Special Issue

Virus Genomics and Diversity

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.

Guest Editors

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Deadline for manuscript submissions

closed (22 October 2024)



Life

an Open Access Journal by MDPI

Impact Factor 3.4
CiteScore 6.0
Indexed in PubMed



mdpi.com/si/201125

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Life (ISSN 2075-1729) is an international, peer-reviewed open access journal that publishes scientific studies related to fundamental themes in life sciences. Some papers are published individually, while others are submitted for inclusion in special issues with guest editors. You are invited to contribute a research article, essay, or a review to be considered for publication.

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