DESCRIPTION

*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 Transcription, protein folding, chaperones, protein degradation and quality control

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INTRODUCTION

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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 Processing and function of biologically important macromolecules and complexes Molecular basis of disease Post-translational modifications, proteomics Nuclear organization Post-translational modifications, proteomics RNA processing, structure and functions of non-coding RNAs, transcription Sorting, spatiotemporal organization, trafficking 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.

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(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.

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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.
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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.

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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.

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**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. The Journal does not publish editorial correspondence concerning published peer-reviewed research articles.

**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...
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Brevia are brief notes that report a specific well-documented result. Brevia are limited to a single
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in total will occupy less than one and a half (1 1/2) printed pages, and less than 50 references.
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Normally, the title of the paper will start with the database/server name. If the requirement to start
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