From lipid bilayers to membrane Proteins

Mini-colloquium *N° 11*

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A biological membrane displays a double leaflet organization including lipids, proteins and sugars. Its role consists in regulating cellular exchange between its exterior and interior, or between cellular compartments. Its mechanical properties at thermodynamic equilibrium are now well understood. Current investigations are directed toward the membrane coupling with external fields (electrical, flows etc.) leading to non-trivial spatiotemporal dynamics, with the underlying challenges to solve: the role of membrane permeabilities, membrane dynamics and vesicles undergoing arbitrarily large deformations (Fig.1, right panel), the interaction between two or more vesicles...

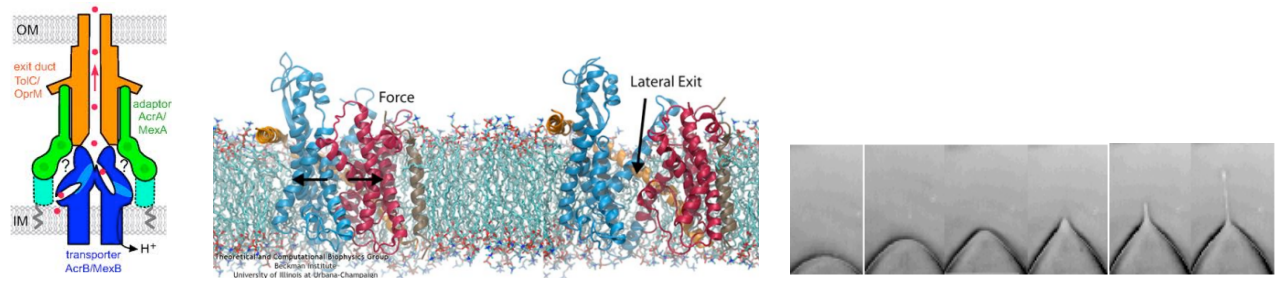

Figure 1: Tripartite multidrug pump mechanism (Koronakis, PNAS 2009), Force-induced protein conformation (Beckman Institute), Vesicle's tether from tip instability (IRPHE)

Membrane proteins permit the exchange of information and cell metabolites with cellular compartments or with the extracellular medium. As such, they constitute pharmacological targets for two thirds of present drugs. A number of hurdles have to be overcome to fully understand their detailed functioning. Among the major problems to be solved, one can mention: (i) the efficient overexpression; (ii) the insertion into supramolecular assemblies such as bilayers, liposomes etc., while maintaining their native structure; (iii) the complete determination of the transmembrane proteins structure and function (Fig.1, middle and left panels respectively); (iv) the study of interactions with other proteins, whether membraneous or not; (v) the collective behaviour at mesoscopic and microscopic scales.

The aim of this minicolloquium is to focus on the wide range of topics in the area of biological membranes, from the microscopic scale with vesicles or proteo-liposomes, to the nanometer scale with membrane proteins. This includes biomimetic models for the study of membrane dynamics within an external field (flow for example), or different model systems, as well as various techniques used for the investigation of membrane proteins. All the above does not exclude combined approaches, such as the transfer of macromolecules by a membrane protein, leading to a collective answer. The presentation dealing with experimental results as well as numerical and/or theoretical results and methods are encouraged. Alternative and original methods are also welcome.