Special Issue

Structure, Function and Dynamics in Proteins: 3rd Edition

Message from the Guest Editor

Dear colleagues, This Special Issue continues on from the previous edition, “Structure, Function and Dynamics in Proteins: 2nd Edition”. The structure–dynamics–function relationship plays crucial roles in the biological function of proteins. High-resolution protein structures can currently be obtained from X-ray crystallography (X-ray), nuclear magnetic resonance (NMR) and cryo-electron microscopy (Cryo-EM) techniques, as well as, under certain conditions, computer molecular modeling. Sometimes, three-dimensional protein structures fail to give a complete understanding of the concerned functional mechanisms. Protein dynamics and conformational transitions, in most biological functions, are the essential link that connects high-resolution structural details with cellular processes ranging from protein folding, enzymatic catalysis to signaling, solute transport and synaptic transmission. This Special Issue of IJMS aims to make a substantial contribution to the understanding of protein structural dynamics and functional relationships by publishing innovative studies in the fields of protein structural dynamics and protein functions.

Guest Editor

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Message from the Editor-in-Chief

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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