Special Issue

Computational Cancer Genomics and Molecular Profile in Breast Cancer

Message from the Guest Editors

Breast cancer is a highly prevalent disease worldwide. Current developments in molecular biology have brought new insights into the nature of this disease, and it is clear that breast cancer is not a unique illness but probably a myriad of entities with distinct biological and clinical behaviors. Such diversity impairs therapeutic strategies, and treating breast cancer patients remains challenging. Computational biology is a powerful field that integrates computer science, mathematics, and statistics to solve complex problems, such as molecular and genomic information from high-throughput technologies. The use of such tools enables a better characterization of breast cancer diversity and has demonstrated that this approach is a successful strategy in the development of more accurately targeted therapies, optimizing cancer treatment, and reducing undesired side effects. Original research, systematic reviews, and new protocols or methodologies of analysis using computational strategies to analyze molecular and genomic data from breast cancer samples—in particular when integrating them with clinical applications—are welcome.

Guest Editors

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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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