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Chromosome-Centric View of the Genome Organization and Evolution

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Deadline for manuscript submissions:
closed (30 April 2021)

Message from the Guest Editors

Dear Colleagues,
The development of next generation sequencing technologies in the last decade has led to obtaining highly-fragmented genome assemblies for numerous organisms. The quality of genome assemblies significantly varies among species, depending of the abundance of the repetitive elements and levels of genetic polymorphism. As a result, many important problems in genome biology remain unresolved, without understanding how the genome is organized at the level of the chromosomes. Recent advances in genome and chromosome technologies, including long-read sequencing, Hi-C scaffoding, chromosome flow sorting, and physical and optical mapping, allow for obtaining genome assemblies at the level of complete chromosomes. Such assemblies provide new opportunities to study chromosome organization and evolution, structural genome variations, sex-biased gene expression, epigenomic modifications, and long-range chromatin interactions.

In this Special Issue, we would like to invite submissions of original research and review articles, with a special focus on chromosomes in our understanding of the genome structure, function, and evolution.

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Special Issue

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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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