

Nucleic Acids Research

Scope and Criteria for Consideration

Nucleic Acids Research (NAR) provides rapid publication of papers on physical, chemical, biochemical and biological aspects of nucleic acids and proteins involved in nucleic acid metabolism, interactions and/or metabolism. All manuscripts must present some novel development and meet the general criteria of originality, timeliness, significance and scientific excellence.

NAR is published online and in print. Methods, Database and Webserver papers only appear in the online version but print copies of the Database and Webserver issues are available for purchase.

The Journal publishes the following types of papers:

Standard papers. Standard papers are published both in print and online in the following subject categories:

- ***Chemistry and Synthetic Biology***
- ***Computational Biology***
- ***Gene Regulation, Chromatin, and Epigenetics***
- ***Genome Integrity, Repair, and Replication***
- ***Genomics***
- ***Molecular Biology***
- ***Nucleic Acid Enzymes***
- ***RNA***
- ***Structural Biology***

Methods papers. Significant new methods can be published in two forms:

1. As methods papers in NAR Methods Online: these papers are published online only but the titles of newly published Methods articles are included in the Table of Contents of the print edition. Methods papers are prepared in exactly the same format as Standard papers, are counted for citation by ISI and Medline and are searchable through all services, such as PubMed and the general *NAR* search page.

or

2. As part of Standard papers that primarily describe novel findings relating to important biological and chemical problems. These papers are listed in the Table of Contents under one standard subject category, and titles are annotated with an ***M***. The full text appears both online and in print.

All Methods papers are indexed in the *NAR Methods* special collection, which includes methods sub-categories (DNA characterisation, nucleic acid modification, microarray etc).

Queries regarding submission of methods papers may be directed to Dr Alan Kimmel (Email:

ark.nar@gmail.com) or Dr Georg Sczakiel (Email: nar@imm.uni-luebeck.de).

Surveys and Summaries. This section accommodates brief formal reviews relevant to nucleic acid chemistry and biology as well as other articles requiring more latitude in subject or format. Presubmission queries to Dr William Dynan are encouraged (Email: nar@mcg.edu). Surveys and Summaries appear both online and in print.

Database papers. In January each year the Journal devotes an entire online issue to biological databases. For an article to be considered, a presubmission query *must* be sent to Dr Michael Galperin by July 1 of the preceding year (Email: nardatabase@gmail.com). Special Database issue submission instructions are available at http://www.oxfordjournals.org/nar/for_authors/msprep_database.html. Papers appear online only but print copies of the Database issue are available for purchase.

Web Server papers. In July each year the Journal devotes a entire online issue to web-based software resources of value to the biological community. For an article to be considered, a presubmission query *must* be sent to Dr. Gary Benson by January 1 of the publication year (Email: narwbsrv@bu.edu). Special Web Server issue submission instructions are available at http://www.oxfordjournals.org/nar/for_authors/submission_webserver.html. Papers appear online only but print copies of the Web Server issue are available for purchase.

Criteria for Consideration

Specific criteria apply in each subject category as outlined below:

Chemistry and Synthetic Biology

The Journal encourages the submission of manuscripts describing:

- chemical synthesis or physical characterization of novel oligonucleotide analogues, where there is a potentially useful biological or structural application.
- novel chemistry applied to nucleic acids (e.g. array technology, cross-linking and modifying agents) that includes demonstration of a significant biological application.
- engineered RNA and DNA molecules (synthetic biology), particularly if they describe application of novel engineering principles or demonstrate cellular or *in vivo* effects. This includes RNAs with new regulatory functions, novel ligand binding properties, or catalytic activities.

Chemical synthesis of novel nucleoside or nucleotide analogues will not be considered unless there is a significant and potentially useful application relating to oligonucleotide or nucleic acids structure or function. Papers that describe molecules that are primarily intended for use as *in vitro* sensors are more appropriate for the Methods category.

Computational Biology

Manuscripts will only be considered if they describe new algorithms that are a substantial improvement over current applications and have direct biological relevance. The performance of such algorithms must be compared with current methods and, unless special circumstances prevail, predictions must be experimentally verified. The sensitivity and selectivity of predictions must be indicated. Manuscripts must be written so as to be understandable to biologists. The extensive use of equations should be avoided in the main text and any heavy mathematics should be presented as supplementary material. All source code must be freely available upon request.

Gene Regulation, Chromatin, and Epigenetics

The Journal encourages manuscripts that describe:

- promoters, enhancers, terminators, silencers, insulators, RNA polymerases, transcription factors and regulators, constitutive and alternative splicing, polyadenylation, editing and RNA turnover.
- novel structural or dynamic features of chromatin.
- new and general insights into mechanisms that modulate covalent modification of DNA or chromatin proteins.
- new information about DNA modifying enzymes and nucleic acid binding proteins.

For consideration, papers should provide new or generally applicable insights, with implications that extend beyond a single gene and new information about the regulation of genes involved in the synthesis, maturation, or degradation of nucleic acids. Findings must demonstrate physiological or cellular relevance to the context in which the process occurs.

Genome Integrity, Repair, and Replication

The Journal encourages manuscripts that focus on systems for the maintenance of genome integrity. In particular we encourage manuscripts that:

- report novel mechanisms for sensing and responding to DNA damage,
- characterize the structural biology of DNA damage sensors and repair enzymes,
- use novel experimental approaches or models.

Manuscripts dealing with DNA replication should provide significant new information about proteins that act by directly contacting the template.

Papers may use physical, genetic, developmental, biochemical, or cell biological approaches.

Genomics

The Journal encourages the submission of manuscripts that:

- report analyses of complete chromosomes or genomes, including comparative studies. Papers should contain complementary data with relevance to genomic organisation, transcription, RNA processing, expression, genetic analysis or other novel biology. Functional characterization of orthologs or paralogs of genes and their products will only be considered if they show novel functions or interesting new properties. Reported sequences must shed significant new light on basic questions of structural or functional interest. Reports that merely summarize information from DNA sequence database annotations, or that focus primarily on topics outside of NAR's core subject areas, are discouraged.
- report application of whole genomic approaches to the analysis of gene regulation (e.g. array and proteomic technologies, or computational methods). Such manuscripts must provide novel insights into biological problems and provide evidence to corroborate and validate hypotheses that have been generated using whole genomic approaches. Purely descriptive accounts of microarray data or sequence characterizations (data mining) that do not lead to a testable hypothesis, or experimentally tested prediction of biological function will not be considered.

Nucleic acid sequences must be deposited in a databank with a release date no later than the date of publication (see General Policies).

Molecular Biology

The Journal encourages the submission of manuscripts that relate to other physical, chemical, or biochemical, or biological characteristics of nucleic acids, which are not readily classifiable in one of the other standard paper categories.

Nucleic Acid Enzymes

The Journal encourages manuscripts that describe detailed enzymological studies of DNA and RNA polymerases, restriction enzymes and other nucleases, DNA methyltransferases and other enzymes that work directly on DNA or RNA substrates. Papers that describe restriction and modification methyltransferases with novel recognition sequences, but do not provide detailed enzymological characterization will be considered for the Methods category.

RNA

The Journal welcomes manuscripts that:

- describe the mechanisms of action, regulation, or assembly of ribosomes, snRNPs and other ribonucleoprotein particles, or other regulatory RNAs, e.g. microRNAs.
- Provide new information about the structural biology of nucleic acid binding proteins that function in RNA biogenesis, particularly if these involve new motifs.

Papers should provide novel structural or functional insights, preferably with implications extending beyond a single gene or organism. Papers that describe natural RNA transcripts (e.g. antisense RNA, miRNA) must provide evidence for their functional significance. This might include mutational data, information on differential control, or other convincing evidence of biological function.

Structural Biology

The Journal encourages manuscripts that describe significant, new, biologically relevant, structural features or principles as determined by X-ray crystallographic or NMR studies. Reports on minor variants of well-established structures are generally not suitable unless significant new insights are obtained. Manuscripts that utilise database and bioinformatics approaches must be firmly related to experimental observations. Papers that describe new biophysical and structural methods, but do not contain novel findings relating to an important biological problem, are more appropriate for the Methods category. Manuscripts that confirm structures previously obtained by other methods, or that contain only an NMR assignment, will not be considered.

Methods

Papers should report novel techniques or significant advances in existing techniques that are relevant to *NAR*'s core subject areas. These should be highly significant and useful, and contain an example of utility.

New applications of existing technologies (e.g. novel diagnostic applications of established techniques) are discouraged.

Emerging or specialized subject areas.

Microarray technology

- Manuscripts dealing with improvements in array technology or array data handling that do not include novel chemistry will be considered in the Methods category.
- Papers reporting novel modes of nucleic acid immobilisation or printing require validation

by genome-wide analyses for superiority at detection, ease of use, or cost as compared to standard approaches.

- Comparative studies among various platforms are generally not appropriate unless they provide insight beyond the conclusion that each may yield different sets of data.
- New statistical and normalisation approaches must offer increased sensitivity, discrimination, or resolution. Papers describing only combinations of standard applications are strongly discouraged.

All microarray data must conform to MIAME guidelines and be submitted to GEO or Array Express (see General Policies).

Molecular dynamics simulations

Manuscripts that describe molecular dynamics simulations will be considered only if they provide valuable insights into biological questions related to nucleic acids. Theoretical results must be put into perspective with available structural and/or biological data, although it is not always essential for them to be accompanied by experimentation. However, theoretical interpretations or speculative ideas should be experimentally testable and, if not backed up by experimental results, should constitute only a small part of the manuscript. Constraints or limitations of the simulation method or theoretical approach used should be identified and discussed. Manuscripts must be written so as to be intelligible to as wide an audience as possible and should avoid jargon and undefined terms.

Small molecule-nucleic acid interactions

The Journal encourages manuscripts describing novel aspects of molecular recognition between DNA and RNA sequences and small molecules where this is biologically relevant. This may include sequence-dependent binding, base recognition and novel recognition motifs. Manuscripts devoted to biologically relevant small molecule-nucleic acid interactions, and their potential applications, will be considered when applied to well-defined DNA or RNA sequences. Studies using emerging biophysical approaches, such as single-molecule methods, to biologically significant systems are strongly encouraged.

Nucleic acid-based delivery systems and reagents for controlling gene expression (e.g. siRNA, miRNA, antisense, ribozymes)

This includes synthetic reagents as well as the endogenous expression of agents produced from recombinant DNA. The Journal encourages manuscripts describing:

- novel nucleic acid derivatives (e.g. conjugates, chemical modifications) where there is a demonstrated significant biological effect or application
- studies that focus on the mechanisms of action of nucleic acid-based gene control reagents
- cellular delivery and intracellular release that is based on novel principles or which cast new light on cellular uptake mechanisms
- novel means for the delivery of nucleic acids including recombinant DNA that are either based on entirely new principles or which demonstrate clearly and significantly improved effectiveness in a relevant biological system.

Derivatives of existing vector systems are not appropriate, and manuscripts describing clinical applications will not be considered.

In vitro nucleic acid selection

The Journal encourages manuscripts describing *in vitro* selection of RNA or DNA or their analogues from random pools (aptamers, selex) that include substantial new information or which have novel applications relevant to nucleic acid structure or function, or to proteins that interact with nucleic acids. Manuscripts dealing primarily with significant improvements in nucleic acid selection methodology will be considered in the Methods category.

ChIP on chip and ChIP-Seq

Manuscripts using ChIP on chip and ChIP-Seq approaches to discover new biological phenomena or provide additional mechanistic insights about known transcriptional processes are encouraged. However, manuscripts that merely catalogue the genomic locations of single transcriptional regulators or chromatin marks but do not provide further biological insights are strongly discouraged. Manuscripts should ideally move beyond mere validation of the dataset. Manuscripts dealing primarily with improvements in methodology will be considered in the Methods category.