INSTRUCTIONS TO AUTHORS

SCOPE

Microbiology Resource Announcements® (MRA) is an online-only, fully open access journal that publishes articles announcing the availability of any microbiological resource deposited in a repository available to the community. In addition to considering genome sequences of prokaryotic and eukaryotic microbes and viruses in public databases, MRA will consider metagenomics sequences, amplicon sequence collections, metabolomics data, proteome data, culture collections, mutant libraries, plasmids and other genetic constructs, publicly available databases and software, and protocols and workflows. Manuscripts submitted to MRA will be peer reviewed for appropriate content and handled by a board of senior editors who will accept manuscripts at their discretion.

MRA will consider manuscripts that announce the resources listed below, for which we have provided instruction. Manuscripts providing an in-depth or comparative analysis of these resources will not be considered by MRA. Such manuscripts are more appropriate for other ASM journals, such as Applied and Environmental Microbiology®, mSphere®, the Journal of Bacteriology®, or the Journal of Virology®.

Genome sequences. MRA will consider papers that announce either a complete, closed genome sequence(s) or a draft whole-genome sequence(s). The manuscript should provide the provenance for the organism sequenced and a brief rationale for sequencing the particular organism, with an emphasis on the detailed methodologies and protocols used in the assembly and annotation of the genome sequence. Accession numbers associated with publicly available data, for both raw reads and assemblies, should be provided with the submission. Announcements of genome sequences, and raw data associated with them, will not be considered for publication until public availability of the sequence(s) in GenBank/ENA/DDBJ has been verified.

Metagenomics and metatranscriptomic data sets. MRA will consider papers that announce metagenomics or metatranscriptomic data sets. The manuscript should provide the source of the material and a brief rationale for the sequencing performed, with an emphasis on the detailed methodologies and protocols used in the generation of libraries, the assembly of the metagenomics or metatranscriptomic data set, and its annotation. Accession numbers associated with publicly available data, for both raw reads and assemblies, should be provided with the submission. Announcements of metagenomics or metatranscriptomic data sets will not be considered for publication until public availability of the data sets in an appropriate database has been verified.

Amplicon sequence collections. MRA will consider papers that announce amplicon data sets—that is, sequences derived from the amplification of genetic material targeting a specific locus. The collection description should provide the source of the material and should include the protocols used to generate the libraries, from extraction to amplification to sequencing. Accession numbers associated with publicly available data should be provided with the submission. Announcements of amplicon sequence collections will not be considered for publication until public availability of the data sets in an appropriate database has been verified.

Metabolomics data sets. MRA will consider papers that announce metabolomics data sets. The manuscript should describe the rationale and study design, including experimental factors, the type of analytical chemistry used to identify metabolites, and a detailed description of protocols (from sample collection and extraction to analysis and metabolite identification). Authors are encouraged to deposit their data set in a public repository such as MetaboLights, the NIH Metabolomics Workbench, or Dryad. The Metabolomics Association of North America includes these repositories along with a list of useful resources. Accession numbers associated with publicly available data should be provided with the submission. Announcements of metabolomics data sets will not be considered for publication until public availability of the data sets in an appropriate database has been verified.

Proteome data sets. MRA will consider papers that announce proteome data sets. The manuscript should describe the rationale and study design, including how samples were digested and processed, the type of chromatography used to identify proteins, and a detailed description of protocols (from sample collection and extraction to analysis and peptide identification). Authors are encouraged to deposit their data set in a public repository such as the PRIDE archive or Dryad. A helpful list of proteomics resources and repositories is available at https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2908408/table/T1/. Accession numbers associated with publicly available data should be provided with the submission. Announcements of proteome data sets will not be considered for publication until public availability of the data sets in an appropriate database has been verified.

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Databases and software. MRA will consider papers that an-

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ETHICS RESOURCES AND POLICIES

Ethics

Please refer to ASM Journals’ Ethics Resources and Policies page (https://journals.asm.org/content/ethics-and-policies) for the ethical standards expected of manuscript submissions, as well as for specific recommendations on the proper use of microbiological information, the use of human subjects or animals in research, publishing ethics (including authorship, plagiarism, and image manipulation), conflicts of interest, and availability of data and materials.

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Submission Process

All submissions to MRA must be made electronically via the eJournalPress (eJP) online submission and peer review system. (E-mailed submissions will not be accepted.) First-time users must create an Author account.

Review Process

All manuscripts are peer reviewed and considered to be confidential. Impersonation of another individual during the review process is considered serious misconduct.

To facilitate the review, each accession number reported in the manuscript must be hyperlinked to the publicly available data record. Copies of in-press and submitted manuscripts that are important for judgment of the present manuscript should be included as related manuscript files. When a manuscript is submitted to the journal, it is given a control number (e.g., MRA00123-20) and assigned to one of the editors. (Always refer to this control number in communications with the editor and the Journals Department.) From there it is assigned to at least one independent expert for peer review. A single-blind review, where authors’ identities are known to reviewers, is applied. It is the responsibility of the corresponding author to inform the coauthors of the manuscript’s status throughout the submission, review, and publication processes. The reviewers operate under strict guidelines set forth in “Reviewer Guidelines” and are expected to complete their reviews expeditiously.

The corresponding author is notified, generally within 6 to 8 weeks after submission, of the editor’s decision to accept, reject, or require modification. When modification is requested, the corresponding author must either submit the modified version within 2 months or withdraw the manuscript. A point-by-point response to the reviews must be uploaded as a separate Revision Response file. Additionally, a Miscellaneous File Not For Publication (without figures) highlighting all of the changes from the original manuscript submission must be uploaded as a separate file if the editor requested one. For the benefit of editors and reviewers assessing revisions, all changes in this file should be highlighted, no matter how minor. Please note that a manuscript may not necessarily be processed editorially until a version with all changes noted has been submitted.

Manuscripts that have been rejected with the option to resubmit, or withdrawn after being returned for modification, may be resubmitted to the same ASM journal if the major criticisms have been addressed. Manuscripts rejected with the option to resubmit may be resubmitted only once unless permission has been obtained from the original editor or the editor in chief.

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Announcements are published in weekly issues (50 issues per year). The articles from issues published in the preceding weeks are moved into the MRA archive.

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Type the manuscript double-spaced, and number all pages in sequence, including the abstract.

Manuscripts may be editorially rejected on the basis of poor English or lack of conformity to the standards set forth in these Instructions.

Authors who are unsure of proper English usage should have their manuscripts checked by someone proficient in the English language or engage a professional language editing service for help.

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If the contributing members of the group associated with the work do not fulfill the criteria of substantial contribution to and responsibility for the paper, the group may not be listed in the author byline. Instead, it and the names of its contributing members may be listed in the Acknowledgments section.

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Abstract. Limit the abstract to 50 words or fewer and concisely summarize the basic content of the paper without presenting extensive experimental details. Avoid abbreviations and references, and do not include diagrams. When it is essential to include a reference, use the format shown under “References” below (see the “Citations in abstracts” section). Because the abstract will be published separately by abstracting services, it must be complete and understandable without reference to the text.

Public availability and accession number(s). The description of how the community can access the announced resource should be provided in a separate paragraph at the end of the text, with the paragraph lead-in “Data availability.” This should include accession numbers for public repositories and Web links for software and databases. Each accession number reported in the manuscript must be hyperlinked to the publicly available data record. For culture collections that cannot be housed within a public repository, authors must provide contact information and a protocol for procuring the described strains. The resource(s) must be made publicly available before the submission will be considered for publication. Authors are encouraged to comply with community metadata standards, such as the “Minimum Information about any (X) Sequence” (MIXS) checklist, when submitting to GenBank, ENA, or DDBJ. For example, for genome sequence submissions, the accession number(s) should be reported in the following format: “Data availability.” This Whole Genome Shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. [XXXX]00000000. The version described in this paper is the first version, [XXXX]01000000.” Please also provide references (with URLs) for the accession numbers.

Acknowledgments. Statements regarding sources of direct financial support (e.g., grants, fellowships, and scholarships, etc.) should appear in the Acknowledgments. A funding statement indicating what role, if any, the funding agency had in your study (for example, “The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.”) may be included. Funding agencies may have specific wording requirements, and compliance with such requirements is the responsibility of the author. In cases in which research is not funded by any specific project grant, funders need not be listed, and the following statement may be used: “This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.” Statements regarding indirect financial support (e.g., commercial affiliations, consultancies, stock or equity interests, and patent-licensing arrangements) are also allowed. It is the responsibility of authors to provide a general statement disclosing financial or other relationships that are relevant to the study.

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in the order in which they are cited in the article. In the text,
references are cited parenthetically by number in sequential
order. Data that are not published are simply cited parenthet-
ically in the text (see section ii below).

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ing types of references must be listed in the References section:

- Journal articles (both print and online)
- Books (both print and online)
- Book chapters (publication title is required)
- Patents and patent applications
- Theses and dissertations
- Published conference proceedings
- Meeting abstracts, posters, and presentations
- Letters (to the editor)
- Company publications
- In-press journal articles, books, and book chapters
- Data sets
- Code

Provide the names of all the authors and/or editors for
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Abbreviate journal names according to the PubMed Journals
Database (National Library of Medicine, National Institutes
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sodic numbers and code/software should be provided if desired; URLs for citations of database accession
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Follow the styles shown in the examples below.

1. Caserta E, Haemig HAH, Manias DA, Tomsic J, Grundy
FJ, Henkin TM, Dunny GM. 2012. In vivo and in vitro
analyses of regulation of the pheromone-responsive prgQ
promoter by the PrgX pheromone receptor protein. J Bac-
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Vibrio cholerae ToxR downregulates virulence factor
production in response to cyclo(Phe-Pro). mBio
4. Falagas ME, Kasiakou SK. 2006. Use of international units
when dosing colistin will help decrease confusion related
to various formulations of the drug around the world. An-
timicrob Agents Chemother 50:2274–2275. (Letter.)
[“Letter” or “Letter to the editor” is allowed but not required
at the end of such an entry.]
5. Cox CS, Brown BR, Smith JC. J Gen Genet, in press.* [Ar-
ticle title is optional; journal title is mandatory.]
6. Forman MS, Valsamakis A. 2011. Specimen collection,
transport, and processing: virology, p 1276–1288. In Ver-
salovic J, Carroll KC, Jorgensen JH, Funke G, Landry ML,
Warnock DW (ed), Manual of clinical microbiology, 10th
ed, vol 2. ASM Press, Washington, DC.
7. da Costa MS, Nobre MF, Rainey FA. 2001. Genus I. Ther-
mus Brock and Freeze 1969, 295, Al, emend. Nobre, Trumper
and da Costa 1996b, 605, p 404–414. In Boone DR, Cas-
tenholz RW, Garrity GM (ed), Bergey’s manual of system-
8. Fitzgerald G, Shaw D. In Waters AE (ed), Clinical micro-
biology, in press. EFH Publishing Co, Boston, MA.*
[Chapter title is optional.]
methylotrophic bacteria, p 251–254. In Crawford RL, Hanson
RS (ed), Microbial growth on C1 compounds. Proceedings of the 4th International Symposium. Ameri-
can Society for Microbiology, Washington, DC.
Abstr 45th Intersci Conf Antimicrob Agents Chemother,
abstr D-1658. [Abstract title is optional.]
11. Smith D, Johnson C, Maier M, Maurer J. 2005. Distribu-
tion of fimbrial, plasmid and phage associated virulence
genes among poultry Salmonella enterica serovars, abstr
American Society for Microbiology, Washington, DC.
[Abstract title is optional.]
C, Vega L, Jara LJ, García-Kutzbach A, Cuellar ML,
Espinoza LR. 1996. Detection of Salmonella DNA in syno-
vial membrane and synovial fluid from Latin American
patients using the polymerase chain reaction. Arthritis
Rheum 39(Suppl 9):S185. [Meeting abstract published in
journal supplement.]
Los Angeles, CA. [Title is optional.]
manual. Stratagene, La Jolla, CA. [Use the company name
as the author if none is provided for a company publication.]
et 484,363,770. [Include the name of the patented item/
process if possible; the patent number is mandatory.]
16. Harrison F, Roberts AEL, Gabrilska R, Rumbaugh KP, Lee
C, Diggle SP. 2015. A 1,000-year-old antimicrobial remedy
with antistaphylococcal activity. mBio 6:e01129–15. [Orig-

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A reference to an in-press ASM publication should state the control number (e.g., MRA00123-20) if it is a journal article or the name of the article if it is a book.

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• Complete name of a data set, including the name of the database or repository and its URL, or the name of the analysis software (if appropriate), including the version and project,
• Publisher (if appropriate), and
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The following template may be helpful.

Author. Year. Description or title of software (version). Repository URL. Retrieved day month year. [Software or code.]

Examples follow.


Nesbitt HK, Moore JW. 2016. Data from “Species and population diversity in Pacific salmon fisheries underpin indigenous food security.” Dryad Digital Repository https://doi.org/10.5061/dryad.ng8pf. [Data set in repository.]

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. . . system was used (J. L. McInerney, A. F. Holden, and P. N. Brighton, submitted for publication).
. . . as suggested by the World Health Organization (http://www.who.int/campaigns/immunization-week/2017/en/).

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For general guidelines on creating acceptable EPS and TIFF files, refer to the KGL Digital Art Support page.

Minimum resolution. Minimum resolution is 300 dpi for all file types. All images imported into a figure file must be at the correct resolution before they are placed in the file. (For instance, placing a 72-dpi image in a 300-dpi EPS file will not result in the placed image meeting the minimum requirements for file resolution.) Note that publication quality will not be improved by using a resolution higher than the minimum.

Size. All graphics should be submitted at their intended publication size; that is, the image uploaded should be 100% of its print dimensions so that no reduction or enlargement is necessary. Resolution must be at the required level at the submitted size. Include only the significant portion of an illustration. White space must be cropped from the image, and excess space between panel labels and the image must be eliminated.

- Maximum figure width: 6.875 inches (ca. 17.4 cm)
- Maximum figure height: 9.0625 inches (23.0 cm)

Contrast. Illustrations should contain sufficient contrast to be viewed easily on a monitor or on the printed page (for reprints).

Labeling and assembly. All final lettering and labeling must be incorporated into the figure. The figure must be supplied as a separate file, and any multipanel figures must be grouped into one file; i.e., rather than uploading a separate file for each panel in a figure, assemble all panels in one piece and supply them as one file.

Fonts. To avoid font problems, set all type in one of the following fonts: Arial, Helvetica, Times Roman, European PI, Mathematical PI, or Symbol. Courier may be used but should be limited to nucleotide or amino acid sequences in which a nonproportional (monospace) font is required. All fonts must be converted to paths (or outlines) in the application with which they were created.

Color illustrations. All figures submitted in color will be processed as color. Adherence to the following guidelines will help to ensure color reproduction that is as accurate as possible.

Color illustrations should be supplied in the RGB color mode, as either (i) RGB TIFF images with a resolution of at least 300 pixels per inch (raster files, consisting of pixels) or (ii) Illustrator-compatible EPS files with RGB color elements (vector files, consisting of lines, fonts, fills, and images). For reprints, ASM’s print provider will automatically create CMYK versions of color illustrations from the supplied RGB versions. Color in the reprints may not exactly match that in the online journal of record because of the smaller range of colors capable of being reproduced by CMYK inks on a printing press.

Preparing figures for those with color vision deficiency. Based on information on color vision deficiency provided by the U.S. National Library of Medicine, we ask that you design your figures with the following considerations in mind.

- Determine whether color elements are absolutely necessary to convey the data.
• Can the data be displayed using symbols or different line thicknesses, shapes, patterns, or font types?
• Avoid the following color combinations whenever possible: red and green; yellow and bright green; light blue and pink; dark blue and violet.
• Magenta can be substituted for red in fluorescent stain images, which typically use a combination of red and green.
• Search the Internet for a color vision deficiency simulator to see how your image might appear to someone who experiences color vision deficiency.

If you have access to Adobe Photoshop or Adobe Illustrator, you can go to View/Proof Setup/Color Blindness, and your images will be transformed to show you how they will appear to someone who has color vision deficiency.

Please refer to the following website for more information: http://jfly.iam.u-tokyo.ac.jp/color/.

**Drawings.** Submit graphs, charts, complicated chemical or mathematical formulas, diagrams, and other drawings as finished products not requiring additional artwork or type-setting. All elements, including letters, numbers, and symbols, must be easily readable, and both axes of a graph must be labeled. When creating line art, please use the following guidelines:

(i) **All art must be submitted at its intended publication size.** For acceptable dimensions, see “Size” above.

(ii) **Avoid using screens (i.e., shading) in line art.** It can be difficult and time-consuming to reproduce these images without moiré patterns. Various pattern backgrounds are preferable to screens as long as the patterns are not imported from another application. If you must use images containing screens,
   (a) Generate the image at line screens of 85 lines per inch or less.
   (b) When applying multiple shades of gray, differentiate the gray levels by at least 20%.
   (iii) Use thick, solid lines that are no finer than 1 point in thickness.
   (iv) Use type that is no smaller than 6 points at the final publication size.
   (v) Avoid layering type directly over shaded or textured areas.
   (vi) Avoid the use of reversed type (white lettering on a black background).
   (vii) Avoid heavy letters, which tend to close up, and unusual symbols, which the printer may not be able to reproduce in the legend.
   (viii) If colors are used, avoid using similar shades of the same color and avoid very light colors.

**Figure Legends**

The figure legend should be placed at the end of the text file. The legend should provide enough information so that the figure is understandable without frequent reference to the text. Define all symbols used in the figure and define all abbreviations that are not used in the text.

**Tables**

The preferred format for tables is Microsoft Word; however, WordPerfect and Acrobat PDF are also acceptable. Tables should be formatted as follows. Arrange the data so that **columns of like material read down, not across.** The headings should be sufficiently clear so that the meaning of the data is understandable without reference to the text. Explanatory footnotes are acceptable, but more-extensive table “legends” are not. Tables must include enough information to warrant table format; those with fewer than six pieces of data will be incorporated into the text by the copy editor. **Table 1** is an example of a well-constructed table.

**NOMENCLATURE**

**Chemical and Biochemical Nomenclature**

The recognized authority for the names of chemical compounds is *Chemical Abstracts* (CAS) and its indexes. *The Merck Index Online* is also an excellent source. For guidelines to the use of biochemical terminology, consult *Biochemical Nomenclature and Related Documents* (Portland Press, London, United Kingdom, 1992) and the Instructions to Authors of the *Journal of Biological Chemistry* and the *Archives of Biochemistry and Biophysics*.

For enzymes, use the recommended (trivial) name assigned by the Nomenclature Committee of the International Union of Biochemistry (IUB) as described in *Enzyme Nomenclature* (Academic Press, Inc., New York, NY, 1992) and its supplements and at https://www.qmul.ac.uk/sbcs/iubmb/enzyme/. If a nonrecommended name is used, place the proper (trivial) name in parentheses at first use in the abstract and text. Use the EC number when one has been assigned. Authors of papers describing enzymological studies should review the standards of the STRENDA Commission for information required for ade-

<table>
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<th>Bacterial species*</th>
<th>Genome size (bp)</th>
<th>No. of contigs</th>
<th>N_c50</th>
<th>Total no. of genes</th>
<th>G+C content (%)</th>
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</table>

*Strain identification by ≥99% similarity with 16S rRNA and by ≥97% with the spoI, recA, and gyrB genes.*
quate description of experimental conditions and for reporting enzyme activity data.

**Nomenclature of Prokaryotes, Eukaryotes, and Viruses**

When the announcement describes the genome of a recognized bacterial species, binary names, consisting of a generic name and a specific epithet (e.g., *Saccharomyces cerevisiae*), must be used. For resources describing genome data from a species that is unculturable and cannot be maintained in a culture collection, the nomenclature “*Candidatus*” preceding the genus name is recommended. Names of categories at or above the genus level may be used alone, but specific and subspecific epithets may not. A specific epithet must be preceded by a generic name, written out in full the first time it is used in a paper. Thereafter, the generic name should be abbreviated to the initial capital letter (e.g., *S. cerevisiae*), provided there can be no confusion with other genera used in the paper. Names of all bacterial taxa (kingdoms, phyla, classes, orders, families, genera, species, and subspecies) are printed in italics and should be italicized in the manuscript; strain designations and numbers are not. The spelling of bacterial names should follow the Approved Lists of Bacterial Names (Amended) & Index of the Bacterial and Yeast Nomenclatural Changes (V. B. D. Skerman et al., ed., American Society for Microbiology, Washington, DC, 1989) and the validation lists and notification lists published in the International Journal of Systematic and Evolutionary Microbiology (formerly the International Journal of Systematic Bacteriology) since January 1989. In addition, two sites on the World Wide Web list current approved bacterial names: Prokaryotic Nomenclature Up-to-Date and List of Prokaryotic Names with Standing in Nomenclature.

Since the classification of fungi is far from complete, it is the responsibility of the author to determine the accepted binomial for a given organism. Sources for these names include *The Yeasts: a Taxonomic Study*, 5th ed. (C. P. Kurtzman, J. W. Fell, and T. Boekhout, ed., Elsevier Science, Amsterdam, Netherlands, 2011), and *Dictionary of the Fungi*, 10th ed. (P. M. Kirk, P. F. Cannon, D. W. Minter, and J. A. Stalpers, ed., CABI International, Wallingford, Oxfordshire, United Kingdom, 2008); see also [http://www.speciesfungorum.org/Names/Fundic.asp](http://www.speciesfungorum.org/Names/Fundic.asp). Names used for viruses should be those approved by the International Committee on Taxonomy of Viruses (ICTV) and reported on the ICTV Virus Taxonomy website ([https://talk.ictvonline.org/](https://talk.ictvonline.org/)). In addition, the recommendations of the ICTV regarding the use of species names should generally be followed: when the entire species is discussed as a taxonomic entity, the species name, as with other taxa, is italic and has the first letter and any proper nouns capitalized (e.g., Tobacco mosaic virus, Murray Valley encephalitis virus). When the behavior or manipulation of individual viruses is discussed, the vernacular (e.g., tobacco mosaic virus, Murray Valley encephalitis virus) should be used. If desired, synonyms may be added parenthetically when the name is first mentioned. Approved generic (or group) and family names may also be used.

Microbial strains, viruses, and plasmids should be given individual designations consisting of letters and serial numbers. It is generally advisable to include a worker’s initials or a descriptive symbol of locale or laboratory, etc., in the designation. Each new strain, mutant, isolate, or derivative should be given a new (serial) designation. This designation should be distinct from those of the genotype and phenotype, and genotypic and phenotypic symbols should not be included.

**Genetic Nomenclature**

Genetic nomenclature should essentially follow the recommendations of Demerec et al. (Genetics 54:61–76, 1966) and those given in the Instructions to Authors of the *Journal of Bacteriology*® (for prokaryotes), *Molecular and Cellular Biology*® (for eukaryotes), and the *Journal of Virology*® (for viruses). To facilitate accurate communication, it is important that standard genetic nomenclature be used whenever possible and that deviations or proposals for new naming systems be endorsed by an appropriate authoritative body. Publication of submitted manuscripts that contain new or nonstandard nomenclature may be delayed by the editor or the Journals Department so that they may be reviewed.