Scientific Style

Availability of viruses, mutants/variants, cells
Submission of a manuscript implies that all viruses, novel mutants and variants, genes, plasmids, vector constructs, and cell lines described in the manuscript will be made freely available for distribution upon request to all qualified members of the scientific community for research purposes.

Nucleotide sequence data
Only in exceptional circumstances will long sequences be published. New nucleotide data must be submitted and deposited in the DDBJ/EMBL/GenBank databases and an accession number obtained before the paper can be accepted for publication. Submission to any one of the three collaborating databanks is sufficient to ensure data entry in all. The accession number should be included in the manuscript e.g., as a footnote on the title page: ‘Note: Nucleotide sequence data reported are available in the DDBJ/EMBL/GenBank databases under the accession number(s)----’. If requested, the database will withhold release of data until publication. The most convenient method for submitting sequence data is by World Wide Web:
- DDBJ via SAKURA: http://sakura.ddbj.nig.ac.jp/
- EMBL via WEBIN: http://www.ebi.ac.uk/embl/Submission/webin.html
  or stand-alone submission tool Sequin:

For special types of submissions (e.g., genomes, bulk submissions, etc.) additional submission protocols are available from the above sites.

Papers dealing mainly with sequences will be considered for publication as " Original Article " or " Brief Report " only if the genomic organisation derived from the reported nucleotide sequence differs fundamentally from those of typical members of the virus genus/family and, preferably, also if the biological significance and functions of certain sequence differences have been experimentally addressed. In the absence of biological data, manuscripts describing only sequences can be submitted as an Annotated Sequence Record.

Database Contact Information
- DDBJ: Center for Information Biology and DNA Databank of Japan. National Institute of Genetics, 1111 Yata, Mishima, Shizuoka 411-8540, Japan; telephone: +81 559 81 6853; fax: +81 559 81 6849; e-mail: ddbj@ddbj.nig.ac.jp; web URL: http://www.ddbj.nig.ac.jp/
- EMBL: EMBL Nucleotide Sequence Submissions, European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB 10 1SD U.K.; telephone: +44 1223494499; fax: +44 1223 494472; e-mail: datasubs@ebi.ac.uk; web URL: http://www.ebi.ac.uk
- GenBank: National Center for Biotechnology Information, National Library of Medicine, Bldg. 38A, Rm 8N-803, Bethesda, MD 20894, U.S.A.; telephone: +1 301 496 2475; fax: +1 301 4809241; e-mail: info@ncbi.nlm.nih.gov; web URL: http://www.ncbi.nlm.nih.gov

Nucleic acid sequences of limited length which are the primary subject of a study may be presented freestyle in the most effective format. In exceptional cases, longer nucleic acid sequences may be presented in the following format to conserve space. Submit the sequence as camera-ready copy in lines of 100 bases, using a nonproportional (monospace) font which is easily legible when published at 100 bases per 16 cm line.

Encoded amino acid sequences may be presented, if necessary, immediately above or below the first nucleotide of each codon, by using the standard single-letter amino acid code.
X-ray crystallographic protein structure data

Manuscripts containing new structure determinations (including X-ray amplitudes and phases and derived atomic coordinates) must be accompanied by (an) accession number(s) from an internationally available depository (such as Brookhaven National Laboratory, Upton, NY 11973, U.S.A.). If structure determinations have been submitted to a depository, but an accession number has not yet been assigned, the manuscript can be submitted for review, but it will not be published until (an) accession number(s) is available for insertion into the manuscript.

Virus nomenclature

Each virus should be identified at least once, preferably in the Introduction or Materials and methods section, using formal family, genus, and species terms, and where possible by using a precise strain designation term as developed by an internationally recognized specialty group or culture collection. Please note that the word type is not used before species designations that include a number. Formal terms used for virus families, genera, and species should be those approved by the International Committee on Taxonomy of Viruses (ICTV): King AMQ, Lefkowitz E, Adams MJ, Carstens EB (eds) (2011) Virus Taxonomy: Ninth Report of the International Committee on Taxonomy of Viruses, Elsevier, 1338 pages or via http://ictvonline.org/virusTaxonomy.asp. Once formal taxonomic names have been given in a paper, vernacular terms may be used.

Formal taxonomic nomenclature:

In formal taxonomic usage, the first letters of virus order, family, subfamily, genus and species names are capitalized and the terms are printed in italics. Other words in the species name are not capitalized unless they are proper nouns or parts of nouns, for example West Nile virus. In formal usage, the name of the taxon should precede the term for the taxonomic unit; for example: "the family Paramyxoviridae", "the genus Morbillivirus". The following represent examples of full formal taxonomic terminology:

2. Family Poxviridae, subfamily Chordopoxvirinae, genus Orthopoxvirus, species Vaccinia virus.
3. Family Picornaviridae, genus Enterovirus, species Enterovirus C.
4. Family Bunyaviridae, genus Tospovirus, species Tomato spotted wilt virus.

Vernacular taxonomic nomenclature:

In formal vernacular usage, virus order, family, subfamily, genus and species names are written in lower case Roman script; they are not capitalized, nor are they printed in italics or underlined. In informal usage, the name of the taxon should not include the formal suffix, and the name of the taxon should follow the term for the taxonomic unit; for example "the picornavirus family", "the enterovirus genus". One particular source of ambiguity in vernacular nomenclature lies in the common use of the same root terms in formal family, genus or species names. Imprecision stems from not being able to easily identify in vernacular usage which hierarchical level is being cited. For example, the vernacular name "paramyxovirus" might refer to the family Paramyxoviridae, the subfamily Paramyxovirinae, or one species in the genus Respirovirus, such as Human parainfluenza virus I. The solution in vernacular usage is to avoid "jumping" hierarchical levels and to add taxon identification wherever needed. For example, when citing the taxonomic placement of Human parainfluenza virus I, taxon identification should always be added: "Human parainfluenza virus I is a species in the genus Respirovirus, family Paramyxoviridae." In this example, as is usually the case, adding the information that this virus is also a member of the subfamily Paramyxovirinae and the order Mononegavirales is unnecessary.

It should be stressed that italics and capital letters must be used only when referring to taxonomic categories like species, genera and families. When referring to the virus being studied rather than to the taxonomic group the virus belongs to, the virus name is written in lower case Roman script without capitals, for instance measles virus or tomato chlorosis virus. It is incorrect to write that the
species *Tobacco mosaic virus* has been sequenced or has been isolated from a host plant, since it is only the virus itself, tobacco mosaic virus, that can be handled in this way and has a sequence. Virus species, like genera or families, are man-made taxonomic constructions and do not have hosts, vectors or sequences. On the other hand, it is correct to write that a member (i.e. a virus), a strain or an isolate of the species *Tobacco mosaic virus* has been isolated or was sequenced. The use of italics when referring to the name of a species signals that it has the status of an official-species recognized by the ICTV.

The 9th ICTV Report (King AMQ, Lefkowitz E, Adams MJ, Carstens EB, Elsevier) or the ICTV web page [http://ictvonline.org/virusTaxonomy.asp](http://ictvonline.org/virusTaxonomy.asp) should be consulted to ascertain which names have been approved as official species names.

**Nomenclature of bacteria:**

Binary names, consisting of a genus and species term (e.g., *Escherichia coli*), should be used for all bacteria. After the first usage, the genus term should be abbreviated (e.g., *E. coli*). All taxonomic terms, including genus, species, and subspecies are printed in italics; strain designations are not.

**Genetic nomenclature:**

Where appropriate for viral genetic systems (e.g., phenotypes, genotypes, wild-type alleles), the nomenclature recommendations of Demerec et al. should be used: Demerec M, Adelberg EA, Clark AJ et al (1966) A proposal for a uniform nomenclature in bacterial genetics. Genetics 54: 61–76.

**Chemical and biochemical nomenclature:**

The names used for chemical/biochemical compounds should be those recommended in Chemical Abstracts and its indices (Chemical Abstracts Service, The Ohio State University, Columbus, Ohio, U.S.A.), Biochemical Nomenclature and Related Documents (The Biochemical Society, London, U.K.), and the Instructions to Authors of leading biochemistry journals. For enzymes, use terms recommended by The International Union of Biochemistry (1984) Enzyme nomenclature. Academic Press, New York.

**Restriction endonucleases:**


**Nucleotide sequence data:**

The sequencing strategy employed should be described, and the sequence itself submitted in the form of "camera ready" copy, following standard conventions of the International Union of Biochemistry.

**Numerical data**

*Units of measurement:*

Standard metric units are used for length, weight, and volume. For these units and for molarity, use standard terms: m, μ, n, and p, for 10–3, 10–6, 10–9, and 10–12, respectively. Use the term k for 103. Avoid compound terms such as mμ or μμ. Avoid the ambiguous term ppm (instead use μg/ml or μg/g). Units of temperature are written as 37°C or 324 K. See standard references for reporting units of illumination, energy, frequency, pressure, etc.
**Molecular mass:**

When indicating the mass of viruses, ribosomes, and other biologically complex entities containing different kinds of molecules, the term molecular mass (Mr), not molecular weight, should be used. (Mr is a dimensionless number representing the ratio of the mass of an entity to onetwelfth the mass of an atom of 12C.) When indicating the mass of proteins, carbohydrates, and other complex molecules, the term Mr is also preferred, but molecular weight may be used. It is acceptable, but not necessary, to use the mass unit dalton with the term Mr, but not with the term molecular weight. For example, it is preferred to state that the Mr of the poliovirus virion is $8.58 \times 10^6$ and that the Mr of poliovirus protein VP-1 is 33,521.

**Isotopically labeled compounds:**

For simple molecules, isotopic labeling is indicated in the chemical formula or name (e.g., $^{14}$CO$_2$, H235SO$_4$, $^{14}$C-amino acids, $^{131}$I-labeled protein). For complex molecules, the symbol for the isotope introduced is placed in square brackets directly preceding the part of the name that describes the labeled entity (e.g., [14C]urea, SV-40 [32P]DNA, [a-14C]lysine). See Instructions to Authors of leading biochemistry journals for further details.

**Patient identification**

When virus isolates are derived from patients in clinical studies, do not identify them by using patients’ names or initials, even as part of a strain designation. Do not use hospital identifiers. Instead, use confidentially coded terms. Note: established designations of some viruses and cells that represent patient initials are acceptable — JC virus, BK virus, HeLa cells, etc. Do not use patient group identifiers pertaining to race, address, occupation, etc., unless relevant to the study.