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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:

- **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
- **Genomic technology** and methodology development, with a focus on new and exciting applications with potential for significant impact in the field and emerging technologies
- **Computational biology**, bioinformatics and biostatistics, including integrative methods, network biology, and the development of novel tools and techniques
- **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.

*Genomics* primarily publishes original research articles but also welcomes proposals for full-length and mini reviews. All [submissions](#) to *Genomics* are subject to rigorous peer review and our goal is to accept only the top 25-30% of submitted manuscripts. Please contact the [Editorial Office](#) with review

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

## IMPACT FACTOR

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## ABSTRACTING AND INDEXING

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## GUIDE FOR AUTHORS

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**To find out more, please visit the Preparation section below.**

### 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
- Functional genomics approaches involving the use of large-scale and/or high-throughput methods to understand genome-scale function and regulation of transcriptomes and proteomes
- Identification of genes involved in disease and complex traits, including responses to drugs and other xenobiotics
- Significant advances in genetic and genomics technologies and their applications, including chemical genomics

In addition to full-length papers, *Genomics* accepts a number of different article types.

As a result of *Genomics*' strict quality measures, the journal rejects as much of 70 % of all submissions received.

**Each manuscript should be accompanied by a Cover letter outlining the basic findings of the manuscript and their significance.** Please submit, with the manuscript, the names and addresses of five potential referees.

### *Full length articles*

Organization should be Abstract, Introduction, Results, Discussion, Materials and methods, Acknowledgments, and References. There is a limit of 8 display items (figures plus tables). Manuscripts should be no more than 7 published pages, excluding references. Accepted papers that are over 8 pages, or 56,000 characters (including spaces), may be returned to the authors for additional editing. To estimate: One published page is approximately 7000 characters; Count each table or figure as 2450 characters and add to the character count of your manuscript text.

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For questions on the submission and reviewing process, please contact the Editorial Office at [genomics@elsevier.com](mailto:genomics@elsevier.com).

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Center for Information Biology and DNA Data Bank of Japan

National Institute of Genetics

1111 Yata

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## PREPARATION

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