Permeability in gram-negative bacteria: A microscopic journey

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New drugs for combating multidrug-resistant bacteria are needed, especially for Gramnegative bacteria. The presence of the outer membrane in this type of bacteria hinders the access of molecules to their internal targets, rendering the development of new drugs even more challenging. To date neither a robust screening method for permeation nor wellestablished physiochemical rules governing permeation through the outer membrane are available.

Starting from high-resolution crystal structures of different porins, we combine all-atom molecular modeling with molecular dynamics to characterize its electrostatic properties. This together with the aid of enhanced sampling techniques for simulating the permeation of antibiotics through them; provide us a microscopic description of the problem that allows us to identify the key molecular parameters involved in successful permeation of known drugs and model it.

Without a strong and accurate experimental method to assess the flux of antibiotics through porins, our model, based on the fluctuations of simple physical properties of porins and trained in the successful analyzed cases, represents a useful tool to explore the chemical space for searching new scaffolds and/or optimize at the molecular level existing molecules for an enhanced permeation through bacterial porins.

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