

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 species in genus *Peropuvirus* (*Mononegavirales*: *Artoviridae*) |
| **Code assigned:** | 2025.005M.Ac.v3.Peropuvirus\_1nsp | |

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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 |  |
| Animal minus-strand and dsRNA viruses | **X** | 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:**. |
| ICTV *Artoviridae* 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** |
| ICTV *Artoviridae* Study Group | 4 |  |  |

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| **Submission date:** | 19/06/2025 |

**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| W - Withdrawn |  |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:** |
| Ac for minor typographical edits and consistent Abstract format across all Subcommittees |

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

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| **Response of proposer:** |
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| **Revision date:** | 19/8/25 |

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

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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** |
| *Peropuvirus crocidurae* | Named after the shrew host genus *Crocidura* |

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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** X |
| NA |  |  |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species in the family *Artoviridae*.  *Description of current taxonomy*:  The family *Artoviridae* currently includes two genera, *Hexartovirus* (4 species) and *Peropuvirus* (9 species).  *Proposed* *taxonomic change(s):*  Create one new species in the genus *Peropuvirus*.  *Justification*:  The virus proposed to be assigned to the novel species encodes an L protein with a minimum amino acid divergence of 51.9 % compared to classified family members and occupies a distinct ecological niche. |

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| **Text of Taxonomy proposal** |
| *Taxonomic rank(s) affected*:  Genus *Peropuvirus*, species.  *Description of current taxonomy*:  The family *Artoviridae* currently includes two genera, *Hexartovirus* (4 species) and *Peropuvirus* (9 species). The viruses of genus *Hexartovirus* infect crustaceans such as barnacles, brine shrimp, and copepods. The viruses of genus *Peropuvirus* infect parasitoid wasps, pillworms, woodlice, odonates, shrews, bats or plants.  *Proposed* *taxonomic change(s)*:  We propose to classify Crocidura shantungensis peropuvirus 1 (CsPV1) in the new species *Peropuvirus crocidurae*.  *Demarcation criteria:*  The virus proposed to be assigned to the novel species encodes an L protein with a minimum amino acid divergence of 51.9 % compared to classified family members and occupies a distinct ecological niche.  *Justification*:  The proteome of CsPV1 is 48.1% identical to those of other members of the family genus *Peropuvirus*. In phylogenetic analysis, the new virus clearly cluster with the established species (Figure 1). The L protein of the virus is at least 51.9% divergent from those of viruses assigned to established species. This significant difference supports the establishment of a new species. In addition, the new virus infects a shrew host (*Crocidura shantungensis* [Miller](https://en.wikipedia.org/wiki/Gerrit_Smith_Miller_Jr.), 1901) that has not been previously associated with peropuviruses. |

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| **References:** |
| Zhang, JT., Hu, ZY., Tang, F. et al. Decoding the RNA viromes in shrew lungs along the eastern coast of China. npj Biofilms Microbiomes 10, 68 (2024). https://doi.org/10.1038/s41522-024-00543-3 |

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

A diagram of a structure

AI-generated content may be incorrect.

**Figure 1** Phylogenetic analysis of virus species in the family *Artoviridae*. Maximum likelihood tree of L protein amino acid sequences utilizing the Jukes-Cantor model and 1,000 bootstraps. *Nyamiviridae* is used as the outgroup. The phylogeny is based on complete deletion of gaps.