Identification of Candidate Genes in Breast and Ovarian Cancer

Guest Editors:

Dr. Nadège Presneau
University of Westminster, Cancer Research Group, School of Life Sciences, College of Liberal Arts & Sciences, London, United Kingdom

Prof. BIGNON Yves-Jean
Centre Jean Perrin, INSERM 1240, Université Clermont Auvergne, France

Dr. Pinar Uysal Onganer
Cancer Research Group, School of Life Sciences, College of Liberal Arts & Sciences, University of Westminster, London, UK

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Message from the Guest Editors

Dear Colleagues,

On a global scale, breast cancer is the most frequently diagnosed cancer in women; there were over 2 million new cases in 2018, contributing to about 11.6% of the total cancer incidence burden (Globocan 2018, International Agency for Research on Cancer). However, although the last decade has seen an increase in breast cancer incidence, there have also been great improvements in its diagnosis and survival with nearly 80% of breast cancer patients surviving for at least 10 years (Cancer Research UK). According to the International Agency for Research on Cancer, in 2018, female breast cancer ranked as the fifth leading cause of death (627,000 deaths, 6.6%) due to the prognosis being relatively favourable, at least in more developed countries.

Novel therapeutics, such as Herceptin (trastuzumab), and hormone-related biological therapies have greatly contributed to the increased survival rate, as has the knowledge acquired in cancer biology, particularly regarding the identification of candidate genes using molecular and computational approaches to interpret the "OMICs" big data generated principally by genomics and transcriptomics.

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Special Issue

Editor-in-Chief

Prof. Dr. Samuel C. Mok
Department of Gynecologic Oncology and Reproductive Medicine, The University of Texas MD Anderson Cancer Center, Houston, TX 77030, USA

Message from the Editor-in-Chief

Cancers is an international online journal addressing both clinical and basic science issues related to cancer research. The journal is publishing in Open Access format, which will certainly evolve to ensure that the journal takes full advantage of the rapidly changing world of information and knowledge dissemination. It publishes high-quality clinical, translational, and basic science research on cancer prevention, initiation, progression, and treatment, as well as other related topics, particularly to capture the most seminal studies in the rapidly growing area of immunology, immunotherapy, and tumor microenvironment.

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