



Virus Discovery, Classification and Characterization

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Message from the Guest Editors

In recent years, viral metagenomics has become an important tool for experts working in the field of virus discovery, classification, and characterization. Improved sample preparation and amplification methods, together with rapidly evolving sequencing technologies and bioinformatics pipelines, have made virus metagenomics a powerful approach for new discoveries. Viral metagenomics can be used to determine viral diversity in the environment or in any microbial community, to reveal the potential viral etiology of disease from pathological/clinical specimens, and to characterize viruses of unknown origin isolated in cell cultures. Using this approach, numerous novel virus species have been described over the past decade from all domains of life. This Special Issue includes all aspects of virus discovery (including new methods, new viruses, and new host–virus relationships) where next-generation sequencing has been central to the process.





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Message from the Editor-in-Chief

Viruses (ISSN 1999-4915) is an open access journal which provides an advanced forum for studies of viruses. It publishes reviews, regular research papers, communications, conference reports and short notes. Our aim is to encourage scientists to publish their experimental and theoretical results in as much detail as possible. There is no restriction on the length of the papers. The full experimental details must be provided so that the results can be reproduced. We also encourage the publication of timely reviews and commentaries on topics of interest to the virology community and feature highlights from the virology literature in the 'News and Views' section.

Electronic files or software regarding the full details of the calculation and experimental procedure, if unable to be published in a normal way, can be deposited as supplementary material.

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