# JOURNAL OF STRUCTURAL BIOLOGY

AUTHOR INFORMATION PACK

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## DESCRIPTION

The *Journal of Structural Biology* publishes papers dealing with the **structural** analysis of living material at every level of organization by all methods that lead to an understanding of **biological** function in terms of **molecular** and **supermolecular structure**.

Techniques covered include:

- Light microscopy including confocal microscopy
- All types of electron microscopy
- X-ray diffraction
- Nuclear magnetic resonance
- Scanning force microscopy, scanning probe microscopy, and tunneling microscopy
- Digital image processing
- Computational insights into structure

The field covered by the journal extends from the structural organization of cells and tissues, their membranes, compartments, organelles and supramolecular assemblies, to the structure and conformation of proteins and nucleic acids from the molecular to the atomic level. !!! Important information for NIH authors !!!

## AUDIENCE

Biochemists, crystallographers, cell biologists, structural biologists

## IMPACT FACTOR

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# GUIDE FOR AUTHORS

## INTRODUCTION

The ***Journal of Structural Biology*** (J. Struct. Biol., JSB) publishes papers dealing with the structural analysis of biological matter at all levels of organization and the functional connotations of such observations. The field covered by the journal extends from individual macromolecules to cells and tissues with emphasis on the supramolecular (e.g. complexes and machines) and subcellular (e.g., membranes, compartments, cytoskeleton) levels of the structural hierarchy.

Novel applications of and methodological innovations in electron microscopy, X-ray diffraction, probe microscopy, and light microscopy as well as aspects of computational biology image processing, bioinformatics and structural prediction, and other biophysical techniques yielding structural information are of interest to the journal. In the context of structural cell biology, papers dealing with cellular architecture and dynamics are particularly welcomed. We see biomineralization as an important emerging area.

Preference will be given to research that correlates structural results with functional, biochemical, biophysical, immunological, or genetic data on the system under study. Purely descriptive contributions should deal with the discovery of novel structural entities of biological significance or novel insights from innovative imaging modalities. A limited number of reviews (usually invited) will be published to keep the reader abreast of recent progress in the various fields of structural biology and advances in methodology.

### *Structural Data*

For papers describing high-resolution structures of biological macromolecules, the coordinates and the related experimental data (structure factor amplitudes/intensities, NMR restraints, density maps obtained by electron microscopy) must be deposited at a member site of the Worldwide Protein Data Bank (http://deposit-next.wwpdb.org/deposition/): RCSB PDB, MSD-EBI, PDBj, BMRB, or EMDB. Similarly, for structures described at intermediate resolution, density maps obtained by electron microscopy or electron tomography must be deposited at EMDB. Manuscripts must carry a statement that coordinates and the supporting experimental data 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. For molecular structures obtained by computational modeling, with or without other constraints applied, authors must provide PDB-format coordinate sets as supplementary material. For simulations of macromolecular dynamics, authors must provide final PDB-format coordinate sets for each system simulated as supplementary material.

It is increasingly common for coordinates to be deposited in the Protein Data Bank without an associated publication. Before submission to JSB, 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 JSB. The primary criteria for publication of a structure in JSB are that it provides novel structural insights or important new functional and biological insights that are likely to be of general interest.

### *Crystallization Notes, Technical Notes and Structure Reports*

In addition to regular full-length papers reporting crystal structures and novel methods and/or mechanisms of crystallization, the *Journal of Structural Biology* publishes three kinds of short communications - Crystallization Notes, Technical Notes and Structure Reports.

The primary consideration for eligibility as a Crystallization Note is that the observations reported should have sufficient significance and originality to merit publication separate from the structure. That significance/originality should be described in the letter of submission. At least one of the following criteria must apply:
i. significant novelty in crystallization method or expression strategy;
ii. crystals of a membrane protein or large macromolecular complex;
iii. 2D crystals (planar or helical/tubular) for EM analysis;
iv. other significant novelty.

For studies in which expression and crystallization have resulted from application of standard procedures, this information is more appropriately reported in the Materials and Methods section of the paper describing structure.

A Technical Note is similar to a Crystallization Note in format and length and gives a succinct description of a major methodological innovation in a domain other than crystallization.

Structure Reports concisely document macromolecular crystal structures, including those emanating from structural genomics. Where no biological role is yet determined, these reports can be presented without such connections. In addition to appropriate quality of the reported structure, it is essential that the procedures used to prepare the protein and to determine the structure should be repeatable with the information provided. The manuscript should begin by describing the source of the protein, the means used to screen for or devise crystallization conditions, and the crystallization procedures and conditions and should include a table with the information listed in Table A.

A Crystallization Note, Technical Note or Structure Report should consist of an abstract, a single passage of text that should not be divided into sections labeled Introduction, Results, etc., but which may include declarative subtitles, and a brief References section, and should not exceed four printed pages (Crystallization Note or Technical Note) or five printed pages (Structure Report) including figures (1 page ~ 900 words/5000 characters). For a paper submitted in one of these three categories, the letter of submission should include a calculation of its length (Number of column-inches for Figures word count).

For 3D crystals, crystal quality should be demonstrated with a crystal photograph as well as the diffraction data used to determine the unit cell parameters and space group symmetry. These data may be given in the form of a table summarizing the data collection statistics and/or precession photographs or pseudo-precession photographs generated from the diffraction data. These data will be reviewed but not necessarily included in the final publication. 2D crystals or helical filaments suitable for analysis by electron microscopy and/or electron crystallography should be documented by optical or computed diffractograms of electron diffractograms and, when possible, by filtered 2D projection images.

### *Minireviews*

JSB will publish minireviews describing emerging concepts, important methodological advances, and research hypotheses on topics related to the journal's sphere of interest (see above). Including graphics, a minreview should be approximately four pages. Minireviews will be subject to the same review process as regular papers. Topics, including a summary of 1-2 paragraphs, may be proposed to either editor.

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The *Journal of Structural Biology* Paper of the Year Award is conferred annually and consists of a cash prize of $1000 and an award certificate. The recipient should be a young scientist (graduate student or postdoctoral fellow) who has been first author or co-first author of a paper that appeared in JSB in the preceding three years or who had that status (graduate student or fellow) at the time the published work was done. Nominations can be made by any reader. A nomination, not exceeding 300 words, should consist of a statement of the particular merit of the paper and should be sent by e-mail to jsb@elsevier.com. The cutoff date for nominations in any year is 31 December. An unsuccessful nomination will remain eligible in the following years, subject to the three-year limitation.

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Strunk Jr., W., White, E.B., 2000. The Elements of Style, fourth ed. Longman, New York.
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Mettam, G.R., Adams, L.B., 2009. How to prepare an electronic version of your article, in: Jones, B.S., Smith , R.Z. (Eds.), Introduction to the Electronic Age. E-Publishing Inc., New York, pp. 281–304.

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