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Quest for Conserved RNAs in Viral Genomes

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Message from the Guest Editor

Dear Colleagues,

Evolutionarily conserved RNAs and their mechanisms are actively investigated across all domains of life. Yet, our general knowledge of conserved, functional RNAs in viruses is restricted to a set of well-studied examples. Novel experimental techniques, together with the increased availability of cheap sequencing technologies, have leveraged the accessibility of viral (meta)genome data in the last couple of years. This has opened new perspectives for the comparative analysis of viral genomes, allowing us to better understand the evolutionary traits associated with functional RNAs, such as virus–host interaction, host range specificity, pathogenicity and immune escape, as well as virus origin.

In the Special Issue ‘The Quest for Conserved RNAs in Viral Genomes’, we would like to bring together both experimental and theoretical research related to the study of evolutionarily conserved (structured and unstructured) RNAs in viruses. Original articles and reviews are welcome, ranging from the analysis of individual species to comparative screens of large-scale datasets.

Dr. Michael T. Wolfinger

Guest Editor



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Special Issue



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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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