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Genetics and Genomics of Leishmania

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Message from the Guest Editors

Leishmania are well-known as causative agents of leishmaniasis, a group of diseases affecting millions of persons living in tropical and subtropical regions. There is currently no acceptable vaccine for humans, and our understanding of the *Leishmania* virulence factors responsible for these diseases is limited. Integrated research into the molecular biology of these pathogens is needed.

In the past fifteen years, great progress has been made in our understanding of *Leishmania*. The advent of high-throughput technologies has led to the accumulation of a massive amount of genomic data. Now, it is time to integrate this information together to decipher particularities in the molecular mechanisms and biosynthetic pathways of this parasite.

This Special Issue welcomes original research articles dealing with topics around the genetics, genomics, transcriptomics, and proteomics of *Leishmania* parasites, pathogen–host interactions, traits of drug resistance, phylogenetics, and evolution of these organisms. Additionally, review articles are welcome which cover the current literature and present a synthesis of our current knowledge of these pathogens.



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Special Issue



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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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