Special Issue

High Throughput Technique use in Animal Genetics and Genomics

Message from the Guest Editors

Over the past decades, there has been a rapid development of high-throughput genome analysis methods, including next-generation sequencing (NGS) and genotyping microarrays. These methods allow genome or population scale screening of single nucleotide polymorphisms (SNPs), insertions or deletions (INDELs), copy number variations (CNVs) or genome-scale gene expression analysis. The methods based on NGS are also applicable for various de novo sequencing applications: sequencing of unknown genomes or transcriptomes, discovery of unknown sequence variants and new splice sites. The most interesting topics in animal's genomics appear to be ones revealing the structure of the genome (especially in species without a known genome), analyzing population genetic structure, mapping of quantitative trait loci, identifying disease related variants and genome responses to inbreeding and artificial selection. The aim of this Special Issue is to present recent original research and reviews concerning various high-throughput techniques in regard to animal genomics and genetics, mostly ones briefly mentioned above.

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Deadline for manuscript submissions

closed (30 April 2022)

Animals

an Open Access Journal by MDPI

Impact Factor 2.7
CiteScore 5.2
Indexed in PubMed

mdpi.com/si/73700

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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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