Biochimica et Biophysica Acta 1788 (2009) 1

Contents lists available at ScienceDirect

Biochimica et Biophysica Acta

journal homepage: www.elsevier.com/locate/bbamem

Lipid interactions, domain formation, and lateral structure of membranes

Biological membranes are crucial structures needed for cellular compartmentalization, signaling, metabolism and interfacial processes. The current knowledge regarding structural and functional aspects of biological and model membranes is large but not complete, partly because the membranes have been found to be extremely complex structures and partly because we still encounter experimental (technical) limitations in assessing the structure of bilayer membranes.

It is the aim of the present special issue to present fresh insight into the recent development of membrane research from both experimental, theoretical and computational work. Many of the contributions will deal with questions and problems relating to lipid interactions in the membrane as pertinent for membrane structure. Some of these papers will focus on sphingolipid behavior in complex membranes. Others will deal with techniques and various intellectual approaches to study domain formation and phase behavior of lipids in fairly complex bilayer membranes. A few papers will discuss the role and impact of proteins for membrane lateral structure and the role of membrane properties for membrane–protein interaction. Contributions reporting on recent advances in the visualization and imaging of membrane structure will also be included. Problems or questions which are difficult or impossible to address experimentally, but which are important for understanding membrane structure, will be discussed in contributions covering recent developments in computational studies on membranes.

Altogether, the contributions of this special issue should give a comprehensive and state-of-the-art view on recent development in membrane structure and function, but should also project where the field is heading.

This issue could not have been put together to such a high standard without the contributions of the many peer reviewers who allocated time and critical thinking in order to improve the quality and impact of each and every contribution. The staff at Elsevier/BBA responsible for Special issues are thanked for helping the guest editor in his work.

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0005-2736/$ – see front matter © 2008 Published by Elsevier B.V.
doi:10.1016/j.bbamem.2008.12.006