Special Issue

Antigenic Drift in Respiratory Viruses

Message from the Guest Editor

Understanding the evolutionary patterns that increase the diversity of viral respiratory pathogens has become paramount. The world faces increasing risks of major infectious outbreaks posed by pathogens such as influenza virus, adenovirus, respiratory syncytial virus and even other members of the *Coronaviridae* family. In this context, technological and analytical approaches have made it possible to simulate in silico, and experimentally characterize in detail, the effects of viral diversity. Such characterizations extend also to predictions regarding diverse variants of viruses, better identification of evolutionary events such as host-switching and recombination/reassortment and methods to surveil viral agents affecting public health. This Special Issue aims to compile scientific reports on these efforts to disseminate best practices aimed to aid in the development of accessible diagnostics and treatments and the prevention of future infectious outbreaks.

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About the Journal

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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