are solid, the ones for 80 monomers micelle are dashed

Average distance from micelle COM to given atoms of the dye

	AN [a]	r(N)	r(O)	r(HG) [b]	r(HG)–r(N)	r(HG)–r(O)
DTAB	50	1.0	1.29	1.86	0.86	0.57
CTAB	80	1.67	1.86	2.38	0.71	0.52
CTAB	95	1.73	1.87	2.52	0.79	0.65

Note: [a] – AN=aggregation number; [b] – HG=the N atom in surfactant head groups.

The dye microenvironment also remains principally the same (Fig. 7). However, the hydration of both the dye molecule as a whole and its oxygen atom appeared to be ~6% lesser in bigger micelles than in the smaller ones. This effect can easily be explained by the abovementioned deeper immersion of the dye into the bigger micelles.

The information about dye microenvironment can be used for explaining the values of the $E_T(30)$ polarity parameter of CTAB and DTAB micellar solutions, which is determined using RD. As supposed in report [4] and discussed in more detail in study [5], the $E_T(30)$ value is likely related to the hydration of the oxygen atom, defined as the number of water atoms around it, because this quantities change in the same order. The results, presented here, support this hypothesis. The measured $E_T(30)$ values of CTAB and DTAB solutions equal 53.0 kcal/mol and 53.9 kcal/mol, respectively, while normalized E_T^N values are 0.688 and 0.716 [9]. At the same time, hydration of the dye O atom in these solutions is 4.8 and 4.9, respectively (if the aggregation number of 95 is taken for CTAB). Still, numbers for DTAB are lower than those for SCS (0.783 and 9.9) [5].

It is important to mention that when the hydration of O atom in CTAB micelles of 80 monomers is used, which equals 5.1, the correlation breaks. However, we consider bigger micelles as more relevant for the conditions of the discussed spectroscopic experiment, where CTAB concentration exceeded critical micellization concentration in ~60 times (0.05 M vs. 0.0008 M [10]). This justifies preferring the MD results of RD in 95 monomers micelle to the ones of RD in 80 monomers micelle. At the same time, this emphasizes that in cases when higher precision of computed characteristics is required, using actual aggregation number of micelles in simulation becomes essential.

Conclusions

Molecular dynamics simulation of the standard solvatochromic Reichardt's dye in micelles of cationic surfactant *n*-dodecyltrimethylammonium bromide was performed. The results show that the localization of the dye molecule in these micelles in close to

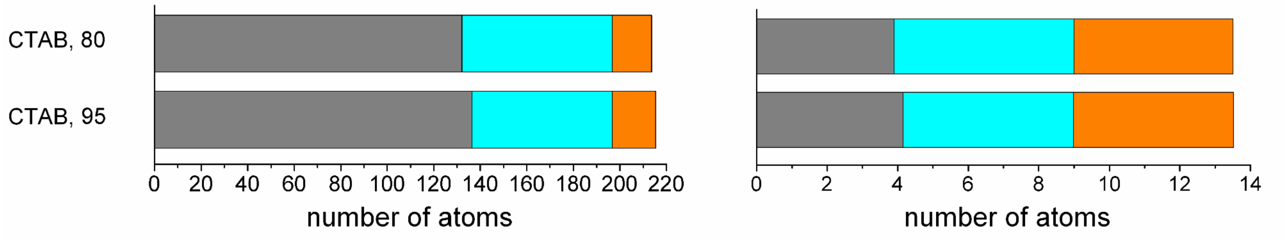

Fig. 7. Microenvironment compositions of RD (left) and its O atom (right) in CTAB micelles of two sizes. The first section (gray) shows the number of hydrocarbon atoms, the second section (light blue) shows the number of water atoms, and the last section (orange) shows the number of head group atoms

that in cetyltrimethylammonium bromide micelles, but the orientation is moderately different. This is in line with the available NMR spectroscopy data. This stays in contrast to the case of sodium dodecyl sulfate and sodium cetyl sulfate micelles, where no difference in orientation was found. Therefore, in general case, not only the head group nature of the surfactant, but the hydrocarbon tail length, as well, is able to affect the state of the adsorbed dye molecule, despite the effect can be negligible in particular cases.

The difference between dye localization in CTAB micelles of 80 and 95 monomers was found to be small: the dye is immersed ~0.1 nm deeper into bigger micelles, and this shift causes a 6% decrease in dye hydration in that micelles. In sum, aggregation number and related micelle properties (size, shape) affect moderately the state of an adsorbed dye molecule. At the same time, MD simulations are able to take these properties into account and reproduce their impact properly. Therefore we can conclude that for receiving a general insight about the state of a probe molecule in micelles, any aggregation number that is pertinent for a given surfactant can be used. However, when more precise information is needed, choosing relevant aggregation number is essential.

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ДОСЛІДЖЕННЯ СОЛЬВАТОХРОМНОГО БАРВНИКА РАЙХАРДТА В КАТІОННИХ МІЦЕЛАХ РІЗНОГО РОЗМІРУ МЕТОДОМ МОЛЕКУЛЯРНОЇ ДИНАМІКИ

В.С. Фарафонов, О.В. Лебідь, М.О. Мчедлов-Петросян

Властивості стандартного сольватохромного барвника Райхардта 4(2,4,6-трифенілпіридиній-1-іл)-2,6-дифенілфенолят у міцелах н*-додецилтриметиламоній броміду досліджені за допомогою молекулярно-динамічного моделювання. Отримані характеристики локалізації та орієнтації молекули, а також природа її мікрооточення. Ці характеристики порівняні з такими в міцелах цетилтриметиламоній броміду (ЦТАБ). Виявлено більш глибоке занурення молекули в міцелу, що відповідає експериментальним даним. Крім того, зіставлені характеристики барвника в міцелах ЦТАБ двох розмірів. Відмінність знайдена невеликою: у великих міцелах барвник занурений глибше в міцелу і дещо менше гідратований. Параметр полярності* $E_T(30)$ *міцелярних розчинів змінюються в тому ж порядку, що гідратація атома Оксигену молекули барвника у відповідних міцелах.*

Ключові слова: *н*-додецилтриметиламонію бромід, цетилтриметиламонію бромід, адсорбція, локалізація, гідратація, параметр полярності.

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