

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create three new species in the genus *Felixounavirus* (class *Caudoviricetes*, family *Andersonviridae*, subfamily *Ounavirinae*) |
| **Code assigned:** | 2025.018B.Ac.v3.Felixounavirus\_3ns | |

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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:** <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:** | 29/08/2024 |

**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| W - Withdrawn |  |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:** |
| Genus in-filling (3 species). There is a potential formatting issue with Excel module |

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

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| **Response of proposer:** |
| Corrected |

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| **Revision date:** | 26/08/2025 |

<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** |
| *Felixounavirus vipecomarii* | Derived from the geographical sites of isolation in the Philippines: *Felixounavirus vipecomarii* isolated from Marikina River |
| *Felixounavirus vipecomesa* | Derived from the geographical sites of isolation in the Philippines: *Felixounavirus vipecomesa* isolated from a drainage site in Sta. Mesa, Manila |
| *Felixounavirus vipecohospii* | Derived from the geographical sites of isolation in the Philippines: *Felixounavirus vipecohospii* isolated from sewage at a public hospital in Manila |
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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*:  Species  *Description of current taxonomy*:  The genus *Felixounavirus* currently includes 97 species.  *Proposed* *taxonomic change(s):*  Add three new species, *Felixounavirus vipecomarii*, *Felixounavirus vipecomesa* and *Felixounavirus vipecohospii* to the genus *Felixounavirus.*  *Justification*:  Three new species within the genus *Felixounavirus* are proposed based on the species demarcation criteria of <95% intergenomic similarity. Escherichia phages vB\_EcoM\_D4, vB\_EcoM\_E9, and vB\_EcoM\_H12 are closely related to *Felixounavirus TP1* (GenBank NC\_041979.1), exhibiting 92.2% intergenomic similarity. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  The genus *Felixounavirus* currently consists of 97 species.  *Proposed* *taxonomic change(s):*  Add three new species, *Felixounavirus vipecomarii*, *Felixounavirus vipecomesa* and *Felixounavirus vipecohospii* to the genus *Felixounavirus.*  *Demarcation criteria:*  Species demarcation: Two phages are classified as the same species if their genomes share more than 95% similarity across their entire genomic content, as determined by VIRIDIC. [1, 2].  *Justification*:  Three novel species within the genus *Felixounavirus* are proposed based on a 95% intergenomic similarity threshold used for species demarcation. Escherichia phages vB\_EcoM\_D4, vB\_EcoM\_E9, and vB\_EcoM\_H12 are closely related to *Felixounavirus TP1* (GenBank NC\_041979.1), exhibiting a maximum of 92.2% intergenomic similarity. |

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| **References:** |
| 1. Turner D., Kropinski AM, Adriaenssens EM (2021) A roadmap for genome-based phage taxonomy Viruses, 13(3), 506. https://doi.org/10.3390/v13030506  2. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC — A Novel Tool to Calculate the Intergenomic Similarities of prokaryote-infecting viruses. Viruses 12(11):1268. https://doi.org/10.3390/v12111268 |

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

<Start here>A screenshot of a computer screen

AI-generated content may be incorrect.Figure 1. Intergenomic similarity scores (VIRIDIC) of three phage isolates against other species included in the genus *Felixounavirus*. The three phage isolates are highlighted with blue font.

Table 1. Summary of genomic features of the proposed new species of bacteriophages.

