

Dynamics and Energetics of Protein Adsorption Processes

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While significant advances in biocompatible and environmentally benign materials have been made, one of the remaining challenges is to understand surface resistance to protein adsorption and cell adhesion. Significant experimental efforts have been made to produce only a relatively small number of nonfouling materials and coatings. Furthermore, the mechanisms for protein resistance are poorly understood at present and the majority of new material breakthroughs are made fortuitously. One method to aid novel material development is molecular simulations. By conducting experiments in-silico, one can perform expensive experimentation after candidates are selected from initial screening. Furthermore, molecular simulations allow direct access of various interactions at the protein-surface-solution interface.

We have performed extensive work on quantifying the resistant forces that non-fouling surfaces generate on proteins and analyzing the resulting hydration structure and dynamics. However, the rigorous thermodynamic criterion of protein adsorption or resistance should be the change in free energy as a protein approaches a surface. In this work, molecular simulations were used to calculate the free energy changes as model peptides in solution approach various surfaces, in order to develop simulation-based surface evaluation criteria. The simulation results were compared directly with those from protein adsorption experiments. By using both simulation and experimental techniques, we were able to directly validate our simulations, as well as evaluate the relative influence of the surface and the hydrating water on the free energy changes. This combined approach provides feedback on our simulation parameters. As the mechanism of protein adsorption and resistance is better understood, it opens the door to rationally design materials for a specific application. By combining molecular simulation and experimental techniques, we are able to develop a fundamental description of the interactions present at both the molecular and macro scales.