

Special Issue

Structure, Function and Dynamics in Proteins

Message from the Guest Editor

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. Over the last decades, experimental techniques such as NMR relaxation, fluorescence spectroscopy, time-resolved X-ray and molecular dynamics have made substantial progress in providing an accurate description, at an atomic level, of protein dynamics on timescales of nano- and microseconds. This Special Issue of IJMS, entitled “Structure, Function and Dynamics in Proteins”, 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)* 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, and molecular biophysics. *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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