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## Computational Oncogenomics

Guest Editor:

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Deadline for manuscript  
submissions:

**closed (31 July 2019)**

### **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.

Prof. Edwin Wang

*Guest Editor*



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# 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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