

APPLIED AND ENVIRONMENTAL MICROBIOLOGY

2007 INSTRUCTIONS TO AUTHORS*

SCOPE

Applied and Environmental Microbiology (AEM) publishes descriptions of all aspects of applied microbial research, basic research on microbial ecology, and research of a genetic and molecular nature that focuses on microbial topics of practical value. Research must address salient microbiological principles, fundamental microbial processes, or basic questions in applied or environmental microbiology. Topics that are considered include microbiology in relation to foods, agriculture, industry, biotechnology, public health, plants, and invertebrates and basic biological properties of bacteria, fungi, algae, protozoa, and other simple eukaryotic organisms as related to microbial ecology. Manuscripts should report new and significant findings that advance the understanding of microbiology and upon which other scientists may build.

The **microbial ecology** section covers a wide range of topics on the ecology of microorganisms, including culture-independent molecular assessments that provide new insights into (i) the structure-function relationships of microorganisms, (ii) the impact of in situ conditions on community structure, and (iii) the effect of changes in microbial community composition on ecosystem function. Archival phylogenetic snapshots that do not provide such insights are not acceptable for publication in AEM.

The **plant microbiology** section covers manuscripts dealing with all aspects of plant-microorganism interactions, including symbiotic and rhizosphere bacteria and phytopathogenic microorganisms.

New microbiological **methods** must provide novel avenues to address fundamental biological questions and will be considered for publication in AEM when accompanied by a demonstrated application. Descriptions of the application of previously described technologies, including the cloning, amplification, and expression of “foreign” genes, to a new genus or species of microbe will generally not be considered for independent publication. Manuscripts that describe the construction of engineered strains for innovative process application, development, or enhancement must present results to authenticate the utility, superiority, and uniqueness of such strains.

Manuscripts submitted to the **mycology** section should be clearly of a microbiological nature and may deal with basic biology, biochemistry, genetics, or physiology of fungi, molds, yeasts, or algae. Papers dealing purely with taxonomy or phylogeny, with fungal or algal structure, or with metabolism/alteration of metabolites/toxins by animal, plant, or insect cells, tissues, or organisms are not suitable. Documentation of the distribution/occurrence of toxins or metabolites in natural samples (foods, cere-

als, grains, soils, etc.) is suitable if the work includes studies involving the isolation, occurrence, or enumeration of the responsible microbes in these samples. The chemical or biochemical elucidation of metabolite or toxin structures is suitable if the work includes aspects of the enzymology or biosynthesis of these compounds.

Invertebrate microbiology manuscripts should address interactions between invertebrates and microorganisms, ranging from commensalism and mutualism to parasitism and pathogenicity. Manuscripts describing work dealing with the metabolites or toxins from animal, plant, or insect cells or the physiology of such cells are not suitable for AEM unless it affects a microbial community or individual microorganisms.

ASM publishes a number of different journals covering various aspects of the field of microbiology. Each journal has a prescribed scope which must be considered in determining the most appropriate journal for each manuscript. The following guidelines may be of assistance.

(i) AEM will consider manuscripts describing properties of enzymes and proteins that are produced by either wild-type or genetically engineered microorganisms and that are significant or have potential significance in industrial or environmental settings. Studies dealing with basic biological phenomena of enzymes or proteins or in which enzymes have been used in investigations of basic biological functions are more appropriate for the *Journal of Bacteriology*.

(ii) AEM will consider papers which describe the use of antimicrobial agents as tools for elucidating aspects of applied and environmental microbiology. Other papers dealing with antimicrobial agents, including manuscripts dealing with the biosynthesis and metabolism of such agents, are more appropriate for *Antimicrobial Agents and Chemotherapy*.

(iii) Papers on the biology of bacteriophages and other viruses are more appropriate for the *Journal of Virology* or the *Journal of Bacteriology*. AEM does, however, consider manuscripts dealing with viruses in relation to environmental, public health, or industrial microbiology.

(iv) Manuscripts dealing with the immune system or with topics of basic medical interest or oral microbiology are more appropriate for *Infection and Immunity*. Reports of clinical investigations and environmental biology applied to hospitals should be submitted to the *Journal of Clinical Microbiology*.

(v) AEM and *Eukaryotic Cell* (EC) accept manuscripts on population dynamics and the ecology of eukaryotic microbes. Studies of microbial communities and of microbial populations with identified economic or ecological significance, e.g., plant pathogens or symbionts, are usually more appropriate for AEM. Studies of single species of eukaryotes, especially “model” organisms or those without identified economic or ecological importance, are usually more appropriate for EC.

(vi) Manuscripts dealing with the purification and char-

* Shading indicates material that has been added or significantly updated.

acterization of enzymes or cloning of genes that have already been extensively described for other organisms will be considered for publication only if they offer experimentally supported new insights into the biological role, properties, or applications of these enzymes. Descriptions of genes or enzymes that differ only in minor ways from the prototypes are not suitable for AEM.

To best serve its readership, the journal must accept only those papers that are most significant to the field of applied and environmental microbiology. Thus, the editors will reject manuscripts that, while scientifically sound, represent only incremental extensions of other studies, are mainly confirmatory, or do not pursue a question in sufficient depth.

Questions about these guidelines may be directed to the editor in chief of the journal being considered.

If transfer to another ASM journal is recommended by an editor, the corresponding author will be contacted.

Note that a manuscript rejected by one ASM journal on scientific grounds or on the basis of its general suitability for publication is considered rejected by all other ASM journals.

EDITORIAL POLICY

Use of Microbiological Information

The Council Policy Committee (CPC) of the American Society for Microbiology affirms the long-standing position of the Society that microbiologists will work for the proper and beneficent application of science and will call to the attention of the public or the appropriate authorities misuses of microbiology or of information derived from microbiology. ASM members are obligated to discourage any use of microbiology contrary to the welfare of humankind, including the use of microbes as biological weapons. Bioterrorism violates the fundamental principles expressed in the Code of Ethics of the Society and is abhorrent to ASM and its members.

ASM recognizes that there are valid concerns regarding the publication of information in scientific journals that could be put to inappropriate use as described in the CPC resolution mentioned above. Members of the ASM Publications Board will evaluate the rare manuscript that might raise such issues during the review process. However, as indicated elsewhere in these Instructions, research articles must contain sufficient detail, and material/information must be made available, to permit the work to be repeated by others. Supply of materials should be in accordance with laws and regulations governing the shipment, transfer, possession, and use of biological materials and must be for legitimate, bona fide research needs. Links to, and information regarding, these laws and regulations can be found at <http://www.asm.org/Policy/index.asp>.

General Requirements

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See p. 15 for nucleic acid sequence formatting instructions.

The URLs of the databases mentioned above are as follows: DNA Data Bank of Japan (DDBJ), <http://www.ddbj.nig.ac.jp>; EMBL Nucleotide Sequence Database (EMBL), <http://www.ebi.ac.uk/embl>; and GenBank, National Center for Biotechnology Information (GenBank), <http://www.ncbi.nlm.nih.gov>.

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The URLs of the databases mentioned above are as follows: Gene Expression Omnibus (GEO), <http://www.ncbi.nlm.nih.gov/geo>; ArrayExpress, <http://www.ebi.ac.uk/arrayexpress>; and Center for Information Biology Gene Expression Database (CIBEX), <http://cibex.nig.ac.jp/index.jsp>.

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- Double space all text, including references and figure legends
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- Present statistical treatment of data where appropriate
- Format references in ASM style
- Indicate journal section for manuscript publication
- Provide accession numbers for all sequences or sequence alignments important for evaluation of the manuscript as supplemental material or make the material available on a website for access by the editor and reviewers
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Abstract. Limit the abstract to **250 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 same format as shown for the References section but omit the article title. Because the abstract will be published separately by abstracting services, it must be complete and understandable without reference to the text.

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Acknowledgments. The source of any financial support received for the work being published must be indicated in the Acknowledgments section. (It will be assumed that the absence of such an acknowledgment is a statement by the authors that no support was received.) The usual format is as follows: "This work was supported by Public Health Service grant CA-01234 from the National Cancer Institute."

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Appendixes. Appendixes, which contain additional material to aid the reader, are permitted. Titles, authors, and References sections that are distinct from those of the primary article are not allowed. If it is not feasible to list the author(s) of the appendix in the byline or the Acknowledgments section of the primary article, rewrite the appendix so that it can be considered for publication as an independent article, either long-form or short-form style. Equations, tables, and figures should be labeled with the letter "A" preceding the numeral to distinguish them from those cited in the main body of the text.

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2. **Cox, C. S., B. R. Brown, and J. C. Smith.** *J. Gen. Genet.*, in press.* {*Article title is optional; journal title is mandatory.*}
3. **da Costa, M. S., M. F. Nobre, and F. A. Rainey.** 2001. Genus I. *Thermus* Brock and Freeze 1969, 295,^{AL} emend. Nobre, Trüper and da Costa 1996b, 605, p. 404–414. *In* D. R. Boone, R. W. Castenholz, and G. M. Garrity (ed.), *Bergey's manual of systematic bacteriology*, 2nd ed., vol. 1. Springer, New York, NY.
4. **Elder, B. L., and S. E. Sharp.** 2003. Cumitech 39, Competency assessment in the clinical laboratory. Coordinating ed., S. E. Sharp. ASM Press, Washington, DC.
5. **Falagas, M. E., and S. K. Kasiakou.** 2006. Use of international units when dosing colistin will help decrease confusion related to various formulations of the drug around the world. *Antimicrob. Agents Chemother.* **50**:2274–2275. (Letter.) {"Letter" or "Letter to the editor" is allowed but not required at the end of such an entry.}
6. **Fitzgerald, G., and D. Shaw.** *In* A. E. Waters (ed.), *Clinical microbiology*, in press. EFH Publishing Co., Boston, MA.* {*Chapter title is optional.*}
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8. **Garcia, C. O., S. Paira, R. Burgos, J. Molina, J. F. Molina, and C. Calvo.** 1996. Detection of salmonella DNA in synovial membrane and synovial fluid from Latin American patients. *Arthritis Rheum.* **39**(Suppl.): S185. {*Meeting abstract published in journal supplement.*}
9. **Green, P. N., D. Hood, and C. S. Dow.** 1984. Taxonomic status of some methylotrophic bacteria, p. 251–254. *In* R. L. Crawford and R. S. Hanson (ed.),

- Microbial growth on C₁ compounds. Proceedings of the 4th International Symposium. American Society for Microbiology, Washington, DC.
10. **Odell, J. C.** April 1970. Process for batch culturing. U.S. patent 484,363,770. {*Include the name of the patented item/process if possible; the patent number is mandatory.*}
 11. **O'Malley, D. R.** 1998. Ph.D. thesis. University of California, Los Angeles. {*Title is optional.*}
 12. **Rotimi, V. O., N. O. Salako, E. M. Mohaddas, and L. P. Philip.** 2005. Abstr. 45th Intersci. Conf. Antimicrob. Agents Chemother., abstr. D-1658. {*Abstract title is optional.*}
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3. **Smith, F. X., H. J. Merianos, A. T. Brunger, and D. M. Engelman.** 2001. Polar residues drive association of polyleucine transmembrane helices. *Proc. Natl. Acad. Sci. USA* **98**:2250–2255. doi:10.1073/pnas.041593698.
4. **Winnick, S., D. O. Lucas, A. L. Hartman, and D. Toll.** 2005. How do you improve compliance? *Pediatrics* **115**:e718–e724.

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... similar results (R. B. Layton and C. C. Weathers, unpublished data).

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... this new process (V. R. Smoll, 20 June 1999, Australian Patent Office). {*For non-U.S. patent applications, give the date of publication of the application.*}

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300 dpi for grayscale and color
600 dpi for lettering
1,200 dpi for line art
600 dpi for combination art (lettering and images)

Size. All graphics **MUST 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 width for a 1-column figure: 3⁵/₁₆ inches (ca. 8.4 cm)
Maximum width for a 2-column figure: 6⁷/₈ inches (ca. 17.4 cm)
Minimum width for a 2-column figure: 4¹/₄ inches (10.8 cm)
Maximum height: 9¹/₁₆ inches (23.0 cm)

Contrast. Illustrations must contain sufficient contrast to withstand the inevitable loss of contrast and detail inherent in the printing process. See also the section on color illustrations below.

Labeling and assembly. All final lettering, labeling, tooling, etc., **MUST** be incorporated into the figures. It cannot be added at a later date. If a figure number is included, it **must** appear well outside the boundaries of the image itself. (Numbering may need to be changed at the copyediting stage.) Each figure must be uploaded as a separate file, and any multipanel figures must be assembled 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: Helvetica, Times Roman, European PI, Mathematical PI, or Symbol. All fonts other than these five must be converted to paths (or outlines) in the application with which they were created. For proper font use in PowerPoint images, refer to the Cadmus digital art website, http://cjs.cadmus.com/da/instructions/ppt_disclaimer.jsp.

Compression. Images created with Macintosh applications may be compressed with Stuffit. Images created with Windows applications may be compressed with WINZIP or PKZIP.

Color illustrations. *The cost of printing in color must be borne by the author.* The current color cost per figure may be accessed from the submission form in Rapid Review. For accepted manuscripts, the total cost of the color will be included in the acceptance letter sent out by ASM. Adherence to the following guidelines, in addition to the general ones below, will help to minimize costs and to ensure color reproduction that is as accurate as possible.

Because of the requirements of print production, color illustrations **must** be in the CMYK (cyan, magenta, yellow, black) color space. The “normal” color mode for most computer software is RGB (red, green, blue), which is also the color space of your computer monitor. Since CMYK is a smaller color space (meaning it can define fewer colors), colors often shift when an RGB file is converted to CMYK. In particular, figures showing red or green fluorescence and those with a significant range of colors may be difficult or impossible to reproduce during the printing process.

Color illustrations must be supplied in the CMYK color mode, as either (i) CMYK TIFF images with a resolution of at least 300 pixels per inch (raster files, consisting of pixels) or (ii) Illustrator-compatible EPS files with CMYK color elements (vector files, consisting of lines, fonts, fills, and images). See the charts above for a list of supported applications.

We cannot accept any Microsoft Office files (PowerPoint, Word, Excel) for color illustrations because they are restricted to the RGB color space.

Drawings

Submit graphs, charts, complicated chemical or mathematical formulas, diagrams, and other drawings as finished products not requiring additional artwork or typesetting. No part of the graph or drawing may be handwritten. *All* elements, including letters, numbers, and symbols, *must* be easily readable, and both axes of a graph must be labeled. Keep in mind that the journal is published both in print and online and that the same electronic files submitted by the authors are used to produce both.

When creating line art, please use the following guidelines:

1. **All art MUST be submitted at its intended publication size.** For acceptable dimensions, see the Size section on p. 14.
2. **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,
 - Generate the image at line screens of 85 lines per inch or lower.
 - When applying multiple shades of gray, differentiate the gray levels by at least 20%.
 - Never use levels of gray below 20% or above 70%

as they will fade out or become totally black upon scanning and reduction.

3. Use thick, solid lines that are no finer than 1 point in thickness.
4. No type should be smaller than 6 points at the final publication size.
5. Avoid layering type directly over shaded or textured areas.
6. Avoid the use of reversed type (white lettering on a black background).
7. Avoid heavy letters, which tend to close up, and unusual symbols, which the printer may not be able to reproduce in the legend.
8. If colors are used, avoid using similar shades of the same color and avoid very light colors.

In figure ordinate and abscissa scales (as well as table column headings), **avoid the ambiguous use of numbers with exponents.** Usually, it is preferable to use the *Système International d'Unités* (SI) symbols (μ for 10^{-6} , m for 10^{-3} , k for 10^3 , M for 10^6 , etc.). A complete listing of SI symbols can be found in the International Union of Pure and Applied Chemistry (IUPAC) publication *Quantities, Units and Symbols in Physical Chemistry* (Blackwell Science, Oxford, United Kingdom, 1993); an abbreviated list is available at <http://www.iupac.org/reports/1993/homann/index.html>. Thus, a representation of 20,000 cpm on a figure ordinate is to be made by the number 20 accompanied by the label kcpm.

When powers of 10 must be used, the journal requires that the exponent power be associated with the number shown. In representing 20,000 cells per ml, the numeral on the ordinate would be “2” and the label would be “ 10^4 cells per ml” (not “cells per ml $\times 10^{-4}$ ”). Likewise, an enzyme activity of 0.06 U/ml would be shown as 6 accompanied by the label 10^{-2} U/ml. The preferred designation would be 60 mU/ml (milliunits per milliliter).

Presentation of Nucleic Acid Sequences

Nucleic acid sequences of limited length which are the primary subject of a study may be presented freestyle in the most effective format. Longer nucleic acid sequences must be presented as figures in the following format to conserve space. Print the sequence in lines of approximately 100 to 120 nucleotides in a nonproportional (monospace) font that is easily legible when published with a line length of 6 inches (ca. 15.2 cm). If possible, lines of nucleic acid sequence should be further subdivided into blocks of 10 or 20 nucleotides by spaces within the sequence or by marks above it. Uppercase and lowercase letters may be used to designate the exon-intron structure, transcribed regions, etc., if the lowercase letters remain legible at a 6-inch (ca. 15.2-cm) line length. Number the sequence line by line; place numerals, representing the first base of each line, to the left of the lines. **Minimize spacing between lines of**

sequence, leaving room only for annotation of the sequence. Annotation may include boldface, underlining, brackets, boxes, etc. Encoded amino acid sequences may be presented, if necessary, immediately above or below the first nucleotide of each codon, by using the single-letter amino acid symbols. Comparisons of multiple nucleic acid sequences should conform as nearly as possible to the same format.

Figure Legends

Legends should provide enough information so that the figure is understandable without frequent reference to the text. However, detailed experimental methods must be described in the Materials and Methods section, not in a figure legend. A method that is unique to one of several experiments may be reported in a legend only if the discussion is very brief (one or two sentences). Define all symbols used in the figure and define all abbreviations that are not used in the text.

Tables

Tables that contain artwork, chemical structures, or shading must be submitted as illustrations in an acceptable format at the modification stage. The preferred format for regular tables is MS Word; however, WordPerfect and Acrobat PDF are also acceptable. Note that a straight Excel file is *not* currently an acceptable format. Excel files must be either embedded in a Word or WordPerfect document or converted to PDF *before* being uploaded. **If your modified manuscript contains PDF tables, select “for reviewing purposes only” at the beginning of the file upload process.**

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. See the Abbreviations section (p. 20) of these Instructions for those that should be used in tables. Explanatory footnotes are acceptable, but more extensive table “legends” are not. Footnotes should not include detailed descriptions of the experiment. 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.

TABLE 1. Distribution of protein and ATPase in fractions of dialyzed membranes^a

Membrane	Fraction	ATPase	
		U/mg of protein	Total U
Control	Depleted membrane	0.036	2.3
	Concentrated supernatant	0.134	4.82
E1 treated	Depleted membrane	0.034	1.98
	Concentrated supernatant	0.11	4.6

^a Specific activities of ATPase of nondepleted membranes from control and treated bacteria were 0.21 and 0.20, respectively.

Cover Photographs and Drawings

AEM publishes photographs and drawings on the front cover. Invitations are issued to authors whose manuscripts are returned for modification or whose manuscripts have been accepted for publication in AEM; material should be related to the work presented in the AEM manuscript. Unsolicited photos will be considered in hard-copy format (two copies) only; if an unsolicited photo is chosen for the cover, the author may be asked to submit digital files. No material submitted for consideration will be returned to the author. Authors will be notified only if their cover art is selected. Copyright for the chosen material must be transferred to ASM. A short description of the cover material will be included at the end of the table of contents or the author index of the issue. Technical specifications for submission are available from the cover editor, Matthew R. Parsek (e-mail: matthew-parsek@uiowa.edu).

NOMENCLATURE

Chemical and Biochemical Nomenclature

The recognized authority for the names of chemical compounds is *Chemical Abstracts* (CAS, Columbus, OH) and its indexes. *The Merck Index*, 14th ed. (Merck & Co., Inc., Whitehouse Station, NJ, 2006), is also an excellent source. For biochemical terminology, including abbreviations and symbols, consult *Biochemical Nomenclature and Related Documents* (Portland Press, London, United Kingdom, 1992), available at <http://www.chem.qmul.ac.uk/iupac/bibliog/white.html>, and the instructions to authors of the *Journal of Biological Chemistry* and the *Archives of Biochemistry and Biophysics* (first issues of each year).

Do not express molecular weight in daltons; molecular weight is a unitless ratio. Molecular mass is expressed in daltons.

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 at <http://www.chem.qmul.ac.uk/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, and express enzyme activity either in katal (preferred) or in the older system of micromoles per minute.

Nomenclature of Microorganisms

Binary names, consisting of a generic name and a specific epithet (e.g., *Escherichia coli*), must be used for all microorganisms. 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., *E. coli*),

provided there can be no confusion with other genera used in the paper. Names of all taxa (kingdoms, phyla, classes, orders, families, genera, species, and subspecies) are printed in italics and should be italicized (or underlined) in the manuscript; strain designations and numbers are not. Vernacular (common) names should be in lowercase roman type (e.g., streptococcus, brucella). For *Salmonella*, genus, species, and subspecies names should be rendered in standard form: *Salmonella enterica* at first use, *S. enterica* thereafter; *Salmonella enterica* subsp. *arizonae* at first use, *S. enterica* subsp. *arizonae* thereafter. Names of serovars should be in roman type with the first letter capitalized: *Salmonella enterica* serovar Typhimurium. After the first use, the serovar may also be given without a species name: *Salmonella* serovar Typhimurium. For other information regarding serovar designations, see *Antigenic Formulas of the Salmonella Serovars*, 8th ed. (M. Y. Popoff, WHO Collaborating Centre for Reference and Research on Salmonella, Institut Pasteur, Paris, France, 2001). For a summary of the current standards for *Salmonella* nomenclature and the Kaufmann-White criteria, see the article by Brenner et al. (J. Clin. Microbiol. **38**:2465-2467, 2000), the opinion of the Judicial Commission of the International Committee on Systematics of Prokaryotes (Int. J. Syst. Evol. Microbiol. **55**:519-520, 2005), and the article by Tindall et al. (Int. J. Syst. Evol. Microbiol. **55**:521-524, 2005).

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., ASM Press, 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: Bacterial Nomenclature Up-to-Date (http://www.dsmz.de/microorganisms/main.php?contentleft_id=14) and List of Prokaryotic Names with Standing in Nomenclature (<http://www.bacterio.cict.fr>). If there is reason to use a name that does not have standing in nomenclature, the name should be enclosed in quotation marks in the title and at its first use in the abstract and the text and an appropriate statement concerning the nomenclatural status of the name should be made in the text. "*Candidatus*" species should always be set in quotation marks.

For guidelines regarding new names and descriptions of new genera and species, see the articles by Tindall (Int. J. Syst. Bacteriol. **49**:1309-1312, 1999) and Stackebrandt et al. (Int. J. Syst. Evol. Microbiol. **52**:1043-1047, 2002). To validate new names and/or combinations, authors must submit three copies of their published article to the *International Journal of Systematic and Evolutionary Microbiology*.

It is recommended that a strain be deposited in at least two recognized culture collections in different countries when that strain is necessary for the description of a new taxon (Int. J. Syst. Evol. Microbiol. **50**:2239-2244, 2000).

Since the classification of fungi is not 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*, 4th ed. (C. P. Kurtzman and J. W. Fell, ed., Elsevier Science Publishers B.V., Amsterdam, The Netherlands, 1998), and *Ainsworth and Bisby's Dictionary of the Fungi*, 9th ed. (P. M. Kirk, P. F. Cannon, J. C. David, and J. A. Stalpers, ed., CABI Publishing, Wallingford, Oxfordshire, United Kingdom, 2001); see also <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 published in *Virus Taxonomy: Eighth Report of the International Committee on Taxonomy of Viruses* (C. M. Fauquet et al., ed., Elsevier Academic Press, San Diego, CA, 2005). 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, like 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.

Microorganisms, viruses, and plasmids should be given designations consisting of letters and serial numbers. It is generally advisable to include a worker's initials or a descriptive symbol of locale, 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. Plasmids are named with a lowercase "p" followed by the designation in uppercase letters and numbers. To avoid the use of the same designation as that of a widely used strain or plasmid, check the designation against a publication database such as Medline.

Genetic Nomenclature

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.** Review and/or 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 by the Genetics and Genomics Committee of the ASM Publications Board.

Before submission of manuscripts, authors may direct questions on genetic nomenclature to the committee's chairman: Maria Costanzo (e-mail: maria@genome.stanford.edu). Such a consultation should be mentioned in the manuscript submission letter.

Bacteria. The genetic properties of bacteria are de-

scribed in terms of phenotypes and genotypes. The phenotype describes the observable properties of an organism. The genotype refers to the genetic constitution of an organism, usually in reference to some standard wild type. The guidelines that follow are based on the recommendations of Demerec et al. (*Genetics* **54**:61–76, 1966).

(i) Phenotypic designations must be used when mutant loci have not been identified or mapped. They can also be used to identify the protein product of a gene, e.g., the OmpA protein. Phenotypic designations generally consist of three-letter symbols; these are *not* italicized, and the first letter of the symbol is capitalized. It is preferable to use Roman or Arabic numerals (instead of letters) to identify a series of related phenotypes. Thus, a series of nucleic acid polymerase mutants might be designated Pol1, Pol2, Pol3, etc. Wild-type characteristics can be designated with a superscript plus (Pol⁺), and, when necessary for clarity, negative superscripts (Pol⁻) can be used to designate mutant characteristics. Lowercase superscript letters may be used to further delineate phenotypes (e.g., Str^r for streptomycin resistance). Phenotypic designations should be defined.

(ii) Genotypic designations are also indicated by three-letter locus symbols. In contrast to phenotypic designations, these are lowercase italic (e.g., *ara his rps*). If several loci govern related functions, these are distinguished by italicized capital letters following the locus symbol (e.g., *araA araB araC*). Promoter, terminator, and operator sites should be indicated as described by Bachmann and Low (*Microbiol. Rev.* **44**:1–56, 1980), e.g., *lacZp*, *lacAt*, and *lacZo*.

(iii) Wild-type alleles are indicated with a superscript plus (*ara*⁺ *his*⁺). A superscript minus is not used to indicate a mutant locus; thus, one refers to an *ara* mutant rather than an *ara*⁻ strain.

(iv) Mutation sites are designated by placing serial isolation numbers (allele numbers) after the locus symbol (e.g., *araA1 araA2*). If it is not known in which of several related loci the mutation has occurred, a hyphen is used instead of the capital letter (e.g., *ara-23*). It is essential in papers reporting the isolation of new mutants that allele numbers be given to the mutations. For *Escherichia coli*, there is a registry of such numbers: *E. coli* Genetic Stock Center, Department of Biology, Yale University, New Haven, CT 06511-5188. For the genus *Salmonella*, the registry is *Salmonella* Genetic Stock Center, Department of Biology, University of Calgary, Calgary, Alberta T2N 1N4, Canada. For the genus *Bacillus*, the registry is *Bacillus* Genetic Stock Center, Ohio State University, Columbus, OH 43210.

(v) The use of superscripts with genotypes (other than + to indicate wild-type alleles) should be avoided. Designations indicating amber mutations (Am), temperature-sensitive mutations (Ts), constitutive mutations (Con), cold-sensitive mutations (Cs), production of a hybrid protein (Hyb), and other important phenotypic properties should follow the allele number [e.g., *araA230*(Am) *hisD21*(Ts)]. All other such designations of phenotype must be defined at the first occurrence. If superscripts

must be used, they must be approved by the editor and defined at the first occurrence in the text.

Subscripts may be used in two situations. Subscripts may be used to distinguish between genes (having the same name) from different organisms or strains, e.g., *his*_{*E. coli*} or *his*_{K-12} for the *his* genes of *E. coli* or strain K-12 in another species or strain, respectively. An abbreviation may also be used if it is explained. Similarly, a subscript is also used to distinguish between genetic elements that have the same name. For example, the promoters of the *gln* operon can be designated *glnAp*₁ and *glnAp*₂. This form departs slightly from that recommended by Bachmann and Low (e.g., *desC1p*).

(vi) Deletions are indicated by the symbol Δ placed before the deleted gene or region, e.g., Δ*trpA432*, Δ(*aroP-aceE*)₄₁₉, or Δ*his*(*dhuA hisJ hisQ*)₁₂₅₆. Similarly, other symbols can be used (with appropriate definition). Thus, a fusion of the *ara* and *lac* operons can be shown as Φ(*ara-lac*)₉₅. Likewise, Φ(*araB'-lacZ*)₉₆ indicates that the fusion results in a truncated *araB* gene fused to an intact *lacZ* gene, and Φ(*malE-lacZ*)₉₇(Hyb) shows that a hybrid protein is synthesized. An inversion is shown as IN(*rrnD-rrnE*)₁. An insertion of an *E. coli his* gene into plasmid pSC101 at zero kilobases (0 kb) is shown as pSC101 Ω(0kb::K-12*hisB*)₄. An alternative designation of an insertion can be used in simple cases, e.g., *galT236*::Tn5. The number 236 refers to the locus of the insertion, and if the strain carries an additional *gal* mutation, it is listed separately. Additional examples, which utilize a slightly different format, can be found in the papers by Campbell et al. and Novick et al. cited below. It is important in reporting the construction of strains in which a mobile element was inserted and subsequently deleted that this fact be noted in the strain table. This can be done by listing the genotype of the strain used as an intermediate in a table footnote or by making a direct or parenthetical remark in the genotype, e.g., (F⁻), Δ*Mu cts*, or *mal::ΔMu cts::lac*. In setting parenthetical remarks within the genotype or dividing the genotype into constituent elements, parentheses and brackets are used without special meaning; brackets are used outside parentheses. To indicate the presence of an episome, parentheses (or brackets) are used (λ, F⁺). Reference to an integrated episome is indicated as described above for inserted elements, and an exogenote is shown as, for example, W3110/F'8(*gal*⁺).

For information about the symbols in current use, consult Berlyn (*Microbiol. Mol. Biol. Rev.* **62**:814–984, 1998) for *E. coli* K-12, Sanderson and Roth (*Microbiol. Rev.* **52**:485–532, 1988) for *Salmonella* serovar Typhimurium, Holloway et al. (*Microbiol. Rev.* **43**:73–102, 1979) for the genus *Pseudomonas*, Piggot and Hoch (*Microbiol. Rev.* **49**:158–179, 1985) for *Bacillus subtilis*, Perkins et al. (*Microbiol. Rev.* **46**:426–570, 1982) for *Neurospora crassa*, and Mortimer and Schild (*Microbiol. Rev.* **49**:181–213, 1985) for *Saccharomyces cerevisiae*. For yeasts, *Chlamydomonas* spp., and several fungal species, symbols such as those given in the *Handbook of Microbiology*, 2nd ed. (A. I. Laskin and H. A. Lechevalier, ed., CRC Press, Inc., Cleveland, OH, 1988) should be used.

Conventions for naming genes. It is recommended that (entirely) new genes be given names that are mnemonics of their function, avoiding names that are already assigned and earlier or alternative gene names, irrespective of the bacterium for which such assignments have been made. Similarly, it is recommended that, whenever possible, homologous genes present in different organisms receive the same name. When homology is not apparent or the function of a new gene has not been established, a provisional name may be given by one of the following methods. (i) The gene may be named on the basis of its map location in the style *yaaA*, analogous to the style used for recording transposon insertions (*zef*) as discussed below. A list of such names in use for *E. coli* has been published by Rudd (Microbiol. Mol. Biol. Rev. **62**: 985–1019, 1998). (ii) A provisional name may be given in the style described by Demerec et al. (e.g., *usg*, gene upstream of *folC*). Such names should be unique, and names such as *orf* or *genX* should not be used. For reference, the *E. coli* Genetic Stock Center's database includes an updated listing of *E. coli* gene names and gene products. It is accessible on the Internet (<http://cgsc.biology.yale.edu/cgsc.html>). The Center's relational database can also be searched via Telnet; for access, send a request to berlyn@cgsc.biology.yale.edu. A list can also be found in the work of Riley (Microbiol. Rev. **57**:862–952, 1993). For the genes of other bacteria, consult the references given above.

“Mutant” versus “mutation.” Keep in mind the distinction between a *mutation* (an alteration of the primary sequence of the genetic material) and a *mutant* (a strain carrying one or more mutations). One may speak about the mapping of a mutation, but one cannot map a mutant. Likewise, a mutant has no genetic locus, only a phenotype.

“Homology” versus “similarity.” For use of terms that describe relationships between genes, consult the articles by Theissen (Nature **415**:741, 2002) and Fitch (Trends Genet. **16**:227–231, 2000). “Homology” implies a relationship between genes that share a common evolutionary origin; partial homology is not recognized. When sequence comparisons are discussed, it is more appropriate to use the term “percent sequence similarity” or “percent sequence identity,” as appropriate.

Strain designations. Do not use a genotype as a name (e.g., “subsequent use of *leuC6* for transduction”). If a strain designation has not been chosen, select an appropriate word combination (e.g., “another strain containing the *leuC6* mutation”).

“Natural” versus “artificial” transformation. Natural transformation is a process whereby the recipient cell has the inherent capacity to take up and integrate exogenous DNA into its genome. As such, natural transformation is part of the biology of the recipient cell line and should not be confused with processes through which integration of DNA is forced upon recipient cells.

Viruses. The genetic nomenclature for viruses differs from that for bacteria. In most instances, viruses have no phenotype, since they have no metabolism outside host cells. Therefore, distinctions between phenotype and genotype cannot be made. Super-scripts are used to indicate hybrid genomes. Genetic symbols may be one, two, or three letters. For example, a mutant strain of λ might be designated λ *Aam11 int2 red114 cI857*; this strain carries mutations in genes *cI*, *int*, and *red* and an amber-suppressible (*am*) mutation in gene *A*. A strain designated λ *att⁴³⁴ imm²¹* would represent a hybrid of phage λ which carries the immunity region (*imm*) of phage 21 and the attachment (*att*) region of phage 434. Host DNA insertions into viruses should be delineated by square brackets, and the genetic symbols and designations for such inserted DNA should conform to those used for the host genome. Genetic symbols for phage λ can be found in reports by Szybalski and Szybalski (Gene **7**:217–270, 1979) and Echols and Murialdo (Microbiol. Rev. **42**: 577–591, 1978).

Eukaryotes. For information about the genetic nomenclature of eukaryotes, see the Instructions to Authors for *Eukaryotic Cell* and *Molecular and Cellular Biology*.

Transposable elements, plasmids, and restriction enzymes. Nomenclature of transposable elements (insertion sequences, transposons, phage Mu, etc.) should follow the recommendations of Campbell et al. (Gene **5**: 197–206, 1979), with the modifications given in section vi above. The Internet site where insertion sequences of eubacteria and archaea are described and new sequences can be recorded is <http://www-is.biotoul.fr/is.html>.

The system of designating transposon insertions at sites where there are no known loci, e.g., *zef-123::Tn5*, has been described by Chumley et al. (Genetics **91**:639–655, 1979). The nomenclature recommendations of Novick et al. (Bacteriol. Rev. **40**:168–189, 1976) for plasmids and plasmid-specified activities, of Low (Bacteriol. Rev. **36**:587–607, 1972) for F' factors, and of Roberts et al. (Nucleic Acids Res. **31**:1805–1812, 2003) for restriction enzymes, DNA methyltransferases, homing endonucleases, and their genes should be used when possible. The nomenclature for recombinant DNA molecules constructed in vitro follows the nomenclature for insertions in general. DNA inserted into recombinant DNA molecules should be described by using the gene symbols and conventions for the organism from which the DNA was obtained.

Tetracycline resistance determinants. The nomenclature for tetracycline resistance determinants is based on the proposal of Levy et al. (Antimicrob. Agents Chemother. **43**:1523–1524, 1999). The style for such determinants is, e.g., Tet B; the space helps distinguish the determinant designation from that for phenotypes and proteins (TetB). The above-referenced article shows the correct format for genes, proteins, and determinants in this family.

ABBREVIATIONS AND CONVENTIONS

Verb Tense

ASM strongly recommends that for clarity you use the **past** tense to narrate particular events in the past, including the procedures, observations, and data of the study that you are reporting. Use the present tense for your own general conclusions, the conclusions of previous researchers, and generally accepted facts. Thus, most of the abstract, Materials and Methods, and Results will be in the past tense, and most of the introduction and some of the Discussion will be in the present tense.

Be aware that it may be necessary to vary the tense in a single sentence. For example, it is correct to say “White (30) demonstrated that XYZ cells *grow* at pH 6.8,” “Figure 2 shows that ABC cells *failed* to grow at room temperature,” and “Air *was* removed from the chamber and the mice *died*, which *proves* that mice *require* air.” In reporting statistics and calculations, it is correct to say “The values for the ABC cells *are* statistically significant, indicating that the drug *inhibited*. . . .”

For an in-depth discussion of tense in scientific writing, see p. 191–193 in *How To Write and Publish a Scientific Paper*, 6th ed.

Abbreviations

General. Abbreviations should be used as an aid to the reader rather than as a convenience to the author, and therefore their **use should be limited**. Abbreviations other than those recommended by the IUPAC-IUB (*Biochemical Nomenclature and Related Documents*, 1992) should be used only when a case can be made for necessity, such as in tables and figures.

It is often possible to use pronouns or to paraphrase a long word after its first use (e.g., “the drug” or “the substrate”). Standard chemical symbols and trivial names or their symbols (folate, Ala, Leu, etc.) may also be used.

It is strongly recommended that all abbreviations except those listed below be introduced in the first paragraph in Materials and Methods. Alternatively, define each abbreviation and introduce it in parentheses the first time it is used; e.g., “cultures were grown in Eagle minimal essential medium (MEM).” Generally, eliminate abbreviations that are not used at least three times in the text (including tables and figure legends).

Not requiring introduction. In addition to abbreviations for Système International d’Unités (SI) units of measurement, other common units (e.g., bp, kb, and Da), and chemical symbols for the elements, the following should be used without definition in the title, abstract, text, figure legends, and tables: DNA (deoxyribonucleic acid); cDNA (complementary DNA); RNA (ribonucleic acid); cRNA (complementary RNA); RNase (ribonuclease); DNase (deoxyribonuclease); rRNA (ribosomal RNA); mRNA (messenger RNA); tRNA (transfer RNA); AMP, ADP, ATP, dAMP, ddATP, GTP, etc. (for the respective 5' phosphates of adenosine and other nucleosides) (add 2', 3', or 5' when needed for contrast); ATPase, dGTPase,

etc. (adenosine triphosphatase, deoxyguanosine triphosphatase, etc.); NAD (nicotinamide adenine dinucleotide); NAD⁺ (nicotinamide adenine dinucleotide, oxidized); NADH (nicotinamide adenine dinucleotide, reduced); NADP (nicotinamide adenine dinucleotide phosphate); NADPH (nicotinamide adenine dinucleotide phosphate, reduced); NADP⁺ (nicotinamide adenine dinucleotide phosphate, oxidized); poly(A), poly(dT), etc. (polyadenylic acid, polydeoxythymidylic acid, etc.); oligo(dT), etc. (oligodeoxythymidylic acid, etc.); UV (ultraviolet); PFU (plaque-forming units); CFU (colony-forming units); MIC (minimal inhibitory concentration); Tris [tris(hydroxymethyl)aminomethane]; DEAE (diethylaminoethyl); EDTA (ethylenediaminetetraacetic acid); EGTA [ethylene glycol-bis(β-aminoethyl ether)-N,N,N',N'-tetraacetic acid]; HEPES (N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid); PCR (polymerase chain reaction); and AIDS (acquired immunodeficiency syndrome). Abbreviations for cell lines (e.g., HeLa) also need not be defined.

The following abbreviations should be used without definition in tables:

amt (amount)	SE (standard error)
approx (approximately)	SEM (standard error of the mean)
avg (average)	sp act (specific activity)
concn (concentration)	sp gr (specific gravity)
diam (diameter)	temp (temperature)
expt (experiment)	tr (trace)
exptl (experimental)	vol (volume)
ht (height)	vs (versus)
mo (month)	wk (week)
mol wt (molecular weight)	wt (weight)
no. (number)	yr (year)
prepn (preparation)	
SD (standard deviation)	

Reporting Numerical Data

Standard metric units are used for reporting length, weight, and volume. For these units and for molarity, use the prefixes m, μ, n, and p for 10⁻³, 10⁻⁶, 10⁻⁹, and 10⁻¹², respectively. Likewise, use the prefix k for 10³. Avoid compound prefixes such as mμ or μμ. Parts per million (ppm) may be used when that is the common measure for the science in that field. Units of temperature are presented as follows: 37°C or 324 K.

When fractions are used to express such units as enzymatic activities, it is preferable to use whole units, such as g or min, in the denominator instead of fractional or multiple units, such as μg or 10 min. For example, “pmol/min” is preferable to “nmol/10 min,” and “μmol/g” is preferable to “nmol/μg.” It is also preferable that an unambiguous form, such as exponential notation, be used; for example, “μmol g⁻¹ min⁻¹” is preferable to “μmol/g/min.” Always report numerical data in the applicable SI units.

Representation of data as accurate to more than two significant figures must be justified by presentation of appropriate statistical analyses.

For a review of some common errors associated with statistical analyses and reports, plus guidelines on how to

avoid them, see the article by Olsen (*Infect. Immun.* **71**:6689–6692, 2003).

For a review of basic statistical considerations for virology experiments, see the article by Richardson and Overbaugh (*J. Virol.* **79**:669–676, 2005).

Statistics

If biological variation within a treatment (coefficient of variation, the standard deviation divided by the mean) is small (less than 10%) and the difference among treatment means is large (greater than 3 standard deviations), it is not necessary to report statistics. If the data do not meet these criteria, however, the authors must include an appropriate statistical analysis (e.g., Student's *t* test, analysis of variance, Tukey's test, etc.). Statistics should represent the variation among biological units (e.g., replicate incubations) and not just the variation due to method of analysis.

Phylogenetic trees based on nucleotide or amino acid sequence alignments must be supported by appropriate statistical analyses of tree stability (e.g., bootstrap analysis), and nonsupported branches (e.g., bootstrap coefficients below 50%) should be collapsed. A copy of the alignment should be available for examination by the editor or the reviewers upon request.

For a review of some common errors associated with statistical analyses and reports, plus guidelines on how to avoid them, see the article by Olsen (*Infect. Immun.* **71**:6689–6692, 2003).

For a review of basic statistical considerations for virology experiments, see the article by Richardson and Overbaugh (*J. Virol.* **79**:669–676, 2005).

Equations

In mathematical equations, indicate the order of operations clearly by enclosing operations in parentheses, brackets, and braces, in that order: $(a + b) \times c$ or $a + (b \times c)$, $100 \times \{[(a/b) \times c] + d\}$ or $100 \times \{a/[(b \times c) + d]\}$. Italicize (or underline) variables and constants (but not numerals), and use roman type for designations: E_0 , E_h , M_r , K_m , K_s , $a + 2b = 1.2 \text{ mM}$, Ca^{2+} , $V_{\max} = \exp(1.5x + y)$, $\text{BOD} = 2.7x^2$.

Isotopically Labeled Compounds

For simple molecules, isotopic labeling is indicated in the chemical formula (e.g., $^{14}\text{CO}_2$, $^3\text{H}_2$, and H^{35}SO_4). Brackets are not used when the isotopic symbol is attached to the name of a compound that in its natural state does not contain the element (e.g., $^{32}\text{S-ATP}$) or to a word that is not a specific chemical name (e.g., ^{131}I -labeled protein, ^{14}C -amino acids, and ^3H -ligands).

For specific chemicals, the symbol for the isotope introduced is placed in brackets directly preceding the part of the name that describes the labeled entity. Note that configuration symbols and modifiers precede the isotopic symbol. The following examples illustrate correct usage.

^{14}C urea	UDP-[U- ^{14}C]glucose
L-[methyl- ^{14}C]methionine	<i>E. coli</i> [^{32}P]DNA
[2,3- ^3H]serine	fructose 1,6-[1- ^{32}P]bisphosphate
[α - ^{14}C]lysine	
[γ - ^{32}P]ATP	

AEM follows the same conventions for isotopic labeling as the *Journal of Biological Chemistry*, and more-detailed information can be found in the instructions to authors of that journal (first issue of each year).