Special Issue

Genomics of Bacterial Pathogens

Message from the Guest Editors

The new genomic technologies together with bioinformatics have resulted in an unprecedented wealth of sequencing data concerning bacterial pathogens. These data can be exploited to answer important questions related to understanding the evolution of these pathogens and their genomic components. It is also important to use this knowledge to advance and transform the fields of biotechnology and clinical practice. This Special Issue of Microorganisms aims to provide a scientific platform for scientists performing fundamental, applied, and translational research related to bacterial pathogens using genomic data. More specifically, it will include original studies, reviews, and method papers related to the application of sequencing technologies, development and/or application of Bioinformatics methods with a focus on bacterial pathogen: i) genome evolution, ii) phylogenomics, iii) core/accessory genome analyses, iv) pathogenicity islands, v) evolution of gene families related to pathogenicity and antimicrobial resistance, vi) genomic epidemiology, vii) genomic forensics, viii) pathogen detection/characterization.

Guest Editors

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About the Journal

Message from the Editor-in-Chief

"Microorganism" merges the idea of the very small with the idea of the evolving reproducing organism is a unifying principle for the discipline of microbiology. Our journal recognizes the broadly diverse yet connected nature of microorganisms and provides an advanced publishing forum for original articles from scientists involved in high-quality basic and applied research on any prokaryotic or eukaryotic microorganism, and for research on the ecology, genomics and evolution of microbial communities as well as that exploring cultured microorganisms in the laboratory.

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manuscripts are peer-reviewed and a first decision is provided to authors approximately 15.2 days after submission; acceptance to publication is undertaken in 2.9 days (median values for papers published in this journal in the first half of 2025).

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