



Genome Analysis of Microbial Communities in the Environment

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Message from the Guest Editor

Dear Colleagues,

Recent achievements in sequencing techniques and bioinformatics tools have greatly expanded the known diversity of Bacteria and Archaea, and postulated the overwhelming majority of uncultured prokaryotes in our planet's environments. Culture-independent genomic analysis and metagenomics are essential to understand microbial diversity, metabolism, and the prospective industrial applications of microorganisms. On the other hand, metabolic reconstructions deduced from metagenome-assembled genomes (MAGs) and single-cell genomes (SAGs) provide clues for improving the cultivation of yet-uncultivated microorganisms.

The aim of this Special Issue of *Microorganisms* is to present a collection of articles that provide insight into genomic analysis in different biotopes, including various types of marine and terrestrial habitats. We also welcome reviews and research articles dedicated to human and animal microbiomes as well as artificial environments.

Prof. Dr. Olga V. Karnachuk

Guest Editor





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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.

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