SCOPE AND CRITERIA FOR CONSIDERATION

***NAR* provides rapid publication of papers on physical, chemical, biochemical and biological aspects of nucleic acids and proteins involved in nucleic acid metabolism and/or interactions. All manuscripts must present some novel development and meet the general criteria of originality, timeliness, significance and scientific excellence.**   To download and print a PDF of the below information, please click [here](http://www.oxfordjournals.org/our_journals/nar/for_authors/scope%20and%20criteria%20for%20consideration.pdf).   *NAR* is published online and in print. Methods, Database and Webserver papers only appear online.

The Journal publishes the following types of papers:

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

Synthetic Biology and Chemistry

Computational Biology

Gene Regulation, Chromatin and Epigenetics

Genome Integrity, Repair and Replication

Genomics

Nucleic Acid Enzymes

RNA

Structural Biology

Molecular Biology

Emerging or specialized subject areas

***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, and are counted for citation by ISI and Medline. They are searchable through all services, such as PubMed and the general *NAR* search page.   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.   All Methods Online papers are subject to the same requirements regarding availability of research materials, and computational executables and/or source code as standard articles, as described for individual categories below and in 'Journal Policies'.    Or

2. As part of Standard papers that primarily report 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/](javascript:encrypt(%20'ark.nar',%20'gmail.com',%20''%20))) or Dr Georg Sczakiel (Email: [nar@imm.uni-luebeck.de](javascript:encrypt(%20'nar',%20'imm.uni-luebeck.de',%20''%20))).

***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: [wsd.nar@gmail.com](javascript:encrypt('wsd.nar',%20'gmail.com',%20''%20);)) . Surveys and Summaries appear both online and in print.

***Database articles***. In January each year the journal devotes a special 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](javascript:encrypt('nardatabase',%20'gmail.com',%20''%20))) Special Database issue submission instructions are available [here](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 articles***. In July each year the Journal devotes an 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](javascript:encrypt('narwbsrv',%20'bu.edu',%20''%20))) Special Web Server issue submission instructions are available [here](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:

***Synthetic Biology and Chemistry***  NAR encourages submission of papers describing the engineering, synthesis, delivery and application of novel nucleic acids, nucleic acid binding proteins, or their derivatives.   Examples of such studies might include:

* novel syntheses or modifications of nucleic acids or their derivatives, or nucleic acid binding proteins, that lead to a desired, beneficial effect in a biological application.
* novel methods of delivery of nucleic acids and their derivatives, or nucleic acid binding proteins, that involve new mechanisms or that demonstrate significantly improved effectiveness, especially in whole organisms.
* cellular and *in viv*o targeting applications of nucleic acids or their derivatives (such as antisense, siRNA or aptamers), or nucleic acid binding proteins, where there is a strong emphasis on understanding their mechanism of action.
* design or selection of nucleic acids, or nucleic acid binding proteins, that leads to a novel ligand binding or catalytic activity, a unique regulatory function, or the ability to selectively modify gene function. Studies that reveal novel principles of biomolecular engineering are particularly encouraged.
* studies that facilitate (i) the creation of novel materials and devices via the manipulation of individual molecules (i.e. nanotechnology development), (ii) genome engineering, and/or (iii) the creation of novel genetic and cellular circuits or systems.

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 may be considered if they fall into one of two descriptions:   1. Description of a new algorithm that represents a substantial improvement over current methodology, and that has direct biological relevance. It should be bench-marked on gold-standard datasets and ideally, be supported by experimental validation where applicable. The performance of such algorithms must be compared with current methods and the relevant statistics (e.g., sensitivity, selectivity, etc) of the performance must be indicated. Limitations of the method and general directions for future improvement should be reported. Small improvements or obvious modifications of existing algorithms will not be considered.   2. Manuscripts that primarily describe the use of existing computational methods to generate significant, novel biological information and insight. Limitations of the approach and issues that may affect the conclusions drawn must be explicitly stated. Purely descriptive 'data mining' studies, (e.g., those that computationally predict biomarkers from disease expression datasets or those that simply compile or catalogue microRNAs from published datasets without providing significant biological or mechanistic insight) are discouraged.

In either case, the manuscript must be written so as to be understandable to biologists. It should ideally report research performed on information pertaining to, or cellular processes that involve, nucleic acids. Extensive use of equations should be avoided in the main text and any detailed mathematics should be presented as supplementary material.   Availability of algorithms and code: If the manuscript describes new software tools or the implementation of novel algorithms the software must be freely available to users at the time of submission (either as executable versions for multiple, common platforms or as source code). Availability must be clearly stated in the article. Authors must ensure that the software is available for a full TWO YEARS following publication, preferably through a download link on a stable URL. Authors are strongly encouraged to make their source code available through an open source license (see [www.opensource.org](http://www.opensource.org/) for examples).   Manuscripts that describe computational methods that primarily focus on protein multi-sequence alignment algorithms, prediction of protein folds or structures, or prediction of protein-protein binding sites or affinities will not be considered by NAR (with the possible exception of papers prepared specifically for the annual NAR special issues on WebServers or Databases, as described above).

Manuscripts describing results from 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.