Bioengineering@CRS4

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SEMINAR: Transport of antibiotics through bacterial porins: Insights from atomistic simulations

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ABSTRACT:

Bacteria's resistance to commonly prescribed antibiotics is challenging the treatment of various infectious diseases today. The very first step in antibacterial activity is the uptake of antibiotics, and the striking presence of outer-membrane in Gram-negative bacteria, constitutes a real barrier for their entry. Thanks to the ubiquitous presence of general diffusion porins, which form a main entry point for the antibiotics to reach their target, located inside the bacteria. One of the most frequently encountered mechanism of bacterial resistance is alteration in the uptake of antibiotics through the porins. For Escherichia coli in particular, outer membrane protein F (OmpF) and outer membrane protein C are the most expressed porins.

The aim of this study is to investigate antibiotic transport through porins, which is based on passive diffusion at a molecular scale. To do so, we use accelerated molecular dynamics calculations to simulate the antibiotic transport through the porin. During the talk, a complete analysis of the translocation of an antibiotic (ampicillin) through the bacterial porin OmpF will be presented, providing insight into the key determinants (preorganization, solvation, entropy-enthalpy compensation) and molecular mechanism for the transport process.

A major current dilemma for the pharmaceutical industry is whether to develop new drugs or promote those presently on the market. In this scenario, the information gathered from our simulations could be used as an input toward designing antibiotics with optimal physicochemical properties, allowing them to translocate with a higher rate through porins.

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BIOGRAPHY:

Education:

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KEYWORDS: Bacterial Resistance, Molecular simulation, Antibiotic transport, OmpF, Preorganization, Entropy-enthalpy compensation, Solvation



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