DESCRIPTION

**Genomics** is a forum for describing the development of **genome-scale technologies** and their application to all areas of biological investigation.

As a journal that has evolved with the field that carries its name, **Genomics** focuses on the development and application of cutting-edge methods, addressing fundamental questions with potential interest to a wide audience. Our aim is to publish the highest quality research and to provide authors with rapid, fair and accurate review and publication of manuscripts falling within our scope. Topics within the scope of **Genomics** include, but are not limited to:

- **Genomics** including genome projects, genome sequencing, and genomic technologies and novel strategies.
- **Functional genomics** including transcriptional profiling, mRNA analysis, microRNA analysis, and analysis of noncoding and other RNAs using established and newly-emerging technologies (such as digital gene expression).
- **Evolutionary** and **comparative genomics**, including phylogenomics.
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- **Modern genetics** on a genomic scale, including complex gene studies, population genomics, association studies, structural variation, and gene-environment interactions.
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- Genomic approaches to understanding the mechanism of **disease pathogenesis** and its relationship to genetic factors, including meta-genomic and the mode and tempo of gene and genome sequence evolution.
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- RNA-seq experiments without three or more biological replicates will not be accepted for differential expression-based articles.

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The goal of Genomics is to promote the understanding of the structure, function, and evolution of genomes in all kingdoms of life and the application of genome sciences and technologies to challenging problems in biology and medicine. The scope of the journal is broad and we welcome original, full-length, and timely papers in all of the following areas:

- Comparative genomics analysis that yields valuable insights into conserved and divergent aspects of function, regulation, and evolution
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