# Special Issue

## 3D Reconstruction of Genome Structures

### Message from the Guest Editor

The Hi-C experiment allows scientists to obtain the proximity relationships between genomic regions in the 3D space, which provides opportunities for computational scientists to infer and reconstruct high-resolution 3D genome structures. These 3D genome structures provide a new perspective to study how genomes function.  Conducting Hi-C experiments at different time points further allows scientists to reconstruct and analyze 4D genome structures. Compared to the bulk Hi-C experiment that is based on a pool of cells, the single-cell Hi-C experiment focuses on each individual cell, which can reveal cell-to-cell variability. A single-cell Hi-C contact matrix (2D) is usually sparse and contains lots of zeros, which creates challenges for reconstructing 3D genome structures. However, the sparseness also creates new research opportunities for developing novel methodologies to impute single-cell Hi-C contacts and infer single-cell 3D genome structures.  The goal of this Special Issue is to collect and publish research for reconstructing and analyzing genome structures.

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### Guest Editor

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### Deadline for manuscript submissions

closed (15 August 2022)

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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

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