Special Issue

Genome Sequencing Technologies Applied in Animal Virology

Message from the Guest Editor

The field of animal virology has been transformed by recent advances in genome sequencing technologies. From classical Sanger methods to high-throughput next-generation sequencing (NGS) and real-time long-read platforms, these innovations have opened new avenues for the detection, characterization, and evolutionary tracking of animal viruses. In both domestic and wild animal populations, genomic tools and sequencing-based approaches are indispensable for understanding viral diversity, pathogenesis, transmission dynamics, outbreak investigation, vaccine development, and the monitoring of viral mutations and recombination events. This Special Issue invites contributions that explore the use of genome sequencing technologies in the study of animal viruses. We welcome original research articles, reviews, and methodological papers that address, but are not limited to, the following topics: metagenomic approaches for virus discovery, viral genome assembly and annotation, sequencing-guided diagnostics, genomic surveillance, phylogenetic and evolutionary analyses, host–virus interactions, and the integration of omics technologies in veterinary virology.

Guest Editor

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Message from the Editor-in-Chief

Animals is an on-line open access journal that was first published in 2011. *Animals* adheres to rigorous peerreview and editorial processes and publishes only high quality manuscripts that address important issues in the many varied disciplines that involve animals, with a focus on animal science, animal welfare and animal ethics. *Animals* is covered in the Science Citation Index Expanded (SCIE) in Web of Science, with the latest Impact Factor: 2.7 (2024, ranks 15/86 (Q1) in 'Agriculture, Dairy & Animal Science'; 21/170 (Q1) in 'Veterinary Sciences'), 5-Year Impact Factor: 3.2.

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