Special Issue

Protein Unfolding Induced by Chemical Agents

Message from the Guest Editors

Protein folding and unfolding has been an important research area since the Anfinsen dogma was established. We know that biologically important proteins work best around room temperature, atmospheric pressure, neutral pH, and in the absence of chemicals (e.g. small, organic molecules). However, the equlibrium that favours folded protein conformation can be shifted by changing any of the conditions mentioned above. Here, we aim at chemical unfolding as it has pharmaceutical importance. Importantly, folding and unfolding time scales are generally too fast for straight experimental (e.g. NMR, AFM, FRET) observations. Therefore, often the equilibria are studied by physical methods as shifted to irreversible „denatured" states. Sometimes even the unfolded states are interesting because they provide insight into the nature of disordered proteins (IDPs). In addition to experimental techniques, in-silico, molecular dynamics simulations may be of help for understanding the mechanism of chemical denaturation.

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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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