Preface

First published online 8 April 2004

This special issue consists of contributions presented at the 2nd International Conference on Structure, Dynamics and Function of Proteins in Biological Membranes held October 5th-10th, 2003 at the Monte Verità in Ascona, Switzerland. At the first conference, which took place in 2001, it had already become clear that the field of membrane protein structure determination had reached a turning point and had entered a phase of impressive growth. This expectation was fully realized in the years between and the progress is impressive indeed. This is reflected by the 2003 Nobel Prize in Chemistry, which was announced on October 8th to go to Roderick MacKinnon and Peter Agre for their discoveries concerning membrane channels, a topic that was at the heart of the second Monte Verità conference on biological membranes.

The enormous progress in our abilities to determine atomic models of integral membrane proteins rests on great improvements in many areas of experimental research. The availability of so many genome sequences together with efficient cloning and expression methods permits us to apply screening technologies for finding the most 'well-behaved' candidates for biophysical studies among many functional homologs. The strongly improved know-how in the solubilization, characterization, handling and crystallization of purified membrane proteins is certainly another important factor. Significant advances in the three major structure determination methods, X-ray and electron crystallography and in particular NMR spectroscopy, also contribute an important share to this overall spectacular progress.

We now know representative structures from many of the major functional classes: photosynthetic reaction centers and photosystems, respiratory complexes, outer membrane porins, ion channels, aquaporins, proton and ion pumps, ABC transporters, secondary transporters, and G-protein coupled receptors. A challenge of the future will be not only to determine more such structures, but to gain more detailed insight into the functional cycles and thus into the different conformational states that most of these proteins assume. This will require the combination of the available techniques, each of which has its special constraints and limitations. Clearly, assessing structural states in a natural lipid membrane environment, even if not at very high resolution, will often be critical. Some of these limitations will never be experimentally overcome and one challenge for bio-computational methods is certainly to extrapolate into experimentally inaccessible states.

The contributions at the conference covered many of these aspects and provided the basis for stimulating exchange between different areas of this research. We thank all the speakers that have kindly contributed articles to this FEBS Letters Special Issue. We hope that it will serve to convey the current excitement of this multidisciplinary research field.

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doi:10.1016/S0014-5793(04)00424-7