Special Issue

Recent Advances in Protein Folding and Misfolding

Message from the Guest Editor

Protein folding and misfolding have been of interest in science for a long time. Recent advances in AI-based tools like AlphaFold and RoseTTAFold have revolutionized 3D-protein structure prediction from amino acid sequences with remarkable accuracy. However, they have limitations in predicting conformational changes or misfolding due to mutations or post-translation modifications. Furthermore, the physics of protein folding and misfolding remains largely unknown. Recent studies have shed light on the relationship between single nucleotide polymorphisms (SNPs) and protein misfolding, revealing significant implications for neurodegenerative diseases and potential therapeutic strategies using CRISPR/Cas9 technology. Thus, the current trends in protein folding and misfolding with diverse techniques, and their applications in revealing protein misfolding mechanisms and diseases at the molecular level, are both significant and interesting. Understanding the clearance mechanisms of misfolded proteins in cells is also a matter of significance.

Guest Editor

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