



## Viral Metagenomic Analysis in Animals

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submissions:

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### Message from the Guest Editors

Dear Colleagues,

At an estimated number of  $10^{31}$  particles, viruses are the most abundant biological entities on Earth. It is assumed that several hundred thousand different viruses exist, but the vast majority of them are yet to be discovered and characterized. The development of next-generation sequencing and bioinformatics pipelines has recently supported the unbiased hypothesis-free detection of viruses and understanding of entire viral communities. However, while the viromes of various samples, species, and diseases have been investigated, the effect of the virome composition on health and disease remains largely elusive.

This Special Issue of *Microorganisms* aims to present viral metagenomic approaches to characterize viral communities in companion animals, livestock and wildlife, as well as bioinformatics pipelines for viral population analyses.

As Guest Editors of this Special Issue, “Viral Metagenomic Analysis in Animals”, we invite you to submit research articles, review articles, and short communications related to these topics.

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## Editor-in-Chief

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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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