

The maximum energy W_{\max} an electron may acquire is given by

$$W_{\max} = mc^2 \Delta g, \approx 2eE_0 c g_r^2 / w, \quad (29)$$

where $g_r^2 = (1 - b^2)^{-1}$. If the length required by an electron to acquire W_{\max} amount of energy is L_A , then we can write $W_{\max} = eE_0 L_A$, which gives $L_A = 2c g_0 / w_p$.

The amplitude of the Langmuir wave, driven by beating a mm wave with a wiggler, scales as one-third power of wiggler strength and one-sixth power of mm wave power density. It is sensitive to cyclotron resonance. The electric field amplitude of the Langmuir wave is $|E| = k f F$, where $F = |f/f_0|$. For a typical case of 36 GHz, mm wave with power density $P = 1 \text{ MW/cm}^2$, wiggler strength $B_w = 1 \text{ kG}$, the value of Langmuir wave electric field amplitude turns out to be 30 MV/m at $w_L/w_C \sim 0.8$. The breaking of the Langmuir wave does not occur here, as the phase velocity of the wave is close to c ; wave breaking occurs when the electron excursion equals a wavelength. The field amplitude could be enhanced near cyclotron resonance, but as one approaches the cyclotron resonance, the phase velocity of the Langmuir wave decreases unless one increases k_w . Alternatively, large phase velocities of the Langmuir wave can be achieved by propagating the Langmuir wave through a plasma of slightly higher density after it has been generated in the wiggler region. The large amplitude Langmuir wave could be utilized for electron acceleration. The length of the plasma column required for maximum particle acceleration scales linearly with the wavelength of the mm wave. The requirement of a large guide field is a serious drawback of the scheme.

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Evidence for bound and free water species in the hydration shell of an aqueous micelle

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Atomistic molecular dynamics simulations revealed the existence of bound and free water molecules in the hydration layer of an aqueous micelle. The bound water molecules can be either singly or doubly hydrogen bonded to the polar head group on the surface of the micelle. The ratio of bound to free water is found to be approximately equal to 9 : 1 at 300 K.

WATER, inevitably present at the surface of biological macromolecules and self-organized assemblies, plays a critical role in the structure, stability and function of these systems¹⁻². However, the layer of water that surrounds these systems is rather thin, typically 1–3 layers thick. Thus, the study of hydration layer has turned out to be rather difficult. Dielectric relaxation studies measure the collective response of the whole system and, therefore, are not a sensitive probe of the dynamics of the hydration water. NMR techniques (NOE and NMRD) have the required spatial resolution, but lack the dynamic resolution. Neutron-scattering techniques are beginning to be applied to study the dynamics of hydration layer in these systems³. Solvation dynamics may be a reasonably good probe because it can have both the temporal and spatial resolution⁴⁻⁶; yet it provides only a collective response. Under these circumstances, computer simulation can play an important role in understanding the nature of the hydration water.

As the hydration layer is spatially heterogeneous even on a molecular-length scale and because the microscopic interactions are quite complex, a purely analytical study of this system is prohibitively difficult. In order to capture some of the basic physics of the dynamics in such systems, a model in terms of a dynamic exchange between bound and free water molecules⁷ has been proposed. The bound water molecules are those which are singly or doubly hydrogen bonded to the protein or to the surface of a self-assembled aggregate, while the free water molecules are not. The microscopic dynamical event is an exchange between these two states of water within the hydration layer. The model predicts the emergence of a slow decay when the binding energy is high.

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In this limit, the time constant of the slow decay is just the inverse of the rate of bound to free transition⁷. Although this model has been semi-quantitatively successful in explaining a wide range of behaviour, the basic assumption of the existence of bound and free water molecules remained unsubstantiated.

In addition to the above, bound and free water molecules give a convenient way to categorize the water molecules in the hydration layer. The bound molecules can be further sub-divided into two categories – singly hydrogen bonded or doubly hydrogen bonded. We shall denote these two by IBW1 and IBW2 respectively. Free water molecules are denoted by IFW (interfacial free water).

Recently, we have presented several studies aimed at understanding various aspects of interfacial water⁸. These were based on detailed atomistic molecular dynamics (MD) simulations of an anionic micelle, CsPFO (cesium pentafluorooctanoate). These studies have confirmed the existence of slow water and ion dynamics in the interfacial region. We have also studied the lifetime of hydrogen bonds that the water molecules form with the micellar polar head groups and found that it becomes considerably longer than those between two water molecules in the bulk.

In the present work, we have extended our previous study to investigate in detail, the equilibrium structure of the interfacial water. Our study has clearly revealed that the water at the interface of CsPFO consists of three different species – IBW2, IBW1 and IFW in the ratio 1.1 : 8 : 0.9, i.e. the bound to free water ratio is 9 : 1. This large ratio is a signature of the highly polar character of the anionic micelle.

As details of the simulation have been discussed elsewhere⁸, we directly proceed to discussion of the results. Figure 1 illustrates the average geometries adopted by IBW1 and IBW2 water species. Figure 1 gives all the details about average bond lengths and bond angles *calculated* from the simulation. There are features which are absent in IBW1 but present in IBW2, such as a well-defined distance between the water and the second (non-bonded) oxygen of the polar head group. This feature at 4.7 Å is prominent for IBW2 water molecules, but is absent for IBW1. An examination of the full distribution of bond lengths and bond angles, and not just their averages, shows that the environment around bound water species is, in general, more well-defined relative to a water molecule in pure water.

Figure 2 presents the monomer energy distribution for all the three species, as also for water molecules in the bulk. It is seen that the interfacial water molecules have peaks at lower energies – the IBW2 species has the lowest potential energy. It is also worth noting that the bound water molecules have considerably lower energy values than the free water molecules. It is this enhanced stability which makes the bound species identifiable, even when they are transient because of the dynamic exchange bet-

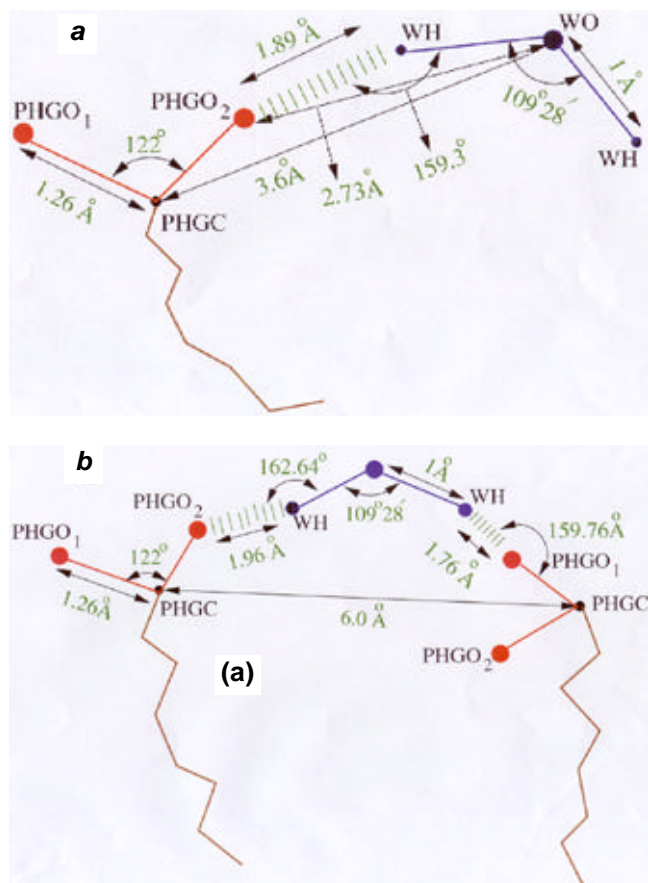


Figure 1. Schematic description of the environment around bound interfacial waters; **a**, IBW1, and **b**, IBW2. Numerical values of the geometrical parameters are average values obtained from the MD run. Water molecules and surfactant head groups are rigid entities in the interaction model. PHGO denotes the oxygen atom of the polar head group of the surfactant, and PHGC denotes the carbon atom in the head group. WO and WH denote the oxygen and hydrogen atoms of the interfacial water respectively. Broken lines between PHGO and WH denote hydrogen bond.

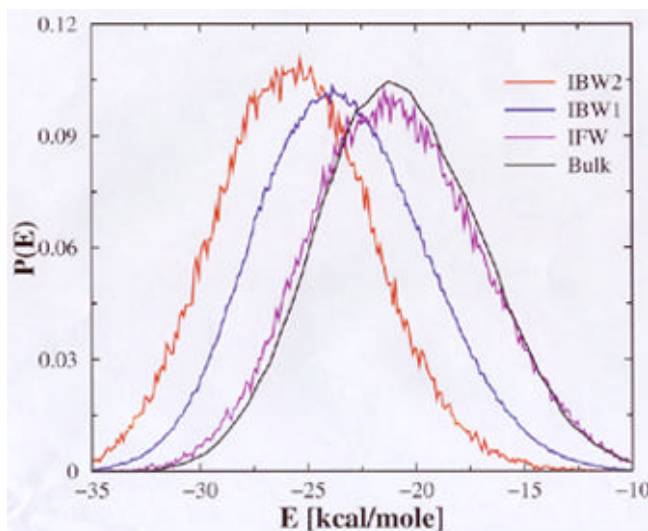


Figure 2. Distribution of monomer energies of interfacial water molecules compared to that of bulk water.

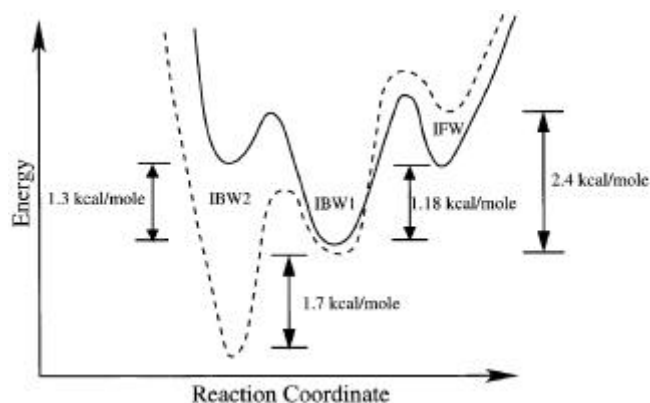


Figure 3. Schematic description of free energy (solid line) and internal energy (dashed line) profiles of interfacial water species. The species are in dynamical equilibrium with themselves and with water present in the bulk region of the micellar solution. The reaction coordinate is arbitrary and does not imply any distance. Barrier heights are also arbitrary.

ween the free and bound species. A large part of this stabilization comes from the stronger hydrogen bonds that bound water molecules form with the surfactant head groups.

Figure 3 provides a schematic of the free energies of the three species, calculated from their average concentrations. Despite the reduced monomer energy arising out of two water-head group hydrogen bonds, the IBW2 state is less stable than the IBW1 state due to entropic considerations (less number of suitable configurations). The reversible reactions between these states of water on such a surface should determine the dynamical response of interfacial water.

Note that Figure 3 describes the free energy and not the binding energy of the three species. The binding energy can be inferred from Figure 2. The total binding energy of the IBW2 species is indeed larger than that of IBW1.

In conclusion, we note that the existence of identifiable bound and free water molecules on the surface can indeed help in developing a phenomenological description of dynamics of water at complex interfaces. The 9 : 1 ratio obtained (for IBW and IFW) is expected to be typical for ionic micelles. However, this ratio is bound to decrease substantially for proteins due to the existence of hydrophobic and less polar amino acid groups on its surface. The water on the protein/membrane surface is expected to play a critical role in the molecular recognition of hydrophobic patches by incoming ligands or drug molecules. Work in this direction is under progress.

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Effect of sodium butyrate on methylation pattern of retinoblastoma (*RBI*) gene in human colon tumour cell line HT29

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Sodium butyrate is known to induce morphological and biochemical changes associated with differentiation in some colon tumour cell lines, including HT29. In this study the HT29 colon carcinoma cells were induced to differentiate with sodium butyrate treatment. High molecular-weight DNA from the untreated and sodium butyrate-treated HT29 cells were isolated at different time periods. The DNA was digested with the restriction enzymes *MspI* and *HpaII* to reveal changes in the methylation pattern at the *RBI* gene locus. Sodium butyrate-treated HT29 cells showed an increase in the level of methylation of retinoblastoma (*RBI*) gene compared to the untreated control. The results suggest that the development of human colonic neoplasia may result from hypomethylation of *RBI* gene.

CYTOSINE methylation in CpG dinucleotides is an important control mechanism of the transcriptional regulation in eukaryotes. The transcriptional activity of several

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