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Genetics and Genomics of Human Pathogens

Guest Editor:

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Deadline for manuscript submissions:
closed (20 April 2024)

Message from the Guest Editor

Past genetic and genomic analyses of viral, bacterial, and parasite genomes have identified various components that play a role in the development, progression, and/or severity of human diseases. In addition, such analyses enable researchers to trace the evolutionary history, identify emerging variants, and predict the future trajectory of these pathogens. The results from such analyses can then be experimentally validated in the wet lab and/or used to inform public health efforts. The continued emergence of novel pathogens, the increased prevalence of drug-resistant genes and variants, and the expanded host range of pathogens capable of infecting humans justify maintaining and expanding comparative genomics research.

This Special Issue will cover novel genetics and genomics findings in viruses, bacteria, and parasites. Specifically, submissions describing novel findings for human pathogens using methods including but not limited to phylogenetic trees, selection pressure, immune epitopes, genotype–phenotype correlations, pathogenicity islands, operons affecting the host range or pathogenicity, and the identification of variants affecting pathogenesis will be evaluated.

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Editor-in-Chief

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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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