

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | ***2023.075B*** |  |
| **Short title:** To abolish three species (*Caudoviricetes*) |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew M. Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

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| Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | May 2023 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2023.075B.N.v1.Caudoviricetes\_ab3sp.xlsx |

**Abstract**

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| The following include a list of taxa which should be abolished. |

**Text of proposal**

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| **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 [1,2] – usually calculated using intergenomic distance calculator VIRIDIC [3].**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. [10] |

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**Supporting evidence**

1. **Delete *Tunavirus tv008*: MK335533.1 Shigella phage vB\_SsoS\_008**

Rationale: Only one representative genome is present in the database for this species. The genome contains an unacceptable numbers of frameshifts.

1. **Delete *Tlsvirus tv36*: KR296690.1 Salmonella phage 36**

Rationale: Only one representative genome is present in the database for this species. It is a partial genome with multiple frameshifts.

1. **Delete *Pecentumvirus WIL1*: KM373208.1 Listeria phage WIL-1**

Rationale: Only one representative genome is present in the database for this species. The genome has a very poor annotation with numerous small CDSs.

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