Special Issue

Advances in Membrane Protein Research

Message from the Guest Editor

Integral membrane proteins represent one-third of all open frames in sequenced genomes. This is in contrast to their immense importance in medicine, where an estimate of 60–70% of current drug targets are based on membrane proteins. To ensure adequate drug design, analysis of the structure and function of membrane proteins is essential. Additionally, the "Resolution Revolution" brought about by single-particle Cryo-EM techniques continues to make progress, with the recently reported 1.7 Å resolution of the GABAA receptor structure. Nevertheless, our ability to take advantage of these methods is hindered in part by a lack of generally applicable methods for overexpression and purification, which are critical steps preceding functional and structural analysis. Thus, the bottlenecks prior to determining a membrane protein's structure or characterizing its function remain. There is also an urgent need to improve the production of a sufficient amount of active membrane proteins. These limitations can be overcome through the development of new ideas, such as cell-free systems or amphipathic nanoparticles.

Guest Editor

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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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