

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create one new species in the genus *Ampunavirus* (Class [*Caudoviricetes*](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Undef&id=2731619&lvl=3&keep=1&srchmode=1&unlock)*;*Order *Autographivirales*, *Family Autonotataviridae*) |
| **Code assigned:** | 2025.003B.Ampunavirus\_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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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | X |
| Animal 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:** |
| 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:** | 17/02/2025 |

**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| W - Withdrawn |  |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 | **×** | 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** |
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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*, order *Autographivirales*, family *Autonotataviridae*  *Description of current taxonomy*:  *Ralstonia* phage LPRS20 is currently unclassified.  *Proposed* *taxonomic change(s):*  Create a new species,  *Ampunavirus LPRS20*  *Justification*:  We isolated a novel *Ralstonia* phage LPRS20. Based on the analysis of VIRIDIC and ViPTree, LPRS20 has the highest identity with 78.7% of intergenomic similarities with *Burkholderia* phage Bp-AMP3 of *Ampunavirus* genus. *Ralstonia* phage LPRS20 shares many properties with *Burkholderia* phage Bp-AMP3 but differs significantly enough (less than 95% identity with *Ampunavirus* *BpAMP1*) to classify it as a separate species of this genus. Thus, this proposal will placeLPRS20 in this genus *Ampunavirus* as a new species*.* |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes,* family *Autonotataviridae*  *Description of current taxonomy*:  The genus *Ampunavirus* encompasses two species. *Ralstonia* phage LPRS20 is currently unclassified.  *Proposed* *taxonomic change(s)*:  This proposal will create a new species, *Ampunavirus* *LPRS20* in the genus *Ampunavirus*.  *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 – usually calculated using intergenomic distance calculator VIRIDIC [1]. 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 [2].  *Justification*:  A tblastx distance tree of *Ralstonia* phage LPRS20 was constructed using VIPTree. LPRS20, along with 12 other phages were selected for VIRIDIC analysis. VIRIDIC analysis computed the pairwise genomic distances and similarities between the phage genomes, revealing that LPRS20 grouped with five other phage genomes at the level required for genus demarcation. LPRS20 exhibited less than 95% similarity to these genomes indicating that it represents a new species. Furthermore, a maximum-likelihood (ML) tree was constructed using the major capsid protein of the 12 phages, with 500 bootstrap replicates. The topology of the ML tree supports the results of VIPTree. In conclusion, we propose a new species, *Ampunavirus LPRS20*, containing a new *Ralstonia* phage LPRS20, within the genus *Ampunavirus*. |

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| **References:** |
| 1. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses 12(11):1268. PMID: 33172115 / PMCID: PMC7694805 doi: 10.3390/v12111268.  2. Turner D, Kropinski AM, Adriaenssens EM (2021) A Roadmap for Genome-Based Phage Taxonomy. Viruses 13(3):506. PMID: 33803862 / PMCID: PMC8003253 doi: 10.3390/v13030506.  3. Nishimura Y, Yoshida T, Kuronishi M et al (2017) ViPTree: the viral proteomic tree server. Bioinformatics 33(15):2379-2380. PMID: 28379287. doi: 10.1093/bioinformatics/btx157.  4. Rohwer F, Edwards R (2002) The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol 184(16):4529-35. PMID: 12142423 / PMCID: PMC135240. doi: 10.1128/jb.184.16.4529-4535.2002.  5. Nishijima S, Nagata N, Kiguchi Y et al (2022) Extensive gut virome variation and its associations with host and environmental factors in a population-level cohort. Nat Commun 13(1):5252. PMID: 36068216 / PMCID: PMC9448778 doi: 10.1038/s41467-022-32832-w.  6. Kozlov AM, Darriba D, Flouri T et al (2019) RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. Bioinformatics 35(21):4453-4455. PMID: 31070718 / PMCID: PMC6821337 doi: 10.1093/bioinformatics/btz305. |

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

<Start here>**Figure 1. ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red box**.

A diagram of a number of samples

AI-generated content may be incorrect.

**Figure 2. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator [1]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes.

**A screenshot of a computer

AI-generated content may be incorrect.**

**Figure 3. Phylogeny:** The phylogenetic tree was constructed using the major capsid protein of phages [5]. MUSCLE was used for multiple alignment and RAxML-NG was used for building phylogenetic tree using maximum-likelihood method with 500 bootstraps [6]. The new species is indicated with red text and star.



**Historical aspects:** *Ralstonia* phage LPRS20 was isolated in 2022 at Huazhong Agricultural University.

**Genome summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| *Ralstonia* phage LPRS20 | PP895304 | 47.6 | 48.8 | 80 | 0 |