

Special Issue

3D Genomics

Message from the Guest Editors

DNA was discovered in 1869. In 1953, the chemical structure of the DNA was elucidated through the double helix model; and the human genome project was declared complete in 2003. Since then, the human genome and many other genomes have been annotated all over. A great deal of information about mammalian genomes is available nowadays, but we are still far from understanding their regulation. A key missing factor is the 3D structure of the genome. Unravelling this information is key to expand our understanding of the biological functionality orchestrated by variables that exceed a unidimensional genome. Microscopy was the main technique used to observe the structure of the chromatin, but the recent advances on chromatin conformation techniques (3C) and derived techniques, especially Hi-C, are starting to allow us to solve part of the puzzle led by the recent discovery of topologically associating domains (TADs), which are keystones in gene regulation with causality in human disease. In this Special Issue, we are most interested in collecting short reviews on 3D genomics.

Guest Editors

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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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