BioMed Research International

Hindawi

Special Issue on

Innovative Membrane Protein Expression and Purification Methods for Structure Determination with Drug Discovery Perspective

CALL FOR PAPERS

Membrane proteins are rewarding drug targets as they constitute about one-third of our proteome and play crucial roles in transport, signaling, and several other intracellular processes. About two-thirds of all current therapeutic targets are membrane proteins; therefore, understanding their structure and mechanism of action and regulation at the molecular level is of great value for drug discovery. Paradoxically, the number of solved membrane protein structures is exceedingly small. There are only about 500 unique membrane protein structures deposited in the Protein Data Bank (PDB), which represent less than 1% of all available structures in the PDB. This underrepresentation stems from the presence of hydrophobic segments in integral membrane proteins that are embedded into lipid bilayers, making membrane proteins difficult to study and crystallize. Therefore, various approaches and techniques are required to express and purify membrane proteins that are naturally weakly abundant. Moreover, pure, monodisperse, and highly concentrated proteins are required for structural approaches such as NMR spectroscopy and X-ray crystallography.

Isolation of membrane proteins from their native lipid environment is a mandatory prior step in order to gather specific structural information. Structural analysis needs to be combined with functional assays for the proper characterization of the molecular mechanisms of native protein. Characterizing their interaction sites with small molecules and other proteins rapidly improves the landscape for the development of highly effective and specific drugs and tool compounds that can advance basic research and medicine.

The methods available for the purification of membrane proteins are basically the same as those used for water-soluble proteins. These methods include precipitation, gel filtration, and techniques such as ion exchange and reversed-phase and affinity chromatography. However, the adaptation of these techniques involving the use of detergents, in addition to several unique characteristics of membrane proteins, such as their hydrophobic tendency and possible associated lipids, makes these methods difficult to apply successfully. Therefore, further development and optimization of these methods are necessary. In parallel, verifying the specific functional properties of the purified protein, such as catalytic activity, ion conductance, substrate transport, or presence of binding partners, is indispensable to determine whether the protein retains its physiological state after purification.

The purpose of this special issue is to publish high-quality research papers as well as review articles addressing questions about expression, purification, and functional validation methods for membrane protein transporters and channels. We encourage peers to submit manuscripts regarding membrane protein expression and purification methods for structural analysis in order to understand molecular mechanisms and contribute to make progress in pharmaceutical research. High-quality contributions that are not published or under review by other journals or peer-reviewed conference proceedings will be accepted.

Potential topics include, but are not limited to:

- Purification methods for membrane protein transporters and channels
- Optimization of expression systems for membrane proteins: bacteria, yeast, insect cells, human cells, and cell-free systems
- Genetic optimization of membrane protein expression
- Biophysics-based methods for functional validation of purified proteins

Authors can submit their manuscripts via the Manuscript Tracking System at http://mts.hindawi.com/submit/journals/bmri/structural.biology/impe/.

Lead Guest Editor
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benjamin.clemencon@ibmm.unibe.ch

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Michael Fine, University of Texas Southwestern Medical Center, Dallas, USA
mfine42@gmail.com

Denis Rousseau, Joseph Fourier University, Grenoble, France
denis.rousseau@ujf-grenoble.fr

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