Special Issue

Protein Folding, Misfolding, and Related Diseases

Message from the Guest Editor

In order to function properly, proteins fold into their native three-dimensional conformations. Protein folding is governed by physico-chemical properties of the amino acids constituting its polypeptide chain, and leads to the minimization of polypeptide chain free energy. Multiple chaperone systems are required to fold proteins correctly in a cellular environment. In addition, degradation pathways participate by destroying improperly folded proteins. However, the intricacy of this multisystem processes provides many opportunities for an error. As a result, many diseases are fundamentally rooted in the protein folding or misfolding problem that all cells need to resolve in order to maintain their function and integrity.

In this Special Issue, you are welcome to address the issues concerning the underlying molecular and cellular mechanisms of protein folding and alternative structural conversion into misfolded species, how these processes may lead to disease or are mitigated by protective cellular mechanisms. The prospective treatments of protein misfolding diseases will be also highlighted.

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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