DESCRIPTION

Transfer News for GPB webpage

Genomics, Proteomics and Bioinformatics (GPB) will no longer be published by Elsevier after December 31st 2023. All articles in 2024 issues will be published by Oxford University Press (OUP) at https://academic.oup.com/gpb. Some of the manuscripts accepted in 2023 will be published by OUP in 2024 issues according to the publication schedule, which will be confirmed by the Editorial Office. GPB remains an open access journal after the publisher transfer. An open access Article Publication Charge (APC) is payable by the author or research funder to cover the costs associated with publication in GPB. All articles published in GPB are freely accessible online by all under CC licenses. Please feel free to contact the Editorial Office at editor@big.ac.cn for questions.

Genomics, Proteomics and Bioinformatics (GPB) is the official journal of the Beijing Institute of Genomics, Chinese Academy of Sciences / China National Center for Bioinformation 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.

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's 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.

**IMPACT FACTOR**

*2022: 9.500 © Clarivate Analytics Journal Citation Reports 2023*

**ABSTRACTING AND INDEXING**

PubMed/Medline
PubMed/Medline
Chemical Abstracts
BIOSIS Previews
Scopus
PubMed Central
Directory of Open Access Journals (DOAJ)
Embase
Index Copernicus
Chinese Science Citation Database (CSCD)
Science Citation Index Expanded

**EDITORIAL BOARD**

**Editor-in-Chief**

*Jun Yu*, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Genomics, bioinformatics

**Executive Associate Editors-in-Chief**

*Songnian Hu*, Institute of Microbiology, Chinese Academy of Sciences, China
Genomics, medical genetics
*Yi Xing*, The Children's Hospital of Philadelphia, United States of America
Bioinformatics, Genomics, RNA Biology

**Associate Editors-in-Chief**

*Alex Bateman*, European Bioinformatics Institute, United Kingdom
*Arndt Benecke*, Pierre and Marie Curie University, France
Host-pathogen interactions, Immune responses, Neurobiology
*Xiangdong Fang*, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Transcriptomics, epigenetic regulation, and markers
*Andreas Keller*, Saarland University, Germany
Non-invasive biomarkers, bacterial resistance, and genetic testing by NGS
*Hongxing Lei*, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Functional genomics of Alzheimer’s disease, big data for stem cell research, and protein folding
**Song Liu**, Roswell Park Comprehensive Cancer Center, United States of America
Transnational bioinformatics, biomarker discovery, and cancer genomics

**Yun-Gui Yang**, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
RNA methylation and DNA damage response

**Zhang Zhang**, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Computational biology, biocuration, and databases

**Fangqing Zhao**, Beijing Institutes of Life Science, Chinese Academy of Sciences, China
Computational biology, metagenomics, and evolutionary genomics of non-model organism

**Heng Zhu**, Johns Hopkins University, United States of America
Biomarker, Diagnostic, High Throughput Screening, Micro Arrays, Protein Modification, Systems biology.

**Editorial Board Members**

**Kin Fai Au**, Ohio State University, United States of America
Third Generation Sequencing

**Brendan Bell**, University of Sherbrooke, Canada
HIV and gene expression

**Kyle K. Biggar**, Western University, ON, Canada
Hypoxia, protein methylation, and microRNAs

**Erik Bongcam-Rudloff**, Swedish University of Agricultural Sciences, Sweden
Medical informatics, Bioinformatics, Animal genomics, Bioinformatics tools and biobanking

**Giacomo Cavalli**, Institute of Human Genetics, Montpellier, France
Epigenetics, polycomb, and genome topology

**Lawrence Wing-Chi Chan**, The Hong Kong Polytechnic University, Hong Kong
MicroRNA, non-small cell lung cancer, survival analysis, radiogenomics, clinical decision support

**Fei Chen**, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
RNA epigenetic modifications and sequencing technologies

**Kaifu Chen**, Harvard Medical School, United States of America
Bioinformatics, Epigenomics, Cardiology, Vascular biology, Prostate cancer

**Luonan Chen**, Shanghai Institutes for Biological Sciences, CAS Center for Excellence in Molecular Cell Science, Chinese Academy of Sciences, China
Systems biology, Bioinformatics

**Ming Chen**, Zhejiang University Library, China
Bioinformatics, systems biology, noncoding RNAs, and protein-protein interaction network

**Runsheng Chen**, Institute of Biophysics, Chinese Academy of Sciences, China
DNA sequence analysis, protein structure and function studies, IncRNAs

**Xiang Chen**, St. Jude Children's Research Hospital, United States of America
Cancer Genomics

**Peng Cui**, Agricultural Genomes Institute at Shenzhen, Chinese Academy of Agricultural Sciences, China
Plant Genomics

**Zhijun Duan**, University of Washington, United States of America
Chromatin, chromosome, epigenomics, genomics, transcription

**Domenica D’Elia**, Institute for Biomedical Technologies National Research Council, Italy
Databases, Transcriptomics, ncRNAs, Micro RNAs, Long non-coding RNAs, Gene regulatory network reconstruction

**Rong Fan**, Yale University, United States of America
Single cell

**Jingyuan Fu**, University of Groningen, Netherlands
Multi-dimensional "omics" integrative analysis towards a better understanding of the development of complex diseases, population-based gut microbiome analyses.

**Feng Gao**, Tianjin University, China
Microbial genomics and bioinformatics

**Ge Gao**, Peking University, China
Bioinformatics tools, genomics, and databases

**Xin Gao**, King Abdullah University of Science and Technology, Saudi Arabia
Bioinformatics, protein structure, NMR, machine learning

**Casey Greene**, University of Pennsylvania, United States of America
Machine learning

**Jin Gu**, Tsinghua University, China
Single cell
Caixia Guo, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
DNA damage tolerance, mutagenesis, and genomics

Bin Han, CAS Center for Excellence in Molecular Plant Sciences, Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, China
Genome sequencing, genome analysis, and rice

Leng Han, The University of Texas Health Science Center at Houston, United States of America
Cancer genomics, computational biology, high-throughput assay, noncoding RNA, post-transcriptional regulation

Jacob Hanna, Weizmann Institute of Science, Israel
Pluripotent Stem Cells, Regulation of pluripotency, Tissue and Organ Development

Henning Hermjakob, European Bioinformatics Institute, Cambridge, United Kingdom
Proteomics, network and systems biology, data curation

Aiilong Ke, Cornell University, United States of America
CRISPR

Arne Klungland, Oslo University Hospital, Norway
Modifications in DNA and RNA

Sanghyuk Lee, Ewha Womans University, Korea
Systems biology, cancer biomarker, microRNA, and genome annotation

Ao Li, University of Science and Technology of China, China
Cancer genome, post-translational modifications (PTM), and ncRNAs

Lei Li, Peking University, China
MicroRNA, gene expression regulation, and plant regulatory network

Shengbin Li, Xi'an Jiaotong University, China
Biodiversity, Genomic diversity, Forensic science, Biosafety, Biometrics recognition

Shuwei Li, China Pharmaceutical University, China
Mass spectrometry, isotope labeling, quantitative proteomics, and protein phosphorylation

Yixue Li, Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences, China
NGS analysis, gene regulatory network, and protein-protein interaction network

Wei Lin, Shanghai Jiao Tong University, China
NGS, autoimmune disease, and cancer vaccine

Tomas Lindahl, The Francis Crick Institute, United Kingdom
Cancer research and DNA repair

Feng Liu, Institute of Zoology, Chinese Academy of Sciences, China
Hematopoiesis, stem cell, epigenetics, transcriptional regulation, and single cell omics

Jiang Liu, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Cancer research and DNA methylation

Mofang Liu, Chinese Academy of Sciences Center for Excellence in Molecular Cell Science, CAS Center for Excellence in Molecular Cell Science, Chinese Academy of Sciences, China
miRNAs in cancer and piRNA regulation in spermatogenesis

P. Paul Liu, National Human Genome Research Institute, United States of America
Cancer genomics, tumor biology, and molecular mechanisms of leukemia

Siqi Liu, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Proteomics

Xiaole Shirley Liu, Dana-Farber Cancer Institute, United States of America
Algorithms

Xiaowen Liu, Indiana University Purdue University Indianapolis, United States of America
Algorithms, proteomics, PTMs, and proteogenomics

Jian Lu, Peking University, China
Evolutionary Biology, Population Genetics, Comparative Genomics, Functional Genomics, Gene regulation, Small non-coding RNAs

Long Mao, Chinese Academy of Agricultural Sciences Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, China
Plant genomics and miRNAs

Antonio Marcilla, University of Valencia, Valencia, Spain
Extracellular vesicles, parasitic disease, and molecular parasitology

Kang Ning, Huazhong University of Science and Technology, China
Metagenomics, genomics, single-cell omics, proteomics, computational biology algorithms

Zemin Ning, Wellcome Sanger Institute, United Kingdom
Genome informatics and data mining

Akimitsu Okamoto, The University of Tokyo, Japan
DNA/RNA imaging, organic chemistry, and functional protein/oligopeptide synthesis,
Jiang Qian, Johns Hopkins University, United States of America
Epigenetics, gene expression, gene regulation, signaling networks

Peter Roepstorff, University of Southern Denmark, Denmark
Mass spectrometry, proteomics, and post translational modifications

Marcel Schulz, Goethe University Frankfurt, Germany
Machine learning

Hui Shen, Van Andel Research Institute, United States of America
DNA methylation, epigenetics/epigenomics, cancer genomics, bioinformatics, ovarian cancer

Erwei Song, Sun Yat-Sen Memorial Hospital, Department of Breast Surgery, China
G protein-coupled receptor (GPCR), microRNA (miRNA), immunotherapy, signal transduction, gene therapy, cancer biology, cancer stem cells, cancer therapy, epigenetics, breast cancer, tumor immunology, epithelial-mesenchymal transition (EMT), membrane protein, NF-kappa B (NF-KB), chemokine, metastasis, macrophage

Jiangning Song, Monash University, Faculty of Medicine Nursing and Health Sciences, Australia
Bioinformatics, Machine learning, Sequence analysis, Artificial intelligence, Pattern recognition, Medical Imaging, Digital Health, Multi-modal data integration

Minjia Tan, Shanghai Institute of Materia Medica, Chinese Academy of Sciences/ China National Center for Bioinformation, China
Fuchou Tang, Peking University, China
Single-cell genomics, human early embryonic development, human germ cell development

Qiang Tian, Shanghai Jiao Tong University, China
Cancer and stem cell biology, immunity, and disease biomarker discovery

Yigang Tong, Beijing University of Chemical Technology, China
Bacteria, metagenomics, microbe, next-generation sequencing, virus

Edwin Wang, University of Calgary, Canada
Bioinformatics, disease biomarker, and systems biology

Hailin Wang, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, China
Homologous recombination, RecA, Rad51, single stranded binding protein, DNA damage detection, ultrasensitive assay, single molecule fluorescence study, protein-DNA interaction, protein assembly and disassembly

Jiguang Wang, Hong Kong University of Science and Technology, China
Precision Oncology

Qianfei Wang, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Genomics, leukemia, and transcriptional network

Ting Wang, Washington University in St Louis, United States of America
Genomics, epigenomics, evolution, computation, and systems biology

Xiangfeng Wang, China Agricultural University, China
Plant genomics, systems biology, and epigenetic modifications

Xiu-Jie Wang, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China
Bioinformatics, Big data, ncRNAs, Stem cells

Zhao-Qi Wang, Leibniz Institute on Aging - Fritz Lipmann Institute, Germany
DNA damage response, epigenetic modification, and aging

Limsoon Wong, National University of Singapore, Singapore
Computational biology, proteomics, transcriptomics, systems biology, database theory, knowledge discovery

Jingfa Xiao, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Bioinformatics, comparative genomics, structure and function of small proteins.

Guo-Liang Xu, Chinese Academy of Sciences, Shanghai Institute of Biochemistry and Cell Biology, China
Gene silencing, Decarboxylase, DNA enzyme, Nucleotide excision repair, Pluripotency, DNA methylation, Base excision repair (BER), Epigenetics, DNA methyltransferase, 5-methylcytosine, Meiosis, Dioxygenase, Fertilization, Transcription enhancer, DNA demethylation, 5-hydroxymethylcytosine (5-hmC)

Yu Xue, Huazhong University of Science and Technology, China
Post-translational modifications, bioinformatics, and comparative proteomics

Kai Ye, Xi'an Jiaotong University, China
Assembly, GWAS, indel, NGS, population sequencing, and structural variant

Chengqi Yi, Peking University, China
Changqing Zeng, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China
Human genomics

Le Zhang, Sichuan University, China
Data mining, Bioinformatics, Artificial intelligence, High performance computing, and Numerical analysis.

**Xiaohua Douglas Zhang**, University of Macau, China  
Artificial Intelligence

**Xue Zhang**, Harbin Medical University, China  
Genomics, monogenic diseases, and mutation profiling

**Xuegong Zhang**, Tsinghua University, China  
Machine learning, computational genomics, and systems biology

**Zhihua Zhang**, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China  
Computational systems biology, histone modification profiles, and transcriptional regulation

**Ziding Zhang**, China Agricultural University, China  
Protein bioinformatics, protein-protein interaction network, and plant-pathogen interaction

**Yi Zhao**, Institute of Computing Technology Chinese Academy of Sciences, China  
Bioinformatics, Transcriptome, Big Data of Medicine, Big Data of Traditional Chinese Medicine, Artificial Intelligence

**Yongliang Zhao**, Beijing Institute of Genomics, Chinese Academy of Sciences/China National Center for Bioinformation, China  
DNA repair, genome stability, and cancer biology

**Zhongming Zhao**, The University of Texas Health Science Center at Houston, United States of America  
NGS data analysis, disease gene network/pathway analysis, cancer bioinformatics

**Weimin Zhu**, Beijing Proteome Research Center, China  
Bioinformatics, databases, and big data

**Zheng-Jiang Zhu**, Chinese Academy of Sciences Shanghai Institute of Organic Chemistry, Chinese Academy of Sciences/China National Center for Bioinformation, China  
Metabolomics, Lipidomics, Mass Spectrometry, Metabolite identification, Metabolic network and pathway
GUIDE FOR AUTHORS

Your Paper Your Way
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
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. 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

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 on Ethics in publishing.

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 certified 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.

Declaration of generative AI in scientific writing

The below guidance only refers to the writing process, and not to the use of AI tools to analyse and draw insights from data as part of the research process.

Where authors use generative artificial intelligence (AI) and AI-assisted technologies in the writing process, authors should only use these technologies to improve readability and language. Applying the technology should be done with human oversight and control, and authors should carefully review and
edit the result, as AI can generate authoritative-sounding output that can be incorrect, incomplete or biased. AI and AI-assisted technologies should not be listed as an author or co-author, or be cited as an author. Authorship implies responsibilities and tasks that can only be attributed to and performed by humans, as outlined in Elsevier’s AI policy for authors.

Authors should disclose in their manuscript the use of AI and AI-assisted technologies in the writing process by following the instructions below. A statement will appear in the published work. Please note that authors are ultimately responsible and accountable for the contents of the work.

**Disclosure instructions**
Authors must disclose the use of generative AI and AI-assisted technologies in the writing process by adding a statement at the end of their manuscript in the core manuscript file, before the References list. The statement should be placed in a new section entitled ‘Declaration of Generative AI and AI-assisted technologies in the writing process’.

*Statement: During the preparation of this work the author(s) used [NAME TOOL / SERVICE] in order to [REASON]. After using this tool/service, the author(s) reviewed and edited the content as needed and take(s) full responsibility for the content of the publication.*

This declaration does not apply to the use of basic tools for checking grammar, spelling, references etc. If there is nothing to disclose, there is no need to add a statement.

**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, a published lecture or academic thesis, see ‘Multiple, redundant or concurrent publication’ 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 compliance, your article may be checked by Crossref Similarity Check and other originality or duplicate checking software.

**Use of inclusive language**
Inclusive language acknowledges diversity, conveys respect to all people, is sensitive to differences, and promotes equal opportunities. Content should make no assumptions about the beliefs or commitments of any reader; contain nothing which might imply that one individual is superior to another on the grounds of age, gender, race, ethnicity, culture, sexual orientation, disability or health condition; and use inclusive language throughout. Authors should ensure that writing is free from bias, stereotypes, slang, reference to dominant culture and/or cultural assumptions. We advise to seek gender neutrality by using plural nouns (“clinicians, patients/clients”) as default/wherever possible to avoid using “he, she,” or “he/she.” We recommend avoiding the use of descriptors that refer to personal attributes such as age, gender, race, ethnicity, culture, sexual orientation, disability or health condition unless they are relevant and valid. When coding terminology is used, we recommend to avoid offensive or exclusionary terms such as "master", "slave", "blacklist" and "whitelist". We suggest using alternatives that are more appropriate and (self-) explanatory such as "primary", "secondary", "blocklist" and "allowlist". These guidelines are meant as a point of reference to help identify appropriate language but are by no means exhaustive or definitive.

**Reporting sex- and gender-based analyses**

**Reporting guidance**
For research involving or pertaining to humans, animals or eukaryotic cells, investigators should integrate sex and gender-based analyses (SGBA) into their research design according to funder/sponsor requirements and best practices within a field. Authors should address the sex and/or gender dimensions of their research in their article. In cases where they cannot, they should discuss this as a limitation to their research's generalizability. Importantly, authors should explicitly state what definitions of sex and/or gender they are applying to enhance the precision, rigor and reproducibility of their research and to avoid ambiguity or conflation of terms and the constructs to which they refer (see Definitions section below). Authors can refer to the Sex and Gender Equity in Research (SAGER) guidelines and the SAGER guidelines checklist. These offer systematic approaches to the use
and editorial review of sex and gender information in study design, data analysis, outcome reporting and research interpretation - however, please note there is no single, universally agreed-upon set of guidelines for defining sex and gender.

**Definitions**

Sex generally refers to a set of biological attributes that are associated with physical and physiological features (e.g., chromosomal genotype, hormonal levels, internal and external anatomy). A binary sex categorization (male/female) is usually designated at birth ("sex assigned at birth"), most often based solely on the visible external anatomy of a newborn. Gender generally refers to socially constructed roles, behaviors, and identities of women, men and gender-diverse people that occur in a historical and cultural context and may vary across societies and over time. Gender influences how people view themselves and each other, how they behave and interact and how power is distributed in society. Sex and gender are often incorrectly portrayed as binary (female/male or woman/man) and unchanging whereas these constructs actually exist along a spectrum and include additional sex categorizations and gender identities such as people who are intersex/have differences of sex development (DSD) or identify as non-binary. Moreover, the terms "sex" and "gender" can be ambiguous—thus it is important for authors to define the manner in which they are used. In addition to this definition guidance and the SAGER guidelines, the resources on this page offer further insight around sex and gender in research studies.

**Author contributions**

For transparency, we require corresponding authors to provide co-author contributions to the manuscript using the relevant CRediT roles. The CRediT taxonomy includes 14 different roles describing each contributor’s specific contribution to the scholarly output. The roles are: Conceptualization; Data curation; Formal analysis; Funding acquisition; Investigation; Methodology; Project administration; Resources; Software; Supervision; Validation; Visualization; Roles/Writing - original draft; and Writing - review & editing. Note that not all roles may apply to every manuscript, and authors may have contributed through multiple roles. More details and an example.

**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 (https://www.elsevier.com/__data/promis_misc/Authorship Agreement.docx) 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, it is recommended to state this.

Open access
Please visit our Open Access page for more information.

Elsevier Researcher Academy
Researcher Academy is a free e-learning platform designed to support early and mid-career researchers throughout their research journey. The "Learn" environment at Researcher Academy offers several interactive modules, webinars, downloadable guides and resources to guide you through the process of writing for research and going through peer review. Feel free to use these free resources to improve your submission and navigate the publication process with ease.

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. Here is a 10% discount for this service by using the code GPB2003.

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

PREPARATION

Peer review
This journal operates a single anonymized 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. Editors are not involved in decisions about papers which they have written themselves or have been written by family members or colleagues or which relate to products or services in which the editor has an interest. Any such submission is subject to all of the journal's usual procedures, with peer review handled independently of the relevant editor and their research groups. 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.

*Research paper*

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

Structure samples for other article types:

*Minireview*

Systems Approaches to Biology and Disease Enable Translational Systems Medicine

*Research 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 article*

FunMod: A Cytoscape Plugin for Identifying Functional Modules in Undirected Protein-Protein Networks

*Technical 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 alone.

**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.

**Highlights**

Highlights are optional yet highly encouraged for this journal, as they increase the discoverability of your article via search engines. They consist of a short collection of bullet points that capture the novel results of your research as well as new methods that were used during the study (if any). Please have a look at the example Highlights.

Highlights should be submitted in a separate editable file in the online submission system. Please use 'Highlights' in the file name and include 3 to 5 bullet points (maximum 85 characters, including spaces, per bullet point).

**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, it is recommended to 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.
• Ensure that color images are accessible to all, including those with impaired color vision.

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.

**Preprint references**

Where a preprint has subsequently become available as a peer-reviewed publication, the formal publication should be used as the reference. If there are preprints that are central to your work or that cover crucial developments in the topic, but are not yet formally published, these may be referenced. Preprints should be clearly marked as such, for example by including the word preprint, or the name of the preprint server, as part of the reference. The preprint DOI should also be provided.

**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:


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 https://www.elsevier.com/__data/promis_misc/GPB-Endnote-Template.ens.

**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 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: www.elsevier.com/authors/author-resources/research-data/data-base-linking.

**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. 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 2018 Elsevier | https://www.elsevier.com