



GENOMICS, PROTEOMICS & BIOINFORMATICS

The official journal of the Beijing Institute of Genomics, the Chinese Academy of Sciences and the Genetics Society of China

AUTHOR INFORMATION PACK

TABLE OF CONTENTS

●	Description	p.1
●	Abstracting and Indexing	p.2
●	Editorial Board	p.2
●	Guide for Authors	p.7



ISSN: 1672-0229

DESCRIPTION

Genomics, Proteomics and Bioinformatics (GPB) is the official journal of Beijing Institute of Genomics, Chinese Academy of Sciences and Genetics Society of China. The goals of GPB are to disseminate new frontiers in the field of omics and bioinformatics, to publish high-quality discoveries in a fast-pace, and to promote open access and online publication via Article-in-Press for efficient publishing.

GPB is interested in submissions across all areas of life science, biology, and biomedicine, focusing on large data acquisition, analysis, and curation. Manuscripts with topics on omics and the related bioinformatics are all welcome to publish with us.

GPB has been indexed/abstracted by PubMed/MEDLINE, PubMed Central, Scopus, BIOSIS Previews, Chemical Abstracts, CSCD, etc.

GPB 's featured research areas include: Genomics: large-scale data acquisition, integrated studies and technology developments, concerning genome structures, variations, repeat contents and evolution. **Genomics, Proteomics and Bioinformatics (GPB)** is the official journal of Beijing Institute of Genomics, Chinese Academy of Sciences and Genetics Society of China. The goals of GPB are to disseminate new frontiers in the field of omics and bioinformatics, to publish high-quality discoveries in a fast-pace, and to promote open access and online publication via Article-in-Press for efficient publishing.

GPB is interested in submissions across all areas of life science, biology, and biomedicine, focusing on large data acquisition, analysis, and curation. Manuscripts with topics on omics and the related bioinformatics are all welcome to publish with us.

GPB has been indexed/abstracted by PubMed/MEDLINE, PubMed Central, Scopus, BIOSIS Previews, Chemical Abstracts, CSCD, etc.

Other 'omics ' fields: epigenomics (DNA modifications, nucleosome positioning, histone modifications, chromosome conformation and 3-D structures, etc.), ribogenomics (transcriptomics, long-non-coding RNA, antisense transcriptomics, miRNAs, other small RNAs, etc.). Proteomics: protein structures, proteomics technology developments, protein expression profiling, protein complexes in terms of structure, function, properties and interactions, metabolomics, homeostasis of macromolecules. Bioinformatics: genome assembling, annotation, and integrated analysis; large data curation and

mining; sequence-based or matrix-based phylogeny, database construction, web-based platforms and tools, novel algorithms, tool boxes and software packages.

GPB 's article types include: Original research articles presenting novel data and findings. Papers describing innovative **method, application note, protocol,** and **database update** as well as **database review** and **resource review** providing primary scientific information to a broad readership. **Comprehensive reviews** as full articles focus on the research history and developments; **mini-reviews** and **life time achievement reviews**, which are invited submissions, adopt limited size and focus on the author' research field and career. **Essays, commentaries, opinions, research highlight, news and views,** and **perspectives** about new discoveries, scientific policies, and research proposals. Other article types including **meeting report, editorial, etc.**

ABSTRACTING AND INDEXING

Chemical Abstracts
MEDLINE®
Index Copernicus
EMBASE
PubMed
BIOSIS Previews
Scopus
CSCD
Directory of Open Access Journals (DOAJ)
PubMed Central

EDITORIAL BOARD

Editor-in-Chief

Jun Yu, Beijing Institute of Genomics (BIG), Chinese Academy of Sciences (CAS), Beijing, China
Genomics and Bioinformatics

Executive Associate Editor-in-Chief

Songnian Hu, BIG, Beijing, China
Functional genomics, Transcriptomics

Associate Editors-in-Chief

Bajic Vladimir, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia
Data modeling and machine learning

Arndt Benecke, Université Pierre et Marie Curie, Paris, France
Host-pathogen interactions, Immune responses, Neurobiology

William Chi-Shing Cho, Queen Elizabeth Hospital (Hong Kong), Hong Kong, China
Cancer biomarker, microRNA, and proteomics

Xiangdong Fang, BIG, CAS, Beijing, China
Transcriptomics, epigenetic regulation, and markers

Andreas Keller, Saarland University, Saarbrücken, Germany
Non-invasive biomarkers, bacterial resistance, and genetic testing by NGS

Hongxing Lei, BIG, CAS, Beijing, China
Functional genomics of Alzheimer's disease, big data for stem cell research, and protein folding

Yun-Gui Yang, BIG, CAS, Beijing, China
RNA methylation and DNA damage response

Zhang Zhang, BIG, CAS, Beijing, China
Computational biology, biocuration, and databases

Heng Zhu, Johns Hopkins University, Baltimore, MD, USA
Proteomics, protein chip, and biomarker identification

Editorial Board Members:

Alex Bateman, EMBL-EBI, Cambridgeshire, UK
Databases, protein families, and ncRNAs

Brendan Bell, Université de Sherbrooke, Sherbrooke, Quebec, Canada
HIV and gene expression

Kyle K. Biggar, Western University, London, ON, Canada

Hypoxia, protein methylation, and microRNAs

Erik Bongcam-Rudloff, Swedish University for Agricultural Sciences, Uppsala, Sweden

Medical informatics, bioinformatics, animal genomics, bioinformatics tools, and biobanking

James Cai, Texas A&M University, College Station, TX, USA

Population genomics, genetic disorders, and computational biology

Murray J. Cairns, University of Newcastle, Callaghan, Australia

Genomics, microRNAs, and brain dysfunction

Giacomo Cavalli, Institute of Human Genetics, CNRS, Montpellier, France

Epigenetics, polycomb, and genome topology

Fei Chen, Beijing Institute of Genomics (BIG), Chinese Academy of Sciences (CAS), Beijing, China

RNA epigenetic modifications and sequencing technologies

Luonan Chen, Shanghai Institutes for Biological Sciences, CAS, Shanghai, China

Disease network, gene regulatory network inference, and protein-protein interaction network prediction

Ming Chen, Zhejiang University, Hangzhou, China

Bioinformatics, systems biology, noncoding RNAs, and protein-protein interaction network

Runsheng Chen, Institute of Biophysics, CAS, Beijing, China

DNA sequence analysis, protein structure and function studies, lncRNAs

Domenica D'Elia, National Research Council of Italy (CNR), Bari, Italy

Databases, Transcriptomics, ncRNAs, Micro RNAs, Long non-coding RNAs, Gene regulatory network reconstruction

Zhijun Duan, University of Washington, Seattle, Washington, USA

Chromatin, chromosome, epigenomics, genomics, transcription

François Fuks, Free University of Brussels, F.D. Roosevelt, Belgium

Histone modifications, DNA modifications, RNA epigenetics, Epigenomics, Cancer

Feng Gao, Tianjin University, Tianjin, China

Microbial genomics and bioinformatics

Ge Gao, Peking University, Beijing, China

Bioinformatics tools, genomics, and databases

Xin Gao, King Abdullah University of Science and Technology, Thuwal, Kingdom of Saudi Arabia

Bioinformatics, protein structure, NMR, machine learning

Caixia Guo, BIG, CAS, Beijing, China

DNA damage tolerance, mutagenesis, and genomics

Bin Han, Shanghai Institutes for Biological Sciences, CAS, Shanghai, China

Genome sequencing, genome analysis, and rice

Jacob Hanna, Weizmann Institute of Science, Rehovot, Israel

Stem cells, Epigenetics, and RNA methylation

Henning Hermjakob, EMBL-EBI, Cambridgeshire, UK

Proteomics, network and systems biology, data curation

Hsien-Da Huang, National Chiao Tung University, HsinChu, China

Biological databases, small RNAs, and clinical bioinformatics

Rong Stephanie Huang, University of Chicago, Chicago, IL, USA

Pharmacogenomics, anti-cancer agents, microRNA, and drug sensitivity model

Marc-Thorsten Hutt, Jacobs University Bremen, Bremen, Germany

Metabolic networks, dynamics on graphs, pattern formation

Zhong Jin, Computer Network Information Center, CAS, Beijing, China

Software, high performance computing, computational chemistry and biology

Arne Klungland, Oslo University Hospital, Oslo, Norway

Demethylation, epigenetic inheritance, and genome instability

Firas Kobaissy, University of Florida, Gainesville, FL, USA

Biomarkers, proteomic analysis, and brain injury

Sanghyuk Lee, Ewha Womans University, Seoul, Korea

Systems biology, cancer biomarker, microRNA, and genome annotation

Tzong-Yi Lee, Yuan Ze University, Taoyuan, China

Database, cancer regulatory network, computational proteomics, and NGS data analysis

Ao Li, University of Science and Technology of China, Hefei, China

Cancer genome, post-translational modifications (PTM), and ncRNAs

Lei Li, Peking University, Beijing, China

MicroRNA, gene expression regulation, and plant regulatory network

Quan-Zhen Li, University of Texas Southwestern Medical Center, Dallas, Texas, USA

Autoimmune diseases, Immunogenetics, immune tolerance and autoantibodies, DNA methylation and transcription regulation

Shuwei Li, University of Maryland, College Park, MD, USA

Mass spectrometry, isotope labeling, quantitative proteomics, and protein phosphorylation
Tongbin Li, AccuraScience, Johnston, IA, USA
 Databases, artificial intelligence, algorithms
Wuju Li, Beijing Institute of Basic Medical Sciences, Beijing, China
 Bioinformatics
Yixue Li, Shanghai Institutes for Biological Sciences, CAS, Shanghai, China
 NGS analysis, gene regulatory network, and protein-protein interaction network
Wei Lin, Baylor Institute for Immunology Research, Dallas, TX, USA
 NGS, autoimmune disease, and cancer vaccine
Tomas Lindahl, Cancer Research UK London Research Institute, London, UK
 Cancer research and DNA repair
Jiang Liu, BIG, CAS, Beijing, China
 Cancer research and DNA methylation
Mofang Liu, Shanghai Institutes for Biological Sciences, CAS, Shanghai, China
 miRNAs in cancer and piRNA regulation in spermatogenesis
P. Paul Liu, National Human Genome Research Institute, Bethesda, MD, USA
 Cancer genomics, tumor biology, and molecular mechanisms of leukemia
Siqi Liu, BIG, CAS, Beijing, China
 Proteomics
Song Liu, Roswell Park Cancer Institute, Buffalo, NY, USA
 Transnational bioinformatics, biomarker discovery, and cancer genomics
Xiaowen Liu, Indiana University-Purdue University Indianapolis, Indianapolis, IN, USA
 Algorithms, proteomics, PTMs, and proteogenomics
Long Mao, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing, China
 Plant genomics and miRNAs
Antonio Marcilla, University of Valencia, Valencia, Spain
 Extracellular vesicles, parasitic disease, and molecular parasitology
Benjamin Meder, Heidelberg University, Heidelberg, Germany
 miRNA biomarkers, acute coronary syndrome, computational cardiology
Amit Meller, Technion - Israel Institute of Technology, Haifa, Israel
 Single molecule DNA sequencing, Single Cell analysis, Nanopores, nano-biotechnology, Translation initiation.
Kang Ning, Huazhong University of Science and Technology, Wuhan, Hubei, China
 Metagenomics, genomics, single-cell omics, proteomics, computational biology algorithms
Zemin Ning, The Wellcome Trust Sanger Institute, Cambridge, UK
 Genome informatics and data mining
Deng-Ke Niu, Beijing Normal University, Beijing, China
 Evolutionary biology, intron, and bioinformatics
Akimitsu Okamoto, The University of Tokyo, Tokyo, Japan
 DNA/RNA imaging, organic chemistry, and functional protein/oligopeptide synthesis
Jiang Qian, Johns Hopkins University, Baltimore, Maryland, USA
 Epigenetics, gene expression, gene regulation, signaling networks
Lianghu Qu, Sun Yat-Sen University, Guangzhou, China
 RNA biology, bioinformatics, miRNAs and cancer
Shaoqi Rao, Guangdong Medical College, Dongguan, China
 Molecular cardiology, statistical genetics, and systems biology
Peter Roepstorff, University of Southern Denmark, Odense, Denmark
 Mass spectrometry, proteomics, and post translational modifications
Patrick Roth, University Hospital Zurich, Zurich, Switzerland
 Biology of malignant gliomas, glioma immune escape, immunogenicity, and anti-glioma therapy
Yijun Ruan, The Jackson Laboratory for Genomic Medicine, Farmington, MO, USA
 3D Genomics, genome structure and genome dynamics
Erwei Song, Sun Yat-Sen University, Guangzhou, China
 Breast cancer, ncRNAs, and personalized medicine
Kenneth B. Storey, Carleton University, Ottawa, ON, Canada
 Freeze tolerance, hibernation, amphibians, and reptiles
Yingli Sun, BIG, CAS, Beijing, China
 Pluripotent stem cells, genomic stabilities, and epigenetic regulation of cancer
Tsutomu Suzuki, The University of Tokyo, Tokyo, Japan
 RNA biochemistry, RNA modification, RNA dysregulation and disease
Fuchou Tang, Peking University, Beijing, China
 Single-cell genomics, human early embryonic development, human germ cell development
Qiang Tian, Institute for Systems Biology, Seattle, WA, USA

Cancer and stem cell biology, immunity, and disease biomarker discovery
Yigang Tong, Beijing Institute of Microbiology and Epidemiology, Beijing, China
 Bacteria, metagenomics, microbe, next-generation sequencing, virus
Edward Wakeland, University of Texas Southwestern Medical Center, Dallas, Texas, USA
 Immunology and autoimmune diseases
Edwin Wang, University of Calgary, Calgary, Alberta, Canada
 Bioinformatics, disease biomarker, and systems biology
Hailin Wang, Research Center for Eco-Environmental Sciences, CAS, Beijing, China
 DNA methylation, LC-MS analysis, DNA modification, highly sensitive nucleic acid analysis, and homologous recombination repair
Qianfei Wang, BIG, CAS, Beijing, China
 Genomics, leukemia, and transcriptional network
Ting Wang, Washington University in St. Louis, St. Louis, MO, USA
 Genomics, epigenomics, evolution, computation, and systems biology
Xiangfeng Wang, China Agricultural University, Beijing, China
 Plant genomics, systems biology, and epigenetic modifications
Xiu-Jie Wang, Institute of Genetics & Developmental Biology, CAS, Beijing, China
 Bioinformatics, big data, ncRNAs, and stem cells
Zhao-Qi Wang, Leibniz Institute for Age Research - Fritz Lipmann Institute, Jena, Germany
 DNA damage response, epigenetic modification, and aging
Andreas Weinhaeusel, Austrian Institute of Technology, Vienna, Austria
 Biomarker development, DNA methylation, autoantibody, microarray technology, and molecular genetic diagnostics
Cesar Wong, The Hong Kong Polytechnic University, HK, China
Limsoon Wong, National University of Singapore, Singapore, Singapore
 Gene expression profile analysis; Proteomic profile analysis; Logical thinking in computational biology; Reproducibility in computational biology
Jingfa Xiao, BIG, CAS, Beijing, China
 Bioinformatics, comparative genomics, structure and function of small proteins.
Yi Xing, University of California Los Angeles, Los Angeles, CA, USA
 Bioinformatics, Genomics, RNA Biology
Guoliang Xu, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China
 HSC; DNA methylation; DNA methyltransferases (Dnmt); DNA demethylases; Tet enzymes; Leukemogenesis; Gametogenesis
Yu Xue, Huazhong University of Science and Technology, Wuhan, China
 Post-translational modifications, bioinformatics, and comparative proteomics
Kai Ye, Xi'an Jiaotong University, Xi'an, China
 Assembly, GWAS, indel, NGS, population sequencing, and structural variant
Haiyuan Yu, Cornell University, Ithaca, USA
 Functional and comparative genomics, molecular and dynamic proteomics, algorithms and tools
Changqing Zeng, BIG, CAS, Beijing, China
 Human genomics
Le Zhang, Southwest University, Chongqing, China
 Computational biology, data mining, and cancer research
Xuegong Zhang, Tsinghua University, Beijing, China
 Machine learning, computational genomics, and systems biology
Xue Zhang, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China
 Genomics, monogenic diseases, and mutation profiling
Zhenhai Zhang, Southern Medical University, Guangzhou, China
 NGS data analysis, autoimmune diseases, and HIV antibody screening
Zhihua Zhang, BIG, CAS, Beijing, China
 Computational systems biology, histone modification profiles, and transcriptional regulation
Ziding Zhang, China Agricultural University, Beijing, China
 Protein bioinformatics, protein-protein interaction network, and plant-pathogen interaction
Fangqing Zhao, Beijing Institutes of Life Science, CAS, Beijing, China
 Computational biology, metagenomics, and evolutionary genomics of non-model organism
Yongliang Zhao, BIG, CAS, Beijing, China
 DNA repair, genome stability, and cancer biology
Zhongming Zhao, The University of Texas Health Science Center at Houston, Houston, TX, USA
 NGS data analysis, disease gene network/pathway analysis, cancer bioinformatics
Fengfeng Zhou, Jilin University, Changchun, China
 Bioinformatics, data mining, and parallel computing
Shuigeng Zhou, Fudan University, Shanghai, China

Data mining, large-scale datasets, spatial database, and GIS

Weimin Zhu, Beijing Proteome Research Center, Beijing, China

Bioinformatics, databases, and big data

Yunping Zhu, Beijing Proteome Research Center, Beijing, China

Proteome bioinformatics, big data, and liver systems biology

Editorial Office

Yuxia Jiao, Genomics, Proteomics & Bioinformatics, BIG, CAS, Beijing, China

Shanshan Xie, Genomics, Proteomics & Bioinformatics, BIG, CAS, Beijing, China

GUIDE FOR AUTHORS

INTRODUCTION

Genomics, Proteomics & Bioinformatics publishes papers from all over the world in the fields of genomics, proteomics and bioinformatics. The Journal aims to achieve fast science broadcasting by publishing efficiently. For manuscripts submitted to GPB, direct rejection, direct acceptance or further review will be decided within 5 days. Besides, GPB offers Article-in-Press, by which all the accepted manuscripts can be freely accessible online ahead of its printed issue print for fast dissemination. Featured areas and particular interests of GPB include but are not limited to:

- Genomics: functional genomics, evolutionary genomics, comparative genomics, epigenetics, transcriptomics
- Proteomics: protein expression profiling, protein complexes in terms of structure, function, properties and interactions, metabolomics
- Bioinformatics: genome analysis, sequence analysis, genetic and population analysis, phylogenetics, gene expression, database, web server, algorithm, tools and software, with emphasis on large-scale data analysis based on high-throughput sequencing technologies

GPB welcomes submissions from all over the world in the following types:

- High-quality research papers presenting novel data and ideas
- Papers describing innovative methods, tools and techniques as well as resources providing primary scientific information to a broad readership
- Comprehensive reviews either as full articles or mini-reviews related with author's own research
- Commentaries and opinions about new discoveries, scientific policies, and research proposals

Sections:

- Editorials
- Essays
- Commentaries
- Reviews
- Research Articles
- Letters
- Methods
- Application Notes
- Research Resources

Page Charges

Genomics, Proteomics & Bioinformatics is an open access journal: all articles will be immediately and permanently free for everyone to read and download. Beijing Institute of Genomics, the Chinese Academy of Sciences and the Genetics Society of China charges a publication fee of USD 50 per published page, color print will be charged extra USD 100 per page for international submissions while Yen 200 per print page and extra Yen 800 per color print page will be charged for submissions from China excluding taxes (also known as an article publishing charge APC) which needs to be paid by the authors or on their behalf e.g. by their research funder or institution. If accepted for publication in the journal following peer-review, authors will be notified of this decision and requested to pay the article processing charge in due time when proofreading is requested after the accepted manuscripts are typeset by Elsevier. Following payment of this charge, the article will be published by Beijing Institute of Genomics, the Chinese Academy of Sciences and the Genetics Society of China in Genomics, Proteomics & Bioinformatics which is made freely available at no further charge through ScienceDirect (Open Access). No article will be published until page fees are paid in full and proof of payment has been received by the Editorial Office. The page charges may be waived under some circumstances, subjected to the editorial justification case by case. The completed form is required for further processing.

Genomics Proteomics and Bioinformatics is under the CC BY license, however if necessary, the authors have a choice of CC BY-NC-ND for their article. The licenses give users the following rights:

Creative Commons Attribution (CC BY): lets others distribute and copy the article, to create extracts, abstracts, and other revised versions, adaptations or derivative works of or from an article (such as a translation), to include in a collective work (such as an anthology), to text or data mine the article, even for commercial purposes, as long as they credit the author(s), do not represent the author as endorsing their adaptation of the article, and do not modify the article in such a way as to damage the author's honor or reputation.

Creative Commons Attribution-NonCommercial-NoDerivs (CC BY-NC-ND): for non-commercial purposes, lets others distribute and copy the article, and to include in a collective work (such as an anthology), as long as they credit the author(s) and provided they do not alter or modify the article.

Submission checklist

You can use this list to carry out a final check of your submission before you send it to the journal for review. Please check the relevant section in this Guide for Authors for more details.

Ensure that the following items are present:

One author has been designated as the corresponding author with contact details:

- E-mail address
- Full postal address

All necessary files have been uploaded:

Manuscript:

- Include keywords
- All figures (include relevant captions)
- All tables (including titles, description, footnotes)
- Ensure all figure and table citations in the text match the files provided
- Indicate clearly if color should be used for any figures in print

Graphical Abstracts / Highlights files (where applicable)

Supplemental files (where applicable)

Further considerations

- Manuscript has been 'spell checked' and 'grammar checked'
- All references mentioned in the Reference List are cited in the text, and vice versa
- Permission has been obtained for use of copyrighted material from other sources (including the Internet)
- 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](#).

CONFLICTS OF INTEREST

A declaration of Conflict of Interest section must be included in the manuscript. A conflict of interest occurs when an individual's objectivity is potentially compromised by a desire for financial gain, prominence, professional advancement or a successful outcome. GPB Editors strive to ensure that what is published in the Journal is as balanced, objective and evidence-based as possible. Since it can be difficult to distinguish between an actual conflict of interest and a perceived conflict of interest, by declaring no conflict of interest, the Journal requires authors to disclose all and any potential conflicts of interest including:

Section I

The authors certify that they have NO affiliations with or involvement in any organization or entity with any financial interest (such as honoraria; educational grants; participation in speakers' bureaus; membership, employment, consultancies, stock ownership, or other equity interest; and expert testimony or patent-licensing arrangements), or non-financial interest (such as personal or professional relationships, affiliations, knowledge or beliefs) in the subject matter or materials discussed in this manuscript.

Section II

The authors report the following details of affiliation or involvement in an organization or entity with a financial or non-financial interest in the subject matter or materials discussed in the manuscript. Please specify the nature of the conflict on a separate sheet of paper.

By submitting to GPB

By submitting to GPB, the corresponding author certifies that all Authors have seen and approved the manuscript being submitted. Authors warrant that the article is the Authors' original work. Authors warrant that the article has not received prior publication and is not under consideration for publication elsewhere. On behalf of all Co-Authors, the corresponding Author shall bear full responsibility for the submission. Authors attest to the fact that all Authors listed on the title page have contributed significantly to the work, have read the manuscript, attest to the validity and legitimacy of the data and its interpretation, and agree to its submission to Genomics, Proteomics & Bioinformatics (GPB). All authors agree that author list is correct in its content and order and that no modification to the author list can be made without the written acceptance of all authors and the formal approval of the Editor-in-Chief. All authors accept that the Editor-in-Chief's decisions over acceptance or rejection or in the event of any breach of the Principles of Ethical Publishing in Genomics, Proteomics & Bioinformatics (GPB) being discovered, of retraction are final.

Submission declaration and verification

Submission of an article implies that the work described has not been published previously (except in the form of an abstract or as part of a published lecture or academic thesis or as an electronic preprint, see '[Multiple, redundant or concurrent publication](#)' section of our ethics policy for more information), that it is not under consideration for publication elsewhere, that its publication is approved by all authors and tacitly or explicitly by the responsible authorities where the work was carried out, and that, if accepted, it will not be published elsewhere in the same form, in English or in any other language, including electronically without the written consent of the copyright-holder. To verify originality, your article may be checked by the originality detection service [CrossCheck](#).

Authorship Policy

All persons who meet authorship criteria are listed as authors, and all authors certify that they have participated sufficiently in the work to take public responsibility for the content, including participation in the concept, design, analysis, writing, or revision of the manuscript. Furthermore, each author certifies that this material or similar material has not been and will not be submitted to or published in any other publication. The manuscript must include the Author Contribution section, which includes the specific contributions made by each author (list the authors' initials and contributions). The name of each author must appear at least once in each of the three categories below.

Category 1

Conception and design of study; acquisition of data; analysis and/or interpretation of data.

Category 2

Drafting the manuscript; revising the manuscript critically for important intellectual content.

Category 3

Approval of the version of the manuscript to be published (the names of all authors must be listed).

Changes to Authorship Policy

This policy concerns the addition, deletion, or rearrangement of author names in the authorship of all submitted manuscripts:

Before the manuscript is accepted by journal editor: Requests to add or remove an author, or to rearrange the author names, must be sent to the Journal Editor from the corresponding author of the submitted manuscript and must include: (a) the reason the name should be added or removed, or the author names rearranged and (b) written confirmation (e-mail, fax, letter) from all authors that they agree with the addition, removal or rearrangement. In the case of addition or removal of authors, this includes confirmation from the author being added or removed. Requests that are not

sent by the corresponding author will be forwarded by the Journal Editor to the corresponding author, who must follow the procedure as described above. Note that: Further process of the manuscript will be halted until authorship has been agreed.

Before the accepted manuscript is published in an online issue: Requests to add or remove an author, or to rearrange the author names, must be sent to the Journal Manager from the corresponding author of the accepted manuscript and must include: (a) the reason the name should be added or removed, or the author names rearranged and (b) written confirmation (e-mail, fax, letter) from all authors that they agree with the addition, removal or rearrangement. In the case of addition or removal of authors, this includes confirmation from the author being added or removed. Please click to download and fill the Authorship Agreement (http://www.elsevier.com/__data/promis_misc/Authorship_Agreement.pdf) with all necessary signatures if any changes made on authorship. Requests that are not sent by the corresponding author will be forwarded by the Journal Manager to the corresponding author, who must follow the procedure as described above. Note that: (1) Journal Managers will inform the Journal Editors of any such requests and (2) publication of the accepted manuscript in an online issue is suspended until authorship has been agreed.

After the accepted manuscript is published in an online issue: Any requests to add, delete, or rearrange author names in an article published in an online issue will follow the same policies as noted above and result in a corrigendum.

Elsevier supports responsible sharing

Find out how you can [share your research](#) published in Elsevier journals.

Role of the funding source

You are requested to identify who provided financial support for the conduct of the research and/or preparation of the article and to briefly describe the role of the sponsor(s), if any, in study design; in the collection, analysis and interpretation of data; in the writing of the report; and in the decision to submit the article for publication. If the funding source(s) had no such involvement then this should be stated.

The open access publication fee for this journal is , excluding taxes. Learn more about Elsevier's pricing policy: <http://www.elsevier.com/openaccesspricing>.

Elsevier Publishing Campus

The Elsevier Publishing Campus (www.publishingcampus.com) is an online platform offering free lectures, interactive training and professional advice to support you in publishing your research. The College of Skills training offers modules on how to prepare, write and structure your article and explains how editors will look at your paper when it is submitted for publication. Use these resources, and more, to ensure that your submission will be the best that you can make it.

Language (usage and editing services)

Please write your text in good English (American or British usage is accepted, but not a mixture of these). Authors who feel their English language manuscript may require editing to eliminate possible grammatical or spelling errors and to conform to correct scientific English may wish to use the [English Language Editing service](#) available from Elsevier's WebShop.

Submission

Our online submission system guides you stepwise through the process of entering your article details and uploading your files. The system converts your article files to a single PDF file used in the peer-review process. Editable files (e.g., Word, LaTeX) are required to typeset your article for final publication. All correspondence, including notification of the Editor's decision and requests for revision, is sent by e-mail.

Submit your article

Please submit your article via <http://ees.elsevier.com/gpb/default.asp>.

PREPARATION

Peer review

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.](#)

Article Structure

General manuscript format: Manuscripts must be written in English. Manuscript sections should be presented in the following order: title page, Abstract (less than 200 words), Introduction, Results, Discussion, Conclusions (optional), Materials and methods, Authors' contributions, Competing interests, Acknowledgments, References, followed by Figure legends and Supplementary materials (if any). Please provide each table and figure separately. [A manuscript template for research articles is available.](#)

Original Article

[Identification of A Novel SBF2 Frameshift Mutation in Charcot-Marie-Tooth Disease Type 4B2 Using Whole-exome Sequencing](#)

Structure samples for other article types:

Life-time Achievement Review

[My Journey to DNA Repair](#)

Comprehensive Review

[N6-methyl-adenosine \(m6A\) in RNA: An Old Modification with A Novel Epigenetic Function](#)

Minireview

[Systems Approaches to Biology and Disease Enable Translational Systems Medicine](#)

Resource Review

[Web Resources for Stem Cell Research](#)

Letter

[Complete Sequence of pABTJ2, A Plasmid from Acinetobacter baumannii MDR-TJ, Carrying Many Phage-like Elements](#)

Method

[FunMod: A Cytoscape Plugin for Identifying Functional Modules in Undirected Protein-Protein Networks](#)

Application Note

[nuMap: A Web Platform for Accurate Prediction of Nucleosome Positioning](#)

Protocol

[Systematic Characterization of Cell Cycle Phase-dependent Protein Dynamics and Pathway Activities by High-content Microscopy-assisted Cell Cycle Phenotyping](#)

Introduction

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

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 a

Essential Title Page Information

A title page should include: the title, all authors' names and complete affiliations, the corresponding author's complete contact information, a running title (50 characters or less, including spaces), 2-6 key words, and sources of grants or funding supports and personal acknowledgments).

Abstract

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.

Keywords

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.

Acknowledgments

All persons who have made substantial contributions to the work reported in the manuscript (e.g., technical help, writing and editing assistance, general support), but who do not meet the criteria for authorship, are named in the Acknowledgments and have given their written permission to be named. If no Acknowledgements was involved, it indicates that no substantial contributions from non-authors were received.

Formatting of funding sources

List funding sources in this standard way to facilitate compliance to funder's requirements:

Funding: This work was supported by the National Institutes of Health [grant numbers xxxx, yyyy]; the Bill & Melinda Gates Foundation, Seattle, WA [grant number zzzz]; and the United States Institutes of Peace [grant number aaaa].

It is not necessary to include detailed descriptions on the program or type of grants and awards. When funding is from a block grant or other resources available to a university, college, or other research institution, submit the name of the institute or organization that provided the funding.

If no funding has been provided for the research, please include the following sentence:

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Artwork

Electronic artwork

General points

- Make sure you use uniform lettering and sizing of your original artwork.
- Embed the used fonts if the application provides that option.
- Aim to use the following fonts in your illustrations: Arial, Courier, Times New Roman, Symbol, or use fonts that look similar.
- Number the illustrations according to their sequence in the text.

- Use a logical naming convention for your artwork files.
- Provide captions to illustrations separately.
- Size the illustrations close to the desired dimensions of the published version.
- Submit each illustration as a separate file.

A detailed [guide on electronic artwork](#) is available.

You are urged to visit this site; some excerpts from the detailed information are given here.

Formats

If your electronic artwork is created in a Microsoft Office application (Word, PowerPoint, Excel) then please supply 'as is' in the native document format.

Regardless of the application used other than Microsoft Office, when your electronic artwork is finalized, please 'Save as' or convert the images to one of the following formats (note the resolution requirements for line drawings, halftones, and line/halftone combinations given below):

EPS (or PDF): Vector drawings, embed all used fonts.

TIFF (or JPEG): Color or grayscale photographs (halftones), keep to a minimum of 300 dpi.

TIFF (or JPEG): Bitmapped (pure black & white pixels) line drawings, keep to a minimum of 1000 dpi.

TIFF (or JPEG): Combinations bitmapped line/half-tone (color or grayscale), keep to a minimum of 500 dpi.

Please do not:

- Supply files that are optimized for screen use (e.g., GIF, BMP, PICT, WPG); these typically have a low number of pixels and limited set of colors;
- Supply files that are too low in resolution;
- Submit graphics that are disproportionately large for the content.

Color artwork

Please make sure that artwork files are in an acceptable format (TIFF (or JPEG), EPS (or PDF), or MS Office files) and with the correct resolution. If, together with your accepted article, you submit usable color figures then Elsevier will ensure, at no additional charge, that these figures will appear in color online (e.g., ScienceDirect and other sites) regardless of whether or not these illustrations are reproduced in color in the printed version. **For color reproduction in print, you will receive information regarding the costs from Elsevier after receipt of your accepted article.** Please indicate your preference for color: in print or online only. [Further information on the preparation of electronic artwork.](#)

Figure captions

Ensure that each illustration has a caption. Supply captions separately, not attached to the figure. A caption should comprise a brief title (**not** on the figure itself) and a description of the illustration. Keep text in the illustrations themselves to a minimum but explain all symbols and abbreviations used.

Tables

Please submit tables as editable text and not as images. Tables can be placed either next to the relevant text in the article, or on separate page(s) at the end. Number tables consecutively in accordance with their appearance in the text and place any table notes below the table body. Be sparing in the use of tables and ensure that the data presented in them do not duplicate results described elsewhere in the article. Please avoid using vertical rules and shading in table cells.

References

The reference style for GPB is Vancouver system. In order to follow the Vancouver system for references, the typesetters requires the full author name list of references in order to implement for your article.

Citation in text

Please ensure that every reference cited in the text is also present in the reference list (and vice versa). Any references cited in the abstract must be given in full. Unpublished results and personal communications are not recommended in the reference list, but may be mentioned in the text. If these references are included in the reference list they should follow the standard reference style of the journal and should include a substitution of the publication date with either 'Unpublished results' or 'Personal communication'. Citation of a reference as 'in press' implies that the item has been accepted for publication.

Reference Style

Text: Indicate references by number(s) in square brackets in line with the text. The actual authors can be referred to, but the reference number(s) must always be given.

List: Number the references (numbers in square brackets) in the list in the order in which they appear in the text.

Examples:

Reference to a journal publication: [1] Van der Geer J, Hanraads JAJ, Lupton RA. The art of writing a scientific article. *J Sci Commun* 2010;163:51-9.

Reference to a book: [2] Strunk Jr W, White EB. *The elements of style*. 4th ed. New York: Longman; 2000.

Reference to a chapter in an edited book: [3] Mettam GR, Adams LB. How to prepare an electronic version of your article. In: Jones BS, Smith RZ, editors. *Introduction to the electronic age*, New York: E-Publishing Inc; 2009, p. 281-304.

Reference to an ebook or online pdf: [4] Smith K. A brief history of NCBI's formation and growth. In: *The NCBI handbook* [Internet]. Bethesda: National Center for Biotechnology Information; 2013, <http://www.ncbi.nlm.nih.gov/books/NBK148949/>

Please do not put webpage links into the reference section. The links can be added in a parenthesis right after the citing materials in the main text.

Note shortened form for last page number. e.g., 51-9, and that for more than 6 authors the first 6 should be listed followed by 'et al.' For further details you are referred to 'Uniform Requirements for Manuscripts submitted to Biomedical Journals' (*J Am Med Assoc* 1997;277:927-34) (see also http://www.nlm.nih.gov/bsd/uniform_requirements.html). A GPB reference style for Endnote is available for downloading http://www.elsevier.com/__data/promis_misc/GPB-Endnote-Template.ens.

Data policy

Data policy

Authors are encouraged to enable other scientists the use of their data that are deposited in public databases on genes, proteins, genomics, diseases, etc. To do so, authors please identify the data accession numbers, tagging identifiers, or any specific IDs generated and/or cited in their papers in parenthesis with the following format:

Database abbreviation accession No: data identifier

eg. The obtained *ITS* and *psbA-trnH* sequences were deposited in the GenBank of NCBI database (GenBank Accessions: HQ386701, HQ386689, HQ386691, HQ386695, HQ386696, HQ407399, HQ386690 and JF423303) at <http://www.sciencedirect.com/science/article/pii/S1672022912000915>.

Authors should check accession numbers, tagging identifiers, or any specific IDs very carefully. An error in a letter or number can result in a dead link. In the final version of the electronic copy, the text for accession number, tagging identifier or other specific ID will be linked to the appropriate source in the databases, enabling the readers to go directly to that source from the article. In the final version of the printed article, the text of accession number, tagging identifier or other specific ID will appear in the same font as regular text.

Detailed information is available regarding the types of data and the corresponding data repositories given in the listing of databases supported by Elsevier at the following link: <http://www.elsevier.com/?a=57755>.

Video data

Elsevier accepts video material and animation sequences to support and enhance your scientific research. Authors who have video or animation files that they wish to submit with their article are strongly encouraged to include links to these within the body of the article. This can be done in the same way as a figure or table by referring to the video or animation content and noting in the body

text where it should be placed. All submitted files should be properly labeled so that they directly relate to the video file's content. In order to ensure that your video or animation material is directly usable, please provide the files in one of our recommended file formats with a preferred maximum size of 150 MB. Video and animation files supplied will be published online in the electronic version of your article in Elsevier Web products, including ScienceDirect: <http://www.sciencedirect.com>. Please supply 'stills' with your files: you can choose any frame from the video or animation or make a separate image. These will be used instead of standard icons and will personalize the link to your video data. For more detailed instructions please visit our video instruction pages at <https://www.elsevier.com/artworkinstructions>. Note: since video and animation cannot be embedded in the print version of the journal, please provide text for both the electronic and the print version for the portions of the article that refer to this content.

Supplementary material

Supplementary material such as applications, images and sound clips, can be published with your article to enhance it. Submitted supplementary items are published exactly as they are received (Excel or PowerPoint files will appear as such online). Please submit your material together with the article and supply a concise, descriptive caption for each supplementary file. If you wish to make changes to supplementary material during any stage of the process, please make sure to provide an updated file. Do not annotate any corrections on a previous version. Please switch off the 'Track Changes' option in Microsoft Office files as these will appear in the published version.

AFTER ACCEPTANCE

Proofs

Accepted articles will be published online on ScienceDirect as an article in press and assigned an issue at a later date. You can track the status of your accepted article throughout this process in our production tracking system (<http://authors.elsevier.com/TrackPaper.html>) using the reference No (e.g. GPB12) we sent to you in the acknowledgement e-mail.

As soon as your article has been typeset, a page proof in the form of a PDF file will be sent to the corresponding author(s) for checking and correction of typographical errors and should be returned before the date specified. This usually happens 4-5 weeks after we receive your completed article. Accurate proofreading and clear marking of corrections are essential for the production of a quality article. Please note that careful proofreading is solely your responsibility. We will do everything we can to have your article corrected and published as quickly and accurately as possible. Therefore, it is important to ensure that all of your corrections are sent back to us in one communication.

AUTHOR INQUIRIES

Visit the [Elsevier Support Center](#) to find the answers you need. Here you will find everything from Frequently Asked Questions to ways to get in touch.

You can also [check the status of your submitted article](#) or find out [when your accepted article will be published](#).

© Copyright 2014 Elsevier | <http://www.elsevier.com>