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ISSN: 0022-2836

### DESCRIPTION

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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: DNA replication, repair and recombination, gene expression, epigenetics and chromatin structure and function, RNA processing, functions of non coding RNAs, transcription Structure, chemistry, processing and function of biologically important macromolecules and complexes Biomolecular interactions, systems biology Computational biology Translation, protein folding, processing and degradation Sorting, spatiotemporal organization, trafficking, signal transduction and intracellular signalling Membrane processes, cell surface proteins and cell-cell interactions Molecular basis of disease Methodological advances, both experimental and theoretical, including databases

### AUDIENCE

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Molecular biologists, biochemists, structural biochemists, geneticists, virologists and cell biologists  
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### INTRODUCTION

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Research areas include but are not limited to: DNA replication, repair and recombination, gene expression, epigenetics and chromatin structure and function, RNA processing, functions of non coding RNAs, transcription Structure, chemistry, processing and function of biologically important macromolecules and complexes Biomolecular interactions, systems biology Computational biology Translation, protein folding, processing and degradation Sorting, spatiotemporal organization, trafficking, signal transduction and intracellular signaling Membrane processes, cell surface proteins and cell-cell interactions Molecular basis of disease Methodological advances, both experimental and theoretical, including databases

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

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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 should indicate a suitable Editor to whom the paper could be allocated. However, the *Journal* reserves the right to reallocate manuscripts to the most appropriate Editor.

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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.

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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.

(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.

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### **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.bmrwisc.edu>). 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.

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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](http://www.elsevier.com/3DMolecularModels).

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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.**

**Articles** should normally be no longer than 15 printed pages with no more than 10 figures and four tables.

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## **PREPARATION**

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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: <http://www.elsevier.com/guidepublication>). 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.

### **Article structure**

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

### **Subdivision**

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.

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