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Integrative Multi-Omics, Single-Cell and Spatial Approaches to Study Complex Diseases

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Deadline for manuscript submissions:
closed (5 December 2022)

Message from the Guest Editors

Dear Colleagues,

In this Special Issue, we hope to bring together a diverse set of experts in genomics from multi-disciplinary backgrounds to share their collective expertise in a broad range of topics related to multi-omics profiling and data integration for various complex human diseases. We expect the themes to cover various topics, such as bulk and single-cell multi-omics and multi-modal data acquisition and analyses (e.g., scRNA-seq, scATAC-seq, CITE-seq), other epigenomic, proteomic and spatial genomics in both healthy and diseased tissues/cells. We will highlight new statistical and machine learning approaches for -omics data harmonization, multi-ancestry analyses, quantitative trait locus mapping, GWAS variant prioritization, as well as web application development for end-to-end analyses, data sharing, visualization, annotation, target validation and precision medicine.

We welcome applications to a broad range of cell/tissue and disease areas, involving either publicly available or custom datasets. We also welcome multiple manuscript formats, including original research articles, reviews or mini-reviews, opinions, hypotheses, or theories.

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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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