# Bioinformatics and Computational Biology of Viruses

Guest Editor:

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Deadline for manuscript submissions:
**closed (28 February 2016)**

## Message from the Guest Editor

Dear Colleagues,

Computational and systems biology, and bioinformatics play an increasingly important role in virology, helping us understand the structure, functioning and interactions of viral molecules, the within-host dynamics of virus infections, the spread of virus epidemics, and the origin and evolution of viruses, as well as the effect and optimal design of human interventions from drug discovery to epidemics control. This Special Issue invites submissions of modelling and bioinformatics papers from all fields of virology at all levels of organization. The scope of methods covers all in silico approaches such as mathematical and simulation models; molecular dynamics; phylogenetic, genomic and network analyses, and analyses of other complex data sets.

Dr. Viktor Müller
*Guest Editor*

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Special Issue

# *viruses*

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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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