Molecular Hydrophobic Attraction and Ion-Specific Effects
Studied by Molecular Dynamics

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Abstract

Much is written about ‘hydrophobic forces’ that act between solvated molecules and non-polar interfaces, but it is not always clear what causes these forces and whether they should be labeled as hydrophobic. Hydrophobic effects roughly fall in two classes, those that are influenced by the addition of salt and those that are not. Bubble adsorption and cavitation effects plague experiments and simulations of interacting extended hydrophobic surfaces and lead to strong almost irreversible attraction that has little or no dependence on salt type and concentration. In this paper, we are concerned with hydrophobic interactions between single molecules and extended surfaces and try to elucidate the relation to electrostatic and ion-specific effects. For these nanoscopic hydrophobic forces bubbles and cavitation effects play only a minor role and even if present cause no equilibration problems. In specific, we study the forced desorption of peptides from non-polar interfaces by means of molecular dynamics simulations and determine the adsorption potential of mean force. The simulation results for peptides compare well with corresponding AFM experiments. An analysis of the various contributions to the total peptide-surface interactions shows that water-structural effects as well as van der Waals interactions between surface and peptide are important. Hofmeister ion effects are studied by separately determining the effective interaction of various ions with hydrophobic surfaces. An extension of the Poisson-Boltzmann equation that includes the ion-specific potential of mean force yields surface potentials, interfacial tensions and effective interactions between hydrophobic surfaces. There, we also analyze the energetic contributions to the potential of mean force and find that the most important factor determining ion-specific adsorption at hydrophobic surfaces can best be described as surface-modified ion hydration.

1 Introduction

Protein folding is a complex process that is closely entangled with the behavior of the water solvent.[1] In the early stage of protein folding a hydrophobic globular molten core is formed which contains most of the non-polar side chains. The reason for this is the mutual attraction of hydrophobic amino acids and hydrophobic patches of the protein surface. This process is closely related to a different phenomenon, namely the adsorption of solvated molecules on non-polar solid surfaces, which is a process of outstanding importance in colloid science, physical chemistry, biology, and atmospheric science. The driving force behind surface adsorption has many origins, depending on the specificities of the solute and surface. In the majority of cases, covalent interactions between the surface and the solute molecule are absent, and the adsorption is governed by non-bonding forces. Out of these non-bonding forces that drive surface adsorption, electrostatic forces have received lot of attention recently.[2, 3] Among the non-electrostatic forces, there is the direct solute-surface van der Waals interaction[4]. Besides this direct interaction, solvent-mediated forces contribute significantly to
the adsorption.[5, 6] For flexible molecules and especially for macromolecules, also the internal degrees of freedom need to be considered. In water, the situation is even more complex, because in nearly all cases the water solvent is in fact an electrolyte solution, and the presence of ions gives rise to various effects. Besides the obvious screening of electrostatic forces, which only depends on the ionic strength, there are effects which strongly depend on the ion type. These effects are commonly called Hofmeister effects.[7] For a complete analysis, the ions themselves have to be considered as solutes, which competitively adsorb at the surface and also at the macromolecule. It has been shown quite recently that large ions (such as iodide or bromide) are attracted to hydrophobic surfaces, in dramatic contradiction to the classical view according to which ions are repelled from non-polar surfaces due to image-charge effects.[8, 9, 10] This implies that the hydrophobic effect in the presence of ions involves ion adsorption and thus induced electrostatic interactions, even if the hydrophobic surfaces themselves are nominally neutral.

In the past, hydrophobic interactions on the molecular scale were experimentally investigated rather indirectly by thermodynamic aggregation and adsorption studies. Not much can be learned from experiments on larger scales,[11] because effects like bubble formation or cavitation become important[12] and because the hydrophobic effect has an intrinsic dependence on the solute size.[5] New insight into the hydrophobic adsorption of macromolecules can be gained by single-molecule AFM experiments.[13] In such studies a polymer chain is covalently attached to a passivated AFM tip. After the polymer is allowed to adsorb on a surface, it is slowly peeled off and the force exerted on the polymer is monitored through the bending of the AFM cantilever. If those single-molecule force measurements are performed with long polymers, direct interactions between the surface and the AFM tip are negligible and one is measuring the free energy of desorption of the polymer.

The diversity of systems which give rise to hydrophobic attraction prevents a general theoretical approach. For surface adsorption, the central quantity is the potential of mean force between the surface and the solvated particles, because it is directly related to the solute density distribution. In the classic DLVO theory,[14] the surface free energy is thought to consist of a sum of electrostatic and dispersion forces only. Another contribution comes from solvent-mediated effects and has in the past been studied for simple, non-polar solutes.[15] While each of these contributions separately is reasonably well understood, it remains to be clarified to what extent they add up to the total potential of mean force. A viable approach that accounts for all interactions present at hydrophobic interfaces are atomistic simulations. They include all present non-bonding forces via force fields that consist of Coulombic and Lennard-Jones interactions, and thus include partial charges, dispersion interactions as well as solvation effects. From simulation results, it is possible to analyze different contributions to the potential of mean force, and thus to assess the validity of different approaches towards the hydrophobic effect.

In this article, we summarize our efforts towards the quantitative description of hydrophobic surface forces by atomistic simulations. We stay close to the geometry employed in AFM experiments with polymers, i.e. we pull a single mildly hydrophobic peptide chain from a flat hydrophobic surface. This setup is advantageous because cavitation effects are avoided and the equilibration is fast. In section 2 we describe the details of modeling the peptide chain and the employed surfaces. We give results for peptides desorbing from hydrophobic surfaces as well as hydrophilic surfaces. For hydrophobic surfaces the single-polymer friction forces are small enough so that equilibrium adsorption forces can be determined (although the pulling velocity is 5 orders of magnitude larger in simulations when compared to AFM experiments). On hydrophilic surfaces, on the other hand, hydrogen bonds give rise to large friction forces and equilibrium cannot be reached with present computer power. Adsorption on hydrophobic surfaces as well as on peptide chains is ion specific, therefore electrolytes modify the hydrophobic attraction in an ion-specific way. Since exploring the full parameter space of different ion types and ionic concentration is prohibitively computer time consuming, one has to resort to more economical ways of investigating the interplay of ion-surface adsorption and hydrophobic interactions. In section 3 we describe simulation results for the adsorption of single ions at hydrophobic surfaces. Here the differences between polarizable and non-polarizable force fields are discussed, and the Hofmeister effect is demonstrated on hydrophobic solid surfaces. In section 4 we show how to carry simulation studies for single ions over to finite ion concentrations based on an extended Poisson-Boltzmann approach. We show results for the surface potential, surface tension and for the effective interaction between hydrophobic surfaces. Our simulations are constrained by the general limitations of atomistic MD, the limited accuracy of force fields as well as the limited computational power available. Including atomistic MD results in an extended Poisson-Boltzmann equation can be viewed as a multiscale approach for the study of systems that are too large for atomistic MD. In the
concluding section we outline possible directions of future work.

2 Protein-Surface forces

The adsorption of proteins on surfaces is interesting as a model for protein folding; it is also important in its own right for many biological and technological systems. However, there is considerable experimental difficulty in the precise determination of surface adsorption affinities. A traditional route towards adsorption free energies is the measurement of bulk/surface distributions, which can be achieved by surface plasmon resonance experiments.[16, 17] With single-molecule atomic force spectroscopy (AFM), the desorption force of a single polymer can be measured directly. In this method, a single polymer is covalently attached to an AFM tip, which is otherwise passivated by, e.g., polyethylene glycole to prevent adsorption on the tip itself. The tip is brought towards the surface, and the attached polymer adsorbs, if it has enough affinity for the surface. For pulling the AFM tip away from the surface, a force has to be applied, which is measured by the deflection of the AFM cantilever. A typical experimental force curve as a function of the separation of the AFM tip from the surface can be roughly separated into three regions: for low separations, there is strong direct tip-surface interaction, which is difficult to interpret and unwanted in the present context. For separations above approximately 50 nm, the force becomes independent of the separation until it drops abruptly to zero when the polymer detaches from the surface. The constant plateau force in the middle region comes from attractive polymer-surface interaction and corresponds to the desorption free energy per unit length. For charged polymers on charged surfaces, the electrostatic part of the interaction is sensitive to the salt concentration, and the charge density of the polymer can be determined.[3] As it turned out, the non-electrostatic part of the desorption force is dominant even in the case of charged polymers on charged surfaces.[18] On uncharged, non-polar surfaces, the adsorption force is commonly labeled as hydrophobic force. Little is known about the hydrophobic desorption force of peptides. Recently, the desorption force of the slightly hydrophobic spider silk protein C16 from a hydrophobic diamond surface has been determined by single-molecule force-spectroscopy.[19] and a value of 58 pN has been found in a 20 mM NaCl electrolyte solution. The C16 protein is well-suited for AFM experiments as well as for simulation studies of desorption. In solution it is typically unfolded and assumes a random coil formation.[20] thus allowing desorption studies without possible interference from folding/unfolding transitions and complications due to secondary structures. In the following, we describe our progress in modeling the AFM experiment.

We study desorption from three different surfaces: hydrophobic H-terminated diamond,[21] hydrophilic OH-terminated diamond, and a hydrophobic alkane SAM, which is modeled with the 30° tilt angle found on a gold (111) surface[22]. The simulation system consists of a 3 nm × 3 nm × 2 nm big surface patch and a short peptide strand arranged in a rectangular box that is subsequently filled with typically 3000 water molecules. After energy minimization, the behavior of the peptide is studied by molecular dynamics simulations at constant temperature (300 K unless otherwise specified) and at a constant pressure of 1 bar using Berendsen’s weak coupling method.[23] All parts of the system are described at atomistic resolution, especially the water molecules, which is important for the correct description of solvent-induced forces. Note that implicit solvent models, despite their popularity, do not always correctly reproduce solvent-mediated forces.[24] We choose the Gromos96[25] force field in combination with the SPC[26] water potential for our study. The charges of the surface COH groups in case of the hydrophilic diamond are the same as the ones in serin, all other surface atoms do not bear a partial charge. The system is treated periodic in all three directions. A cut-off of 0.8 nm is used for the van der Waals forces, and the electrostatics are calculated by particle-mesh Ewald summation (PME). The AFM tip, whose position is an external control parameter, is modeled by a restrain potential that is acting on the center of mass of the first amino acid of the peptide chain.

2.1 Lateral pulling

The pulling rates applied in molecular dynamics simulations, typically of the order of meter per second, exceed the experimental pulling rates (which are in the micrometer per second range) by orders of magnitude, a direct comparison of desorption forces from simulation and experiment is thus only justified if thermal equilibrium is achieved in the pulling simulations[27]. However, the friction contribution to the desorption force is hard to identify from simulations where the polymer is moved vertically away from the surface, since desorption forces and friction forces are mixed together. Friction is more directly studied by lateral pulling, where the force has no equilibrium contribution.[28] Pulling a peptide laterally along a hydrophobic surface is achieved by restraining the lateral position of the center of mass of the first amino acid and moving the restrain at
a constant rate. The force applied through this restrain is monitored as a function of time and averaged after a steady state is established.

The first system we study is a monomer of C_{16} spider silk, which we split into three pieces for computational efficiency; the sequences of the individual fragments are shown in Fig. 3, and the structures of the amino acids are shown in Fig. 4. Note that fragment two and three overlap by 6 residues. In Fig. 1 we show the lateral mean friction force $\langle F_L \rangle$ for fragment three consisting of 15 amino acids as a function of the pulling rate $v_0$ on a hydrophobic diamond surface. Anticipating a desorption force of the order of the experimentally measured 58 pN, this plot reveals that in order for the friction force to be smaller than the desorption force a pulling velocity smaller than about $v_0 \approx 1 \text{ m/s}$ should be used. For pulling rates of the order of $v_0 \approx 0.1 \text{ m/s}$ the friction force is only a small fraction. Forced desorption at this rate is within the reach of current computational abilities, allowing for the accurate simulation of peptide desorption experiments on a hydrophobic surface. It becomes clear that for efficient simulation of forced desorption, the peptide strand should not be longer than necessary for it to stay attached on the surface; since the total friction force is proportional to polymer length, the friction force would otherwise dominate the measured desorption force.

On the hydrophilic surface on the other hand, friction effects are much stronger, and we cannot reach equilibrium conditions with our current capabilities. The equilibrium rupture of hydrogen bonds between the peptide and surface hydroxyl groups requires much longer time scales than available in simulations[28].

2.2 Vertical Pulling

AFM desorption simulations from hydrophobic diamond are performed in close analogy to the lateral pulling simulations, the only difference is that instead of the lateral position the vertical position of the terminal peptide group, i.e. the separation between the center of mass of the first amino acid and the surface, is restrained. We study peptide desorption by two types of simulations: in the first type, ‘dynamic’ pulling, the restrain potential is vertically moved away from the surface at a constant rate. Here we obtain a continuous force curve as a function of the tip-surface separation. In the second, ‘static’ type, we take configurations from dynamic simulations, let the system evolve for 8 ns with a fixed restrain position, and average the pulling force during the second half of the simulation.

In Fig. 2 we show the vertical force as a function of the tip separation for the desorption of fragment three at constant vertical pulling rates of 10, 1, and 0.1 m/s. The average force from static simulations is also shown as data points.
ence for thermal equilibrium: starting conformations with slightly different forces acting on the terminal peptide group relax to a state with the same average force within less than 4 ns, and the desorption force $F$ only depends on the position of the restrain potential $z$. Thus, the static simulations give the equilibrium pulling force for a discrete set of surface separations. The desorption force increases only weakly when the peptide is desorbed at a rate of 0.1 m/s, in qualitative agreement with the predictions from the lateral pulling simulations. For 1 and 10 m/s the force increases drastically, which we trace back to an increased contribution from polymer/surface friction, demonstrating a transition to non-equilibrium conditions. The results from lateral pulling simulations and from desorption simulations both predict that friction effects dominate for pulling rates above 0.1 m/s. The desorption simulations show that thermal equilibrium is still not generally ensured for a pulling rate of 0.1 m/s, but that static simulations reach equilibrium, if the restrain potential is fixed and the system is allowed to relax for 4 ns.

AFM experiments typically give a constant plateau force, whereas our static simulations predict distinct variations in $F(z)$ with prominent force peaks of approximately 100 pN. These peaks occur when strongly hydrophobic amino acids like tyrosine are detached from the surface. In the experiments, the peptide chain is much longer than in our simulations. Thermal fluctuations are much stronger, and the fingerprint of the individual amino acids is washed out. We calculate the average desorption force from the static simulations as the spatial average over the desorption force profile $F(z)$. The averaging starts with the completely adsorbed peptide and is done in steps of $\Delta z = 0.2$ nm until all but the end of the peptide chain is desorbed from the surface. This is the quantity to be compared to experimentally determined plateau forces.

By averaging over all three fragments, we find an average desorption force of $C_{16}$ on hydrophobic diamond of $F = 54$ pN, which is in good agreement with the experimentally observed desorption force $F = 58$ pN at similar, low salt conditions[19]. Considering that the force fields involved were never designed for a study of hydrophobic adsorption, the agreement between experiment and simulation is excellent, but we also note that the near-quantitative agreement might be partly fortuitous. In Table 1 we summarize the average desorption forces for different systems.

It is commonly assumed that the specific chemical nature of a hydrophobic surface is of minor importance as long as it cannot form hydrogen bonds. In order to check this assumption, we study desorption from an alkane SAM in addition to the desorption from the diamond surface. There, we restrict the study to the third fragment of $C_{16}$ and show only static simulations. Fig. 5 compares static desorption forces at the SAM and at the hydrophobic diamond surface. We find an average desorption force of 35 pN on the SAM, slightly less than the 40 pN found on the hydrophobic diamond surface. The reduced force is mostly due to less pronounced force peaks for the strongly hydrophobic residues, which we trace back to less favorable steric interactions; otherwise the desorption forces are similar.

To understand better the dependence of peptide desorption forces on the chemical nature of the peptide chain, we also study homopeptides. Decamers of phenylalanine, F, and asparagine, N, are desorbed from a hydrophobic diamond surface. We choose
these two amino acids as the most hydrophobic one (F) and the most hydrophilic one with a non-ionic sidechain (N).[29] Using static simulations, we find equilibrium desorption forces of 88 pN for F and 51 pN for N. As expected, the hydrophobic amino acid has a higher desorption force from the hydrophobic diamond surface than the hydrophilic one. Surprisingly, the desorption force for the hydrophilic asparagine chain is also quite high. Since the interaction between a hydrophobic surface and a hydrophilic peptide can neither be classified as hydrophobic or hydration induced, this casts some serious doubts on this force classification scheme.

2.3 Contributions to the hydrophobic attraction

Even more interesting, the interaction between poly-asparagine and the surface is stronger than for the third spider silk fragment, which is on average more hydrophobic than poly-N. It transpires that there is no simple rule according to which adsorption strength should correlate with hydrophobicity. Without doubt, the diamond surface is hydrophobic in the simulations, since it is modeled with all partial charges set to zero. Accordingly, the simulations yield a water contact angle of 106°. Our finding suggests that the peptide-surface interaction is rather complicated and contains not only solvent-mediated forces. To gain deeper understanding of this, we analyze the energetics of the peptide desorption process for the third C16 fragment in more detail. We define the initial state of the desorption process as the state where the peptide is completely adsorbed, and the final state as the state where the peptide is still attached to the surface with one end and is stretched by the terminal peptide group in the solution. We label this as process I, which is relevant for AFM experiments, see also Fig. 6. Additionally, we study a process starting at the same initial state, but ending in a state in which the peptide is completely detached from the surface and assumes a coil conformation in water. This process, which is related to the spontaneous adsorption/desorption equilibrium, but is not studied in AFM experiments, is labeled as process II.

The free energy change $\Delta$ of process I is obtained from the integral of the desorption force over the length of the desorbed peptide chain. To obtain the corresponding free energy change for process II, the second end of the peptide is restrained by a second restrain potential. We transform the peptide from the final state of process I (chain stretched between surface and terminal peptide group in solution) to a state in which both ends of the peptide are in bulk with no relative force acting between them. This state corresponds to an unconstrained relaxed bulk conformation. By integrating the force acting on the second end of the polymer, the free energy difference for process II is obtained along a path which includes the detachment from the surface and the subsequent bulk relaxation. The internal energy change $U$ is evaluated as the difference between the initial and final internal energies, $U = U_f - U_i$, and the entropy change $S$ is obtained from the thermodynamic relation $S = (U - A)/T$. The internal energy change is decomposed into groupwise con-

Figure 4: Structural formulas of the amino acids used in our simulations. The amino acids are distinguished by their side chains, which are shown separated from the amino acid backbone. In proline, P, the amino acid functional group is part of the cyclic structure, and the whole residue is shown. Also shown is the hydrophobicity index of the amino acids.[29] Note that glutamic acid, E, bears a negative charge which in our simulations is neutralized by a sodium ion.

Figure 5: Desorption force of the third C16 monomer fragment on hydrophobic diamond and on a hydrophobic alkane self-assembled monolayer obtained from simulations, where the restrain potential acting on the first amino acid is at a constant position for 8 ns. The sequence of the third C16 fragment is shown in Fig. 3.
tributions according to

\[ U = U_{PP} + U_{PW} + U_{WW} + U_{PS} + U_{WS} \]

with the subscripts P for peptide, W for water, and S for surface. Fig. 6 shows a bar diagram of the energy decomposition for processes I and II for 280, 300, and 320 K.

Figure 6: Energy decomposition for the desorption of the third C₁₆ fragment from a hydrophobic diamond surface at temperatures 280, 300, and 320 K. Shown is the change of internal energy \( U \) and free energy \( A \) per monomer for the forced desorption scenario (process I, top), which terminates with the peptide fully stretched between the forced end and the surface, and for spontaneous desorption scenario (process II, bottom), where the peptide is fully relaxed in the final state. The interactions are divided into contributions from peptide (P), surface (S), and water (W) groups, and the internal energy change \( U \) is accordingly split into five contributions.

The main observation from this analysis is that the individual contributions to \( U \) are all larger in magnitude than \( U \) itself. The total energy change thus is a result of near-compensation. Therefore, no theory focusing on a single contribution like the hydrophobic cavitation energy, which is related to the water-water interactions, or the excess van der Waals energy, can give a satisfying explanation of the adsorption process. The contributions from \( U_{WW}, U_{PW}, \) and \( U_{PP} \) are very different for the processes I and II. This is not surprising, since the final states of the two processes are very different. In the extended state at the end of process I, the peptide cannot build stabilizing intramolecular hydrogen bonds and van der Waals contacts, as it can in the coil formation at the end of process II, and to a lesser extent in the initial state. Therefore, \( U_{PP} \) is positive for process I and negative for process II. The interaction between the water molecules, \( U_{WW}, \) increases with the water surface. In both processes, the surface area increases, and \( U_{WW} \) is positive. \( U_{PW} \) is a measure for the solvation of the peptide and is related to its solvent accessible surface, which is largest for the extended conformation. Upon coil formation of the peptide, \( U_{PW} \) is substantially reduced. The interactions where the surface is involved behave as expected: \( U_{PS} \) is positive, because peptide-surface contacts are removed, and \( U_{WS} \) is negative, because the water accessible surface on the diamond is increased. There is only a small difference in \( U_{PS} \) and \( U_{WS} \) between processes I and II, because the peptide-surface contact is already very small at the end of process I. It is amusing that by adding both surface contributions \( U_{PS} \) and \( U_{WS}, \) which add up to the excess surface van der Waals contribution, one obtains a fair description of the total internal energy change. In other words, solvent and peptide contributions almost cancel out to zero. This might be an explanation why calculations of the dispersion contributions alone often give acceptable results for effective interactions. However, our results show that solvation effects are always large and important, and the near-cancellation of non-surface contributions is possibly merely coincidental.

The total free energy \( A \) does not differ as drastically as the individual internal energy terms be-
between processes I and II. In both cases $U$ and $A$ are positive. The entropic contribution, estimated from the difference of $U$ and $A$, amounts to roughly a quarter of the total free energy. The entropy change is unfavorable in process I, but favorable in process II, as would be expected: in the final state of process I, the peptide is in a stretched state with low entropy, whereas the coil state at the end of process II has a higher entropy than the surface-adsorbed state. However, a separation of the entropy into individual contributions is difficult, and therefore the origin of the entropic difference between processes I and II cannot be determined.

### 2.4 Salt effects on hydrophobic attraction

So far our simulations are performed in pure water. A single counterion is present to neutralize the single negative charge of the second $C_{16}$ fragment. The electrolyte concentration of this counterion amounts to about 20mM. Experiments with $C_{16}$ in pure water are not possible, because the solubility is too low. The reported AFM measurements were performed in a 20 mM NaCl buffer. For a better understanding of the salt influence on the hydrophobic attraction, we perform an additional series of simulations of the $C_{16}$ fragment 3 on hydrophobic diamond in a 1 M NaCl electrolyte solution. Fig. 7 shows a snapshot of a simulation with NaCl included. Fig. 8 compares the static desorption forces of the third $C_{16}$ fragment obtained in simulations with pure water and 1 M NaCl. By the addition of salt, the average desorption force increases from 40 to 49 pN. This increase of approximately 20% shows that the desorption force at the hydrophobic surface is sensitive towards the presence of ions. This is consistent with recently reported AFM desorption experiments in concentrated salt solutions.[30] Clearly, further simulation studies are required for the understanding of salt effects on the hydrophobic attraction. A thorough investigation of the influence of salt for different salt concentrations, different salt types and varying surfaces and peptides is not feasible in such a complex system. Even the relatively simple case of a salt solution in contact with a hydrophobic surface is not fully understand and ion-specific effects have only recently moved into the focus of attention.[31] We now turn our focus on the much simpler problem of the adsorption of a single ion at a hydrophobic surface.

### 3 Ion-Specific Adsorption at Hydrophobic Surfaces

The term ‘Hofmeister series’ is commonly used for a broad class of ion specific effects that influence aqueous solubility of various solutes.[32] More specifically, it was originally developed in the context of protein denaturation, and classifies ions according to their ability to precipitate proteins from solution. Anions are ordered as $SO_4^{2-} > F^- > Ac^- > Cl^- > Br^- > I^- > SCN^-$, the respective order of cations is $K^+ \approx Na^+ > Li^+ > NH_4^+ >> GuH^+$.\[7\] In other words, added fluoride salt precipitates proteins at a much lower concentration than does the corresponding iodide salt. Ions interact both with the polar and non-polar surface patches of a protein. While there is a strong Coulombic interaction of ions with polar groups, their direct interaction...
with the non-polar, hydrophobic parts is commonly assumed to be weak. Remarkably, there is a strong similarity to the influence ions have on the surface tension of water.[33] The key to the understanding of Hofmeister effects is therefore thought to be related to the ion-induced change of the thermodynamics of the interfacial water layers. Indeed, good progress was made for the air-water interface, and the experimentally observed trends for the surface tension and the surface potential are well understood by now.[9, 10].

At solid surfaces, on the other hand, the Hofmeister series is unexplained so far, even for flat model surfaces. The reason is the complexity of the interfacial system, where forces of various origin act. Attempts to model ion specificity have focused on certain specific contributions to the total energy.[34, 35, 36] The understanding of ion specific effects mandates that all acting forces at the solid/water interface are considered. The method of choice for this is the use of molecular dynamics simulations, which consider all relevant forces including solvent-mediated effects on a realistic footing. We study adsorption of Cl\(^-\), Br\(^-\), I\(^-\), and Na\(^+\) ions at a hydrophobic self-assembled alkane monolayer (SAM) as a model hydrophobic surface by molecular dynamics simulations.[31] The SAM is modeled by the general Amber force field,[37] with polarizabilities of the SAM atoms set to zero. Water molecules are described with the polarizable POL3 water model.[38] In Table 2 we summarize the force field parameters used for the simulations. The choice of a polarizable force field is motivated by studies of ion adsorption at the water/vapor interface, for which it has been shown that polarizable terms in the force fields are required to get a correct description of ion adsorption.[9, 10, 39] Owing to the fact that hydrophobic surfaces lack sites for strong electrostatic interactions with water molecules, such surface not only share certain properties when they are in contact with water, but behave in many respects similarly to the air/water interface. To understand the influence of polarizabilities, we study the adsorption of ions at the hydrophobic diamond/water interface,[40] using non-polarizable force fields, similar to the force fields used for the study of peptide adsorption described in the previous section. The non-polarizable water model (SPC/E[41]) and non-polarizable ion parameters,[42] are summarized in Table 3.

First, we study the properties of the interfacial systems with simulations of pure water at the hydrophobic surface. The system size is similar to the size in the study of peptide adsorption: a simulation system consists of a 3 nm \(\times\) 3 nm \(\times\) 2 nm surface patch and approximately 2000 water molecules, resulting in a roughly 7 nm thick water film. The simulation protocol is the same as the one used for the study of peptide adsorption. All simulations are done at 300 K and 1 bar.

In Fig. 9 we show the density \(\rho\) and electrostatic potential \(\Phi\) at both interfaces. The profiles look very similar. Due to the interruption of the water hydrogen bonding network, the water molecules reorient, causing an average polarization of the solvent in the direction normal to the interfacial plane. Similarly to many other studies of the air/water interface[44] and hydrophobic/water interfaces[48] an interfacial potential drop of approximately 500 mV is observed at both interfaces. Polarizable force fields (SAM surface) and non-polarizable force fields (diamond surface) give very similar results, showing that for the correct description of interfacial water effects atomic polarizability is not crucial, even though the polarizable contribution to the surface potential is significant for polarizable water models.[45] The oscillations of the water density[46]
and the electrostatic potential[47] at the diamond surface seem more pronounced compared to the SAM surface. These profiles result from a convolution of the density and potential profiles with the interface positional distribution, which is sharper for the diamond surface than for the SAM.

![Figure 9: Simulation results for the SAM/water and the diamond/water interface. The force field parameters for both systems are shown in Table 2 and Table 3. Shown are the density profiles $\rho(z)$ and the electrostatic potential profiles $\Phi(z)$. The profiles are very similar for both interfaces. The oscillations of the water density and potential at the diamond surface are more pronounced because the diamond surface is flatter than the alkane SAM.](image)

The polarizable anions are attracted to the interface, while all non-polarizable ions are repelled. The polarizability of atomistic simulations on the underlying force fields[9, 10]. Finally, we stress the similarity of the potentials of mean force obtained at the SAM/water interface and potentials of mean force obtained at the air/water interface, which are based on similar polarizable force field parameters.[43] This suggests that the energetic effects are similar for the two cases. However, ion adsorption at the SAM/water interface is more complex than at the air/water interface, even if the total potentials of mean force are similar for both interfaces: in addition to the forces acting at the air/water interface, there are van der Waals forces between the SAM on one side and the water molecules and ions on the other. In order to gain more insight into the adsorption energetics, we attempt to split up the total potential of mean force according to

$$V_{\text{PMF}} = V^\Phi + \Delta V^{vdW} + V^{\text{pol}} + V^{\text{img}}, \quad (1)$$

where the individual terms are discussed in the following. Assuming that the presence of an ion of charge $q$ does not alter the electrostatic potential caused by interfacial water orientation, $\Phi_W$, the electrostatic energy of an ion in the interfacial water layer is given as

$$V^\Phi(z) = q\Phi_W(z).$$

The electrostatic water potential $\Phi_W(z)$ is accurately described by the fitted expression

$$\Phi_W(z)/V = 0.228 + 0.029 \tanh[18(z - 0.512)] - 0.089 \tanh[18(z - 0.365)] + 0.177 \tanh[18(z - 0.225)] - 0.347 \tanh[13(z - 0.019)]$$

where the distance is measured in units of nm. The excess polarization energy of an ion in the water electric field, $E_W(z)$, is given by

$$V^{\text{pol}}(z) = -\frac{1}{2}(\alpha - n\omega_W)E_W^2(z)$$

where the polarization energy of $n\omega_W$ replaced water molecules with polarizability $\alpha_W$ is subtracted.

![Figure 10: Potential of mean force for ion adsorption at the hydrophobic SAM/water interface, calculated with a polarizable force field (Table 2) and at the hydrophobic diamond/water interface, calculated with a non-polarizable force field (Table 3). The polarizable anions are attracted to the interface, while all non-polarizable ions are repelled.](image)
The electric field follows from the water potential as $E_W(z) = -d\Phi_W(z)/dz$. The van der Waals interaction of a particle (either ion or water molecule) with the SAM is obtained at zero temperature performing an explicit sum over Lennard-Jones interactions between SAM-sites and the particle using a cutoff radius of 9 Å. An average over several lateral positions of the ion is performed. The obtained energy is fitted to a 9-6 Lennard-Jones potential

$$V^{vdW}(z) = 4\varepsilon L J \left[ (\sigma/(z-z_0))^9 - (\sigma/(z-z_0))^6 \right]$$

with different parameters for every ion type and water. The $z^{-6}$ dependence of the attractive term compared to the usual $z^{-3}$ dependence of surface van der Waals forces is a result of the cutoff used for the calculation. The excess potential is defined as

$$\Delta V^{vdW} = V^{vdW} - n_W V^{vdW}_{W}$$

accounting for the substitution of $n_W$ water molecules.

The image charge repulsion of the ions from the SAM is described based on an expression $V^{img}(z)$ for finite-size charged spheres and a dielectric boundary at $z = 0$ with a dielectric constant of $\varepsilon_A$ for $z < 0$ and $\varepsilon_W$ for $z > 0$. For completely solvated ions with radius $a$, $V^{img}$ is given as

$$V^{img}(z) = \frac{q^2e^2}{32\pi\varepsilon_0\varepsilon_W a} \left[ 4 + \varepsilon_W - \varepsilon_A \frac{2a}{z} + \left( \frac{\varepsilon_W - \varepsilon_A}{\varepsilon_W + \varepsilon_A} \right)^2 \right]$$

$$\times \left( \frac{2}{1 - (2z/a)^2} + \frac{a}{2z} \ln \left( \frac{2z + a}{2z - a} \right) \right),$$

and the expression for $a > z > 0$ is

$$V^{img}(z) = \frac{q^2e^2}{32\pi\varepsilon_0\varepsilon_W a} \left\{ (2 + \frac{2z}{a}) + \varepsilon_W - \varepsilon_A \left( 4 - \frac{2z}{a} \right) \right. $$

$$\left. + \left( \frac{\varepsilon_W - \varepsilon_A}{\varepsilon_W + \varepsilon_A} \right)^2 \left[ (1 + z/a)(1 - 2z/a) \right] \right\}$$

$$\times \left( 1 + \frac{a}{2z} \right),$$

For $z < 0$, $V^{img}$ is obtained exchanging $\varepsilon_A$ and $\varepsilon_W$. For the ion radius we take $\sigma/2$, the Lennard-Jones radius of the particle, and $\varepsilon = 80$ and $\varepsilon = 1$ for the relative dielectric constants in the water and SAM half spaces.

In Fig. 11 we show the four separate terms for $\Gamma^-$ and their sum according to Eq. (1). Also shown is the simulation result for the complete potential of mean force as shown in Figure 10. Clearly, the presented approximation (solid line) is not even in qualitative agreement with the simulation results (triangles). The four presented terms do not account for the potential of mean force, and it is not clear how to improve this theoretical description. Probably the most severe shortcoming is that ion-water interactions are not included in an accurate fashion, although they are the origin of the terms $V^\phi$, $V^{pol}$, and $V^{img}$. We assign this failure to an incomplete description of the surface-modified solution of the ions. Further analytical work along this direction is clearly needed.

Figure 11: Comparison of the potential of mean force $V^{PMF}$ for a single iodide ion obtained in simulations (triangles) with an analytical approximation (solid line) which is a sum of physically motivated contributions. $V^\phi$ is the Coulombic ion energy due to the electrostatic water potential, $\Phi_W$, shown in Fig. 9. $V^{pol}$ is the polarization energy in this electric field, $E_W = -d\Phi_W/dz$. $V^{img}$ is the image repulsion due to the low-dielectric substrate, and $V^{vdW}$ is the $z$-dependent ion-surface excess van der Waals energy. The analytic approximation is qualitatively wrong, suggesting that neglected contributions like the surface-modified ion hydration dominate the ion-surface interaction.

For the usage in multiscale methods, a simple analytical representation of our potentials of mean force is mandatory. Since the parametrization in physical terms failed, we present a numerical fit of the potentials of mean force for ion adsorption at the SAM/water interface[31] and at the air water interface.[43] For SAM/water, we use the fitting expression

$$V^{fit}(z) = A/(z-z')^{12} - B/(z-z')^8$$

$$+ C_1 (z-C_2)e^{-C_3(z-C_2)^2}$$

$$+ D_1 e^{-D_2(z-D_2)^2},$$

(2)
The units of the parameters for the SAM/water interface, defined by Eq. 2, the lower entries are the parameters for the LJ interaction between the surface and the ion (\( n = 1 \)) for the attractive \( \text{Br}^- \) and \( \Gamma^- \), and \( n = 2 \) for \( \text{Cl}^- \) and \( \text{Na}^+ \). The numerical fit functions give a good representation of the simulation data for all potential of mean force.[31] The obtained parameters are shown in Table 4.

<table>
<thead>
<tr>
<th>SAM</th>
<th>A</th>
<th>B</th>
<th>( z' )</th>
<th>( C_1 )</th>
<th>( C_2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \text{I}^- )</td>
<td>50.73</td>
<td>18.99</td>
<td>-1.09</td>
<td>-10.22</td>
<td>0.54</td>
</tr>
<tr>
<td>( \text{Br}^- )</td>
<td>0.51</td>
<td>0.92</td>
<td>-0.74</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>( \text{Cl}^- )</td>
<td>1.20</td>
<td>-1.05</td>
<td>-0.99</td>
<td>-7.74</td>
<td>0.48</td>
</tr>
<tr>
<td>( \text{Na}^+ )</td>
<td>-2.22</td>
<td>-7.33</td>
<td>-0.89</td>
<td>10.28</td>
<td>0.37</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>SAM</th>
<th>( C_3 )</th>
<th>( D_1 )</th>
<th>( D_2 )</th>
<th>( D_3 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \text{I}^- )</td>
<td>200</td>
<td>-2.51</td>
<td>0.21</td>
<td>60.24</td>
</tr>
<tr>
<td>( \text{Br}^- )</td>
<td>0</td>
<td>2.33</td>
<td>0.18</td>
<td>46.41</td>
</tr>
<tr>
<td>( \text{Cl}^- )</td>
<td>200</td>
<td>-2.26</td>
<td>0.12</td>
<td>60.61</td>
</tr>
<tr>
<td>( \text{Na}^+ )</td>
<td>100</td>
<td>-0.28</td>
<td>0.12</td>
<td>2.58</td>
</tr>
</tbody>
</table>

Table 4: Fit parameters for the numerical parametrization of the potentials of mean force in Fig. 10. The upper entries are the parameters for the SAM/water interface, defined by Eq. 2, the lower entries are the air/water parameters, defined by Eq. 3. The units of the parameters for the SAM/water potentials are: \( A \): \( k_B T \)nm\(^2\), \( B \): \( k_B T \)nm\(^3\), \( z' \): nm, \( C_1 \): \( k_B T \)nm, \( C_2 \): nm, \( C_3 \): nm\(^{-2}\), \( D_1 \): \( k_B T \), \( D_2 \): nm, \( D_3 \): nm\(^{-2}\). For the air/water potentials the units for \( A \) (\( k_B T \)) and \( B \) (nm\(^{-1}\)) differ.

and for air/water the expression

\[
V_{\text{fit}}(z) = A \left[ e^{-B(z-z')} + (-1)^n z'^2 - 1 \right] + C_1 (z - C_2) e^{-C_3(z-C_3)^2} + D_1 e^{-D_2(z-D_2)^2}, \tag{3}
\]

with \( n = 1 \) for the attractive \( \text{Br}^- \) and \( \Gamma^- \), and \( n = 2 \) for \( \text{Cl}^- \) and \( \text{Na}^+ \). The numerical fit functions give a good representation of the simulation data for all potential of mean force.[31] The obtained parameters are shown in Table 4.

Although the quantitative theoretical description of the potential of mean force fails, insight into the physics of ion adsorption can be gained from the simulations by separating the contribution due to dispersion interactions off from the total PMF. In Fig. 12 we show simulation results for the total ionic potential of mean force for an iodide ion, together with the internal-energy contributions from the LJ interaction between the surface and the ion (\( \star \)), the ion and the water (\( + \)), and the surface and the water (\( \times \)). The sum of these three terms (\( \circ \)) is repulsive. To completely account for the Lennard-Jones part of the internal energy, the water-water interactions are missing. They can only be determined with a much large statistical error than the other three parts. Due to these errors, we do not include them in the sum of the LJ terms. The total water-water interaction, also known as solvent reorganization energy, does not contribute to solvation free energies.[53] Therefore, the solvent reorganization energy is also not a driving force of ion adsorption, and we neglect the LJ part of it in our analysis. Thus, we represent the total LJ energy as the sum given above. As can be seen, the surface-ion LJ interaction is attractive and shows a behavior that roughly resembles the total PMF. This might be a hint as to why calculations of ion-surface vdW interactions often give good results when compared with experiments. However, adding the ion-water and SAM-water LJ interactions (which are difficult to estimate analytically as the hydration layers of the ion and SAM change in a subtle manner when the ion approaches the surface), the total LJ contribution to the PMF becomes purely repulsive. Therefore, the dispersion or van der Waals interaction, which is parameterized in the simulations via LJ potentials, is not responsible for the attraction of iodide ions to the surface. The attraction must be caused by Coulombic contributions to the internal energy and by entropic terms, which are both included in the total PMF. This conclusion is in accord with the observation that the heavier halide ions are attracted to the air-water and the hydrophilic substrate-water interface in a similar manner.[31] Since the dispersion interactions are quite different in both cases, they have to be ruled out as the driving force behind ion-specific surface adsorption.

### 4 Poisson-Boltzmann approach including ion-specific effects

Although the results on single-iod adorption at solid hydrophobic surfaces gives a hint as to how Hofmeister effects come about, the real challenge is to predict ion-specific effects at finite ion concentration. Performing MD simulations at finite ion concentration is time consuming but in principle possible. The main problem is that such an approach is unlinked to the bulk of analytic work on charged systems performed previously and might easily miss the essential physical insight into such effects. Excellent experimental data exist for surface potentials and surface tension at the air-water interface that clearly exhibits the Hofmeister trends. For predicting such data, we have to extend our work described so far, which gives potentials of mean force at infinite dilution, to finite ion concentra-
The water bulk (ary conditions that the potential is zero inside the hydrophobic surface, the extended Poisson-Boltzmann equation for unpo

tions where ion-ion interactions have to be included. If the inter-ionic interaction is purely electrostatic, the Poisson-Boltzmann equation gives a mean field description for finite concentrations. For ion adsorption at hydrophobic surfaces, non-electrostatic ion-surface potentials need to be included. Having the potential of mean force from MD, this can be achieved including the potential of mean force into an extended Poisson-Boltzmann equation for unpolarizable particles:[55, 31]

\[
\varepsilon \frac{d^2 \Phi(z)}{dz^2} = - \sum_i q_i c_i^0 e^{-V_{\text{PMF}}^\text{PMF}(z) + q_i \Phi(z)/k_BT},
\]

where \(q_i\) is the charge of ions of type \(i\), \(c_i^0\) is their bulk concentration, and \(\varepsilon\) is the dielectric constant. Provided with accurate ionic potentials of mean force, \(V_{\text{PMF}}^\text{PMF}(z)\), the Poisson-Boltzmann equation yields correct concentration profiles for not too high ionic concentrations, unless the mean-field approximation becomes invalid because of ionic correlation effects.

### 4.1 Single hydrophobic surface

For modeling ion concentration profiles at a single hydrophobic surface, the extended Poisson-Boltzmann equation is solved using the potentials of mean force obtained from MD, with the boundary conditions that the potential is zero inside the water bulk \((z \to -\infty)\) and constant outside \((z \to \infty)\). The numerical solution is done on a one-dimensional grid with a lattice constant small enough so that discretization effects are negligible. The solution of the extended Poisson-Boltzmann equation yields the ionic contribution to the surface potential \(\Phi\), shown in Fig. 13 as a function of salt concentration for NaCl, NaBr, and NaI. The calculations are done with our potentials of mean force for the SAM/water interface[31] (solid symbols) and with Dang’s potentials of mean force[43] for the air/water interface (open symbols). For NaCl at the air/water interface, there is only a small potential change, because both ions are repelled from the surface, and there is no charge separation at the interface. For the other cases, there is a significant drop of the surface potential, ranging from −20 mV for NaCl at SAM/water to −58 mV for NaI at air/water for a 1 M electrolyte, depending on the attraction strength of the anion to the interface.

As a third quantity, the surface tension change is typically not observed in experiments at the air-water interface[56], for reasons that are not clear at present. On the other hand, the calculated slope of \(\Delta \Phi(c^0)\) at \(c^0 \approx 1\) M agrees well with experiments for concentrated solutions: the experimental and predicted slopes in mV/M in the high concentration range are −20/−18 (NaI), −14/−15 (NaBr), and −8/−1 (NaCl) at the air-water interface. Only for NaCl, the ionic surface potential is strongly underestimated, which might have to do with a too small polarizability of the employed force fields (see the discussion in Refs. [54]).

The second quantity obtained from the extended Poisson-Boltzmann equation are the ionic concentration profiles at finite bulk salt concentration. The results are shown in Fig. 14 for NaI for four different bulk salt concentrations. The main effects of finite bulk concentration are: i) the adsorption peak of the anion is diminished with increasing bulk concentration, and ii) electrostatic screening leads to a more pronounced double-layer structure with an increased concentration of cations and a depletion of anions close to the peak in anion concentration.

The effect of finite salt concentration can also be studied directly by a MD simulations. For this we study a 1 M solution of NaI by MD. The obtained concentration profiles are shown in Fig 15. In the direct simulation at 1 M concentration, the reduction of the anion adsorption peak is less pronounced than predicted by the extended Poisson-Boltzmann results, and the screening peak of Na\(^+\) is higher than predicted. Still, the qualitative trends are captured by the extended Poisson-Boltzmann equation.

As a third quantity, the surface tension change is
accessible through the Gibbs adsorption equation from the ionic concentration profiles. For ideal solutions, activity can be replaced by concentration, and the Gibbs adsorption equation reads

$$\Delta \gamma = -k_B T \int_0^{c^0} dc' \sum_i \Gamma_i(c')c', \quad (4)$$

where the surface excess $\Gamma_i$ of ions of type $i$ is related to their concentration profile with respect to the position of the Gibbs dividing surface, $z_{GDS}$, by

$$\Gamma_i = \int_{-\infty}^{z_{GDS}} c_i(z)dz + \int_{z_{GDS}}^{\infty} (c_i(z) - c^0_i)dz.$$  

The results for polarizable ions at the SAM/water interface are shown in Fig. 13 in comparison to results at the air/water interface based on Dang’s potentials of mean force.[43] The interfacial tensions increase nearly linearly with addition of NaCl, because the repulsion of Na$^+$ is stronger than the attraction of Cl$^-$ over the whole concentration range. Experimentally, NaCl addition gives a linear increase of the air/water surface tension with a slope of 1.7 mN/m/M,[56] which is only ∼30% higher than our prediction. An attractive PMF does not necessarily lead to a decrease of the surface tension: only for $c^0 \to 0$, $d\gamma/dc^0$ is negative for the strongly adsorbing bromide and iodide ions, for larger concentrations the slope changes due to ion-ion interactions which are taken into account by the Poisson-Boltzmann formalism. For larger concentration our results agree with the experimentally found linear increase of the interfacial tension for NaBr at the air-water interface with a slope of 1.4 mN/m/M[56] within ∼30%. For NaI at the air-water interface the experimental slope of 1.2 mN/m/M is not reproduced by our calculations, which might indicate the failure of our mean field analysis or the inadequateness of the underlying force field.

4.2 Interaction between two hydrophobic surfaces

We now turn back to the problem of protein folding and protein adsorption, which is related to the force between two hydrophobic moieties. One contribution to this force is the hydration force, which has been studied between solid walls.[57] We study the force acting between two planar hydrophobic surfaces with our extended Poisson-Boltzmann equation approach, including specific adsorption of ions on both interfaces. A second surface is easily included in the extended Poisson-Boltzmann equation; now the total ionic potential is the sum of two potential of mean force terms coming from each surface,

$$V_{2\text{planes}}(z) = V_{\text{PMF}}(z) + V_{\text{PMF}}(d-z),$$

where $d$ is the separation between the two surfaces. The boundary conditions for the correct solution of the differential equation for the laterally averaged electrostatic potential $\Phi$ are $\Phi(z < 0) =$.
Figure 15: Ion concentration profiles of 1 M NaI at the SAM interface obtained from the extended Poisson-Boltzmann modeling (PBE) and from a simulation of a 1 M electrolyte (MD). The peak height of the $c/c_0$ curve for iodide is reduced compared to infinite dilution (see Fig. 14) in both methods. The extended Poisson-Boltzmann modeling overestimates this reduction compared to the explicit MD result.

$\Phi(z > d) = \text{const}$. This is most easily implemented by complementing the boundary condition $\Phi(z < 0) = \text{const}$ by the symmetry condition at the mid-plane $E(z = d/2) = -\Phi'(z = d/2) = 0$. The ionic pressure between the two plates follows from the surface tension change $\Delta \gamma$ as

$$P(d, c^0) = -\frac{d \Delta \gamma(d, c^0)}{dd},$$

where we obtain $\Delta \gamma$ from the the Gibbs adsorption equation (Eq. 4) with the surface excesses $\Gamma_i$ obtained as

$$\Gamma_i = 2 \left[ \int_{-\infty}^{z_{\text{GDS}}} c_i(z) dz + \int_{z_{\text{GDS}}}^{d/2} (c_i(z) - c^0_i) dz \right].$$

The differentiation with respect to $d$ is done numerically.

In Fig. 16 we show the ionic pressure between two hydrophobic walls obtained from the extended Poisson-Boltzmann equation for NaCl, NaBr, and NaI. The bulk salt concentration is always fixed at 0.1 M. The repulsive pressure is caused by specific adsorption of anions on both surfaces and thus by a resulting electrostatic repulsion between the effectively charged surfaces.

5 Summary and outlook

Molecular simulations constitute a powerful tool for the study of intermolecular interactions and molecular adsorption at the solid/liquid interface. We specifically considered hydrophobic surfaces, for which adsorption effects involve the interplay of i) the water structure at the hydrophobic surface, ii) hydration of the adsorbing solute, and iii) direct solute-surface interactions. Analytical theories that include all these effects are not available. Peptide desorption from a hydrophobic surface can be successfully studied by simulations, leading to desorption forces that agree quantitatively with AFM experimental results. The mechanism for the hydrophobic attraction involves both dispersion interactions between peptide and surface, which are parameterized via the Lennard-Jones interaction po-
tentative, as well as hydration effects. As a detailed analysis of the interaction energies from the simulations shows, massive cancellation of individual contributions from the surface, peptide and water takes place, showing that the hydrophobic attraction results from a subtle balance of these terms. The good agreement of equilibrium desorption forces between simulation and experiment is traced back to very low friction forces of peptides adsorbed on hydrophobic surfaces, which allows adsorbed peptides to equilibrate very quickly on simulation time scales. The situation is very different on hydrophilic surfaces, where equilibration is not achieved on the nano-second time scale and equilibrium desorption free energies cannot be determined by simulations. Simulations and AFM experiments show that hydrophobic interactions are modified by the addition of salt in an ion-specific fashion.

To understand these ion-specific effects at hydrophobic surfaces in more detail, we determine single-ion adsorption potentials of mean force. The trends on hydrophobic solid surfaces are similar as for the air-water interface: large anions (such as bromide or iodide) readily adsorb on hydrophobic surfaces, smaller anions like chloride are only weakly adsorbed, and cations are repelled. The van der Waals or dispersion interaction is repulsive for all ions and therefore not responsible for the observed adsorption of ions on surfaces. Finite ion concentration effects are reasonably described by an extension of Poisson-Boltzmann theory, where we include the potentials of mean force from MD simulations. This leads to negative surface potentials that increase in magnitude with increasing bulk salt concentrations, surface tensions that change with salt concentration according to the Hofmeister series, and interactions between hydrophobic surfaces that are screened by addition of salt and get more repulsive the more the anion is attracted to the surface.

Several controversial issues remain. i) The change of surface tension of the air-water interface found in experiments[58] can at present not be explained quantitatively by simulations, even if one simulates finite ion-concentrations directly without the recourse to the extended Poisson-Boltzmann equation. This points to the inability of the underlying force fields to model concentrated electrolyte solutions. Along the same lines, simulations and some experiments suggest that the surface of pristine water is acidic,[59] while the traditional view favors the specific adsorption of OH$^-$ ions at the water surface.[60, 61]. ii) As shown here, the extended Poisson-Boltzmann approach gives the right trends for finite ion concentration, but the agreement with simulations is not perfect. It seems that ion-ion interactions have to be included in the approach, possibly beyond the mean-field level. iii) As discussed in Section 2.4, simulations and AFM experiments show that salt strengthens the peptide-hydrophobic surface attraction and leads to an increase in the desorption force. For interactions between similarly hydrophobic surfaces, the adsorption of ions should lead to a repulsive contribution to the interaction. It follows that ion adsorption on surfaces is more complicated and depends on ion interactions with polar and charged surface groups[62] as well as on the modified properties of water in concentrated salt solutions.

References


