

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

<https://ictv.global/taxonomy/templates>**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create a new subfamily, *Alvaradovirinae,* with three genera in the Class *Caudoviricetes* |
| **Code assigned:** | 2025.002B.Alvaradovirinae\_1nsf\_3ng\_9ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
| Andrew M. | Kropinski | Department of Pathobiology, The Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada | Phage.Canada@gmail.com |  |
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| Johannes | Wittmann | Leibniz Institute DSMZ, | Johannes.wittmann@dsmz.de | 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> |
| Caudoviricetes 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 |  |
| 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| W - Withdrawn |  |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:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

**Part 2:** **GENERAL PROPOSAL**

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| **Abstract for General Proposal:** |
| *Brief description of current situation:*  *Proposed changes:*  *Justification:* |

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| **Text of General Proposal:** |
| *Background:*  *Proposed* *changes:*  *Justification:* |

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| **References:** |
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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
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| **Tables, Figures:** |

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**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** |
| *Alvaradovirinae* | Named after a major route through the SDSU campus |
| *Amaduovirus* | Named after *Achromobacter* phage AMA2 |
| *Nyaakvirus* | Named after *Achromobacter* phage nyaak\_TL1 |
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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*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  Achromobacter phage JWX belongs to the genus *Steinhofvirus* which was created via Taxonomy Proposals 2018.007B.A.v4.rename137gen6sp and 2016.020a-dB.A.v1.Jwxvirus. This genus currently contains two species: *Steinhofvirus JWX* and *Steinhofvirus* sv8324  *Proposed* *taxonomic change(s):*  To create a new subfamily “*Alvaradovirinae”* with three genera “*Steinhofvirus”,* “*Amaduovirus”* and *“Nyaakvirus”*; and move *Steinhofvirus sv8324* to the genus “*Amaduovirus”*  *Justification*: In accord with our established criteria for establishing a subfamily, of a new genus and species [3] |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  Achromobacter phage JWX belongs to the genus *Steinhofvirus* which was created via Taxonomy Proposals 2018.007B.A.v4.rename137gen6sp and 2016.020a-dB.A.v1.Jwxvirus. This genus currently contains two species: *Steinhofvirus JWX* and *Steinhofvirus* sv8324  *Proposed* *taxonomic change(s):*  To create a new subfamily “*Alvaradovirinae”* with three genera “*Steinhofvirus”,* “*Amaduovirus”* and *“Nyaakvirus”*; and move *Steinhofvirus sv8324* to the genus “*Amaduovirus”*  *Demarcation criteria:*  Genus demarcation criteria: An intergenomic similarity cut-off of 70%, a combination of average nucleotide identity and alignment fraction is used to determine genera demarcation. Members of the same genus have >70% intergenomic similarity and cluster tightly in marker gene phylogenies.  Species demarcation criteria: A demarcation value of 95% intergenomic similarity was used to define different species according to intergenomic similarity. Members of the same species have >95% intergenomic similarity.  *Justification*: In accord with our definition of a new subfamily, genus and species [3] |

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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. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| Alvaradovirinae VIRIDIC\_heatmap.xlsx | VIRIDIC intergenomic similarity data |
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| **Tables, Figures:** |

**Table 1A.** To add one new species to the genus *Steinhofvirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Achromobacter phage SE2 | *Achromobacter sp.* | Siphovirus | Lytic | OQ817844.1 | 45648 bp | 71 | 1 |

**Table 1B.** To create a new genus (*Amaduovirus*) with two species

|  |  |  |  |  |  |  |  |
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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Achromobacter phage AMA2 | *Achromobacter marplatensis* | Siphovirus | Lytic | MT241607.1 | 45901 bp | 68 | 1(\*) |
| Achromobacter phage 83-24 (\*\*) | *Achromobacter xylosoxidans* | Siphovirus | Lytic | KP202970.1 | 48216 bp | 61 | 1 |

**(\*) discovered using tRNAscan-SE (**[**https://lowelab.ucsc.edu/tRNAscan-SE/**](https://lowelab.ucsc.edu/tRNAscan-SE/)**)**

**(\*\*) transferred from *Steinhofvirus* due to the level of DNA sequence similarity**

**Table 1C.** Characteristics of the phages belonging to the genus *Nyaakvirus*

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Achromobacter phage tuull (partial) | *Achromobacter ruhlandii* | Siphovirus | Lytic | OR396896.1 | 47460 bp | 87 | 1 |
| Achromobacter phage vB\_AxyS\_19-32\_Axy06 (\*) | *Achromobacter xylosoxidans* I2BC | Siphovirus | Lytic | MK962627.1 | 45830 bp | 55 | 1 |
| Achromobacter phage ehaak\_LB5 | *Achromobacter sp.* | Siphovirus | Lytic | OQ817833.1 | 46435 bp | 64 | 1 |
| Achromobacter phage emuu\_LB7 | *Achromobacter sp.* | Siphovirus | Lytic | OQ817834.1 | 46012 bp | 63 | 1 |
| Achromobacter phage AMA1 | *Achromobacter marplatensis* | Siphovirus | Lytic | MT241605.2 | 46328 bp | 62 | 1(\*\*) |
| Achromobacter phage maay\_LB1 | *Achromobacter sp.* | Siphovirus | Lytic | OQ817838.1 | 46086 bp | 63 | 1 |
| Achromobacter phage vB\_AxyS\_19-32\_Axy14 | *Achromobacter xylosoxidans* I2BC | Siphovirus | Lytic | MK962633.1 | 46703 bp | 60 | 1 |
| Achromobacter phage nyaak\_TL1 | *Achromobacter sp.* | Siphovirus | Lytic | OQ817839.1 | 46478 bp | 67 | 1 |

**(\*) genome has 2978 bp direct terminal repeats**

**(\*\*) discovered using tRNAscan-SE (https://lowelab.ucsc.edu/tRNAscan-SE/)**

Achromobacter phage vB\_Ade\_ART (MH746817.1; host: Achromobacter denitrificans PR1) should be considered a member of this subfamily but its genome is 95343 bp i.e. twice as big as most of the phages in this proposal. Examination of the sequence reveals two copies of the major capsid and terminase large subunit proteins leading to the conclusion that it is chimeric. It is in the process of being corrected.

**A screen shot of a chart

AI-generated content may be incorrect.**

**Figure 1.** VIRIDIC heat map (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) heatmap for this group of phages. It computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: Achr = *Achromobacter*; phg = phage. Because of the size of this diagram we have included the original Excel spreadsheet to render the numbers more visible (Alvaradoviridae\_VIRIDIC heatmap).

A close-up of a document

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

AI-generated content may be incorrect.**Figure 2:** ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages of interest are indicated with **red stars**. Abbreviations: Achr = *Achromobacter*; phg = phage.

**CoreGenes 5 Analysis** [7]: revealed that the phages listed in Table 1A-C share 41 protein homologs, including tape measure domain protein, terminase large subunit, transcriptional regulator, dCMP deaminase, and thymidylate synthase. This indicates that approximately 62.4% of the phage-encoded proteins are conserved.