Interactions of biomolecules with the surfaces of solids in molecular dynamics simulations

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Interactions between proteins and solid surfaces belong to the fundamental phenomena and are at the heart of many potential applications in biotechnology and medicine. They include biosensing, biomaterials, drug delivery and industrial chemistry. Many of these applications rely on recognition of the surfaces by specific proteins or peptides. It is thus important to investigate the role of the sequential makeup of the biomolecules in binding. We used all-atom classical molecular dynamics simulations to study single amino acids, analogues of their side chains, dipeptides and small proteins in the vicinity of solid surfaces of distinct physicochemical properties: ZnO, ZnS, Au, and crystalline cellulose.

We determined potentials of the mean force for interactions of 20 amino acids with 4 common surfaces of ZnO in aqueous solutions. We found that the profiled nature of the density of water with the strongly adsorbed first layer affects the approach of amino acids to the surface and generates either repulsion or weak binding. The largest binding energy was determined for tyrosine interacting with the surface in which the Zn ions are at the top. It is equal to 7 kJ/mol which is comparable to that of the hydrogen bonds in a protein. In the absence of water, binding energies are more than 40 times stronger. Among the four considered surfaces the one with Zn at the top was recognized as binding almost all amino acids with an average binding energy of 2.60 kJ/mol. Another (O at the top) is non-binding for most amino acids. For binding situations the average energy is 0.66 kJ/mol. The remaining two surfaces bind nearly as many amino acids as they do not and the average binding energies are 1.46 and 1.22 kJ/mol. For all of the surfaces the binding energies exhibit large specificity. Finally, we observed that tryptophan cage, a protein of 20 residues, adsorbs onto ZnO only intermittently, with only a small deformation and various adsorption events lead to different patterns in mobilities of amino acids within the protein.

For the ZnS (110) surface in aqueous solutions we found that 5 of 20 amino acids do not bind at all and the binding energy of the remaining amino acids does not exceed 4.3 kJ/mol. Such energies are comparable to those found for ZnO but the nature of the specificity is distinct. Since cysteine can bind with ZnS in a covalent way we included this effect within a model incorporating the Morse potential, and found that the binding energy was close to 98 kJ/mol. We then considered tryptophan cage and characterized its adsorption to ZnS. Our simulations indicate that ZnS is more hydrophobic than ZnO which leads to a different density profile of water.

In the case of Au, we compared results obtained within three different force fields: one hydrophobic (appropriate for a contaminated surface) and two hydrophilic - with and without polarization. In the hydrophobic case, we determined the contact angle that a water droplet makes with the surface. We found that all of these fields led to good binding with very different specificities and different patterns in the density and polarization of water. We demonstrated that binding energies of dipeptides were different than the combined binding energies of their amino acidic components. We also found that relative affinity of the side chains analogues was consistent with that of the corresponding residues. For the hydrophobic gold, adsorption events of a small protein are driven by attraction to the strongest binding amino acids. This is not so in the hydrophilic cases - a result of the smaller specificities combined with the difficulty for proteins (but not for single amino acids) to penetrate the first layer of water.

Finally, we determined the binding free energies between amino acids and the surface of crystalline cellulose. Our results show that all twenty standard amino acids adsorb on the surface of cellulose with binding energies ranging from 2 to 11 kJ/mol with the specificity of approximately 30 %. The amino acid discriminating capacity of the surface of cellulose can be valuable information towards the rational design and re-engineering of the cellulosome in order to improve its catalytic properties.

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