**Instructions to Authors**

**The ICTV Report on Virus Classification and Taxon Nomenclature**

**Aims and Scope**

**General scope**

The ICTV Report is being produced as an online, open access publication provided on the ICTV web site ([ictv.global/report](https://ictv.global/report)). Individual chapters of the Report will be cited through a two page, freely accessible summary published as an “ICTV Virus Taxonomy Profile” in the Journal of General Virology. These Profiles will be indexed by NCBI, assigned a PubMed ID, and republished on a roughly five-year cycle. There will be no charge for authors to contribute Report chapters or JGV Profiles. Chapters from the 9th Report (2012) are also available on the ICTV website (<https://ictv.global/report_9th>).

**Length and focus**

Each Report chapter will summarize the features and structure of a particular family or higher taxon and its relationship to other virus taxa as they exist at the time of publication. Major differences from the 9th Report format are that citations can now be included in the text, and that lists of species in a genus are now automatically generated from the ICTV Master Species List (MSL: <https://ictv.global/msl>) and Virus Metadata Resource (VMR: <https://ictv.global/vmr>) spreadsheets. The online format means that chapters can be corrected and updated to accommodate future advances in taxonomy.

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**Editorial Process**

General enquiries should be made to the Managing Editor. Authors should submit Report chapters, JGV Profiles, and associated files by email to the Managing Editor who will check and forward them to the appropriate Associate Editor and an Editor for review. The Managing Editor will upload the final version of the chapter to the ICTV Report web site and submit the finalised Profile to JGV and coordinate the approval of page proofs. Queries about editorial policies should be directed to the Editor-in-Chief.

**Report Text**

#### Format

* Request family-specific Profile and Report templates from the Managing Editor – this has all the subfamily and genus pages required, and the taxonomy section of Table 1 pre-filled
* Alternatively, use the template [**Chapter\_template.v6.docx**](https://ictv.global/files/templates)
* Text and figures from the 9th Report are available to use as a starting point
* To avoid unnecessary repetition between genus and family sections, use the phrase “See discussion under family description.” to refer back to the family section as needed.

#### Authorship

#### Authors need not be members of a Study Group. The list of authors may be followed by acknowledgment of the contribution of the authors of previous versions of the Online Report and of the 9th Report when appropriate.

#### Spelling

* Authors may use British or American (Merriam-Webster’s Collegiate Dictionary) spelling.
* Do not use hyphenation to split words between lines.

#### Emphasis

* Do not use italics, bold or underlining for emphasis within the text.
* For information and examples on how to write virus and species names, see <https://ictv.global/faq/names>

#### Tables

* Each table should be numbered consecutively and integrated within the text in the most appropriate position. Explanatory material can be placed in footnotes.
* Table 1 is identical to Table 1 of the JGV Profile
* “Member species” tables are not numbered and are automatically generated from information provided on the Isolate spreadsheet (Family isolate–list.xlsx – see below).

#### Figures

* Figures should not be inserted within the text but provided individually as separate files.
* Each figure should be numbered consecutively for each family, subfamily or genus page with the figure legend inserted below the paragraph in which it is first cited.
* Phylogenetic trees should be supported by alignment and tree files (see below).

#### Units and nomenclature

* SI units (https://www.nist.gov/pml/weights-and-measures/metric-si/si-units ) should be used and expressed in the form m s–1 (not m/s).

**Literature Citations**

For the Online Report, in contrast to previous Reports, citations can now be included in the text. In order to minimize the effort required to generate chapter bibliographies, please supply these as in-text citations using PubMed Unique Identifiers (PMIDs) as described below:

* Non-Endnote Users: To cite a reference, simply add the PubMed ID (listed below each reference in PubMed - e.g. PMID: 12345678) within braces (squiggly brackets), e.g.{12345678} or as {Smith, 2001, 12345678}. Separate multiple citations by a semicolon, e.g. {Smith, 2001, 12345678; Davison 2014 87654321}. Do not use “et al.,” or “&”.
* EndNote Users*.* Embed citations using the format you prefer. Your citations will be merged with the ICTV Endnote library.
* To cite material such as book chapters that lack PMIDs, give the references in full in the Reference section with full bibliographic information and numbered sequentially as “Ref\_1”, “Ref\_2”, etc and cite in the text as [Ref\_1], [Ref\_2; Ref\_3].

**Website citations:** Websites may not remain active for the life of a publication and may not be peer-reviewed; for this reason, you should be careful about using them within the text of your chapter. A web site should be cited in-line with the text and bracketed by parentheses. Please also provide a short title with each web address as guidance for the reader: (e.g. Current ICTV TaxonomyBrowser: https://ictv.global/taxonomy).

**Artwork**

Do not place figures within the text of the document, but submit them as separate files in the following formats and using the palette of standard colours (<https://ictv.global/files/templates>). Please remember that photos and halftones that are embedded in an EPS, PDF or AI file remain as raster images that cannot be edited. Figures may be edited by the Editorial Board to conform to the Report style.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **File Format** | **Line drawings, trees** | | **Halftones/photographs** | |
| AI (Adobe Illustrator) |  | As an editable drawing object |  | Min 300dpi |
| SVG (Inkscape) |  | As an editable drawing object |  | Min 300dpi |
| EPS |  | As an editable drawing object |  | Min 300dpi |
| PDF |  | As an editable drawing object |  | Min 300dpi |
| PPT (Powerpoint) | () | Possible, but not preferred |  | Min 300dpi |
| Tiff | X |  |  | Min 300dpi |
| PSD (Adobe Photoshop) | X |  |  | Min 300dpi |
| JPEG | X |  | () | Resolution often too low |

Editable line drawings and images from the 9th Report can be provided to you if needed. The sources of illustrations, tables and multimedia should be cited in the legend. Permission must be obtained again to use previously published material, even if it was included in the 9th Report.

**Phylogenetic trees**

Most chapters will include a figure that depicts the phylogenetic relationships among virus sequences. In order to ensure that phylogenetic trees are informative and follow a consistent format, we suggest that trees are presented as phylograms, with branch lengths proportional to distance with a scale provided. The rooting method should be described, preferably using an outgroup. Tip labels should comprise first, the primary GenBank nucleotide accession number, followed by the virus name written in full. The distribution of sequences between different virus taxa can be indicated by the addition of bars, brackets or coloured areas with taxonomic names italicized. Bootstrap support and the position of any root should be indicated. All text should be coloured black and use the Arial font family.

For each phylogenetic tree, provide a FASTA alignment file and a tree file in Newick format. This is to support reproducibility and provide a standard to which additional sequences can be added and from which updated trees can be constructed. These files will be linked to the Report chapter in the Resources section. It is helpful if the sequence labels in these files are identical to those in the trees, with any spaces replaced with underscores. Use GenBank nucleotide accession numbers rather than RefSeq numbers as the latter can change.

We recommend that alignment files consist of nucleic acid sequences even where phylogenies are based on amino acid sequences. Information should be provided on the alignment program (e.g. MUSCLE, Clustal, MAFFT or T-Coffee), any truncation or concatenation of sequences used to produce the alignment, and the phylogenetic method (e.g. Maximum Likelihood or Bayesian), evolutionary model (e.g. Jukes-Cantor distances) and package (e.g. MEGAX, RaxML or MrBayes) used to generate the trees. Bootstrap re-sampling or other methods should be employed to demonstrate the robustness of groupings.

We recognize that the generation of standard sequence alignments and phylogenetic trees represents a potential burden for authors. For assistance, please contact the Managing Editor.

**Isolate spreadsheet**

The list of exemplar and additional isolates belonging to each species covered by your chapter should be entered into the family-specific Excel spreadsheet provided; this information will be used to update the Virus Metadata Resource (VMR: <https://ictv.global/vmr>). Please note:

1. This spreadsheet will have been prepopulated with information compiled from the current Master Species List and the ICTV database. Update and extend it as necessary, but DO NOT enter any species that are not recognized in the current taxonomy. If you believe the list of species is in error, please contact Stuart Siddell.
2. **Organization**: Each row of the table includes information for one species. Columns in each row are provided for the species name (with parent taxa); the name of a chosen exemplar, indicated as E (i.e. the name of a representative isolate belonging to that species–see 3 below); the sequence accession number(s) that link the exemplar isolate to its genomic sequence in GenBank/ENA/DDBJ; and the RefSeq accession number if available. There are also columns to indicate the virus name abbreviation; the isolate designation; how complete the genome sequence is; the genome composition; and the host(s) or source of the virus. The names and abbreviations used to refer to viruses within the species may represent common or historical names and more than one name and abbreviation may be entered for a virus isolate. Separate multiple names and abbreviations using a semicolon. Additional isolates, indicated as A, for a species, can be entered by duplicating the rows for a species as many times as needed. This is especially desirable when members of a species have been informally organized into well-recognized subspecies level groups of viruses (types, clusters, clades, etc.). The same information should be provided as for exemplar isolates.
3. **Choice of exemplar**: One virus isolate should be listed as the exemplar for each species. This may be the virus listed in the original taxonomic proposal, the NCBI RefSeq virus or a different virus of your choice, but should, if possible, have a complete genome or complete coding sequence.
4. **Accession numbers**: For viruses with multiple genomic segments, separate accession numbers for each segment using a semicolon in a single spreadsheet cell. Please indicate the genome segments using the conventional designations; for example, L: KX884758; M: KX884759; S: KX884760
5. **Complete, coding-complete and partial genome sequences**: Exemplar strains and additional isolates should, if possible, have complete or coding-complete genome sequences. Only select an exemplar virus isolate with a partial genome sequence if none of the viruses belonging to a species have been completely sequenced.
6. **Genome composition**: Please indicate the genome composition of the exemplar and additional viruses using the categories shown on the column definitions page
7. **Hosts/Source**: Please indicate the natural host or hosts of the exemplar and additional viruses using the categories shown on the column definitions page

**Submission**

Submit material to the Managing Editor via email with the following files:

* Chapter text
* JGV Profile
* Individual files for each Figure (Chapter and Profile)
* Isolate spreadsheet (Family Isolate\_list.xlsx)
* Sequence alignments (FASTA format) and tree files (Newick format)
* Permissions to publish

After the Online Report chapter and Profile texts have been reviewed and approved by ICTV Report Editors, the Managing Editor will upload the Chapter text and Figures and Resource files to the ICTV website, and submit the Profile text, figures and permissions to JGV. Page proofs will be forwarded to the corresponding author and Editors for approval before publication.

**Chapter Revisions**

**Revisions to Report chapters will be required in the event of taxonomic changes being ratified by the ICTV, or in case of new discoveries. In these circumstances, or should you wish to make a revision for other reasons, you should advise the Managing Editor so that a text version of the current web content can be made available to you. Any changes made to this document should be tracked so as to facilitate their transfer to the web pages. Extensive modifications may require Subcommittee Chair or Editorial Board review.**

**JGV Profile**

**Aim and Scope**

The means by which individual chapters of the ICTV Report will be cited is through the publication of a taxon-specific summary entitled “ICTV Virus Taxonomy Profile: <taxon name> 2023” that will be published in the Journal of General Virology (JGV) and that will be freely available to access. These Profiles will also provide an accessible overview of the virus family (or higher taxon) and so should be readable in their own right.

There is a two published page limit for each Profile. In order to achieve this, it is important that you follow the specified word limits and choose figures that will fit legibly within one of the two printed columns. Examples of published Profiles can be accessed on the JGV website at: [https://www.microbiologyresearch.org/content/collections/i](https://www.microbiologyresearch.org/content/collections/i%20)

Profiles will usually only be updated when there have been significant changes to the taxonomy. Consequently, you should try to “time-proof” the profile by avoiding specific statements that are likely to become inaccurate within a short time period. For example, there is usually no need to state the exact number of current species in a family or genus.

**Profile Content**

The Profile should be prepared using the family-specific template provided by the Managing Editor or using the general template ([Profile\_template.v6.docx](https://ictv.global/files/templates)). Virus names should not be abbreviated. The Profile should contain the following elements:

**Title**: This is fixed to: “ICTV Virus Taxonomy Profile: <insert italicized taxon name> 2023”.

**Authors**: This is the authors of the Report chapter followed by “and the ICTV Report Consortium”. This Consortium comprises the Editor-in-chief, Editors, Managing Editor, and the appropriate Associate Editor. Consortium members (listed in the acknowledgments section) are not authors of the published Profile.

**Author Affiliations**: List all authors and abbreviated addresses (department, university or other institution, city, postcode and country).

**Corresponding author(s)**: Add the name of the corresponding author(s) with telephone and email contact details.

**Twitter quote:** Short sentence to be used by the Microbiology Society to promote the Profile

**Author Twitter handles:** If available, to help promote the Profile.

**Abstract**: The abstract (maximum 100 words) will appear in PubMed, should not include citations, and should be understandable without reference to the full Profile. The last line of the abstract (included within the word count) is “This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the order/family/genus <*insert name of taxon in italics*> which is available at ictv.global/report/<insert taxon name>.”

**Table 1. Characteristics of members of the family *XXXXX*:** This table (maximum 100 words) follows the Abstract and should contain rows labelled:

* Example: virus isolate (Accession number), species *YYYYY*, genus *ZZZZZZ* (generally, the isolate listed here will be an exemplar isolate).
* Virion
* Genome
* Replication
* Translation
* Host range
* Taxonomy (including higher taxa)

**Main Section**: This is divided into a series of standard headings (maximum 500 words in total):

Virion: Brief description of the virion including citation of Table 1. This section may contain a figure showing a typical virion either diagrammatically or as an EM.

Genome: Brief description of the genome, noting any differences between members of genera. A figure providing a map of the genome may be helpful.

Replication: Brief account of the main features of virus replication. Please include replication (genome amplification), transcription (mRNA synthesis) and translation in this section

Pathogenicity: An optional section.

Taxonomy: Begins with “Current taxonomy: ictv.global/taxonomy.” followed by a brief description of the higher taxonomy as well as the taxa and the principal viruses within the family. To avoid the Profile becoming outdated, do not give precise numbers of subfamilies, genera, subgenera or species.

**Additional sections**

Resources: “Current ICTV Report on the order/family/genus XXXX: [ictv.global/report/<insert](http://www.ictv.global/report/%3cinsert) taxon name>” Other links can be added as required.

Funding Information: This section should also include the text “Production of this Profile, the ICTV Report, and associated resources was supported by the Microbiology Society.”

Acknowledgements: This section can be used to acknowledge any assistance with preparing the Profile and perhaps previous Report authors or SG members. This section must also contain the text “Members of the ICTV (10th) Report Consortium are Stuart G. Siddell, Elliot J. Lefkowitz , Sead Sabanadzovic, F. Murilo Zerbini, Peter Simmonds, Donald B. Smith and <name of Associate Editor>.”

Conflicts of interest: Suggested form of words “The authors declare that there are no conflicts of interest.”

**References**: For a Profile to be included in the major publication indexes (e.g. PubMed, Science Citation Index and Google Scholar) it must contain five or more citations of the original literature. Each Profile must therefore include at least 5 but no more than 10 citations. These will be published in Vancouver format, but should be provided in the same manner as described in the Report instructions using EndNote or as {PMID} or {PMID; PMID} for in-text citations.

**Figures**: Figures and associated figure legends should be formatted as for the Report chapter and should be a subset of those. Figures should be legible when printed at a single published column. Figure files should be provided separately from the text. Refer to figures and tables in the text as “Fig. 1” and “Table 1”, and label subsidiary panels “a”, “b” etc.

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