

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

Dr. Umesh Kalathiya

International Centre for Cancer Vaccine Science, University of Gdansk,
ul. Kladki 24, 80-822 Gdańsk, Poland

Dr. Monikaben Padariya

International Centre for Cancer Vaccine Science, University of Gdansk,
ul. Kladki 24, 80-822 Gdańsk, Poland

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Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
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Editor-in-Chief

Prof. Dr. José L. Quiles
Department of Physiology, Institute of Nutrition and Food Technology
"Jose Mataix", Biomedical Research Center, University of Granada,
Avda. Conocimiento s/n, 18100 Armilla, Granada, Spain

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