SCOPE

Clinical and Vaccine Immunology (CVI) is devoted to the advancement and dissemination of new knowledge about all aspects of the immune response in health, in disease, and after vaccination. CVI will welcome studies of (i) cellular and humoral immunity in humans and animals; (ii) immunological and immune-mediated disorders, including relevant new animal models for immunologic diseases; (iii) microbial immunology; (iv) viral immunopathogenesis; (v) assay development, standardization, quality control, normal reference values, and biostatistical issues; and (vi) immunoepidemiology.

In addition, the journal will publish articles on all aspects of immunization and vaccine research, including (i) development and evaluation of vaccines; (ii) mechanisms of vaccine action; (iii) the immune response to vaccines in humans and animals; (iv) studies of vaccine vectors, adjuvants, and immunomodulators; (v) immunological correlates of vaccine efficacy; and (vi) clinical trials, including phases 1 through 3.

ASM publishes a number of journals covering various aspects of microbiology. Each journal has a prescribed scope that must be considered in determining where to submit a manuscript. Papers with a primary immunological or vaccine focus are suitable for CVI; those with a primary focus on a microbe, an infectious process, a mechanism of microbial pathogenesis or host response, or animal models for microbial diseases are best directed to one of the other ASM journals. The following guidelines may be of assistance.

(i) Papers developing or evaluating animal models for human immune disease and dysfunction are appropriate for CVI; those dealing with development of animal models of microbial pathogenesis should be sent to Infection and Immunity.

(ii) Papers with a primary focus on the immunology and immunopathogenesis of human viral infections are appropriate for CVI; those using an immunologic approach to basic virology research are more appropriate for the Journal of Virology.

(iii) Papers that focus on the immunologic aspects of development and evaluation of vaccines in humans and animals, including clinical trials, may be sent to CVI; studies that focus on establishing a proof of principle using nonviral microbial antigens as immunogens or that describe the construction and initial evaluation of novel bacterial vectors are suitable for Infection and Immunity.

Commentaries, intended to raise issues and engender discussion, will occasionally be solicited by the CVI editors.

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.

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EDITORIAL POLICY

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Newly determined nucleotide and/or amino acid sequence data must be deposited and GenBank/EMBL/DDBJ accession numbers must be included in the manuscript no later than the modification stage of the review process. It is 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 Notes. 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.

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See “Presentation of Nucleic Acid Sequences” for nucleic acid sequence formatting instructions.

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To comply with recommendations from the International Nucleotide Sequence Database (INSD) Collaborators and to avoid conflicts in gene identification, researchers should implement the following two fundamental guidelines as standards for utilization of locus tags in genome analysis, annotation, submission, reporting, and publication. (i) Locus tag prefixes are systematic gene identifiers for all of the replicons of a genome and as such should be associated with a single genome project submission. (ii) New genome projects must be registered with INSD, and new locus tag prefixes must be assigned in cooperation with INSD to ensure that they conform to the agreed-upon criteria. Locus tag prefixes that are currently in use may be searched at the NCBI locus tag database (http://www.ncbi.nlm.nih.gov/genomes/lftp.cgi).

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SUBMISSION, REVIEW, AND PUBLICATION PROCESSES

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1. Alexander, T. W., et al. 2008. Effect of subtherapeutic administration of antibiotics on the prevalence of antibiotic-resistant Escherichia coli bacteria in feedlot cattle. Appl. Environ. Microbiol. 74:4405–4416.
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, 295Al 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.}
7. Forman, M. S., and A. Valsamakis. 2003. Specimen collection, transport, and processing: virology, p. 1227–1241. In P. R. Murray, E. J. Baron, M. A. Pfaller, J. H. Jorgensen, and R. H. Yolken (ed.), Manual of clinical microbiology, 8th ed. ASM Press, Washington, DC.
8. Garcia, C. O., et al. 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 methylo trophic 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, CA. {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.}
13. Smith, D., C. Johnson, M. Maier, and J. J. Maurer. 2005. Distribution of fimbrial, phage and plasmid associated virulence genes among poultry Salmonella enterica serovars, abstr. P-038, p. 445. Abstr. 105th Gen. Meet. Am. Soc. Microbiol. American Society for Microbiology, Washington, DC. {Abstract title is optional.}
14. Stratagene. 2006. Yeast DNA isolation system: instruction manual. Stratagene, La Jolla, CA. (Use the company name as the author if none is provided for a company publication.)

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nine and polyamines. In R. Curtiss III et al. (ed.), EcoSal—Escherichia coli and Salmonella: cellular and molecular biology. ASM Press, Washington, DC. http://www.ecosal.org/. {Note that each chapter has its own posting date.}

2. Dionne, M. S., and D. S. Schneider. 2002. Screening the fruity immune system. Genome Biol. 3: REVIEWS1010. http://genomebiology.com/2002/3/4/reviews/1010.

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. U. S. A. 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).
... system was used (J. L. McInerney, A. F. Holden, and P. N. Brighton, submitted for publication).
... as described previously (M. G. Gordon and F. L. Rattner, presented at the Fourth Symposium on Food Microbiology, Overton, IL, 13 to 15 June 1989). {For nonpublished abstracts and posters, etc.}
... 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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600 dpi for combination art (lettering and images)
1,200 dpi for line art

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

Maximum width for a 1-column figure: 3\(\frac{3}{16}\) inches (ca. 8.4 cm)
Maximum width for a 2-column figure: 6\% inches (ca. 17.4 cm)
Minimum width for a 2-column figure: 4 1/4 inches (10.8 cm)
Maximum height: 9 3/16 inches (23.0 cm)

Contrast. Illustrations must contain sufficient contrast to be viewed easily on a monitor or on the printed page.

Labeling and assembly. All final lettering and labeling must be incorporated into the figures. On initial submission, illustrations should be provided as PDF files, with the legend beneath each image, to assist review. At the modification stage, production quality digital figure files must be provided, along with text files for the legends. Put the figure number 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: Arial, Helvetica, Times Roman, European PI, Mathematical PI, or Symbol. Courier may be used but should be limited to nucleotide or amino acid sequences, where 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. When figure files are uploaded to the manuscript submission and peer review system, they may be compressed with WinZip.

Color illustrations. Color costs must be borne by the author. See “Publication Fees.” All figures submitted in color will be processed as color. Adherence to the following guidelines will help to minimize costs and to ensure color reproduction that is as accurate as possible.

The online version is considered the version of record for CVI and all other ASM journals. 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). CMYK files are also accepted. Other than in color space, CMYK files must meet the same production criteria as RGB files. The RGB color space is the native color space of computer monitors and of most of the equipment and software used to capture scientific data, and it can display a wider range of colors (especially bright fluorescent hues) than the CMYK (cyan, magenta, yellow, black) color space used by print devices that put ink (or toner) on paper. For reprints, ASM’s print provider will automatically create CMYK versions of color illustrations from the supplied RGB versions. Color in the reprints may not match that in the online journal of record because of the smaller range of colors capable of being reproduced by CMYK color. For additional information on RGB versus CMYK color, refer to the Cadmus digital art site, http://art.cadmus.com/da/guidelinesRgb.jsp.

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.

When creating line art, please use the following guidelines:

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

(ii) Avoid using screens (i.e., shading) in line art. It can be difficult and time-consuming to reproduce these images without moiré patterns. Various pattern backgrounds are preferable to screens as long as the patterns are not imported from another application. If you must use images containing screens,

(a) Generate the image at line screens of 85 lines per inch or less.

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

(c) Never use levels of gray below 5% or above 95%, as they are likely to fade out or become totally black when output.

(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 ap-
propriate Système International d’Unités (SI) symbols (μ for 10⁻⁶, m for 10⁻³, k for 10³, and M for 10⁶, 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://old.iupac.org/reports/1993/homann/index.html. Thus, a representation of 20,000 cpm on a figure ordinate should be “2” and the label should be represented 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 of the ordinate should be “2” and the label should be “10⁴ cells per ml” (not “cells per ml x 10⁻⁴”). Likewise, an enzyme activity of 0.06 U/ml might be shown as 6 accompanied by the label 10⁻² U/ml. The preferred designation is 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 closely as possible to the same format.

Figure Legends

On initial submission, to assist review, the legend should be incorporated in the image file and appear beneath the figure. At the modification stage, figure legends must be provided as text files separate from the image file.

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). De-

| Antibody | No. of samples with V-Z virus-neutralizing antibody | Correlation (%) |
|----------|-----------------------------------------------------|-----------------|
| EIA      |                                                    |                 |
| Positive | 50                                                  | 94              |
| Negative | 3                                                   | 64              |
| IAHA     |                                                    |                 |
| Positive | 37                                                  | 87              |
| Negative | 16                                                  |                 |

* Sera from individuals without evidence of a current V-Z virus infection.
* Titer of >1/4.
* Titer of >1/8.

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 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 instruc-
tions 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. Authors of papers describing enzymological studies should review the standards of the STRENDA Commission for information required for adequate description of experimental conditions and for reporting enzyme activity data (http://www.beilstein-institut.de/en/projekte/strenda/guidelines/).

Drugs

Whenever possible, use generic names of drugs; the use of trade names is generally not permitted.

Amino Acid Sequences

Single-letter designations, rather than three-letter designations, should be used for sequences of amino acids.

Leukocyte Antigen Nomenclature

For clusters of differentiation nomenclature for leukocytes, refer to Leucocyte Typing (D. Mason et al., ed., Oxford University Press, New York, NY, 2002). For HLA nomenclature, refer to the work of Bodmer et al. (Hum. Immunol. 53:98–128, 1997).

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., it is used in a paper. Thereafter, the generic name should be used in the abstract and text. Use the EC number when one has been assigned. Authors of papers describing enzymological studies should review the standards of the STRENDA Commission for information required for adequate description of experimental conditions and for reporting enzyme activity data (http://www.beilstein-institut.de/en/projekte/strenda/guidelines/).

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 Typhimurium, S. Typhimurium, or 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/ip/portal/action/WebdriveActionEvent/oid/01s-000036-089). 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., American Society for Microbiology, Washington, DC, 1989) and the validation lists and notification lists published in the International Journal of Systematic and Evolutionary Microbiology (formerly the International Journal of Systematic Bacteriology) since January 1989. In addition, two sites on the World Wide Web list current approved bacterial names: 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.

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, 5th ed. (C. P. Kurtzman, J. W. Fell, and T. Boekhout, ed., Elsevier Science, Amsterdam, Netherlands, 2010), and Dictionary of the Fungi, 10th ed. (P. M. Kirk, P. F. Cannon, and J. A. Stalpers, ed., CABI Publishing, Wallingford, Oxfordshire, United Kingdom, 2008); see also http://www.speciesfungorum.org/Names/Fundic.asp.

Names used for viruses should be those approved by
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 chairperson: Maria Costanzo (maria@genomed.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) 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 OprA 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, 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. Lower-case 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 only a single such locus exists or if it is 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: the Coli Genetic Stock Center (http://cgsc.biology.yale.edu/). For the genus Salmonella, the registry is the Salmonella Genetic Stock Centre (http://people.ucalgary.ca/~kesander/). For the genus Bacillus, the registry is the Bacillus Genetic Stock Center (http://www.bgsc.org/).

(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 hisK-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., ΔnpA432, Δ(aroP-aceE)y419, 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(rmD-rmE)]. An insertion of an E. coli his gene into plasmid pSC101 at zero kilobases (0 kb) is shown as pSC101 0(0kb::K-12hisB)4. An alternative designation of an insertion can be used in simple cases, e.g., galT236::Tn3. 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−), ΔMu 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, parentheticals (or brackets) are used (λ, F−). Reference to an integrated episome is indicated as described for inserted elements, and an exogenote is shown as, for example, W3110/F’8(gal8)).

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.

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 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). 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 CaURA4); 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. 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 the 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 the 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”).

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 methyltransf erases, homing endonucleases, and their genes should be used. 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.

**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.

**Eukaryotes.** When naming genes for *Aspergillus* species, the nomenclature guidelines posted at http://www.aspergillus.org.uk/indexhome.htm?secure/sequence_info/nomenclature.htm~main should be followed, and the *Aspergillus* Genome Database (http://www.aspgd.org) should be searched to ensure that any new name is not already in use. For information about the genetic nomenclature of other eukaryotes, see the Instructions to Authors for *Eukaryotic Cell* and *Molecular and Cellular Biology*.

### 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 introduc-

ation 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 for 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.

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); eRNA (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 dGTPase, 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. (oligodeoxythymidyl 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:

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

**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 mm or μm. Use μg/ml or μg/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 "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 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).

**Statistics**

Statistical analysis of data is a crucial component of scientific publication. Authors who are unsure of proper statistical analysis should have their manuscripts checked by a qualified statistician.

The following is a list of important items that must be considered before manuscript submission. Deficiencies in any of these areas may delay review and/or publication.

(i) Statistical analyses should be performed on all quantitative data regardless of how significant the differences look in the tables or figures.

(ii) Data should be appropriately analyzed as parametric (normally distributed) or nonparametric data.

(iii) Parametric and nonparametric data should be presented appropriately. Means and standard deviations or standard errors are appropriate ways of presenting data analyzed by parametric analyses (i.e., t test and analysis of variance [ANOVA]), but only medians and surrounding levels (quartiles, quintiles, and 10th and 90th percentiles, etc.) are appropriate for nonparametric statistics (Mann-Whitney test and Kruskal-Wallis test, etc.). Means have no meaning in nonparametric analyses.

(iv) For any data in which there are more than two comparisons (i.e., between one control and more than one experimental group), an analysis must be done for multigroup comparisons. Such an analysis would usually be an ANOVA for parametric data or a Kruskal-Wallis test for nonparametric data. t tests cannot be used when more than two groups are being compared (except as indicated below). Failure to use multigroup tests generates type 1 errors: concluding that two data sets within the overall data set being compared are different when in fact they are not. Exception: some statisticians argue that two-group comparisons can be used on multigroup data if the expected outcomes are appropriately anticipated before the experiment. For example, data generated by individually testing two unrelated factors for their effects on a target with only a single, untreated target as a control could be appropriately analyzed by t tests instead of ANOVA.

(v) For all appropriate multigroup comparisons, two P values must be generated and provided in the manuscript. The main P value applies to the overall data set and indicates that within that data set at least two groups differ from each other. The overall P value does not indicate which two groups are different. The main P value and the overall P value should be computed by using a post hoc test. For ANOVA, these post hoc tests are usually Dunnett’s test (used to compare multiple experimental groups to a single control), the Fisher protected least significant difference (PLSD) test, the Tukey-Kramer test, and the Games-Howell test. Others may be used. Note that each post hoc test has certain underlying assumptions that may not be applicable to the data under analysis. For a Kruskal-Wallis nonparametric ANOVA, the Dunn procedure
is appropriate to generate $P$ values for two-group comparisons.

(vi) Data presented as endpoints (i.e., LD$_{50}$ and ID$_{50}$, etc.) contain both the calculated value and a confidence interval with a statistical significance associated with it (95%, 99%, or similar confidence interval), calculated by logit or probit analysis. Simple LD$_{50}$ values such as Reed-Muench calculations may not be used alone.

(vii) When samples are taken multiple times from one experimental entity (i.e., multiple serum samples from one animal, gross pathology scores measured for the same animal over time, and growth curves, etc.), one cannot use analyses such as $t$ tests, ANOVA, and the Mann-Whitney test, etc., because these tests assume that each measure is independent. An entity with a high score on day 1 is more likely to have a high score on day 2 than is an entity with a low score. It is likely that some expert statistical help will be needed for these situations, usually involving regression analysis or survival analysis, etc.

(viii) Statistical significance and biological significance are not the same. There is nothing magical about a $P$ value of 0.05. When results from large sample sizes are compared, a $P$ value of <0.05 will often be obtained, as $P$ value is a function of both sample size and effect size. If sample sizes are large, then more-rigorous (i.e., smaller) $P$ values may be desirable. If sample sizes are small, $P$ values of >0.05 may still be important. There should be both statistical and biological significance to the results and conclusions in the manuscript.

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).

Isotopically Labeled Compounds

For simple molecules, labeling is indicated in the chemical formula (e.g., $^{14}$CO$_2$, $^3$H$_2$O, and $H_2^{35}$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., $^{32}$S-ATP) or to a word that is not a specific chemical name (e.g., $^{131}$I-labeled protein, $^{14}$C-amino acids, and $^3$H-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
- L-$[^{methyl-^{14}$C}$]methionine
- $[2,3-^{3}$H$]$serine
- $[^{1}$H$]$lysine
- UDP-$[^{U-^{14}$C}$]glucose
- E. coli $[^{32}$P]$]$DNA
- fructose 1,6-$[^{1-^{32}$P}$]bisphosphate
- $[^{γ-^{32}$P}$]ATP

Because of the possibility of impurities in commercially available radiochemicals and the sensitivity of isotope detection, the purity of the radiochemicals must be determined when tracers are used.

CVI 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).