

## Special Issue

# Quest for Conserved RNAs in Viral Genomes

### Message from the Guest Editor

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.

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### Guest Editor

Dr. Michael T. Wolfinger

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### Deadline for manuscript submissions

closed (30 June 2021)

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## Genes

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### Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan  
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