



Virus Comparative Genomics

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Message from the Guest Editor

Dear Colleagues,

In the last two decades, there has been a tremendous increase in the number of novel viruses discovered in human and animals using molecular technologies. Some of the novel viruses have been found by conventional PCR/RT-PCR, using conserved primers. With the advancement of sequencing technologies, a number of the previously-undescribed viruses have been discovered using a metagenomic approach. The discovery of these novel viruses has expanded our knowledge of the diversity of viruses, and has filled a number of the phylogenetic gaps. It has also revealed unprecedented models of evolution in different families of viruses. This Special Issue welcomes original or review articles related to any aspects of the comparative genomics of viruses.

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Guest Editor





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Message from the Editor-in-Chief

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