Special Issue

Emerging Topics in Structural Biology

Message from the Guest Editors

In the last few years, two events have revolutionized the field of structural biology: the “resolution revolution” of cryo-electron Microscopy (cryo-EM), which allows the visualization of single particles at a near-atomic resolution without the need of growing them in a crystalline form, and the recent development of AlphaFold 2, an AI system able to predict the 3D structure of a single protein with high reliability. This last event will strongly influence crystallography since that most of the future crystal structures will be solved using the molecular replacement technique. In parallel, new techniques/methods are emerging in crystallography, such as new crystal growing methods, more intense and focused X-ray beams, novel data collection methods, ultra-sensitive detectors, advanced computational algorithms, and new software.

The present Special Issue is aimed at summarizing frontier technologies and methodological advances in the field, as well as structures and functions of special proteins or protein complexes, to take stock of the present situation and to create a virtual forum for the future of Structural Biology.

Guest Editors

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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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