

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create a new genus (*Peggyvirus*) with a single species in the order *Autographivirales* |
| **Code assigned:** | 2025.059B.Ac.v3.Peggyvirus\_1ng\_1ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
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| Hany | Anany | Guelph Research and Development Centre, Agriculture and Agri-Food Canada, Guelph, Ontario, Canada | hany.anany@agr.gc.ca | X |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | **x** |
| xAnimal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** <https://ictv.global/sc> |
| Caudoviricites Study Group |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** | 15/06/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required | **x** |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
| The genbank record has to be available publicly to move to “Accept”. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| GenBank record now available. |

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| **Revision date:** | 2025/08/27 |

**Part 3:** **TAXONOMIC PROPOSAL**

<https://ictv.global/taxonomy/templates>

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **x** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| **Peggyvirus** | **Name directly derived from first virus of its type, Cronobacter phage Peggy** |
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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: Subfamily, Genus  *Description of current taxonomy*: The family *Autographiviridae* (T7-like phages) has recently been replaced by the order *Autographivirales* which consists of four families, 13 subfamilies, 228 genera, and 968 species (ICTV Taxonomy Proposal 2024.045B.Autographivirales). This proposal affects the subfamily *Slopekvirinae*  *Proposed* *taxonomic change(s):* Addition of a new genus, “*Peggyvirus*” to this subfamily  *Justification*: In accordance with our definition of what constitutes a new genus and species [3] this Cronobacter phage is sufficiently different from other viruses to constitute a new genus in the subfamily *Slopekvirinae.* |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: Genus/Subfamily  *Description of current taxonomy*: The family Autographiviridae (T7-like phages) has recently been replaced by the order Autographivirales which consists of four families, 13 subfamilies, 228 genera, and 968 species (ICTV Taxonomy Proposal 2024.045B.Autographivirales). This proposal affects the subfamily *Slopekvirinae*  *Proposed* *taxonomic change(s)*: Addition of a new genus, “*Peggyvirus*” to this subfamily  *Demarcation criteria:* Species demarcation criteria: Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates. These values can be calculated by a number of tools, such as BLASTn [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **Genus demarcation criteria**: In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [3]  **Subfamily demarcation criteria:** Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny [8]  *Justification*: In accord with our definition of what constitutes a new genus and species [3] this Cronobacter phage is sufficiently different from other viruses to constitute a new genus in the subfamily *Slopekvirinae* |

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| **References:** |
| 1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2021 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 33095870  2. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. http://kronos.icbm.uni-oldenburg.de/viridic/  3. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.  4. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287. https://www.genome.jp/viptree/  5. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PubMed PMID: 12142423  6. Lemoine F, Correia D, Lefort V, Doppelt-Azeroual O, Mareuil F, Cohen-Boulakia S, Gascuel O. NGPhylogeny.fr: new generation phylogenetic services for non-specialists. Nucleic Acids Res. 2019 Jul 2;47(W1):W260-W265. doi: 10.1093/nar/gkz303. PMID: 31028399; PMCID: PMC6602494.  7. Letunic I, Bork P. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. Nucleic Acids Res. 2021 Jul 2;49(W1):W293-W296. doi: 10.1093/nar/gkab301. PMID: 33885785; PMCID: PMC8265157.  8. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253 |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| **Peggyvirus\_1ng\_1ns** | **Data for this proposal** |
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| **Tables, Figures:** |

**Table 1.** Characteristics of the phage described in the proposal

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| *Cronobacter*  phage Peggy | *Cronobacter sakasakii* | Podovirus | Lytic | PV796109 | 43797 bp | 55 | 0 |

**A chart with text and numbers

AI-generated content may be incorrect.**

**Figure 1:** Partial VIRIDIC heatmap of this group of phages. VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; Kleb = *Klebsiella*; Ente = *Enterobacter;* Salm = *Salmonella*; Cron = *Cronobacter*. The complete VIRIDIC heatmap accompanies this proposal as Peggyvirus\_VIRIDIC heatmap.xlsx.

A close-up of a diagram

AI-generated content may be incorrect.A screenshot of a computer screen

AI-generated content may be incorrect.**Figure 2:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [5]. The phage of interest is indicated with **red arrowhead**.

A diagram of a tree

AI-generated content may be incorrect.

**Figure 3.** The phylogenetic tree was constructed using the DNA polymerase from *Cronobacter* phage Peggy and related phages with NGPhylogeny.fr in “one click” mode [6]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. The alignment was exported to iTOL v7 [7]. The red arrowhead indicates the phage of interest