

## Special Issue

# Computational Oncogenomics

### Message from the Guest Editor

Dear colleagues, Omic studies of tumors have generated a lot of data, including data from new genome sequencing, transcriptomes, proteomes, ATAC-seq and genome-wide association studies (GWAS). The sampling for omics data generation have been applied to primary and metastasis tumors, with or without treatment. Furthermore, single-cell genomics data have been generated in the past two-to-three years. We would like to collect a set of research papers, methods and reviews in a broad range of topics, including but not limited to: cancer genomics, transcriptomics and methylome analysis, tumor genetics and evolution, CNV studies, cancer biomarkers discovery, immunotherapy, network analysis, single-cell genomics, translational studies and computational oncogenomics.

### Guest Editor

Prof. Dr. Edwin Wang

Cumming School of Medicine, University of Calgary, Calgary, AB T2N 1N4, Canada

### Deadline for manuscript submissions

closed (31 July 2019)

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### Message from the Editor-in-Chief

*Genes* is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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### Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan  
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