Special Issue

Bacteriophage Genomes and Genomics: News from the Wild

Message from the Guest Editor

In the jungle of the phage world, genomes analyses have started to bring some order: Genomics becomes a reliable tool to classify phages, and ICTV has recently begun implementing taxonomic classifications, based primarily on genomic data. The raising interest in phage therapy has launched phage discoveries for a variety of bacterial species, allowing to reduce the over-representation of model phage-like coliphages in databases, and to reach a more equilibrated view on the phage world. Teaching on its side has opened an unprecedented view on mycophages, and new teaching projects now tackle other genera, such as Bacilli or Streptomycetes. Finally, (meta)viromics and single whole genome amplification are also bringing to the shore a wealth of new genomes. As such, the time is ready to collect the most striking features of the recent discoveries into a single issue.

Guest Editor

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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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