

Special Issue

Comparative Genomics of Human Pathogens

Message from the Guest Editor

A number of genetic mechanisms that contribute to human pathogenesis have been previously identified, including pathogenicity islands and variants that affect invasiveness, fitness, host range, and evading the host immune response. In addition, genomic analyses enable researchers to trace the evolutionary history, identify emerging variants, and predict the future trajectory of these pathogens. The results from such computational analyses can then be experimentally validated in the wet lab. The continued emergence of novel pathogens, the increased prevalence of drug-resistance genes and variants, as well as the expanded host range of pathogens capable of infecting humans justify maintaining and expanding comparative genomics research. This Special Issue will cover comparative genomics analyses of viral, bacterial, and parasite sequence data. Submissions describing novel findings for human pathogens using methods 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.

Guest Editor

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Deadline for manuscript submissions

closed (20 May 2022)

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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.

Why not consider *Genes* for your next genetics paper?

Editor-in-Chief

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