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# High Throughput Technique use in Animal Genetics and Genomics

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Deadline for manuscript submissions:
**closed (30 April 2022)**

## 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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## Message from the Editor-in-Chief

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