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## Virus Genomics and Diversity

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Deadline for manuscript  
submissions:

**22 October 2024**

### **Message from the Guest Editors**

Our understanding of virus genomics and diversity has always been limited by available technology. Consequently, eras of virus discovery have been heralded by new technologies. The advent of multiple high-throughput genome sequencing technologies (Illumina, Nanopore, PacBio, and others) and the enhanced computing capacity now available have increased our resolution of virus diversity and simultaneously ushered in an era of virus discovery in both common and unusual places. The accompanying insights continue to expand our understanding of virus genome sizes, architecture, host range, and genotypes in both commonly explored and previously unexplored ecosystems.

In this Special Issue, we explore virus genomes and what they show us about the possibilities that exist. We welcome articles describing the use of any nucleotide sequencing technology to catalogue novel virus genomes (in terms of genome size, architecture, host range, families, species, and genotypes) in any sample type (environmental, vertebrate, or invertebrate hosts, reservoirs, healthy or diseased subjects) and/or ecosystem. Articles describing novel phage genomes are also welcome.



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## Message from the Editor-in-Chief

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