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Transcriptome Analysis of Viruses

Guest Editor:

Dr. Dóra Tombácz
Department of Medical Biology,
Faculty of Medicine, University of
Szeged, Somogyi B. u. 4., 6720
Szeged, Hungary

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Message from the Guest Editor

Dear Colleagues,

The current COVID-19 pandemic underscores the importance of the RNA-level analysis of viruses. Understanding the molecular mechanisms of small pathogens is essential for developing a defense strategy against them. Rapidly evolving sequencing technologies (including RNA sequencing) and bioinformatics have revolutionized the field of molecular virology. Next- and third-generation sequencing approaches enable us to analyze thousands of transcripts simultaneously. Third-generation long-read sequencing (LRS) has opened new avenues for a comprehensive understanding of how genes are expressed and connected with each other. Such as the single-molecule real-time (SMRT) technique from Pacific Biosciences, the nanopore sequencing method from Oxford Nanopore Technologies, and LoopSeq synthetic long-read sequencing from Loop Genomics allows distinguishing between transcript length variants, including splice and length variants, embedded RNAs, polycistronic transcripts, and alternatively spliced transcript isoforms.

This Special Issue aims to provide in-depth knowledge and an overview of the current results, focuses, and future directions of current research projects.

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Editor-in-Chief

Prof. Dr. Lawrence S. Young
Warwick Medical School,
University of Warwick, Coventry
CV4 7AL, UK

Message from the Editor-in-Chief

The worldwide impact of infectious disease is incalculable. The consequences for human health in terms of morbidity and mortality are obvious and vast but, when infections of animals and plants are also taken into account, it is hard to imagine any other disease that has such a significant impact on our lives—on healthcare systems, on agriculture and on world economics. *Pathogens* is proud to continue to serve the international community by publishing high quality studies that further our understanding of infection and have meaningful consequences for disease intervention.

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Contact Us

Pathogens Editorial Office
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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pathogens@mdpi.com
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