

The role of electrostatics in the protein adsorption process on nanostructured surfaces: a multiscale approach based on the Poisson-Boltzmann equation and molecular dynamics

Speaker

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Protein adsorption on nanostructured surfaces is a critical process in the design and development of biotechnological applications such as biosensors and biocatalytic surfaces. These devices are widely used to detect target molecules through a bioreceptor immobilized on a surface, and their performance is closely related to variables such as orientation of the bioreceptor, the number of adsorbed proteins, and conformational changes during immobilization. Although the adsorption arises due to a competition between different processes, under a specific conditions, mean-field electrostatic plays a dominant role with direct influence on the coverage and orientation of adsorption. In this talk, I will present a multiscale strategy coupling Molecular Dynamics and the Poisson-Boltzmann equation to study the effect of electrostatics and structural rearrangement in protein-surface interaction through an MMPBSA approach¹.

Under this methodology, the structure conformational changes due to adsorption on a surface are predicted with a molecular mechanics model, and the solvation free energy landscape is computed with an implicit solvent model. The computational workflow will be based on Amber24² to perform molecular dynamic simulations, PyGBe³ to solve Poisson-Boltzmann equation, that allows us to evaluate the electrostatic solvation free energy for different orientations; and MDTraj to calculate the molecular surface (SASA) of each of the configuration, variable required to compute the non-polar solvation free energy. We will focus on discussing the role of electrostatics in an experimental/computational application case: the interaction of trypsin with a carbon electrode under external electric fields, and how these polar effects might affect enzyme activity in the context of biosensor design⁴.

In addition, I will introduce how conformational changes due to temperature would affect the interaction with nanostructure surfaces, taking as an example L-lysine oxidase interacting with graphene oxide.

(1) Wang, C.; Nguyen, P. H.; Pham, K.; Huynh, D.; Le, T. B. N.; Wang, H.; Ren, P.; Luo, R. Calculating Protein-Ligand Binding Affinities with MMPBSA: Method and Error Analysis. *J Comput Chem* 2016. <https://doi.org/10.1002/jcc.24467>.

(2) Case, D. A.; Cheatham, T. E.; Darden, T.; Gohlke, H.; Luo, R.; Merz, K. M.; Onufriev, A.; Simmerling, C.; Wang, B.; Woods, R. J. The Amber Biomolecular Simulation Programs. *J Comput Chem* 2005, 26 (16), 1668–1688. <https://doi.org/10.1002/jcc.20290>.

(3) Cooper, C. D.; Clementi, N. C.; Barba, L. A. Probing Protein Orientation near Charged Nanosurfaces for Simulation-Assisted Biosensor Design. *Journal of Chemical Physics* 2015. <https://doi.org/10.1063/1.4931113>.

(4) Urzúa, S. A.; Saucedo-Oloño, P. Y.; García, C. D.; Cooper, C. D. Predicting the Orientation of Adsorbed Proteins Steered with Electric Fields Using a Simple Electrostatic Model. *Journal of Physical Chemistry B* 2022. <https://doi.org/10.1021/acs.jpcc.2c03118>.

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