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Breast Cancer Ecosystem: Genomic and Proteomic Profiling

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Deadline for manuscript
submissions:

closed (15 April 2024)

Message from the Guest Editor

Breast cancer is a heterogeneous disease. The classification of breast cancer ranges from various histopathological subtypes based on cell morphology and biomarker expressions to molecular intrinsic subtypes according to gene expression patterns. Previously, genetic testing was conducted to determine the presence of mutations of certain breast cancer susceptibility genes. Nowadays, molecular prognostic assays are conducted to predict long-term outcomes of the disease. In this Special Issue, we aim to build a collection of research works that focus on advances in our understanding of the initiation and progression of breast cancer, particularly on the characterization of cancer and the surrounding micro-environment and their role in driving aggressiveness and recurrence risk. Research studies related to the identification of genetic modifications, genomics, proteomics, epigenetics, biomarker testing, prognostic assays and multi-omic signatures in any stage of breast cancer development are welcomed.



mdpi.com/si/185743

Special Issue



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Editor-in-Chief

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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