Special Issue

Virus Detection and Metagenomics

Message from the Guest Editor

Viruses can spread very quickly, something humanity has been convinced of many times - and again in 2019, when the SARS-CoV-2 virus struck and spread rapidly around the world, causing the COVID-19 pandemic worldwide.

The idea of using NGS to identify viral pathogens was proposed about 10 years ago, shortly after the advent of sequencing techniques, and the concept rapidly gained momentum as technology evolved. Currently, the use of NGS to study viral diversity is clearly one of the most promising approaches, as evidenced by the active use of this method in similar projects in recent years. Researchers primarily use metagenomic sequencing, as it is a powerful tool for detecting the entire spectrum of viruses. However, in recent years, approaches, both experimental and bioinformatic, have been actively developed to enhance the capabilities of NGS sequencing in the detection of viruses.

The purpose of this special issue is to provoke a discussion aimed at integrating knowledge and to present a variety of methods and approaches to meet the challenge of finding and identifying viral pathogens in biological material using NGS sequencing and original bioinformatic approaches.

Guest Editor

Dr. Kamil Khafizov
Central Research Institute of Epidemiology of Rospotrebnadzor, Moscow, Russia

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Microorganisms
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
microorganisms@mdpi.com

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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

Dr. Nico Jehmlich
Department of Molecular Toxicology, UFZ-Helmholtz Centre for Environmental Research, 04318 Leipzig, Germany

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