

## Special Issue

# Decoding Protein Structure and Protein Dynamics in Cancer

### Message from the Guest Editors

Malfunctioning genes are often recognized as the common driver of cancer, which can manipulate these essential molecules, promoting disease progression. Understanding protein modifications in the context of cancer is crucial for advancing therapeutic strategies. Protein structure is key to deciphering molecular mechanisms, including those exploited by cancer cells. Advancements in proteomics such as affinity purification, proximity labeling, cross-linking, and co-fractionation mass spectrometry have revolutionized protein identification, quantification, and post-translational modification analysis (e.g., phosphorylation, glycosylation, ubiquitination). Bridging experimental and computational methods, this Special Issue features state-of-the-art techniques in structural biology, proteomics, and bioinformatics for analyzing protein interactomes. We invite original research and reviews exploring dynamic protein structural changes and their role in cancer progression. Combining proteomics and bioinformatics techniques is aimed at accelerating breakthroughs in biomarker discovery and drug target identification, driving innovations in medicine and biotechnology.

### Guest Editors

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### Deadline for manuscript submissions

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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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### Editor-in-Chief

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