EUKARYOTIC CELL

2011 INSTRUCTIONS TO AUTHORS*

SCOPE

Eukaryotic Cell (EC) publishes reports of basic research on eukaryotic microorganisms such as yeasts, fungi, algae, protozoa, and social amoebae. Topics include but are not limited to basic biology; molecular and cellular biology; mechanisms, and control, of developmental pathways; structure and form inherent in basic biological processes; cellular architecture; metabolic physiology; comparative genomics, biochemistry, and evolution; ecology; and population dynamics.

Manuscripts should make genuine and novel contributions to understanding the molecular, cellular, or organismal biology or genetics of a eukaryotic microbe. The journal will consider manuscripts reporting results from the use of genome-, transcriptome-, or proteome-wide screening approaches when the experiments address a specific question or working hypothesis and when the results are used to illuminate mechanisms of gene regulation or interactions of signal transduction pathways via additional experiments. Studies that only catalog differences and similarities between genotypes or responses to stimuli are not likely to be reviewed favorably.

In addition, EC will consider manuscripts dealing with the viruses of these organisms and their organelles and with interactions with other living systems, where the focus is clearly on the eukaryotic cell.

Questions about these guidelines may be directed to the editor in chief.

ASM publishes a number of different journals covering various aspects of microbiology. Each journal has a prescribed scope that must be considered in determining the most appropriate journal for each manuscript. If transfer to another ASM journal is recommended by an editor, the corresponding author will be contacted.

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See “Presentation of Nucleic Acid Sequences” 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, http://www.ebi.ac.uk/EMBL/; and GenBank, National Center for Biotechnology Information, http://www.ncbi.nlm.nih.gov/.

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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/lLetter.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, 295, 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 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, CA. {Title is optional.}

12. Rotimi, V. O., N. O. Salako, E. M. Mohaddas, and L. P. Philip. 2005. Abstr. 45th Intersci. Conf. Anti-microb. 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 *Salmo-nella 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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2. Dionne, M. S., and D. S. Schneider. 2002. Screening the fruity immune system. Genome Biol. **3:**REVIEWS1010. http://genomewebiology.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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...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.}

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(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 appropriate Système International d'Unités (SI) symbols (µ for 10⁻⁶, m for 10⁻², k for 10³, and M for 10⁶, etc.). A complete listing of SI symbols can be found in the International...
TABLE 2. Specific activity of β-galactosidase produced from an integrated YIFBP1 promoter-lacZ fusion in Y. lipolytica grown in different carbon sources

| Strain and relevant genotype | YNB | YP | YNB | YP | YNB | YP | YNB | YP |
|-----------------------------|-----|----|-----|----|-----|----|-----|----|
| RJM007 YIFBP1              | 36 ± 5 | 14 ± 4 | 47 ± 4 | 12 ± 1 | 83 ± 6 | 36 ± 3 | 70 ± 5 | 23 ± 5 |
| RJM008 Ylfip1::URA3         | 97 ± 13 | 33 ± 2 | 94 ± 15 | 23 ± 5 | 297 ± 15 | 182 ± 6 | 372 ± 13 | 189 ± 10 |

*Y. lipolytica* strains RJM007 and RJM008, wild type and Ylfip1::URA3, respectively, bearing a fusion of the YIFBP1 promoter to *E. coli* lacZ integrated into the chromosomal YLEU2 locus (see Materials and Methods) were cultured in minimal or rich medium with the indicated carbon sources, and β-galactosidase was assayed as described in Materials and Methods. Results are the mean values ± the standard errors of the means of the results from four independent cultures.

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/RSC/Publishing/1993/homann/index.html. Thus, representation of 20,000 cpm on a figure ordinate should be made by the number 20 accompanied by the label kcpm.

Where 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 should be “2” and the label should be “10^4 cells per ml” (not “cells per ml × 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 nearly 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). 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 Microsoft 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 and is being submitted in Rapid Review, 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 of these Instructions for those that should be used in tables. Explanatory footnotes are acceptable, but more-extensive table “legends” are not. Footnotes should not include detailed descriptions of the experiment. Tables must include enough information to warrant table format; those with fewer than six pieces of data will be incorporated into the text by the copy editor. Table 2 from Eukaryot. Cell 7:1742–1749, 2008, is an example of a well-constructed table.

Cover Photographs and Drawings

EC publishes photographs and drawings on the front cover. Invitations are issued to authors whose manuscripts are returned for modification or whose manuscripts have been accepted for publication in EC; material should be related to the work presented in the manuscript. Unsolicited photos will also be considered. No material submitted for consideration will be returned to the author. Authors will be notified only if their cover art is selected. Copyright for the chosen material must
be transferred to ASM. A short description of the cover material will be included. Technical specifications for submission are available from the cover editor, Michael Lorenz (Michael.Lorenz@uth.tmc.edu).

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/biblog/white.html, and the instructions to authors of the Journal of Biological Chemistry and the Archives of Biochemistry and Biophysics (first issues of each year).

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

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

Nomenclature of Mice

For mouse strain and genetic nomenclature, ASM encourages authors to refer to the guidelines set forth by the International Committee on Standardized Genetic Nomenclature for Mice, available on the Mouse Genome Database home page at http://www.informatics.jax.org/ and in Genetic Variants and Strains of the Laboratory Mouse, 3rd ed. (M. F. Lyon et al., ed., Oxford University Press, Oxford, England, 1996).

Nomenclature of Microorganisms

Binary names, consisting of a generic name and a specific epithet (e.g., Saccharomyces cerevisiae), 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., S. cerevisiae), 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 in the manuscript; strain designations and numbers are not.

The spelling of bacterial names should follow the Approved Lists of Bacterial Names (Amended) & Index of the Bacterial and Yeast Nomenclatural Changes (V. B. D. Skerman et al., ed., American Society for Microbiology, Washington, DC, 1989) and the validation lists and notification lists published in the International Journal of Systematic and Evolutionary Microbiology (formerly the International Journal of Systematic Bacteriology) since January 1989. In addition, two sites on the World Wide Web list current approved bacterial names: 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/).

Since the classification of fungi is far from complete, it is the responsibility of the author to determine the accepted binomial for a given organism. Sources for these names include The Yeasts: a Taxonomic Study, 5th ed. (C. P. Kurtzman, J. W. Fell, and T. Boekhout, ed., Elsevier Science, Amsterdam, Netherlands, 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 the International Committee on Taxonomy of Viruses (ICTV) and reported on the ICTV Virus Taxonomy website (http://www.ictvonline.org/index.asp). In addition, the recommendations of the ICTV regarding the use of species names should generally be followed: when the entire species is discussed as a taxonomic entity, the species name, as with other taxa, is italic and has the first letter and any proper nouns capitalized (e.g., Tobacco mosaic virus, Murray Valley encephalitis virus). When the behavior or manipulation of individual viruses is discussed, the vernacular (e.g., tobacco mosaic virus, Murray Valley encephalitis virus) should be used. If desired, synonyms may be added parenthetically when the name is first mentioned. Approved generic (or group) and family names may also be used.

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

Genetic Nomenclature

To facilitate accurate communication, it is important that standard genetic nomenclature be used whenever possible and that deviations or proposals for new nam-
ing 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@genome.stanford.edu). Such a consultation should be mentioned in the manuscript submission letter.

Eukaryotes. The nomenclature used for the genetics of lower eukaryotic microorganisms has not been as well formalized as that for bacteria and bacteriophages. Generally, authors should conform to current practices in identifying mutants and their genotypes. For organisms not mentioned below, it is advisable to consult the Handbook of Microbiology, 2nd ed. (A. I. Laskin and H. A. Lechevalier, ed., CRC Press, Boca Raton, FL, 1988) or the Handbook of Genetics, vol. 1, Bacteria, Bacteriophages, and Fungi (R. C. King, ed., Plenum Publishing Corp., New York, NY, 1974).

Gene names may begin with prefixes to indicate the genus and species from which the gene is derived only when needed 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. The genetic nomenclature of Dictostelium is summarized in the Trends in Genetics “Genetic Nomenclature Guide” (p. S.5–S.6; Elsevier Science Ltd., Cambridge, United Kingdom, 1998; out of print). The most recent modifications can be found at http://dictybase.org/.

For Saccharomyces cerevisiae, a gene name should always be indicated in italics and, for the wild-type locus (or dominant alleles), capital letters (e.g., URA3). Loss-of-function (hypomorphic) or altered-function (neomorphic) alleles of the same locus should always be indicated in italics and, for the wild-type locus designated in italics and lowercase letters (e.g., ura3Δ). The product of a gene (i.e., a protein) should be indicated in roman type with an initial capital letter (e.g., Ura3). There is generally no need to add the suffix “p” to the symbol for a protein; however, in rare instances where it may be deemed necessary to indicate unambiguously that the symbol refers to a protein, the “p” suffix may be added (e.g., Ura3p). For the most recent information on S. cerevisiae gene names, consult the Saccharomyces Genome Database (SGD) at http://www.yeastgenome.org/. Details on the format of S. cerevisiae locus and allele designations are provided in the SGD and are also described by Cherry (Trends Genet. March:11–12, 1995) (available for download as a PDF file at SGD, http://www.yeastgenome.org/sgdup/Saccharomyces_cerevisiae.pdf). Authors should use standard S. cerevisiae gene names, as listed in the SGD, in their submitted manuscripts and register new gene names with the SGD no later than the modification stage.

The most recent information for Neurospora crassa can be found in The Neurospora Compendium: Chromosomal Loci (D. R. Perkins et al., Academic Press, San Diego, CA, 2001). When naming genes for Aspergillus species, the nomenclature guidelines posted at http://www.aspergillus.org.uk/indexhome.htm?secure/sequence_info/nomenclature.html—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. The 1998 Trends in Genetics “Genetic Nomenclature Guide” (Elsevier Science Ltd., Cambridge, United Kingdom; out of print) contains nomenclature guidelines for several eukaryotic microbes: Schizosaccharomyces pombe (p. S.7–S.9), Chlamydomonas reinhardtii (p. S.18–S.19), Neurospora crassa (p. S.14–S.15), and Aspergillus nidulans (p. S.12–S.13). In addition, for S. pombe, the websites http://www.sanger.ac.uk/Projects/S_pombe/SP_Name_FAQ.shtml and http://www-bcf.usc.edu/~forsburg/plasmids.html may be helpful, and for C. reinhardtii, use http://www.chlamy.org/nomenclature.html.

For Trypanosoma and Leishmania, consult the article by Clayton et al. (Mol. Biochem. Parasitol. 97:221–224, 1998).

FlyBase (http://flybase.org/) is the genetic nomenclature authority for Drosophila melanogaster. WormBase (http://wormbase.org/) is the genetic nomenclature authority for Caenorhabditis elegans.

For the most recent information on Candida albicans, consult the Candida Genome Database (CGD) at http://www.candidagenome.org. Details on the format of C. albicans gene nomenclature are described at http://www.candidagenome.org/Nomenclature.shtml. Authors should use standard C. albicans gene names, as listed in the CGD, in their submitted manuscripts and should register new gene names with the CGD no later than the modification stage.

Prokaryotes. The genetic properties of prokaryotes 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. Use the recommendations of Demerec et al. (Genetics 54:61–76, 1966) as a guide to the use of these terms. If your manuscript contains genetic nomenclature, please refer to the Instructions to Authors in the January issue of the Journal of Bacteriology.

Viruses. In most cases, viruses have no phenotype, since they have no metabolism outside host cells. Therefore, distinctions between phenotype and genotype are not made. Superscripts are used to indicate hybrid genomes. Genetic symbols may be one, two, or three letters. For example, a mutant strain of lambda may be designated cI857 int2 red11A Aam11; this strain carries mutations in genes cI, int, and red and an amber-suppressible (am) mutation in gene A. 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.
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 organism 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, the GenBank locus tag may be used to designate the gene; it should not be 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.

“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.

“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.

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 referred to in the Instructions to Authors in the Journal of Bacteriology.

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). Use 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. 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.

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 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);
cRNA (complementary RNA); RNase (ribonuclease); DNase (deoxyribonuclease); tRNA (ribosomal RNA); mRNA (messenger 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. (polyadenylcylic 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'-tetraacetic acid]; HEPES (N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid); PCR (polymerase chain reaction); and AIDS (acquired immunodeficiency syndrome). Abbreviations for cell lines (e.g., HeLa) also need not be defined.

The following abbreviations should be used without definition in tables:

- **amt**: amount
- **approx**: approximately
- **av**: average
- **concn**: concentration
- **diam**: diameter
- **expt**: experiment
- **exptl**: experimental
- **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 10³.

Avoid compound prefixes such as mµ or µµ. 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 “mmol/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.

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, isotopic labeling is indicated in the chemical formula (e.g., 14CO₂, 3H₂O, and H₂35SO₄). 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., 32S-ATP) or to a word which is not a specific chemical name (e.g., 131I-labeled protein, 14C-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. Abbreviation symbols and modifiers precede the isotopic symbol. The following examples illustrate correct usage:

- [14C]urea
- [1-14C]methionine
- [32P]ATP
- UDP-[U-14C]glucose
- E. coli [13C]DNA
- [2,3-3H]serine
- [α-14C]lysine
- [5-32P]bisphosphate

EC 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).