Special Issue

Next-Generation Sequencing in Antimicrobial Resistance

Message from the Guest Editors

Antimicrobial resistance (AMR) is a serious threat with impacts on public health, food sustainability and security, environmental wellbeing, and socio-economic development. Today, the improvements of diagnostic methods have deeply transformed our ability to address AMR. Next-generation sequencing (NGS) offers the possibility to sequence microbial genomes either from colonies (genome of bacteria and fungi) or directly from clinical samples (metagenome). The NGS data analyzed by bioinformatics tools enable the rapid and accurate detection of a variety of known and new genes or mutations conferring resistance of microorganisms (bacteria, viruses, fungi and parasites) to antimicrobial agents. The introduction of NGS in "One Health" appears to be a new perspective in the diagnostic field of AMR, with a focus on personalized therapy and on the limitation of the spread of resistant pathogens.

In this Special Issue entitled "Next-Generation Sequencing and Antimicrobial Resistance", we welcome reviews, original research, and short communications that share new insights into the application of NGS in human, animal and environmental samples for detecting AMR.

Guest Editors

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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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