



Microbiota: From the Environment to Humans 2.0

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Message from the Guest Editor

Dear Colleagues,

Microbiomes are the genomes associated with these microbial communities, and the metaproteome is the whole proteome expressed by these genomes. Thanks to the “omic” technologies, it is now possible to investigate both the genetic traits and the biological functions expressed by these complex microbial systems. Although the relationship between the host’s characteristics and its associated microbial communities has been extensively studied, the effects of one on the other are largely unknown.

The aim of this Special Issue is to provide an overview of the significance of microbial community fluxes from natural and built environments to humans, microbial community fluxes across foods, the effects of microbiota on host biology, and the integrated functions operating inside the holobiont.

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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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