Special Issue

Whole-Genome Sequencing of Pathogenic Bacteria - New Insights into Antibiotic Resistance Spreading

Message from the Guest Editor

Antibiotic resistance acquisition by pathogenic and opportunistic bacteria has become a major problem worldwide. Whole-genome sequencing (short- and long-read) is currently attracting increasing attention since it allows one to accurately and rapidly obtain the data regarding the presence of specific antibiotic resistance genes and their locations in a bacterial genome (chromosomal or plasmid). we invite you to contribute original research and review papers describing the application of the whole-genome sequencing of bacterial pathogens to revealing antimicrobial resistance genes, comparing phenotypic and genomic resistance profiles, reconstructing plasmids, performing epidemiological surveillance and elucidating the mechanisms and/or ways of antimicrobial resistance spreading and being acquired. Novel computational approaches and pipelines for performing such investigations are particularly welcome.

Guest Editor

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Deadline for manuscript submissions

closed (31 December 2022)

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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.

Editor-in-Chief

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