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Genomic Medicine in Cancer

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Message from the Guest Editors

Cancer is a disease of the genome, and enormous efforts are directed toward a clearer understanding of this heterogeneous collection of diseases. The expansion of our insight into cancer genomes is mostly driven by the rapid development in sequencing technologies all the way from the early identification of oncogenes and tumor suppressors to the full annotation of the most common cancers resulting in the so-called genomic landscapes of cancer. The major advances in sequencing technologies followed by the development of computational tools have enabled analyses such as whole-exome, whole-genome, and RNA sequencing to be implemented in routine clinical settings, thus supporting the emerging clinical relevance of genomics in cancer medicine. The cancer genome is somewhat dynamic, and each cancer evolves with the accumulation of several types of somatic mutations, copy number alterations, epigenetic factors, and structural variants. These changes can occur in a predisposed genetic background, such as hereditary cancers which again cause diverse patterns for the individual tumor genome.

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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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