

#### **AUTHOR INFORMATION PACK**

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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

2016: 2.801 © Clarivate Analytics Journal Citation Reports 2017

# ABSTRACTING AND INDEXING

Scopus

**EMBASE** 

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**BIOBASE** 

**BIOSIS** 

Biological and Agricultural Index

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We now differentiate between the requirements for new and revised submissions. You may choose to submit your manuscript as a single Word or PDF file to be used in the refereeing process. Only when your paper is at the revision stage, will you be requested to put your paper in to a 'correct format' for acceptance and provide the items required for the publication of your article.

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.

Please note that there is no limit on the number of References. *Genomics* feels strongly that authors should be able to give credit where credit is due.

Readers are invited to submit ideas and proposals for reviews and minireviews; they should not submit complete or finished manuscripts prior to consultation with the editor-in-chief or one of the associate editors.

# Contact details for submission

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For questions on the submission and reviewing process, please contact the Editorial Office at genomics@elsevier.com.

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# Ensure that the following items are present:

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All necessary files have been uploaded:

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Supplemental files (where applicable)

#### Further considerations

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- A competing interests statement is provided, even if the authors have no competing interests to declare
- Journal policies detailed in this guide have been reviewed
- Referee suggestions and contact details provided, based on journal requirements

For further information, visit our Support Center.

# **BEFORE YOU BEGIN**

# Ethics in publishing

Please see our information pages on Ethics in publishing and Ethical guidelines for journal publication.

## Human and animal rights

If the work involves the use of human subjects, the author should ensure that the work described has been carried out in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki) for experiments involving humans; Uniform Requirements for manuscripts submitted to Biomedical journals. Authors should include a statement in the manuscript that informed consent was obtained for experimentation with human subjects. The privacy rights of human subjects must always be observed.

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Genomics follows the ICMJE recommendations regarding conflict of interest disclosures. All authors are required to report the following information with each submission: (1) All third-party financial support for the work in the submitted manuscript. (2) All financial relationships with any entities that could be viewed as relevant to the general area of the submitted manuscript. (3) All sources of revenue with relevance to the submitted work who made payments to you, or to your institution on your behalf, in the 36 months prior to submission. (4) Any other interactions with the sponsor of outside of the submitted work should also be reported. (5) Any relevant patents or copyrights (planned, pending, or issued). (6) Any other relationships or affiliations that may be perceived by readers to have influenced, or give the appearance of potentially influencing, what you wrote in the submitted work. As a general guideline, it is usually better to disclose a relationship than not. This information will be acknowledged at publication in a Transparency Document link directly in the article. Additional information on the ICMJE recommendations can be found at: <a href="http://www.icmje.org/coi\_disclosure.pdf">http://www.icmje.org/coi\_disclosure.pdf</a> (if this link does not display properly in your browser, please right-click the link and select "Save Target As..." or "Save Link as..." from the pop-up menu).

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Please submit the names and institutional e-mail addresses of several potential referees. For more details, visit our Support site. Note that the editor retains the sole right to decide whether or not the suggested reviewers are used.

# Additional Information

# Sharing information and materials

It is expected that all new biological or other reagents described in papers published in Genomics will be made available freely to all qualified members of the scientific community upon written request. If delays in strain or vector distribution are anticipated, or if these are available from sources other than the author(s), this must be indicated and, if the editor thinks it necessary, explained.

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The editorial policy of *Genomics* is to require the use of databases. Deposit of data in the appropriate database(s) is a condition of publication. New nucleotide data must be submitted and deposited in the DDBJ/EMBL/GenBank databases and an accession number obtained before the paper can be accepted for publication. Submission to any one of the three collaborating databanks is sufficient to ensure data entry in all.

The accession number should be included in the manuscript as a footnote on the title page: "Sequence data from this article have been deposited with the DDBJ/EMBL/GenBank Data Libraries under Accession No. .... If requested, the database will withhold release of data until publication. The most convenient method for submitting sequence data is by the World Wide Web:

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# **PREPARATION**

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If your article includes any Videos and/or other Supplementary material, this should be included in your initial submission for peer review purposes.

Divide the article into clearly defined sections.

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This journal operates a single blind review process. All contributions will be initially assessed by the editor for suitability for the journal. Papers deemed suitable are then typically sent to a minimum of two independent expert reviewers to assess the scientific quality of the paper. The Editor is responsible for the final decision regarding acceptance or rejection of articles. The Editor's decision is final. More information on types of peer review.

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#### Introduction

State the objectives of the work and provide an adequate background, avoiding a detailed literature survey or a summary of the results.

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Provide sufficient details to allow the work to be reproduced by an independent researcher. Methods that are already published should be summarized, and indicated by a reference. If quoting directly from a previously published method, use quotation marks and also cite the source. Any modifications to existing methods should also be described.

# Theory/calculation

A Theory section should extend, not repeat, the background to the article already dealt with in the Introduction and lay the foundation for further work. In contrast, a Calculation section represents a practical development from a theoretical basis.

#### Results

Results should be clear and concise.

#### Discussion

This should explore the significance of the results of the work, not repeat them. A combined Results and Discussion section is often appropriate. Avoid extensive citations and discussion of published literature.

#### Conclusions

The main conclusions of the study may be presented in a short Conclusions section, which may stand alone or form a subsection of a Discussion or Results and Discussion section.

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A concise and factual abstract is required. The abstract should state briefly the purpose of the research, the principal results and major conclusions. An abstract is often presented separately from the article, so it must be able to stand alone. For this reason, References should be avoided, but if essential, then cite the author(s) and year(s). Also, non-standard or uncommon abbreviations should be avoided, but if essential they must be defined at their first mention in the abstract itself.

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Immediately after the abstract, provide a maximum of 6 keywords, using American spelling and avoiding general and plural terms and multiple concepts (avoid, for example, 'and', 'of'). Be sparing with abbreviations: only abbreviations firmly established in the field may be eligible. These keywords will be used for indexing purposes.

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Define abbreviations that are not standard in this field in a footnote to be placed on the first page of the article. Such abbreviations that are unavoidable in the abstract must be defined at their first mention there, as well as in the footnote. Ensure consistency of abbreviations throughout the article.

# Acknowledgements

Collate acknowledgements in a separate section at the end of the article before the references and do not, therefore, include them on the title page, as a footnote to the title or otherwise. List here those individuals who provided help during the research (e.g., providing language help, writing assistance or proof reading the article, etc.).

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#### Artwork

# Electronic artwork

# General points

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- Use a logical naming convention for your artwork files.
- Indicate per figure if it is a single, 1.5 or 2-column fitting image.
- For Word submissions only, you may still provide figures and their captions, and tables within a single file at the revision stage.
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