Special Issue

Protein Aggregation: From Molecular Biology to Human Disease

Message from the Guest Editor

Cells have evolved multiple pathways to control the synthesis, folding, and degradation of proteins. These pathways contain thousands of components and are collectively called the proteostasis network (PN). The PN balances the synthesis and degradation of proteins to prevent the buildup of toxic protein aggregates in the cell. It is recognized that a disruption in the PN leads to a variety of human diseases such as neuromuscular and neurodegenerative disorders, cancers, and diabetes. Important pathways that contribute to the PN include ribosomal translation, the ubiquitin–proteasome system, the unfolded protein response, autophagy, and the heat shock response. Recent data from multiple studies suggest that the robustness of the PN varies depending on the cell and tissue type, and the activity of the PN appears to decline with age. There is a great deal still unresolved concerning the regulation and decline of PN activity with age or human disease. This Special Issue focus on the regulation of the PN molecular mechanisms involved in the prevention or clearance of protein aggregates in health, disease, and aging.

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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