Special Issue

Molecular Advances in Bioinformatics Analysis of Protein Properties

Message from the Guest Editor

The paradigm of sequence–structure relationships was introduced more than half a century ago and has since been associated with the functions carried by proteins. The highly complex nature of these relationships is a consequence of the interaction between physics and evolution, which has been studied using a wide range of experimental and theoretical techniques. In addition, this paradigm has become more complex by taking into account the dynamics of proteins, an essential element for understanding their functions, along with the pathological problems that may be associated with them. This Special Issue will therefore deal with the study of this entire sequence–structure–function–dynamics paradigm of proteins, which can range from the most sophisticated sequence analyses to the conservation of essential residues, the dynamics of proteins through both atomistic and simplified approaches (coarse-grained, normal modes, etc.) or quantum analyses. However, the ultimate goal of these studies must be the biological question being asked and the link with experimental data.

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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