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

Guest Editor:

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Deadline for manuscript submissions: closed (31 December 2022)

Message from the Guest Editor

Antibiotic resistance acquisition by pathogenic and opportunistic bacteria has become a major problem worldwide. Whole-genome sequencing (short- and longread) 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.



Specialsue





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Message from the Editor-in-Chief

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