Journal of Molecular Biology (JMB) provides high quality, comprehensive and broad coverage in all areas of molecular biology. The journal publishes original scientific research papers that provide mechanistic and functional insights and report a significant advance to the field. The journal encourages the submission of multidisciplinary studies that use complementary experimental and computational approaches to address challenging biological questions.

Research areas include but are not limited to: Biomolecular interactions, signaling networks, systems biology Cell cycle, cell growth, cell differentiation Cell death, autophagy Cell signaling and regulation Chemical biology Computational biology, in combination with experimental studies DNA replication, repair, and recombination Development, regenerative biology, mechanistic and functional studies of stem cells Epigenetics, chromatin structure and function Gene expression Receptors, channels, and transporters Membrane processes Cell surface proteins and cell adhesion Methodological advances, both experimental and theoretical, including databases Microbiology, virology, and interactions with the host or environment Microbiota mechanistic and functional studies Nuclear organization Post-translational modifications, proteomics Processing and function of biologically important macromolecules and complexes Molecular basis of disease RNA processing, structure and functions of non-coding RNAs, transcription Sorting, spatiotemporal organization, trafficking Structural biology Synthetic biology Translation, protein folding, chaperones, protein degradation and quality control

Important benefits for authors

Since 1959, JMB is ensuring some basic principles in the services it provides to all authors: Fast-track option of time-sensitive research articles (please consult the Guide for Authors for details). Anti-scooping policy: if a competitor paper has been published while yours is under peer-review in JMB, that will not affect the editorial outcome. All editorial decisions are made by active scientists who are leading experts in the field. Manuscripts are reviewed by leading experts in the field. JMB also supports mentoring of early career researchers in peer-review (please consult our VolunPeers program). Availability: contact the Editor-in-Chief or the scientific editors via the Editorial Board page for any questions you may have. See the impact, speed and readership of JMB here. We provide upon request free PDFs to all authors who may not have access to their articles via their institution or library. Publication is free to authors (no color or page charges) Supporting open access: if your funding body or institution requires your article to be open access, JMB offers that option. Please see details here. Reuse figures from any JMB article via "get rights and content" hyperlink available within each article (below author names and affiliations) on ScienceDirect.
Please click here for more information on more general author services Elsevier offers.

AUDIENCE
Molecular biologists, biochemists, structural biochemists, geneticists, virologists and cell biologists.

IMPACT FACTOR
2020: 5.469 © Clarivate Analytics Journal Citation Reports 2021

ABSTRACTING AND INDEXING
Scopus
EMBiology
Biochemistry and Biophysics Citation Index
Biological and Agricultural Index
Biological Abstracts
Biotechnology Citation Index
Chemical Abstracts
Current Contents - Life Sciences and Clinical Medicine
Biostatistica
Embase
FSTA (Food Science and Technology Abstracts)
Genetics Abstracts
Immunology Abstracts
PubMed/Medline
Reference Update
Research Alert
Science Citation Index
Web of Science
BIOSIS Citation Index

EDITORIAL BOARD
Editor-in-Chief
Peter Wright, The Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla, CA 92037, U.S.A.

Senior Scientific Editor
Denise Wells, Elsevier Inc Cambridge, MA 02139, Cambridge, Massachusetts, United States of America

Senior Managing Editor
Jasmin Bakker, Elsevier B.V., 1043 NX, Amsterdam, Netherlands

Social Media Editor
Rebecca Berlow, The Scripps Research Institute, La Jolla, California, United States of America

Founding Editor
Sir John Kendrew†

Associate Editors
Anna M. Pyle, Yale University, New Haven, Connecticut, United States of America
Structure, folding and function of long noncoding RNAs, molecular mechanism of RNA helicase proteins and RNA-triggered mechanical devices
Sheena E. Radford, University of Leeds, Leeds, United Kingdom
Protein folding and misfolding mechanisms
Michael J.E. Sternberg, Imperial College London, London, United Kingdom
Bioinformatics, systems biology, computational biology, web servers
Michael F. Summers, University of Maryland Baltimore, Baltimore, Maryland, United States of America
Structural biology, RNA, proteins, structure, retroviruses, HIV
Moshe Yaniv, Institut Pasteur, Paris, France
Chromatin, epigenetic and gene expression, oncogenic viruses and cancer, cell growth control

Editorial Board Members
James M. Berger, Johns Hopkins University School of Medicine, Baltimore, Maryland, United States of America
DNA replication, nucleic acid-dependent motors, chromosome organization and topology

Philip C. Bevilacqua, The Pennsylvania State University, University Park, Pennsylvania, United States of America
RNA enyzymology and structural genomics

Johannes Buchner, Technical University of Munich Department of Chemistry, Garching, Germany
Antibody engineering, heat shock protein 90 (Hsp90), molecular chaperone, small heat shock protein (sHsp), chaperone

Rita Casadio, University of Bologna Biocomputing Group, Bologna, Italy

Eric Cascales, Laboratory of Macromolecular Systems Engineering, Marseille, France
Microbiology, microbial pathogenesis, protein secretion, peptidoglycan, prolyl isomerase, membrane biogenesis, bacteria, cell surface, protein translocation, bacterial conjugation, protein export, protein targeting, bacteriophage, bacterial toxin, cell wall, secretion

Bill Clemons, California Institute of Technology Division of Chemistry and Chemical Engineering, Pasadena, California, United States of America
Tail-anchored protein targeting, membrane protein expression, bacterial glycoendocrinology

Yamini Dalal, Center for Cancer Research, Frederick, Maryland, United States of America
Chromatin/nucleosome structure, epigenetics, atomic force and electron microscopy, cancer chromatin biology

Eric O. Freed, NCI at Frederick, Frederick, Maryland, United States of America
Virology, assembly and release of HIV-1/retroviruses

Mónica Fuxreiter, University of Padua Department of Biomedical Sciences, Padova, Italy
Computational biology, intrinsically disordered proteins, protein dynamics, structure-function relationship

Ruben L. Gonzalez, Columbia University, New York, New York, United States of America
Ribosome structure and function, mechanism of protein synthesis, single-molecule biophysics

Max Gottesman, Columbia University, New York, New York, United States of America
Transcription elongation regulation in E. coli

Patrick R. Griffin, Scripps Research Institute Department of Molecular Medicine, Jupiter, Florida, United States of America
Metabolic control of inflammation and immunity, structural and chemical biology of enzymes and receptors, H/D exchange mass spectrometry

Mitchell Guss, The University of Sydney, Sydney, New South Wales, Australia
Structural biology, metallocproteins

Barry Honig, Columbia University, New York, New York, United States of America
Computational and theoretical methods to study the structure and function of proteins, nucleic acids and membranes, software tools

Anne Houdusse, Institute Curie, Paris, France
Cytoskeleton, intracellular traffic, molecular motors, myosins, small GTPases, X-ray crystallography

Gerhard Hummer, Max Planck Institute of Biophysics Department of Theoretical Biophysics, Frankfurt am Main, Germany
Theory and molecular simulation, protein dynamics

Urs Jenal, University of Basel, Basel, Switzerland
Molecular basis of chronic bacterial signaling and infections in humans, cGMP

Charalampos G. Kalodimos, St Jude Children's Research Hospital, Memphis, Tennessee, United States of America
Molecular chaperones, protein kinases, protein allostery, type III Secretion in bacteria

Achillefes Kapanidis, University of Oxford, Oxford, United Kingdom
Transcription, DNA repair, protein-DNA interactions, single-molecule fluorescence spectroscopy

Amy Keating, Massachusetts Institute of Technology, Cambridge, Massachusetts, United States of America
Protein-protein interactions, protein engineering and design, computational structural biology

Sepideh Khorasanizadeh, University of Oxford, Oxford, United Kingdom
Epigenetic mechanisms, transcriptional regulation, therapeutics discovery with small molecules

Shohei Koide, NYU Langone Health, New York, New York, United States of America
Protein design and engineering, drug discovery, protein-protein interactions, cellular signaling, structural biology, synthetic biology

Richard Kriwacki, St Jude Children's Research Hospital, Memphis, Tennessee, United States of America
Cell division and apoptosis, Intrinsically disordered proteins, signal transduction

**Gabriel C. Lander**, Scripps Research, Integrative Structural and Computational Biology, San Diego, California, United States of America
Cryo-EM, AAA+ motors

**Edward A. Lemke**, Johannes Gutenberg University Mainz, Mainz, Germany
Chemical biology, synthetic biology, single molecule spectroscopy, super-resolution microscopy, protein engineering, intrinsically disordered proteins, structure and dynamics, phase separation, FRET, nuclear function.

**Zhi-Jie (James) Liu**, ShanghaiTech University, Shanghai, China
G protein coupled receptors (GPCR), signal transduction, drug development

**Karolin Luger**, University of Colorado Boulder, Boulder, Colorado, United States of America
Chromatin structure and dynamics, molecular biophysics, proteins and enzymology, structural biology

**Sascha Martens**, University of Vienna, Vienna BioCenter (VBC), Max Perutz Labs, Wien, Austria
Autophagy

**David H. Mathews**, University of Rochester Medical Center Department of Biochemistry & Biophysics, Rochester, New York, United States of America
Computational biology, bioinformatics

**Anthony Maxwell**, John Innes Centre Department of Biological Chemistry, Norwich, United Kingdom
Structure and function of DNA topoisomerases, antibiotic and herbicide development

**Daniel L. Minor, Jr.**, University of California San Francisco, San Francisco, California, United States of America
Structure, chemistry, mechanisms and function of ion channels

**Daniel Otzen**, Aarhus University, Aarhus, Denmark
Protein aggregation, deposition diseases, protein folding and misfolding, membrane proteins, protein-lipid and protein-surfactant interactions

**Anna Panchenko**, Queen's University Department of Pathology and Molecular Medicine, Kingston, Ontario, Canada
Computational and hybrid approaches to study protein interactions, chromatin and nucleosome dynamics

**Bert Poolman**, University of Groningen Groningen Biomolecular Sciences and Biotechnology Institute, Haren, Netherlands
Synthetic biology, enzymology, membrane biology, transport, signal transduction

**Owen Pornillos**, University of Virginia Department of Molecular Physiology and Biological Physics, Charlottesville, Virginia, United States of America
Structure and assembly of HIV, virus/host interactions, structural biology of the innate immune system

**Raul Rabada**, Columbia University, New York, New York, United States of America
Computational biology

**Lutz Schmitt**, Heinrich Heine University Düsseldorf, Dusseldorf, Germany
ABC transporters, bacterial secretion, type 1 secretion system, multi-drug resistance, structural biology

**Georg E. Schulz**, University of Freiburg, Freiburg im Breisgau, Germany
Membrane protein x-ray crystallography, structure, function and mechanism of enzymes and other proteins, protein engineering

**James R. Sellers**, National Heart Lung and Blood Institute, Bethesda, Maryland, United States of America
Structure, function, and regulation of myosins, single molecule microscopy

**Louise Serpell**, University of Sussex, Brighton, United Kingdom
Structure and function of amyloidogenic proteins, neurodegenerative diseases

**Konstantin Severinov**, Waksman Institute of Microbiology, Piscataway, New Jersey, United States of America
Transcription initiation and regulation in bacteria, RNA polymerases, bacteriophage development, temporal regulation of gene expression

**Feng Shao**, National Institute of Biological Sciences Beijing, Beijing, China
Inflammasome, innate immunity and cell death

**Yigong Shi**, Westlake University, Hangzhou, China
Apoptosis structural biology, Structural mechanisms of macromolecular machineries, Apoptotic pathways, Proteasome

**Ichio Shimada**, RIKEN Center for Biosystems Dynamics Research, Yokohama, Kanagawa, Japan
Structural biology of membrane receptors and ion channels, NMR

**Sachdev Sidhu**, University of Toronto, Toronto, Ontario, Canada
Antibody engineering, protein engineering, phage display technology, protein-protein interactions

**Titia Sixma**, Antoni van Leeuwenhoek Netherlands Cancer Institute, Amsterdam, Netherlands
Structural biology of DNA repair, ubiquitin and SUMO modification, chromatin remodeling

**Arne Skerra**, Technical University of Munich Chair of Biological Chemistry, Freising, Germany
Protein engineering and design, biological chemistry
Thomas Smith, The University of Texas Medical Branch at Galveston Sealy Center for Structural Biology and Molecular Biophysics, Galveston, Texas, United States of America
Structural biology, cryo-EM, X-ray

Igor Stagljar, University of Toronto, Toronto, Ontario, Canada
Cancer signalling, Chemical biology, Cancer therapeutics, Protein-protein interactions, Proteomics, Systems biology, Membrane transport

Dylan J. Taatjes, University of Colorado Boulder Department of Chemistry, Boulder, Colorado, United States of America
Structure and mechanisms of eukaryotic transcription machinery

Sarah A. Teichmann, Wellcome Sanger Institute, Saffron Walden, UK
Transcriptional regulatory networks, gene expression regulation and protein complex assembly

Yanli Wang, Institute of Biophysics Chinese Academy of Sciences, Chaoyang District, China
Protein-nucleic acid interaction, structural biology, CRISPR/Cas, DNA binding protein, RNA-protein interaction, cryo-electron microscopy, RNA interference (RNAi), microRNA mechanism, crRNA, RNA structure, small interfering RNA (siRNA), protein-DNA interaction, Argonaute, Cas6, crystal structure

Ronald Wetzel, University of Pittsburgh, Pittsburgh, Pennsylvania, United States of America
Amyloids, protein aggregation, neurodegenerative diseases

Sarah A. Woodson, Johns Hopkins University, Baltimore, Maryland, United States of America
RNA folding, ribosome assembly, RNA-chaperone interactions

Nieng Yan, Princeton University, Princeton, New Jersey, United States of America
Membrane transporters, mechanisms of substrate recognition and transport

Kai Zhang, University of Illinois Urbana-Champaign, Champaign, Illinois, United States of America
Imaging, neurobiology, optogenetics, signal transduction

Mingjie Zhang, Southern University of Science and Technology, Shenzhen, China
Structural biology of neuronal signaling complex organization and regulation, protein complexes governing cell polarity, screening and development of small molecules with therapeutic potentials
GUIDE FOR AUTHORS

INTRODUCTION
The *Journal of Molecular Biology* provides high quality, comprehensive and broad coverage in all areas of molecular biology. The journal publishes original scientific research papers that provide functional and mechanistic insights and report a significant advance to the field. The journal encourages the submission of multidisciplinary studies that use complementary experimental and computational approaches to address challenging biological questions.

In addition to research Communications and Articles, the journal welcomes submission of Methods Notes, Databases/ Web Servers, Brevia, Perspectives, and Reviews

Research areas include but are not limited to: Biomolecular interactions, signaling networks, systems biology Cell cycle, cell growth, cell differentiation Cell death, autophagy Cell signaling and regulation Chemical biology Computational biology, in combination with experimental studies DNA replication, repair, and recombination Development, regenerative biology, mechanistic and functional studies of stem cells Epigenetics, chromatin structure and function Gene expression Membrane processes, cell surface proteins and cell-cell interactions Methodological advances, both experimental and theoretical, including databases Microbiology, virology, and interactions with the host or environment Microbiota mechanistic and functional studies Nuclear organization Post-translational modifications, proteomics Processing and function of biologically important macromolecules and complexes Molecular basis of disease RNA processing, structure and functions of non-coding RNAs, transcription Sorting, spatiotemporal organization, trafficking Structural biology Synthetic biology Translation, protein folding, chaperones, protein degradation and quality control

The Journal, as a rule, will not publish papers which fall outside the areas defined above.

**Editorial policy**
The *Journal* aims to publish novel and significant research in the general areas of molecular genetics and structural biology. Acceptance of papers for publication in the *Journal* is at the discretion of the Editors. All manuscripts are reviewed initially by the Editorial Board and only those papers that meet the scientific and editorial standards of the *Journal* will be sent for outside review. Authors may indicate in their cover letter a suitable Editor to whom the paper could be allocated. However, the *Journal* reserves the right to reallocate manuscripts to the most appropriate Editor.

In general, Editors will seek advice from two or more expert reviewers about the scientific content, biological significance, and clarity of presentation of papers. Authors are required to suggest the names, affiliations, and contact information for up to six individuals who could serve as referees and indicate their specific areas of scientific expertise. Suggested referees should be established scientists with expertise in the field of the paper. Members of the Editorial Board of JMB must not be suggested as referees as well as people who have a potential conflict of interest, such as recent collaborators, close colleagues at your academic institution, personal friends or family members. If a revision of the manuscript is required, authors will be provided with the comments of the reviewers and specific instructions from the Editor handling the manuscript.

Many acceptable papers require minor revision or condensation. It is in the mutual interest of both the authors and the journal that amended manuscripts are returned promptly. A paper requiring major revision will retain its original date of receipt only if it is received by the Editor within 60 days of the date of return to the author. Extensions to the 60 days limit may be granted at the discretion of the Editor. Papers requiring minor revision must be returned to the Editor within 30 days.

As soon as the paper has been reviewed, the corresponding author will receive a decision letter from the Editor. Revised manuscripts and correspondence concerning such manuscripts should be addressed to the Editor at the address indicated on the decision letter.

The *Journal of Molecular Biology* discourages authors from submitting multiple manuscripts on closely related topics. Submission of two or more related manuscripts intended for simultaneous publication will be permitted only under exceptional circumstances. Authors wishing to submit related manuscripts must obtain prior permission from the Editors.
The Board will editorially reject papers, without outside review, if in their opinion the paper falls outside the scope of papers normally published by JMB, if the paper lacks originality, or if the paper fails to meet expected technical standards. The following specific points are brought to the attention of authors:

(a) **Originality.** The Board will reject those papers that it considers to provide only slight or incremental advances over previously published material.

(b) **Methodology papers.** Papers that deal only with new methods and do not contain important new results discovered by means of these methods will be accepted only when the general applicability and interest of the method are immediately obvious and clearly documented in the manuscript. Improvements on existing methods will in general be viewed as appropriate to more specialized journals unless it can be shown that they lead to important new insights that were not accessible with current technologies. Please consult the guidelines for the dedicated **Methods Notes** article type below, under the section **Types of Paper.**

(c) **Sequences.** Papers describing new members of a gene family will not ordinarily be accepted unless they contain results of particular importance for studies of evolution or of the function of the gene. In general, papers describing the cloning and sequencing of new genes will be acceptable only if there is experimental evidence for the function of the gene.

(d) **Structural studies.** Communications describing preliminary crystallographic data (crystallization conditions and diffraction pattern and space group) will not, in general, be accepted. Papers of this type will be considered only if, in the judgment of the Editorial Board, they contain results of exceptional interest and importance. Low-resolution structural studies will be acceptable only if they have clear biological implications and exhibit features of special interest. Papers describing structures of mutant proteins are appropriate if the mutations have been successfully designed to provide new insights into structural principles or biological function. Similar criteria apply to structures of proteins from variant species. In the particular case of unliganded antibody Fab fragments, papers would not normally be acceptable unless they provide novel structural or biological insight.

(e) **Modeled structures.** Papers describing modeled structures will in general be considered only if they provide novel and important biological insights. The reliability of the model must be clearly documented, including evidence that the expected accuracy level of the model is consistent with the application that is described. This could be based, for example, on the known success rate of the modeling procedure at specified levels of sequence identity, or the application of model validation procedures. Validation of the model through experimental tests is always desirable.

(f) **Theory and computer simulation.** Papers reporting theoretical studies should have direct applicability to experimental work in a field normally represented in papers published in JMB or should address issues of current interest to the broader biological community. As a general rule, all theory papers should deal directly with experimental data; the papers should provide predictions that are testable experimentally or provide an interpretation of experimental observations. Papers describing computer simulations are generally acceptable only if they provide new insights of high biological significance or lead to novel interpretations of experimental data. As is the case for modeled structures, evidence must be provided that the accuracy level of the method is consistent with the application that is described. This might involve, for example, control simulations on systems that have been well-characterized experimentally.

(g) **Database papers.** Papers describing biological or molecular databases will be considered if they report important new results discovered by means of that database, or if the database permits novel integration of biological information that will be of general applicability and lead to important new insights. The biological principles used in the construction of the database must be clearly documented in the paper.

**Sharing of reagents and data**

To allow others to build on work published in JMB, the Editors strongly encourage authors to share reagents (e.g., cloned DNAs; antibodies; bacterial, animal, or plant cells; viruses), data, algorithms, computer codes, and detailed scientific protocols with their colleagues in the scientific community. Authors are also encouraged to deposit as much of their data as possible in publicly accessible databases to facilitate the free exchange of scientific information.
**Sequence data**

Papers dealing with amino acid sequences of proteins or with nucleotide sequences must carry a statement that the data have been deposited with an appropriate data bank, e.g., the European Molecular Biology Laboratory (EMBL) or GenBank Data Libraries. The data base accession number must be given at the end of the Materials and Methods section of the manuscript under the separate heading 'Accession numbers'. For example: Coordinates and structure factors have been deposited in the Protein Data Bank with accession number 2XYZ. Lengthy nucleotide sequences will be published only if, in the judgement of the Editorial Board, these results are of general interest and importance.

**Structural data**

For papers describing structures of biological macromolecules, the atomic coordinates and the related experimental data (structure factor amplitudes/intensities and/or NMR restraints) must be deposited at a member site of the Worldwide Protein Data Bank (http://www.wwpdb.org): RCSB PDB (http://www.pdb.org), MSD-EBI (http://www.ebi.ac.uk/pdbe/), PDBj (http://www.pdbj.org), or BMRB (http://www.bmrb.wisc.edu). The full PDB validation report must be submitted with all manuscripts reporting crystal or NMR structures. Manuscripts must carry a statement that coordinates and structure factors (or NMR restraints) have been deposited in the Protein Data Bank. The accession number(s) must be cited in the manuscript at the end of the Materials and Methods section. Authors must agree to release the atomic coordinates and experimental data immediately upon publication. Small angle scattering (Small angle X-ray and neutron scattering (SAXS and SANS)) data and structural models must be deposited at SASBDB (https://www.sasbdb.org/) prior to submission. The database accession numbers must be cited in the manuscript and authors must agree to release the experimental data and structural models immediately upon publication.

For papers reporting structures determined by electron microscopy, the 3D map must be deposited at either the EMBL-EBI or RCSB EMDB site (http://www.emdatabank.org). The fitted atomic coordinates must be deposited at a member site of the Worldwide Protein Databank (see links above). The full PDB validation report must be submitted with all manuscripts reporting cryo-electron microscopy structures. The database accession numbers must be cited in the manuscript and authors must agree to release the atomic coordinates and experimental data immediately upon publication.

It is increasingly common for coordinates to be deposited in the Protein Data Bank without an associated publication. Before submission to JMB, authors are expected to search the Protein Data Bank for related structures using one or more alignment programs and report the outcome. Prior deposition of related coordinates, without an associated publication, does not necessarily preclude publication in JMB. The primary criteria for publication of a structure in JMB are that it provides novel structural insights or important new functional and biological insights that are likely to be of general interest.

You can enrich your online articles by providing 3D molecular models (optional) in PDB, PSE or MOL/MOL2 format, which will be visualized using the interactive viewer embedded within the article. Using the viewer, it will be possible to zoom into the model, rotate and pan the model, and change display settings. Submitted models will also be available for downloading from your online article on ScienceDirect. Each molecular model will have to be uploaded to the online submission system separately, via the “3D molecular models” submission category. For more information see: www.elsevier.com/3DMolecularModels.

**NMR assignments**

NMR assignment data must be deposited in the BioMagResBank (BMRB; http://www.bmrb.wisc.edu). The accession number(s) must be cited in the manuscript at the end of the Materials and Methods section. Tables listing resonance assignments will not be published in the Journal but may be deposited as Supplemental data that will be actively linked to the online version of the paper. Supplemental data must be included with the manuscript submitted for review (see below for full instructions).

**Machine learning in bioinformatics**

Authors must ensure that algorithms using supervised machine learning do not overestimate the accuracy of the approach as a result of an inappropriate selection of examples in the training and testing sets. For protein modelling, the default position is that one must ensure that even remote homologues are either in a training or a testing set but cannot span both sets. Low percent sequence identity is insufficient to identify remote homologies. Authors should identify homologues based on a structure-based classification such as the superfamily classification of the SCOP, CATH or homology...
(or even better possible homology) in ECOD. For non-coding RNAs the Rfam classification can be used for the same purpose. For prediction of the impact of missense variants, variants from a particular protein must be in either the training or the testing data set and the authors need to consider the extent to which homology could also confound their study. Similar considerations and approaches are required for other studies. On no account must the test data be used for parameterisation, including deciding on the learning algorithm, for example a network architecture. If such parameterisation is required, then training, validation and test sets must be used. Authors should fully explain their approach in the paper and if they do not follow the above guidelines, they should provide a detailed justification for this.

Computational studies: deposition of code and data or provision of a web server
All papers describing computational studies must provide sufficient information so that the research can be verified. JMB strongly encourages authors to deposit source code and data files for use by the community on an appropriate resource such as GitHub or Zenodo. Alternatively, algorithms and data can be made accessible to the community via a web server; in many circumstances the availability of a web server can enhance community use. Authors should plan to keep a web server operational for several years; otherwise, they should consider depositing the code or data. Code and web servers must be freely available to the academic community. Trajectories from molecular dynamics simulations should be deposited within open access resources such as Zenodo. The extent to which the community can benefit from the deposition of code, data or the provision of a web resource will be an important factor in editorial decisions. Authors should also consult, where appropriate, the sections on Machine learning in bioinformatics and Editorial policy: "Methodology papers", "Theory and computer simulation" and "Database papers."

Cell lines
In keeping with NIH guidelines, the Journal considers it to be good practice for cultured cell lines to be authenticated. A description of the methods used to authenticate cells should be included in the Materials and Methods section. Authors are expected to check that cell lines used in their experiments are free from mycoplasma infections.

Types of paper
The Journal of Molecular Biology will publish full Articles, Communications, Reviews, Perspectives, Brevia, Methods Notes, Databases, Web Servers and Fast Track.

Articles are not limited in length but the editors recommend that in most cases they should be no longer than 15 printed pages with no more than 10 figures and 4 tables. Note that 1 printed page is roughly equivalent to 2.5 pages in a Word document using double spacing and Arial Font 11.

Communications are brief papers that make a specific well-documented point. In general, a Communication should include no more than four figures and tables. The text will be continuous, with technical and methodological detail printed in the legend to the tables and figures.

Reviews are typically upon invitation only. You must obtain a pre-approval by an Editor before submitting your review. These are the criteria for consideration: We would like to ask you to approach it as a critical overview of the field, with a strong focus on current challenges and the bottlenecks to future major advances. Please make sure to emphasize the molecular mechanistic aspects where possible, otherwise please feel free to decide the exact scope of your review and the depth of coverage, keeping in mind that the overall message should be accessible to the broad readership of the journal. The review must represent a fair and unbiased coverage of the most recent advances and relevant approaches and research groups working in the field and accommodate different points of view. The scope of the review should stand out from other recently published reviews on the same theme. Please also feel free to highlight areas that you think deserve more attention from the scientific community. We strongly encourage use of summary illustrations which may serve as an easy reference to readers to understand the message of the overall messages relayed in the review. Finally, we would encourage you to include a ‘perspectives’ paragraph at the end of your review that proposes the direction you personally consider the field should take and the prospects for useful applications you might expect to see in the near future and beyond. Typically, authors choose to have 2-4 figures and 8-12 printed pages of text (22-32 pages in Word, double spacing, Arial font 11, not counting the references pages), but this can greatly vary and we leave
the length entirely up to you. We would like to discourage listing too many References, but only cite directly relevant literature. A primary research result used in a review should reference the original research article, not another review.

**Perspectives** are brief reviews that present a sharply focused view of a rapidly advancing area of research. Authorship is normally by invitation: the Editor-in-Chief or Scientific Editor should be consulted in advance by anyone wishing to submit an unsolicited Perspective.

**Brevia** are brief notes that report a specific well-documented result. Brevia are limited to a single page, including references and captions, and contain only one figure or table. Details of methods must be provided as Supplemental Material.

**Methods Notes** report novel methods of immediate and general interest and applicability. Methods Notes are limited to 5 pages, including references and captions, with a maximum of 3 displayed items (figures or tables). Additional details required to implement the new method must be provided as Supplemental Material. Preliminary enquiries about the suitability of a submission to this section are encouraged.

**Databases** and **web servers** are descriptions of new or updated databases and web servers of broad interest to the general readership of the journal. The database/server must be freely available to the academic community. The journal has set some limits on the length of the database/server. The journal requires that database/server articles should have less than 5000 words including title, abstract, legends, acknowledgements and references, a maximum of 3 displayed items (figures or tables) that in total will occupy less than one and a half (1 1/2) printed pages, and less than 50 references. Additional details required to implement the new method must be provided as Supplemental Material. Normally, the title of the paper will start with the database/server name. If the requirement to start with a name is not appropriate, please consult with the journal. On submission, the authors must in their covering letter identify any previous publications reporting this (or a closely related) database/server and explain why this paper presents a substantial advance. Related databases/servers must be reported and referenced in the article.

**Fast Track** articles are only available to authors whose paper is in a highly competitive field and facing direct competition. You must include a statement in your cover letter to justify the need for fast-track. Fast-track papers will be examined immediately and require prior approval by the editorial board before they are sent for peer-review. You do not need to contact an Editor directly prior to submitting, but we highly recommend it to expedite the handling of your submission. You should provide prior reviewer reports and the name of the journal(s) from which your paper was rejected. **Junior Investigators** have priority to be fast-tracked.

**Contact details for submission**
Please submit your manuscript for the Journal of Molecular Biology via the web site at [https://www.editorialmanager.com/jmb](https://www.editorialmanager.com/jmb). If you are unable to provide an electronic version of your paper, please contact the Editorial Office prior to submission (email: jmb@elsevier.com).

**BEFORE YOU BEGIN**

**Ethics in publishing**
Please see our information on Ethics in publishing.

**Declaration of interest**
All authors must disclose any financial and personal relationships with other people or organizations that could inappropriately influence (bias) their work. Examples of potential competing interests include employment, consultancies, stock ownership, honoraria, paid expert testimony, patent applications/registrations, and grants or other funding. Authors must disclose any interests in two places: 1. A summary declaration of interest statement in the title page file (if double anonymized) or the manuscript file (if single anonymized). If there are no interests to declare then please state this: 'Declarations of interest: none'. 2. Detailed disclosures as part of a separate Declaration of Interest form, which forms part of the journal's official records. It is important for potential interests to be declared in both places and that the information matches. More information.
**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 originality, your article may be checked by the originality detection service Crossref Similarity Check.

**Preprints**
Authors are required to disclose in their cover letter if their manuscript has been previously posted on a preprint server.

Please note that preprints deposited on SSRN, bioRxiv or other servers can be shared anywhere at any time, in line with Elsevier's sharing policy. Sharing your preprints e.g. on a preprint server will not count as prior publication (see 'Multiple, redundant or concurrent publication' for more information).

**Preprint posting on SSRN**
In support of Open Science, this journal offers its authors a free preprint posting service. Preprints provide early registration and dissemination of your research, which facilitates early citations and collaboration.

During submission to Editorial Manager, you can choose to release your manuscript publicly as a preprint on the preprint server SSRN. Your choice will have no effect on the editorial process or outcome with the journal. Please note that the corresponding author is expected to seek approval from all co-authors before agreeing to release the manuscript publicly on SSRN.

You will be notified via email when your preprint is posted online and a Digital Object Identifier (DOI) is assigned. Your preprint will remain globally available free to read whether the journal accepts or rejects your manuscript.

For more information about posting to SSRN, please consult the SSRN Terms of Use and FAQs.

**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.

**Author contributions**
For transparency, we encourage authors to submit an author statement file outlining their individual contributions to the paper using the relevant CRediT roles: Conceptualization; Data curation; Formal analysis; Funding acquisition; Investigation; Methodology; Project administration; Resources; Software; Supervision; Validation; Visualization; Roles/Writing - original draft; Writing - review & editing. Authorship statements should be formatted with the names of authors first and CRediT role(s) following. More details and an example.
**Authorship**
All authors should have made substantial contributions to all of the following: (1) the conception and design of the study, or acquisition of data, or analysis and interpretation of data, (2) drafting the article or revising it critically for important intellectual content, (3) final approval of the version to be submitted.

**Changes to authorship**
Authors are expected to consider carefully the list and order of authors before submitting their manuscript and provide the definitive list of authors at the time of the original submission. Any addition, deletion or rearrangement of author names in the authorship list should be made only before the manuscript has been accepted and only if approved by the journal Editor. To request such a change, the Editor must receive the following from the corresponding author: (a) the reason for the change in author list and (b) written confirmation (e-mail, 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.

Only in exceptional circumstances will the Editor consider the addition, deletion or rearrangement of authors after the manuscript has been accepted. While the Editor considers the request, publication of the manuscript will be suspended. If the manuscript has already been published in an online issue, any requests approved by the Editor will result in a corrigendum.

**Article transfer service**
This journal is part of our Article Transfer Service. This means that if the Editor feels your article is more suitable in one of our other participating journals, then you may be asked to consider transferring the article to one of those. If you agree, your article will be transferred automatically on your behalf with no need to reformat. Please note that your article will be reviewed again by the new journal. More information.

**Copyright**
Upon acceptance of an article, authors will be asked to complete a 'Journal Publishing Agreement' (see more information on this). An e-mail will be sent to the corresponding author confirming receipt of the manuscript together with a 'Journal Publishing Agreement' form or a link to the online version of this agreement.

Subscribers may reproduce tables of contents or prepare lists of articles including abstracts for internal circulation within their institutions. Permission of the Publisher is required for resale or distribution outside the institution and for all other derivative works, including compilations and translations. If excerpts from other copyrighted works are included, the author(s) must obtain written permission from the copyright owners and credit the source(s) in the article. Elsevier has preprinted forms for use by authors in these cases.

For gold open access articles: Upon acceptance of an article, authors will be asked to complete a 'License Agreement' (more information). Permitted third party reuse of gold open access articles is determined by the author's choice of user license.

**Author rights**
As an author you (or your employer or institution) have certain rights to reuse your work. More information.

**Elsevier supports responsible sharing**
Find out how you can share your research published in Elsevier journals.

**Open access**
Please visit our Open Access page from the Journal Homepage 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 Author Services.

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.

PREPARATION

Queries
For questions about the editorial process (including the status of manuscripts under review) or for technical support on submissions, please visit our Support Center.

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.

In their cover letter, authors are encouraged to recommend an Associate Editor and one or more board members to handle their paper.

Authors are asked to suggest 6 expert referees. Where appropriate, authors should suggest 2 to 3 referees who are expert in the methodology as well as 2 to 3 referees who are expert on the biological system. Authors should avoid suggesting as referees people who, within the past 3 years, they have had a collaborative relationship, have mentored, or have been mentored by.

In rare instances, authors may also request that conflicted individuals be excluded from the review process. However, the editors reserve the right to choose as referees individuals who in their opinion are best qualified to review the paper.

Use of word processing software
It is important that the file be saved in the native format of the word processor used. The text should be in single-column format. Keep the layout of the text as simple as possible. Most formatting codes will be removed and replaced on processing the article. In particular, do not use the word processor's options to justify text or to hyphenate words. However, do use bold face, italics, subscripts, superscripts etc. When preparing tables, if you are using a table grid, use only one grid for each individual table and not a grid for each row. If no grid is used, use tabs, not spaces, to align columns. The electronic text should be prepared in a way very similar to that of conventional manuscripts (see also the Guide to Publishing with Elsevier). Note that source files of figures, tables and text graphics will be required whether or not you embed your figures in the text. See also the section on Electronic artwork.

To avoid unnecessary errors you are strongly advised to use the 'spell-check' and 'grammar-check' functions of your word processor.

Submission checklist
The following list will be useful during the final checking of an article prior to finalizing your submission at the journal's website (https://www.editorialmanager.com/JMB). Please consult this Guide for Authors for further details of any item.

Ensure that the single, complete PDF file contains, in the following order:

Cover letter Graphical Abstract Highlights Title page Abstract (and Keywords) Marked manuscript (optional for Revisions) Manuscript References Figure captions Tables Figures
Please make sure that:

Your manuscript has been checked for correct spelling and grammar. References are in the correct format for the journal. All references mentioned in the Reference list are cited in the text, in correct order. Permission has been obtained for use of copyrighted material from other sources.

For any other information please visit our customer support site at https://service.elsevier.com

**Article Structure and Subdivisions**

Manuscripts should be submitted as a word processing file, with one-inch margins and double-spaced lines.

The conventions used in current issues of the Journal for headings, references etc. should be used in preparing manuscripts. **Articles, Methods Notes and Databases/Web Servers are divided into sections in the following order: Introduction; Results; Discussion; Materials and Methods.** Other section headings (e.g., Theory, Results and Discussion) may be used if this improves the clarity of presentation. **Communications** should not be divided into sections but should include topic headings where appropriate.

**Cover letter**

Each manuscript is to be accompanied by an electronic cover letter outlining the basic findings of the paper, their significance, and the compatibility of the paper with the journal's scope. The authors are asked to suggest 6 referees and may also suggest a handling editor from the journal's editorial board (please consult the section **Peer Review**).

**Revision notes (required for Revisions)**

The authors should provide a separate **Revision Notes** file for revisions. The file should include a point-by-point response to each reviewer's comments, which the authors have received alongside the initial decision letter from the handling editor. Revision notes should clearly state the revisions the authors made to the manuscript, preferably including the subdivision title and page/line numbers to indicate where the manuscript has been edited.

**Graphical abstract**

A Graphical abstract is required for this journal and should summarize the contents of the article in a concise, pictorial form designed to capture the attention of a wide readership online. Authors must provide images that clearly represent the work described in the article. A Graphical Abstract should as much as possible provide a visual indication of the context of the results depicted and should contain simple labels.

Specifications: The maximum size of the image should be 200(H) x 500(W) pixels with a minimum resolution of 300 dpi, using Arial font with a size of 10-16 points; Preferred file types: TIFF, EPS, PDF or MS Office files.

Preparation Guidelines: A Graphical Abstract should be one image and should not contain multiple panels; visualize one process or make one point clear; for ease of browsing, images should have a clear start and end, preferably ‘reading’ from top to bottom or left to right. No additional text, outline or synopsis should be included. Any text or label must be part of the image file. Graphical Abstracts should be submitted as a separate file in the online submission system. Graphical Abstracts can be uploaded in Editorial Manager by selecting "Graphical Abstract" from the drop-down list when uploading files.

In case of Review or Perspective articles, you may reuse one of your figures as graphical abstract.

The graphical abstract will be displayed in online search result lists, the Contents List and the online article, but will not appear in the article PDF file or print.

**Highlights**

Highlights are required for this journal. Specifications: include 3 to 5 bullet points (max. 85 characters per bullet point including spaces); only the core results of the paper should be covered. The first bullet point should state the background or context of the question. One to three bullet points should...
describe the principal results. The last bullet point should conclude on a clear description of the conceptual advance and significance of the work. Highlights should be submitted as a separate file in Editorial Manager by selecting 'Highlights' from the drop-down list when uploading files.

In case of Review or Perspective articles, simply state in a few bullet points the main points you are discussing. This will help the readers to easily grasp the content.

Highlights will be displayed in online search result lists, the contents List and in the online article, but will not appear in the article PDF file or print.

**Title page**
The title page should include the title, author names and affiliations, corresponding author information, and the present/permanent address of the researchers.

**Title.** The title should convey the concept and the importance of the paper to non-specialist readers. Titles may occupy no more than three lines of type. Each line should contain no more than 50 characters, including spaces. Titles are often used in information-retrieval systems. Avoid abbreviations and formulae where possible.

**Author names and affiliations.** Where the family name may be ambiguous (e.g., a double name), please indicate this clearly. Present the authors' affiliation addresses (where the actual work was done) below the names. Indicate all affiliations with a lower-case superscript letter immediately after the author's name and in front of the appropriate address. Provide the full postal address of each affiliation, including the country name, and, if available, the e-mail address of each author.

**Corresponding author.** Clearly indicate who will handle correspondence at all stages of refereeing and publication, also post-publication. Ensure that telephone numbers (with country and area code) are provided in addition to the e-mail address and the complete postal address.

**Present/permanent address.** If an author has moved since the work described in the article was done, or was visiting at the time, a "Present address" (or "Permanent address") may be indicated as a footnote to that author's name. The address at which the author actually did the work must be retained as the main, affiliation address. Superscript Arabic numerals are used for such footnotes.

All pages should be numbered serially.

**Abstract**
The abstract must be concise (limit of 250 words) and factual. It should convey the concept and the importance of the paper to non-specialist readers. The abstract should state briefly the background of the question, the principal results and conclude on a clear description of the conceptual advance and significance of the work. Detailed descriptions of the study or of the findings should not be included in the abstract. An abstract is required for all papers; the abstract for Brevia should be limited to 100 words whereas the abstract of Methods Notes, Databases and Servers should be limited to 150 words.

An abstract is often presented separately from the article, so must be able to stand alone. 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**
Authors should supply five keywords after the Abstract. Keywords should not be words from the title.

**Abbreviations**
Define non-standard abbreviations in a footnote to be placed on the first page of the article. Abbreviations that are unavoidable in the abstract must be defined at their first mention there, as well as in the footnote. Ensure consistency of abbreviations throughout the article.

**Marked manuscript (optional for Revisions)**
The authors may choose to provide an additional Marked Manuscript file, where the portions of the manuscript which have been edited during revision are highlighted or marked by the word processing software. The authors should make sure that the Marked Manuscript and the responses made in Revision Notes thoroughly match and are justified accordingly.
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.

Materials and methods
Provide sufficient detail to allow the work to be reproduced. Methods already published should be indicated by a reference: only relevant modifications should be described.

Accession numbers
Accession numbers must be cited immediately following the Materials and Methods section. Accession numbers are unique identifiers in bioinformatics allocated to nucleotide and protein sequences to allow tracking of different versions of that sequence record and the associated sequence in a data repository [e.g., databases at the National Center for Biotechnical Information (NCBI) at the National Library of Medicine (‘GenBank’) and the Worldwide Protein Data Bank]. There are different types of accession numbers in use based on the type of sequence cited, each of which uses a different coding. Authors should explicitly mention the type of accession number together with the actual number, bearing in mind that an error in a letter or number can result in a dead link in the online version of the article. Please use the following format: accession number type ID: xxxx (e.g., MMDB ID: 12345; PDB ID: 1TUP). Note that in the final version of the electronic copy, accession numbers will be linked to the appropriate database, enabling readers to go directly to that source from the article.

For each and every accession number cited in an article, authors should type the accession number in bold, underlined text. Letters in the accession number should always be capitalised.

Example 1: "GenBank accession nos. AI631510, AI631511, AI632198, and BF223228, a B-cell tumor from a chronic lymphatic leukemia (GenBank accession no. BE675048, and a T-cell lymphoma (GenBank accession no. AA361117)."

Glossary
Please supply, as a separate list, the definitions of field-specific terms used in your article.

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

Footnotes
Footnotes should be used sparingly. Designate them throughout the article, using an asterisk (*). Many wordprocessors build footnotes into the text, and this feature may be used. Should this not be the case, indicate the position of footnotes in the text and present the footnotes themselves separately at the end of the article. Do not include footnotes in the Reference list.

References
Reference style
References should be listed at the end of the manuscript. They should be listed in the order in which they appear in the text, tables, and figure legends and numbered sequentially. When cited in the text, reference numbers should be given in square brackets. Only papers that have been published or accepted should be cited in the reference list (see suggestion for preprints). All the authors' surnames and initials, year of the article (in parenthesis), title of the article, journal title (abbreviated and italicized), the volume number, and first and last pages should be cited.

Examples:

For articles which use Article Numbering (introduced from Volume 432, Issue 24 in December 2020):

For all articles which have page numbers:


Articles in books should include the title of the article, the name of the book, editor(s), edition number, first and last page numbers, the name and the location of the publisher, e.g.:


Posted preprints may be included in the Reference list with appropriate identification of the object type (e.g. Preprint) and the Digital Object Identifier (DOI).


Reference management software

Most Elsevier journals have their reference template available in many of the most popular reference management software products. These include all products that support Citation Style Language styles, such as Mendeley or EndNote. Using citation plug-ins from these products, authors only need to select the appropriate journal template when preparing their article, after which citations and bibliographies will be automatically formatted in the journal’s style. If no template is yet available for this journal, please follow the format of the sample references and citations as shown in this Guide. If you use reference management software, please ensure that you remove all field codes before submitting the electronic manuscript. More information on how to remove field codes from different reference management software.

Citation in text

Please ensure that every reference cited in the text is also present in the reference list (and vice versa). 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 and a copy of the title page of the relevant article must be submitted.

Web references

As a minimum, the full URL should be given. Any further information, if known (DOI, author names, dates, reference to a source publication, etc.), should also be given. Reference to material which is available on the Internet but has not been published elsewhere should be made in the text only and should not be included in the reference list.

Data references

This journal encourages you to cite underlying or relevant datasets in your manuscript by citing them in your text and including a data reference in your Reference List. Data references should include the following elements: author name(s), dataset title, data repository, version (where available), year, and global persistent identifier. Add [dataset] immediately before the reference so we can properly identify it as a data reference. The [dataset] identifier will not appear in your published article.

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.
Figures and Artwork

Figures and figure captions
Ensure that you include lower resolution figures in your Manuscript Word file and place a caption below each 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. This is designed to help the reviewers evaluate your work more efficiently.

When you are ready to submit your revised manuscript, please make sure you also upload ALL your figures as individual high resolution files. These will be used to format the final version of your paper.

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.
• Size the illustrations close to the desired dimensions of the published version.
• Provide captions next to each illustration.
A detailed guide on electronic artwork is available on our website: https://www.elsevier.com/artworkinstructions.

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.
For any other application, please convert the images to:
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.

Composite figures. In general, no more than four sections should appear in a single figure. If more than four sections are required, it is better to create several separate figures. Label individual sections in composite figures clearly with lower case letters, using (a), (b), (c).

Stereo pairs. Stereo pairs should be in divergent (wall-eye) view and should be supplied at the same size as they are to appear in the Journal. Before submitting figures, authors should check carefully that stereo figures are correct and give the proper stereo image.

Color artwork
Please make sure that artwork files are in an acceptable format (TIFF, EPS 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 on the Web (e.g., ScienceDirect and other sites) in addition to color reproduction in print. For further information on the preparation of electronic artwork, please see https://www.elsevier.com/artworkinstructions.

Journal abbreviations source
SI units and the system of abbreviations and symbols formulated by the IUPAC-IUB Combined Commission on Biochemical Nomenclature should be followed. When non-SI units are used, their equivalent SI units should be given. Genetic names should be described according to the appropriate conventions. Genus and species names should be written in full at first use and in italics (e.g., Escherichia coli, Caenorhabditis elegans).
**Data visualization**
Include interactive data visualizations in your publication and let your readers interact and engage more closely with your research. Follow the instructions [here](#) to find out about available data visualization options and how to include them with your article.

**Supplemental data**
The acceptance of supplemental material is at the Editor’s discretion. Supplemental information must be submitted with the manuscript for review by the editor and referees. Manuscripts must be complete and stand-alone. Supplemental material should complement the printed paper and may include figures and figure legends, tables, supporting data, sequence alignments, primers, derivation of equations, and videos. The availability of supplemental information will be indicated in the printed paper and the supplemental data will be directly linked to the online version of the paper. Reference to the supplemental information may be made at appropriate places in the text.

With the exception of videos, the supplemental information must be submitted electronically in the form of a single PDF file. Very large tabulations of supporting data may be submitted as Microsoft Excel files.

To ensure that the majority of potential users are able to access, view and playback the data, Elsevier recommends the submission of material in the specified ‘preferred’ formats.

**Audio**

1. **Format**
   - MP3
2. **Extension**
   - MP3
3. **Details**
   - MPEG-1 or MPEG-2 format required; highest possible quality required; audio bit rate at least 128 kbps

**Video**

1. **Format**
   - MP4
2. **Extension**
   - MP4
3. **Details**
   - Preferred video format; H.264+AAC, max target 720p MPG
   - MPG Acceptable video format; MPEG-1 or MPEG-2 format required; highest possible quality required
   - Apple QuickTime MOV Acceptable video format
   - Microsoft Audio/Video Interlaced AVI Acceptable video format
   - Compuserve GIF Expected to be non-photographic animation-based data

**Research data**
This journal encourages and enables you to share data that supports your research publication where appropriate, and enables you to interlink the data with your published articles. Research data refers to the results of observations or experimentation that validate research findings. To facilitate reproducibility and data reuse, this journal also encourages you to share your software, code, models, algorithms, protocols, methods and other useful materials related to the project.

Below are a number of ways in which you can associate data with your article or make a statement about the availability of your data when submitting your manuscript. If you are sharing data in one of these ways, you are encouraged to cite the data in your manuscript and reference list. Please refer to the "References" section for more information about data citation. For more information on depositing, sharing and using research data and other relevant research materials, visit the research data page.

**Data linking**
If you have made your research data available in a data repository, you can link your article directly to the dataset. Elsevier collaborates with a number of repositories to link articles on ScienceDirect with relevant repositories, giving readers access to underlying data that gives them a better understanding of the research described.

There are different ways to link your datasets to your article. When available, you can directly link your dataset to your article by providing the relevant information in the submission system. For more information, visit the database linking page.

For supported data repositories a repository banner will automatically appear next to your published article on ScienceDirect.
In addition, you can link to relevant data or entities through identifiers within the text of your manuscript, using the following format: Database: xxxx (e.g., TAIR: AT1G01020; CCDC: 734053; PDB: 1XFN).

**Mendeley Data**

This journal supports Mendeley Data, enabling you to deposit any research data (including raw and processed data, video, code, software, algorithms, protocols, and methods) associated with your manuscript in a free-to-use, open access repository. During the submission process, after uploading your manuscript, you will have the opportunity to upload your relevant datasets directly to Mendeley Data. The datasets will be listed and directly accessible to readers next to your published article online.

For more information, visit the Mendeley Data for journals page.

**Data in Brief**

You have the option of converting any or all parts of your supplementary or additional raw data into a data article published in Data in Brief. A data article is a new kind of article that ensures that your data are actively reviewed, curated, formatted, indexed, given a DOI and made publicly available to all upon publication (watch this video describing the benefits of publishing your data in Data in Brief). You are encouraged to submit your data article for Data in Brief as an additional item directly alongside the revised version of your manuscript. If your research article is accepted, your data article will automatically be transferred over to Data in Brief where it will be editorially reviewed, published open access and linked to your research article on ScienceDirect. Please note an open access fee is payable for publication in Data in Brief. Full details can be found on the Data in Brief website. Please use this template to write your Data in Brief data article.

**Data statement**

To foster transparency, we encourage you to state the availability of your data in your submission. This may be a requirement of your funding body or institution. If your data is unavailable to access or unsuitable to post, you will have the opportunity to indicate why during the submission process, for example by stating that the research data is confidential. The statement will appear with your published article on ScienceDirect. For more information, visit the Data Statement page.

**Additional information**

**Suggestions for cover illustrations.**

Cover illustrations should illustrate a key point raised by the paper and be immediately recognizable. The authors are encouraged to propose original covers that represent their work in a symbolic and creative manner. Please consult the journal’s Cover Gallery for recent examples. The specifications required for the cover are: W 213 mm x H 286 mm. The resolution should be 300 dpi minimum in JPEG or GIF formats. A short descriptive legend should be supplied including any authorship references. The legend should be no longer than a couple of sentences and usually supplies information about the general topic rather than detailed information about the figure. If your cover is selected as the most appealing among other suggested covers we receive, it could be chosen as the cover of the same issue as your manuscript or one of the following issues.

**AFTER ACCEPTANCE**

**Online proof correction**

To ensure a fast publication process of the article, we kindly ask authors to provide us with their proof corrections within two days. Corresponding authors will receive an e-mail with a link to our online proofing system, allowing annotation and correction of proofs online. The environment is similar to MS Word: in addition to editing text, you can also comment on figures/tables and answer questions from the Copy Editor. Web-based proofing provides a faster and less error-prone process by allowing you to directly type your corrections, eliminating the potential introduction of errors. If preferred, you can still choose to annotate and upload your edits on the PDF version. All instructions for proofing will be given in the e-mail we send to authors, including alternative methods to the online version and PDF.

We will do everything possible to get your article published quickly and accurately. Please use this proof only for checking the typesetting, editing, completeness and correctness of the text, tables and figures. Significant changes to the article as accepted for publication will only be considered at this
stage with permission from the Editor. It is important to ensure that all corrections are sent back to us in one communication. Please check carefully before replying, as inclusion of any subsequent corrections cannot be guaranteed. Proofreading is solely your responsibility.

**Offprints**
The corresponding author will, at no cost, receive a customized Share Link providing 50 days free access to the final published version of the article on ScienceDirect. The Share Link can be used for sharing the article via any communication channel, including email and social media. For an extra charge, paper offprints can be ordered via the offprint order form which is sent once the article is accepted for publication. Both corresponding and co-authors may order offprints at any time via Elsevier's Author Services. Corresponding authors who have published their article gold open access do not receive a Share Link as their final published version of the article is available open access on ScienceDirect and can be shared through the article DOI link.

**Increasing discoverability of your work**
Title, keywords, abstract but also metadata, image and video descriptions are crucial for search-engine optimisation. Please read these tips on how to optimize the discoverability of your work. In summary:

Choose your keywords carefully
Make your title short and relevant
Repeat keywords in your abstract and throughout the article
Caption everything
Use subheadings
Link as much as possible

We encourage you to Tweet about your work and include @JMolBiol. We will share it further!

**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