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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:

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- **Genomic technology** and methodology development, with a focus on new and exciting applications with potential for significant impact in the field and emerging technologies
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- **Modern genetics** on a genomic scale, including complex gene studies, population genomics, association studies, structural variation, and gene-environment interactions
- **Epigenomics**, including DNA methylation, histone modification, chromatin structure, imprinting, and chromatin remodeling
- **Genomic regulatory analysis**, including DNA elements, locus control regions, insulators, enhancers, silencers, and mechanisms of gene regulation
- 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.
- **Medical Genomics**, Personal Genomics, and other applications to human health
- Application of **Genomic techniques** in model organisms that may be of interest to a wide audience.

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proposals or any inquiries regarding the scope of the journal or the suitability of a manuscript for publication.

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INTRODUCTION

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
- Bioinformatics and computational biology with particular emphasis on data mining and improvements in data annotation and integration
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- Identification of genes involved in disease and complex traits, including responses to drugs and other xenobiotics
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