

ANTIMICROBIAL AGENTS AND CHEMOTHERAPY

2009 INSTRUCTIONS TO AUTHORS

SCOPE

Antimicrobial Agents and Chemotherapy (AAC) is an interdisciplinary journal devoted to the dissemination of knowledge relating to all aspects of antimicrobial and antiparasitic agents and chemotherapy. Within the circumscriptions set forth below, any report involving studies of or with antimicrobial, antiviral (including antiretroviral), or antiparasitic agents is within the purview of AAC. Studies involving animal models, pharmacological characterization, and clinical trials are appropriate for consideration.

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

(i) Papers which describe the use of antimicrobial agents as tools for elucidating the basic biological processes of bacteria are considered more appropriate for the *Journal of Bacteriology*.

(ii) Manuscripts that (a) describe the use of antimicrobial or antiparasitic agents as tools in the isolation, identification, or epidemiology of microorganisms associated with disease; (b) are concerned with quality control procedures for diffusion, elution, or dilution tests for determining susceptibilities to antimicrobial agents in clinical laboratories; and (c) deal with applications of commercially prepared tests or kits to assays performed in clinical laboratories to measure the activities of established antimicrobial agents or their concentrations in body fluids are considered more appropriate for the *Journal of Clinical Microbiology*. Manuscripts concerned with the development or modification of assay methods and the validation of their sensitivity and specificity are considered appropriate for AAC.

(iii) Manuscripts describing new or novel methods or improvements in media and culture conditions will not be considered for publication in AAC unless these methods are applied to the study of problems related to the production or activity of antimicrobial agents. Such manuscripts are more appropriate for *Applied and Environmental Microbiology* or the *Journal of Clinical Microbiology*.

(iv) Manuscripts dealing with properties of unpurified natural products, or with entities that are primarily anti-tumor agents, or with immunomodulatory agents that are not antimicrobial agents are not appropriate for AAC.

(v) Manuscripts dealing with novel small molecular antimicrobials must provide at least some data showing that the proposed new agents or scaffolds have the potential to become therapeutic agents. Appropriate demonstrations will vary but generally should be some combination of data on physical properties (solubility,

protein binding, $\log P$ [logarithm of the ratio of the concentrations of un-ionized solute in solvents]), pharmacological properties (Caco2 predictions of bioavailability, pharmacokinetics in an animal species), or tolerability (mammalian cell toxicity, likelihood of hepatic metabolism, potential for receptor interactions, potential for human ERG liability). Initial presentations of compounds are not expected to address all these areas but rather to show an appropriate initial subset. For example, the first publication of a novel compound or compound series might address selected physical properties plus mammalian cell toxicity. Subsequent publications are expected to add progressively to the proof of the agent's therapeutic potential.

(vi) Biochemical analyses for β -lactamases that determine kinetic parameters (e.g., K_m , K_{cat}) must be performed on purified enzyme preparations. The enzyme must be in its native form, without any leader sequences or fusions used for purification (e.g., His tag). The determination of relative rates of hydrolysis may be performed on crude extracts.

(vii) A manuscript limited to the nucleic acid sequence of a gene encoding an antibiotic target, receptor, or resistance mechanism may be submitted as a short-form paper (see "[Short-Form Papers](#)" below) or a New-Data Letter to the Editor (see "[Letters to the Editor](#)" below), depending on its length. Formatting instructions for nucleic acid sequences are given below (see "[Presentation of Nucleic Acid Sequences](#)"). Repetition of sequences already in a database should be avoided.

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 fundamen-

tal 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

Manuscripts submitted to the journal must represent reports of original research, and the original data must be available for review by the editor if necessary.

All authors of a manuscript must have agreed to its submission and are responsible for its content (initial submission and any subsequent versions), including appropriate citations and acknowledgments, and must also have agreed that the corresponding author has the authority to act on their behalf in all matters pertaining to publication of the manuscript. The corresponding author is responsible for obtaining such agreements and for informing the coauthors of the manuscript's status throughout the submission, review, and publication process. For Authors' Corrections and Retractions, signed letters of agreement from all of the authors must be submitted (see "[Authors' Corrections](#)" and "[Retractions](#)" below).

By submission of a manuscript to the journal, **the authors guarantee that they have the authority to publish the work and that the manuscript, or one with substantially the same content, was not published previously, is not being considered or published elsewhere, and was not rejected on scientific grounds by another ASM journal.**

It is expected that the authors will provide written assurance that permission to cite unpublished data or personal communications has been granted.

By publishing in the journal, the authors agree that, subject to requirements or limitations imposed by laws or governmental regulations of the United States, any DNAs, viruses, microbial strains, mutant animal strains, cell lines, antibodies, and similar materials newly described in the article are available from a national collection or will be made available in a timely fashion, at reasonable cost, and in limited quantities to members of the scientific community for noncommercial purposes. The authors guarantee that they have the authority to comply with this policy either directly or by means of material transfer agreements through the owner.

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Posting of a method/protocol on a nonpersonal website should not interfere with the author's ability to have a manuscript utilizing that technique considered for publication in an ASM journal; however, ultimately, it is an editorial decision whether the method constitutes the substance of a paper.

Posting of a limited amount of original data on a personal/university/company website or websites of small collaborative groups working on a problem does not preclude subsequent submission to, and publication by, an ASM journal. The posted data, however, may not constitute the substance of the submission. Specific questions about this policy may be referred to the Publications Board chairman on a case-by-case basis.

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Posting of unpublished sequence data on the Internet is usually not considered prior publication; however, the address (URL) where the sequence is posted should be included in the text.

Preliminary disclosures of research findings webcast as meeting presentations or published in abstract form as adjuncts to a meeting, e.g., part of a program, are not considered prior publication.

It is incumbent upon the author to acknowledge any prior publication, including his/her own articles, of the data contained in a manuscript submitted to an ASM journal. A copy of the relevant work should be submitted with the paper as supplemental material.

Ultimately, it is an editorial decision whether the material constitutes the substance of a paper.

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A study group, surveillance team, working group, consortium, or the like (e.g., the Active Bacterial Core Surveillance Team) may be listed as a coauthor in the byline if its contributing members satisfy the requirements for authorship and accountability as described in these Instructions. The names (and institutional affiliations if desired) of the contributing members only may be given in a footnote keyed to the study group name in the byline or as a separate paragraph in the Acknowledgments section.

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The use of human subjects or other animals for research purposes is regulated by the federal government and individual institutions. Manuscripts containing information related to human or animal use should clearly state that the research has complied with all relevant federal guidelines and institutional policies. Copies of these guidelines and policy statements must be available for review by the editor if necessary.

Patient Identification

When isolates are derived from patients in clinical studies, do not identify them by using the patients' initials, even as part of a strain designation. Change the initials to numerals or use randomly chosen letters. Do not give hospital unit numbers; if a designation is needed, use only the last two digits of the unit. (Note: established designations of some viruses and cell lines, although they consist of initials, are acceptable [e.g., JC virus, BK virus, and HeLa cells].)

Nucleotide and Amino Acid Sequences

It is expected that newly determined nucleotide and/or amino acid sequence data will be deposited and GenBank/EMBL/DDBJ accession numbers will be included in the manuscript no later than the modification stage of the review process. It is also expected that the sequence data will be released to the public no later than the publication (online posting) date of the accepted manuscript. The accession numbers should be included in a separate paragraph at the end of the Materials and Methods section for full-length papers or at the end of the text for short-form papers. If conclusions in a manuscript are based on the analysis of sequences and a GenBank/EMBL/DDBJ accession number is not provided at the time of the review, authors should provide the sequence data as supplemental material.

It is expected that, when previously published sequence accession numbers are cited in a manuscript, the original citations (e.g., journal articles) will be included in the References section when possible or reasonable.

Authors are also expected to do elementary searches and comparisons of nucleotide and amino acid sequences against the sequences in standard databases (e.g., GenBank) immediately before manuscripts are submitted and again at the proof stage.

Analyses should specify the database, and the date of each analysis should be indicated as, e.g., January 2009. If relevant, the version of the software used should be specified.

See "Presentation of Nucleic Acid Sequences" below 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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It is expected that coordinates for new structures of macromolecules determined by X-ray crystallography or cryo-electron microscopy will be deposited in the Protein Data Bank and that assigned identification codes will be included in the manuscript no later than the modification stage of the review process. It is also expected that the coordinates will be released to the public no later than the publication (online posting) date of the accepted manuscript. Authors are encouraged to send coordinates with their original submission, however, so that reviewers can examine them along with the manuscript. The accession number(s) should be listed in a separate paragraph at the end of the Materials and Methods section for full-length papers or at the end of the text for short-form papers.

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

Culture Deposition

AAC expects authors to deposit strains used in therapeutic activity assessments and studies of mechanisms of action, resistance, and cross-resistance in publicly accessible culture collections and to refer to the collections and strain numbers in the text. Since the authenticity of

subcultures of culture collection specimens that are distributed by individuals cannot be ensured, authors should indicate laboratory strain designations and donor sources as well as original culture collection identification numbers.

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The editorial style of ASM journals conforms to the *ASM Style Manual for Journals* (American Society for Microbiology, 2009, in-house document) and *How To Write and Publish a Scientific Paper*, 6th ed. (Greenwood Press, Westport, CT, 2006), as interpreted and modified by the editors and the ASM Journals Department.

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All manuscripts are considered to be confidential and are reviewed by the editors, members of the editorial board, or qualified ad hoc reviewers. To expedite the review process, authors must recommend at least three reviewers who have expertise in the field, who are not members of their institution(s), who have not recently been associated with their laboratory(ies), and who could not otherwise be considered to pose a conflict of interest regarding the submitted manuscript. At least one recommended reviewer must be a member of the journal's editorial board. Please provide, where indicated on the submission form, contact information for suggested reviewers who are not editorial board members.

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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.}
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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.}
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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.}*
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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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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 other than these must be converted to paths (or outlines) in the application with which they were created.

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.

To maximize online reproduction, 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). Color illustrations may also be supplied in the CMYK color mode; other than in color space, CMYK files must meet the same production criteria as RGB files.

Drawings

Submit graphs, charts, complicated chemical or mathematical formulas, diagrams, and other drawings as finished products not requiring additional artwork or typesetting. 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:

(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 lower.

(b) When applying multiple shades of gray, differentiate the gray levels by at least 20%.

(c) Never use levels of gray below 20% or above 70% as they will fade out or become totally black upon scanning and reduction.

(iii) Use thick, solid lines that are no finer than 1 point in thickness.

(iv) No type should be 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.

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 , and 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* (RSC Publishing, Cambridge, United Kingdom, 2007); an abbreviated list is available at <http://www.oid.iupac.org/reports/1993/homann/index.html>. Thus, a representation of 20,000 cpm on a figure ordinate should 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 "10⁴ 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

Long 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 or 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, and 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 set forth in a legend only if the description 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 (below) 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 de-

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.

scriptions 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 (below) is an example of a well-constructed table.

Avoid tables (or figures) of raw data on drug susceptibility, therapeutic activity, or toxicity. Such data should be analyzed by an approved procedure, and the results should be presented in tabular form.

NOMENCLATURE

Chemical and Biochemical Nomenclature

The recognized authority for the names of chemical compounds is *Chemical Abstracts* (CAS; <http://www.cas.org>) and its indexes. *The Merck Index*, 14th ed. (Merck & Co., Inc., Whitehouse Station, NJ, 2006), 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), 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).

Molecular weight should not be expressed in daltons; molecular weight is a unitless ratio. Molecular mass is expressed in daltons.

For enzymes, use the recommended (trivial) name as 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 <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 Formulae of the Salmonella Serovars*, 9th ed. (P. A. D. Grimont and F.-X. Weill, WHO Collaborating Centre for Reference and Research on Salmonella, Institut Pasteur, Paris, France, 2007; see http://www.pasteur.fr/sante/clre/cadrecnr/salmoms/WKLM_2007.pdf). 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.

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 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.

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 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. 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 described 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) Phenotype 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. Phenotype 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, and 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). Phenotype designations should be defined.

(ii) Genotype designations are also indicated by three-letter locus symbols. In contrast to phenotype 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 only a single such locus exists or 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* gene of *E. coli* or strain K-12, respectively, may be used to distinguish this gene from the *his* gene in another species or strain. 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 *glnAp₁* and *glnAp₂*. 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., *ΔtrpA432*, *Δ(aroP-*

aceE)419, or Δ (*hisQ-hisJ*)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(*rnd-rmE*)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., *galT*236::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*:: Δ Mu *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 genetic maps of locus 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, orthologous 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/index.php>). 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.

For prokaryotes, gene names should not begin with prefixes indicating the genus and species from which the gene is derived. (However, subscripts may be used where necessary to distinguish between genes from different organisms or strains as described in section v of "Bacteria" above.) For eukaryotes, such prefixes may be used for clarity when discussing genes with the same name from two different organisms (e.g., *ScURA3* versus *CaURA3*); the prefixes are not considered part of the gene name proper and are not italicized.

Locus tags. Locus tags are systematic, unique identifiers that are assigned to each gene in GenBank. All genes mentioned in a manuscript should be traceable to their sequences by the reader, and locus tags may be used for this purpose in manuscripts to identify uncharacterized genes. However, since locus tags are not genetic names, they should appear in roman type rather than in italics. In addition, authors should check GenBank to make sure that they are using the correct, up-to-date format for locus tags (e.g., uppercase versus lowercase letters and presence or absence of an underscore, etc.). Locus tag formats vary between different organisms and also may be updated for a given organism, so it is important to check GenBank at the time of manuscript preparation.

"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 have 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").

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. Superscripts 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 *att*⁴³⁴ *imm*²¹ would represent a hybrid of phage λ that 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, and phage Mu, etc.) should follow the recommendations of Campbell et al. (*Gene* 5:197–206, 1979), with the modifications given in section vi of "Bacteria" 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 whenever 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 also gives 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, and 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, and GTP, etc. (for the respective 5' phosphates of adenosine and other nucleosides) (add 2', 3', or 5' - when needed for contrast); ATPase and dGT-Pase, etc. (adenosine triphosphatase and 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) and poly(dT), etc. (polyadenylic acid and 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-hydroxyethyl-piperazine-*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)	
concn (concentration)	sp act (specific activity)
diam (diameter)	sp gr (specific gravity)
expt (experiment)	temp (temperature)
exptl (experimental)	tr (trace)
ht (height)	vol (volume)
mo (month)	vs (versus)
mol wt (molecular weight)	wk (week)
no. (number)	wt (weight)
prepn (preparation)	yr (year)
SD (standard deviation)	

Drugs and pharmaceutical agents. Should an author decide to abbreviate the names of antimicrobial agents in a manuscript, the following standard abbreviations are strongly recommended.

(i) Antibacterial agents. Amikacin, AMK; amoxicillin, AMX; amoxicillin-clavulanic acid, AMC; ampicillin, AMP; ampicillin-sulbactam, SAM; azithromycin, AZM; azlocillin, AZL; aztreonam, ATM; carbenicillin, CAR; cefaclor, CEC; cefadroxil, CFR; cefamandole, FAM; cefazolin, CFZ; cefdinir, CDR; cefditoren, CDN; cefepime, FEP; cefetamet, FET; cefixime, CFM; cefmetazole, CMZ; cefonicid, CID; cefoperazone, CFP; cefotaxime, CTX; cefotetan, CTT; cefoxitin, FOX; cefpodoxime, CPD; cefprozil, CPR; ceftazidime, CAZ;

ceftibuten, CTB; ceftizoxime, ZOX; ceftriaxone, CRO; cefuroxime (axetil or sodium), CXM; cephalixin, LEX; cephalothin, CEF; cephalirin, HAP; cephradine, RAD; chloramphenicol, CHL; cinoxacin, CIN; ciprofloxacin, CIP; clarithromycin, CLR; clinafloxacin, CLX; clindamycin, CLI; colistin, CST; daptomycin, DAP; dicloxacillin, DCX; dirithromycin, DTM; doxycycline, DOX; enoxacin, ENX; erythromycin, ERY; fleroxacin, FLE; fosfomycin, FOF; gatifloxacin, GAT; gentamicin, GEN; grepafloxacin, GRX; imipenem, IPM; kanamycin, KAN; levofloxacin, LVX; linezolid, LZD; lomefloxacin, LOM; loracarbef, LOR; meropenem, MEM; methicillin, MET; mezlocillin, MEZ; minocycline, MIN; moxalactam, MOX; moxifloxacin, MXF; nafcillin, NAF; nalidixic acid, NAL; netilmicin, NET; nitrofurantoin, NIT; norfloxacin, NOR; ofloxacin, OFX; oxacillin, OXA; penicillin, PEN; piperacillin, PIP; piperacillin-tazobactam, TZP; polymyxin B, PMB; quinupristin-dalfopristin (Synercid), Q-D; rifabutin, RFB; rifampin, RIF; rifapentine, RFP; sparfloxacin, SPX; spectinomycin, SPT; streptomycin, STR; teicoplanin, TEC; telithromycin, TEL; tetracycline, TET; ticarcillin, TIC; ticarcillin-clavulanic acid, TIM; tigecycline, TGC; tobramycin, TOB; trimethoprim, TMP; trimethoprim-sulfamethoxazole, SXT; trovafloxacin, TVA; and vancomycin, VAN.

(ii) β-Lactamase inhibitors. Clavulanic acid, CLA; sulbactam, SUL; and tazobactam, TZB.

(iii) Antifungal agents. Amphotericin B, AMB; clotrimazole, CLT; flucytosine, 5FC; fluconazole, FLC; itraconazole, ITC; ketoconazole, KTC; nystatin, NYT; terbinafine, TRB; and voriconazole, VRC.

(iv) Antiviral agents. Acyclovir, ACV; cidofovir, CDV; famciclovir, FCV; foscarnet, FOS; ganciclovir, GCV; penciclovir, PCV; valacyclovir, VCV; and zidovudine, AZT.

The use of “nonstandard” abbreviations to designate names of antibiotics and other pharmaceutical agents generally will not be accepted, because the use of different abbreviations for a single agent has often caused confusion. If, on occasion, a nonstandardized abbreviation for a drug or pharmaceutical substance is used, it will be accepted under the following conditions: (i) it must be defined in an abbreviation paragraph in Materials and Methods or at the first use in the text, (ii) it must be unambiguous in meaning, and (iii) it must contribute to ease of assimilation by readers.

Chemical or generic names of drugs should be used; the use of trade names is not permitted. Designation of β-lactam antibiotics by generation is discouraged. When code names or corporate proprietary numbers are to be used, either the chemical structure of the compound or a published literature reference illustrating the chemical structure, if known, must be provided at the first occurrence of the code name or number. For compounds not identified by generic nomenclature, all previous or concurrent identification numbers or appellations should be listed in the manuscript.

Pharmacodynamic terminology. Pharmacodynamic indices (PDIs) must be introduced at their first occurrence in the text and follow guidelines set forth by Mouton et al. (*J. Antimicrob. Chemother.* **55**:601–607, 2005). In Materials and Methods, it should be clearly stated how the PDIs were derived. The most common indices used are the following: AUC/MIC ratio (the area under the concentration-time curve over 24 h in steady state divided by the MIC), AUIC (the area under the inhibitory curve; note that the AUC/MIC ratio is not equal to the AUIC), $\%T_{\text{MIC}}$ (the cumulative percentage of a 24-h period that the drug concentration exceeds the MIC under steady-state pharmacokinetic conditions), $C_{\text{max}}/\text{MIC}$ ratio (the peak level divided by the MIC), PTA (probability of target attainment), and CFR (cumulative fraction of response). Clear distinction should be made between $\%T_{\text{MIC}}$, which is expressed as a percentage of the dosing interval, and T_{MIC} , expressed in hours. It is strongly recommended that the prefix *f* be used with an index (e.g., *f*AUC) if the free, unbound fraction of the drug is meant.

β -Lactamases

Studies performed to characterize a β -lactamase or the interaction of a compound with a β -lactamase (i.e., as a substrate, inhibitor, or inducer) should follow the guidelines set forth by Bush and Sykes (*Antimicrob. Agents Chemother.* **30**:6–10, 1986). Assays that measure the hydrolysis of β -lactam antibiotics must be appropriate for the substrate examined (e.g., iodometric methods are not appropriate quantitative assays for substrates whose products are unknown). Reproducibility of results must be shown. When referring to β -lactamases, please use the functional designations defined by Bush et al. (*Antimicrob. Agents Chemother.* **39**:1211–1233, 1995). Alternatively, if the amino acid sequence for the enzyme is known, the β -lactamases may be described by molecular class as initiated by Ambler (*Phil. Trans. R. Soc. Lond.* **289**:321–331, 1980).

A database of defining amino acid alterations for new β -lactamases is maintained at the Internet address <http://www.lahey.org/studies/> and is also accessible via the ASM home page at <http://www.asm.org/>. It should be consulted before a new designation is proposed.

In Vitro Susceptibility Tests

Tabulate results of determinations of minimal inhibitory and bactericidal concentrations according to the range of concentrations of each antimicrobial agent required to inhibit or kill the members of a species or of each group of microorganisms tested, as well as the corresponding concentrations required to inhibit 50 and 90% of the strains (MIC_{50} and MIC_{90} , respectively) and those required to kill 50 and 90% of the strains (MBC_{50} and MBC_{90} , respectively). The MIC_{50} and MIC_{90} reported should be the actual concentrations tested that inhibited 50 and 90%, respectively, of the strains. They should not be values calculated from the actual data obtained. When only six to nine isolates of a species are

tested, tabulate only the MIC range of each antimicrobial agent tested.

If more than a single drug is studied, insert a column labeled “Test agent” between the columns listing the organisms and the columns containing the numerical data and record data for each agent in the same isolate order. Cumulative displays of MICs or MBCs in tables or figures are acceptable only under unusual circumstances.

The percentage of strains susceptible and/or resistant to an antibiotic at its breakpoint concentration may be given only if an appropriate breakpoint has been approved, as by the Clinical and Laboratory Standards Institute, 940 W. Valley Rd., Suite 1400, Wayne, PA 19087-1898. In the absence of approved breakpoints, authors cannot assign breakpoints or use breakpoints from related antibiotics. An exploratory analysis tabulating the percentage of strains inhibited over a range of concentrations is acceptable.

Bactericidal tests must be performed with a sufficient inoculum ($>5 \times 10^5$ CFU/ml) and subculture volume (0.01 ml) to ensure accurate determination of the 99.9% killing endpoint, as described by Pearson et al. (*Antimicrob. Agents Chemother.* **18**:699–708, 1980) and Taylor et al. (*Antimicrob. Agents Chemother.* **23**:142–150, 1983). Inoculum size and subculture volume are also critical to studies of combinations of antimicrobial agents.

Synergy is defined in two-dimensional or checkerboard tests when the fractional inhibitory concentration (FIC) or fractional bactericidal concentration (FBC) index (Σ) is ≤ 0.5 . In killing curves, synergy is defined as a ≥ 2 -log₁₀ decrease in CFU per milliliter between the combination and its most active constituent after 24 h, and the number of surviving organisms in the presence of the combination must be ≥ 2 log₁₀ CFU/ml below the starting inoculum. At least one of the drugs must be present in a concentration which does not affect the growth curve of the test organism when used alone. Antagonism is defined by a ΣFIC or ΣFBC of >4.0 .

When standard twofold-dilution schemes are used to determine checkerboard interactions, the inherent variability of the method casts doubt on the significance of interactions represented by ΣFICs or ΣFBCs of >0.5 but ≤ 4 . Therefore, such interactions, if labeled at all, should be termed “indifferent.” Alternatively, indices in this range may be described as “nonsynergistic” or “nonantagonistic,” as appropriate. The technically imprecise term “additive” should be avoided as it is too easily misunderstood. See reports by W. R. Greco et al. (*Pharmacol. Rev.* **47**:331–385, 1995), F. C. Odds (*J. Antimicrob. Chemother.* **52**:1, 2003), and M. D. Johnson et al. (*Antimicrob. Agents Chemother.* **48**:693–715, 2004) for further discussion of these issues.

For killing curve tests, the minimal, accurately countable number of CFU per milliliter must be stated and the method used for determining this number must be described. In the absence of any drug and with a sample size of 1 ml, this number is 30 (1.5 in log₁₀) CFU. If

procedures for drug inactivation or removal have not been performed, the author must state how drug carryover effects were eliminated or quantified. For drugs showing an inoculum effect, mere dilution below the MIC obtained in standard tests is not sufficient.

Clinical Trials

(i) Criteria for enrollment. The methods used to find and enroll patients and the criteria for enrollment in a clinical trial should be stated. In addition, the time period (month/year to month/year) of the enrollment should be specified. It should be indicated, if appropriate, that written informed consent was obtained and that the trial was approved by the pertinent committee on human subjects.

(ii) Method of randomization. Randomized, double-blind studies are preferred. Comparisons using historical controls are usually regarded as questionable unless the differences in outcome between the groups are dramatic and almost certainly the result of the new intervention. The rationale for the choice of the control group should be explained. The sample size should be justified, and the method of randomization should be stated.

(iii) Criteria for determining whether a case is evaluable. The minimum criteria for evaluability should be stated explicitly. For example, it should be stated that the minimum criterion for evaluability was *a* or the combination of *b* and *c* rather than *a*, *b*, and *c* without designating which were the minimum criteria. The criteria for evaluability are usually different from those for enrollment.

(iv) Reasons for nonevaluability. State the number of patients in each group who were excluded from evaluation and the reason(s) for each exclusion.

(v) Criteria for assessment. Define each outcome for each category of assessment (e.g., "clinical outcomes were classified as cure, improvement, and failure; microbiological outcomes were classified as eradication, persistence, and relapse"). The frequency and timing of such assessments in relation to treatment should be stated. Specify any changes made in the study regimen(s) during the trial; the results for regimens with and without such modification generally should be stated separately. The criteria (questionnaires, results of specific laboratory tests) for evaluation of adverse effects should be stated, as should the period encompassed in the assessment and the time of assessment in relation to the time of treatment (e.g., daily during treatment). Some authors prefer to consider superinfections as failures of treatment, whereas others prefer to consider them separately or even as adverse effects. In any event, the manuscript should state the number of superinfections with each regimen and should differentiate between superinfections and colonization. The duration of follow-up should be mentioned.

(vi) Statistical analyses. The type of statistical test should be stated and, when appropriate, the reason for the choice of test should be given. References should be given for statistical procedures other than the *t* test, chi-square test, and Wilcoxon rank sum test. The comparability of the treatment groups at the baseline should be evaluated statistically.

For a review of some common errors associated with statistical analyses and reports, plus guidelines on how to avoid them, see the article by C. 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).

(vii) Beta error. For trials which show no statistically significant difference between regimens, the authors should calculate the probability (β) of a type II error and the power of the study ($1 - \beta$) to detect a specified clinically meaningful difference in efficacy between the regimens. For further details, see Freiman et al. (*N. Engl. J. Med.* **299**:690–694, 1978). Alternatively, or in addition, the authors should indicate the magnitude of difference between the regimens that could have been detected at a statistically significant level with the number of evaluable patients studied.

For further details, see the editorial on guidelines for clinical trials (*Antimicrob. Agents Chemother.* **33**:1829–1830, 1989).

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 10^3 . Avoid compound prefixes such as m μ or $\mu\mu$. Use $\mu\text{g/ml}$ or $\mu\text{g/g}$ in place of the ambiguous ppm. Units of temperature are presented as follows: 37°C or 324 K.

When fractions are used to express units such 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 " $\mu\text{mol/g}$ " is preferable to "nmol/ μg ." It is also preferable that an unambiguous form such as exponential notation be used; for example, " $\mu\text{mol g}^{-1} \text{min}^{-1}$ " is preferable to " $\mu\text{mol/g/min}$." Always report numerical data in the appropriate 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).

Isotopically Labeled Compounds

For simple molecules, labeling is indicated in the chemical formula (e.g., $^{14}\text{CO}_2$, $^3\text{H}_2\text{O}$, and $\text{H}_2^{35}\text{SO}_4$). 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 square 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- $[\text{U-}^{14}\text{C}]$ glucose
L- $[\text{methyl-}^{14}\text{C}]$ methionine	<i>E. coli</i> $[\text{P-}^{32}]$ DNA
$[\text{2,3-}^3\text{H}]$ serine	fructose 1,6- $[\text{1-}^{32}\text{P}]$ bisphosphate
$[\alpha\text{-}^{14}\text{C}]$ lysine	
$[\gamma\text{-}^{32}\text{P}]$ ATP	

AAC 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).