



Whole-Genome Sequencing of Pathogenic Bacteria - New Insights into Antibiotic Resistance Spreading 2.0

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Message from the Guest Editor

Antibiotic resistance acquisition by pathogenic and opportunistic bacteria has become a major problem worldwide. However, the mechanisms of antibiotic resistance acquisition and spreading among different bacterial species cannot be easily revealed by the traditional phenotypic analyses. Whole-genome sequencing (short- and long-read) is currently attracting increased attention since it allows for accurately and rapidly obtain data regarding the presence of specific antibiotic resistance genes and their locations in a bacterial genome (chromosomal or plasmid).

For this Special Issue, we therefore invite you to contribute original research and review papers describing the application of the whole-genome sequencing of bacterial pathogens for revealing antimicrobial resistance genes, comparing phenotypic and genomic resistance profiles, reconstructing plasmids, performing epidemiological surveillance, and elucidating the mechanisms and/or methods of the spreading and acquisition of antimicrobial resistance. Novel computational approaches and pipelines for performing such investigations are particularly welcome.





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Message from the Editor-in-Chief

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