

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

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| **Code assigned:** | **2021.012B** |  |
| **Short title:** Create one new subfamily (*Boydwoodruffvirinae*) including two existing genera (*Caudoviricetes*) | | |
|  | | |

**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew Kropinski |

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

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| Actinobacteriophages Study Group, Bacterial and Archaeal Viruses Subcommittee |

**ICTV study group comments and response of proposer**

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**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**

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

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

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

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

**Name of accompanying Excel module**

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| 2021.012B.R.Boydwoodruffvirinae |

**Abstract**

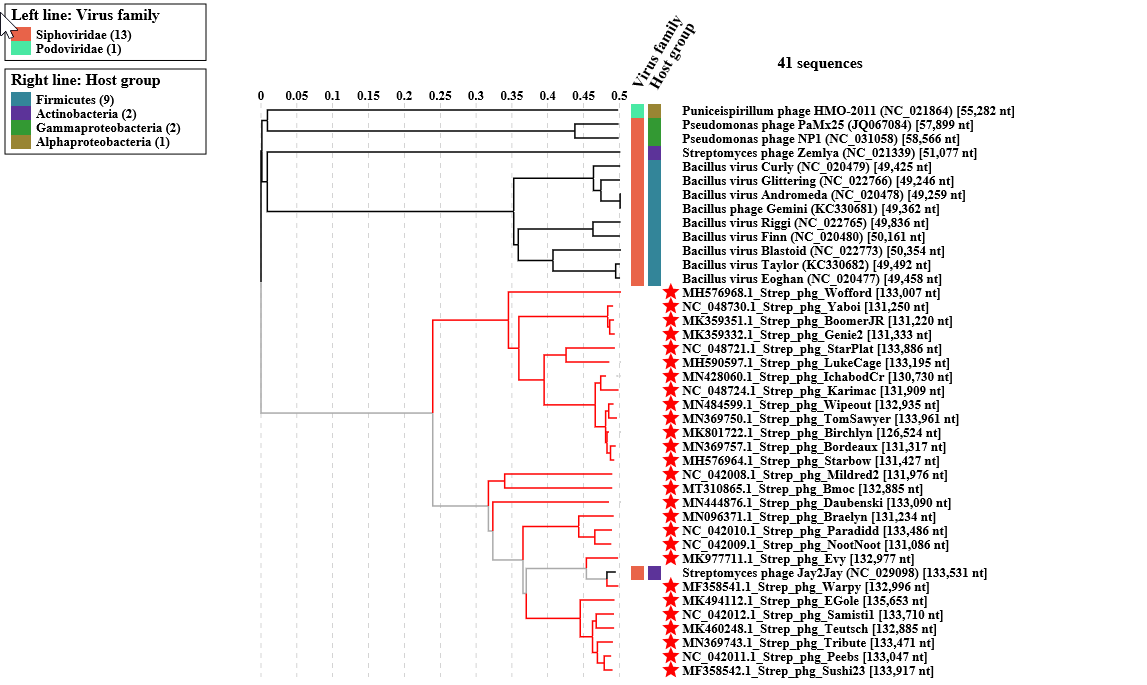
|  |
| --- |
| We have chosen to create a new subfamily named in honour of the American soil microbiologist H. Boyd Woodruff to contain two existing related genera - *Karimacvirus* (Taxonomy Proposal 2020.081B) and *Samistivirus* (Taxonomy Proposal 2018.055B). |

**Text of proposal**

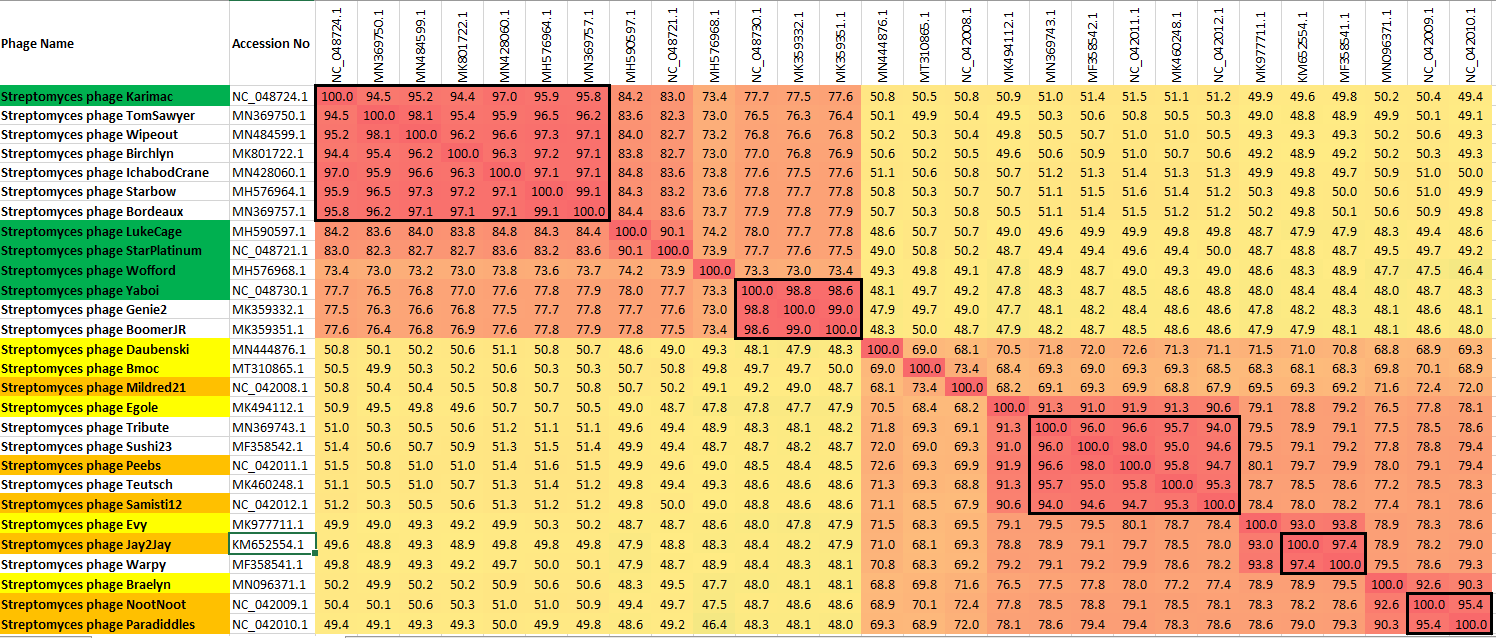
|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic 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.  **Subfamily demarcation criteria:** Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity and that the genera form a clade in a marker tree phylogeny. [9] | |

**Supporting evidence**

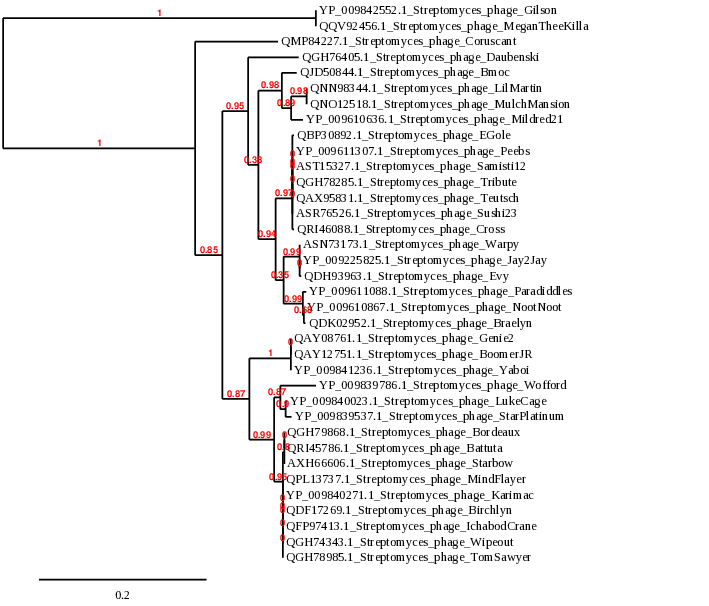
**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. The phages of interest are indicated with **red lines**.



**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. Strains are indicated by boxes. The green and gold enhanced names are of recognized species, while the yellowed named are new species.



**Phylogeny:** The phylogenetic tree was constructed using the major capsid proteins of *Boydwoodruffvirinae* phages with phylogeny.fr in “one click” mode [5]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [6] for details."

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**Source of the name of this taxon:** This subfamily is named in honour of American soil microbiologist and member of the National Academy of Sciences Harold Boyd Woodruff (1917 – 2017). He obtained his Ph.D. from Rutgers University where his advisor was Selman Waksman. In his doctoral work, he discovered the antibiotics actinomycin and streptothricin. He spent his career as a researcher at Merck & Co.



(Woodruff (right) in 1940; from: <https://www.nytimes.com/2017/02/03/science/h-boyd-woodruff-dead-antibiotics-researcher.html>).

**History:** This subfamily contains two genera: *Karimacvirus* (Taxonomy Proposal 2020.081B) and *Samistivirus* (Taxonomy Proposal 2018.055B). Phages belonging to the latter genus belong to The Actinobacteriophage Database Cluster BE/Subcluster BE1, while the *Karimacvirus* members are part of Cluster BE/Subcluster BE2. Here we proposed five new species in the genus *Samistivirus*.

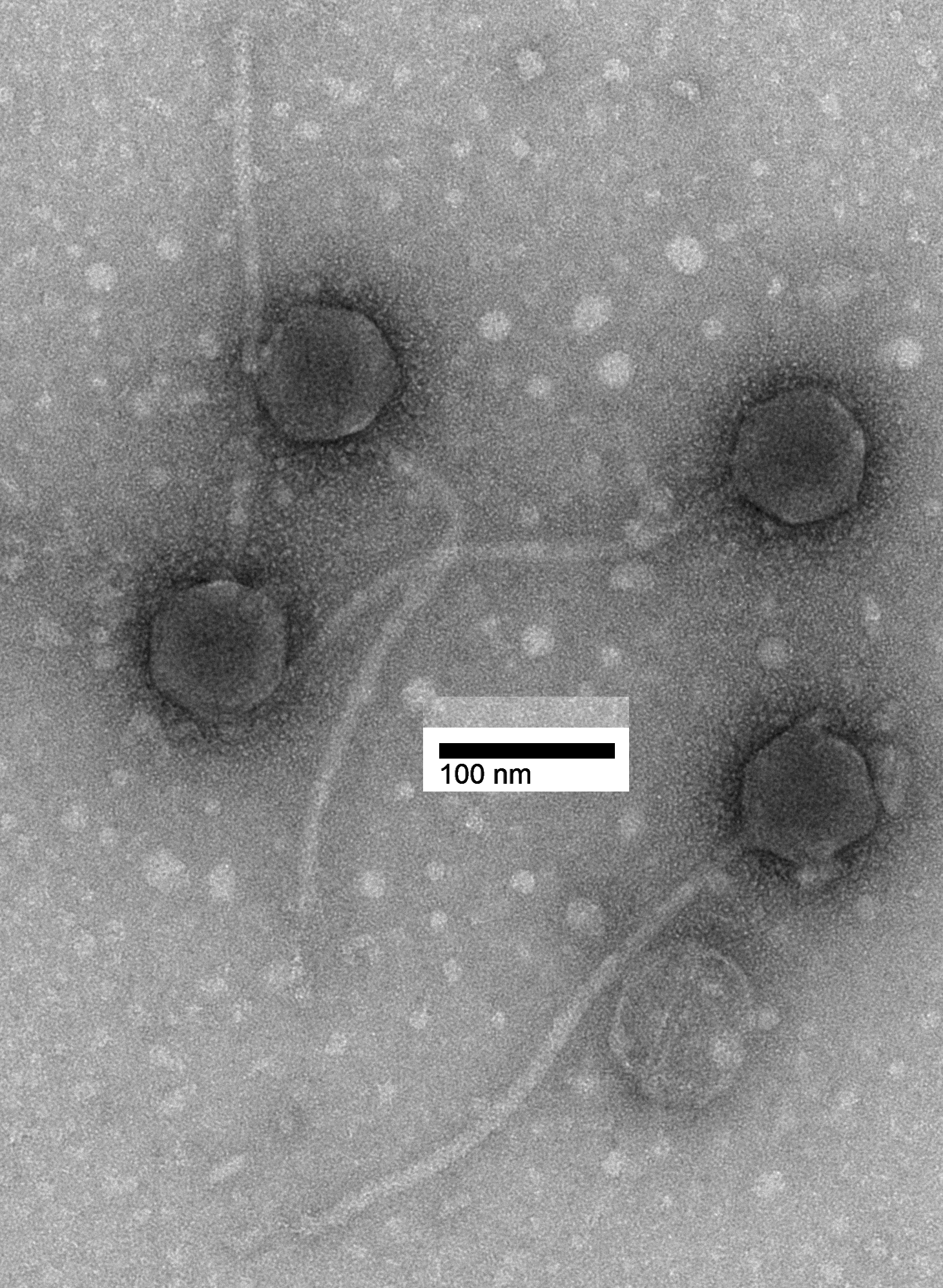
**Specific Reference:** Woodruff HB. A soil microbiologist's odyssey. Annu Rev Microbiol. 1981;35:1-28. doi: 10.1146/annurev.mi.35.100181.000245. PMID: 7027897.

**GenBank Summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Streptomyces phage Samisti12 | [NC\_042012.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_042012.1) | [MF347639.1](https://www.ncbi.nlm.nih.gov/nuccore/MF347639.1) | 133.71 | 49.9 | [226](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63760/466381%7CStreptomyces%20phage%20Samisti12/viral%20segment/) | 44 | 100 | 100 |
| Streptomyces phage Daubenski |  | [MN444876.1](https://www.ncbi.nlm.nih.gov/nuccore/MN444876.1) | 133.09 | 49.4 | [226](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85555/743714%7CStreptomyces%20phage%20Daubenski/viral%20segment/) | 39 | 71.1 | 78.8 |
| Streptomyces phage Bmoc |  | [MT310865.1](https://www.ncbi.nlm.nih.gov/nuccore/MT310865.1) | 132.89 | 49.6 | [235](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89549/893411%7CStreptomyces%20phage%20Bmoc/viral%20segment/) | 41 | 68.5 | 78.3 |
| Streptomyces phage Egole |  | [MK494112.1](https://www.ncbi.nlm.nih.gov/nuccore/MK494112.1) | 135.65 | 49.9 | [228](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/78113/478566%7CStreptomyces%20phage%20EGole/viral%20segment/) | 47 | 90.6 | 84.1 |
| Streptomyces phage Evy |  | [MK977711.1](https://www.ncbi.nlm.nih.gov/nuccore/MK977711.1) | 132.98 | 49.6 | [226](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82597/609665%7CStreptomyces%20phage%20Evy/viral%20segment/) | 33 | 78.4 | 78.8 |
| Streptomyces phage Braelyn |  | [MN096371.1](https://www.ncbi.nlm.nih.gov/nuccore/MN096371.1) | 131.23 | 50.1 | [228](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82673/614449%7CStreptomyces%20phage%20Braelyn/viral%20segment/) | 38 | 77.4 | 81.0 |

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**Electron micrograph:** Electron micrographs of negatively stained Streptomyces phage Daubenski (https://phagesdb.org/phages/Daubenski/). Limited permission was granted by The Actinobacteriophages Database (https://phagesdb.org/), funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.

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**References**

1: 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.

2: 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

3: 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://rhea.icbm.uni-oldenburg.de/VIRIDIC/>

4: Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.

5: Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.

6: Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.

7: Lowe, T.M. and Chan, P.P. (2016) tRNAscan-SE On-line: Search and Contextual Analysis of Transfer RNA Genes. Nucl. Acids Res. 44: W54-57.

8: Zimmermann L, Stephens A, Nam SZ, et al. A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core. J Mol Biol. 2018;430(15):2237-2243. doi:10.1016/j.jmb.2017.12.007

9: Turner D, Kropinski AM, Adriaenssens EM. 2021. A Roadmap for Genome-Based Phage Taxonomy. Viruses 2021, 13, 506. https://doi.org/10.3390/v13030506