

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

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| **Code assigned:** | **2021.063B** |  |
| **Short title:** Create one new family (*Peduoviridae*) including 20 new genera and 21 new species (*Caudoviricetes*) | | |
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**\***The views expressed in this article reflect the results of research conducted by the author and do not necessarily reflect the official policy or position of the Department of the Navy, Department of Defense, nor the United States Government. This work was supported/funded by work unit number A1417

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

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| *Peduovirinae* Study Group |

**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**

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| --- | --- |
| Date first submitted to SC Chair | May 2021 |
| 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. |

**TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| --- |
| 2021.063B.R.Peduoviridae |

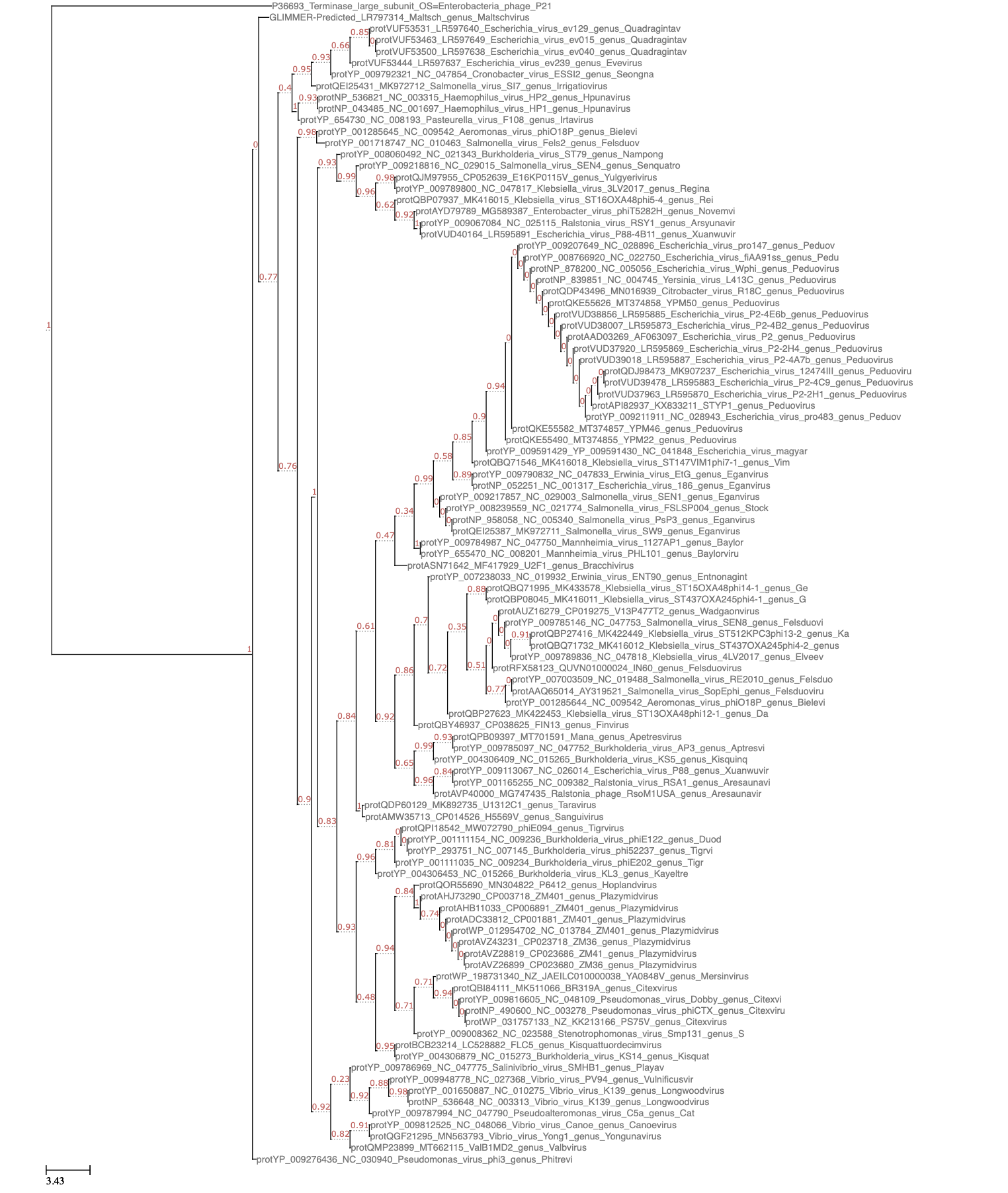
**Abstract**

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| In this proposal, we suggest to elevate the subfamily *Peduovirinae* to a family, becoming *Peduoviridae*. We also change the genus demarcation criteria from 50% nucleotide identity to 70%, in line with other new families. This change requires splitting a number of previously defined genera and renaming them. Finally, we add new genera and species to the family. |

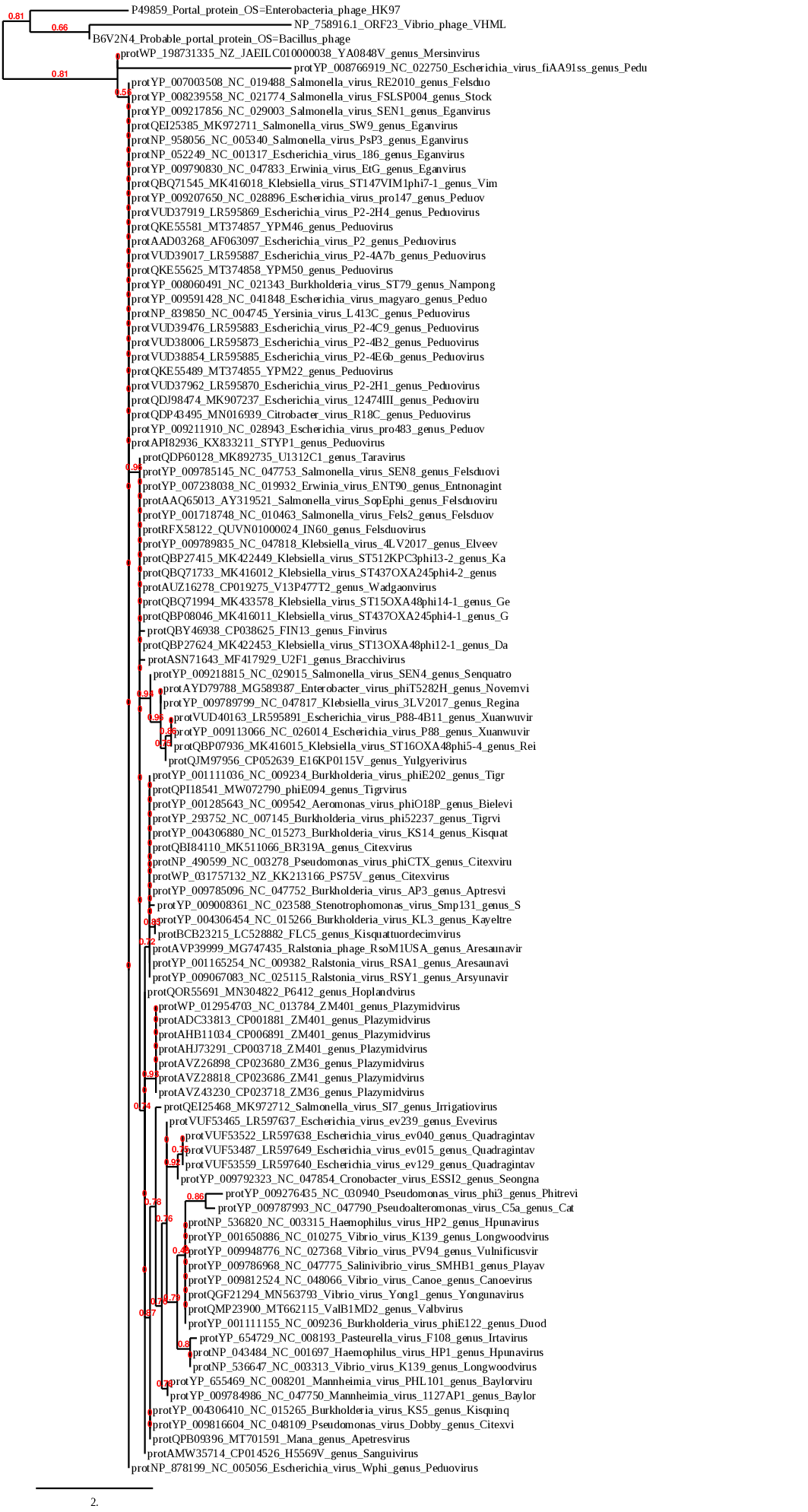
**Text of proposal**

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Each of the proposed species differs from the others by more than 5% at the DNA level as confirmed with the BLASTN algorithm.  **Genus demarcation criteria (updated):** The defining criterion for membership in a genus is that the species display 70-95% DNA sequence identity to one another. This was previously set to 50-95%. Membership to existing genera is adjusted to meet this new criterion within this proposal. All genera are monophyletic in the marker gene trees.  **Family demarcation criteria:** All members of *Peduoviridae* encode a set of 6 orthologous core genes:   |  |  | | --- | --- | | Orthogroup 1 | Terminase, large subunit | | Orthogroup 2 | Portal protein | | Orthogroup 3 | Capsid scaffolding protein | | Orthogroup 4 | Major capsid protein | | Orthogroup 5 | Terminase, small subunit | | Orthogroup 6 | Capsid completion/stabilization protein |   Members of *Peduoviridae* have genome sizes between 28 kb and 41kb.  **Proposal 1:** To promote the subfamily *Peduovirinae* creating a new family, *Peduoviridae,* retaining the membership*.*  **Background/History:** The subfamily *Peduovirinae* was first defined as a subfamily in 2011. At that time phages were assigned to families based on morphology. New ICTV guidelines allow new families to be defined by genomic and proteomic evidence. The diversity within *Peduovirinae* is consistent with other recently defined families in the order *Caudovirales*.  **Source of name of this taxon:** The name of this taxon is derived from the name of the original subfamily.  Members of *Peduoviridae* contain the following characteristic features:     |  |  | | --- | --- | | Genome | Linear dsDNA, 28-41 kb in length | | Morphology | Myovirus-like morphology | | Host range | Proteobacteria | | Core Genes | Large and small terminase subunits, portal protein, capsid scaffolding protein, major capsid protein, capsid completion/stabilization protein. |   The following proposals (2-29) all describe the creation of new genera and species within the newly elevated family *Peduoviridae*.  **Proposal 2:** To create a new genus, *Evevirus,* and to reassign *Seongnamvirus ev239* to it.  **Background/History:** This species was originally assigned to the genus*Seongnamvirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** The name of this genus comes from the species name ‘***ev****239*’.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | LR597637 | NC\_049392 | *Evevirus ev239* | 29,203 bp | 51.4% | 0 | 48 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 3:** To create a new genus, *Quadragintavirus*, and to reassign *Seongnamvirus ev015, Seongnamvirus ev040,* and *Seongnamvirus ev129* to it.  **Background/History:** These three species were originally assigned to the genus*Seongnamvirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. These species are getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** The name of this genus comes from the species *Seongnamvirus ev040.*  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | LR597649 | NC\_049395 | *Quadragintavirus ev015* | 30,584 | 50.9% | 0 | 49 | | LR597638 | NC\_049393 | *Quadragintavirus ev040* | 30,597 | 50.8% | 0 | 46 | | LR597640 | NC\_049394 | *Quadragintavirus ev129* | 30,927 | 51.5% | 0 | 45 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 4:** To create a new genus, *Gemsvirus*, and to reassign *Xuanwuvirus gv5004652* to it.  **Background/History:** This species was originally assigned to the genus *Xuanwuvirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** The exemplar for *Gemsvirus gv5004652* was collected as part of GEMS, Global Enteric Multicenter Study.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | CP025901 | NC\_049343 | *Gemsvirus gv5004652* | 33,041 | 52.4% | 0 | 59 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 5:** To create a new genus, *Dagavirus*, and to reassign *Felsduovirus ST13OXA48phi121* to it.  **Background/History:** This species was originally assigned to the genus *Felsduovirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** The last four residues of the exemplar genome for *Dagavirus ST13OXA48phi121’s* major capsid protein are DAGA.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | CP025901ß | NC\_049343 | *Dagavirus ST13OXA48phi121* | 33,041 | 52.4% | 0 | 59 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 6:** To create a new genus, *Wadgaonvirus*, to reassign *Felsduovirus wv5004651* to it, and to assign a new species, *Wadgaonvirus V13P477T2*, to it.  **Background/History:** *Wadgaonvirus wv5004651* was originally assigned to the genus *Felsduovirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity. *Wadgaonvirus V13P477T2* was deposited to GenBank as a plasmid of *Escherichia coli* strain *13P477T*. However, this sequence is the correct size to belong to *Peduoviridae*, has all *Peduoviridae* core genes, and has other phage genes suggesting that it is a plasmid prophage.  **Source of name of this taxon:** *Wadgaonvirus wv5004651* sample from Wadgaon, India. The species ‘*V13P477T2’* is derived from the name of its exemplar’s GenBank entry, Escherichia coli strain 13P477T plasmid p13P477T-2.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | CP025900 | NC\_049342 | *Wadgaonvirus wv5004651* | 39,179 | 52.7% | 1 | 70 | | CP019275 | N/A | *Wadgaonvirus V13P477T2* | 37,446 | 51.3% | 1 | 81 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 7:** To create a new genus, *Elveevirus*, and to reassign *Felsduovirus 4LV2017* to it.  **Background/History:** This species was originally assigned to the genus *Felsduovirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** *Elveevirus* is named after its first species, *4LV2017* (pronounced ‘LVvirus’)  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | KY271398 | NC\_047818 | *Elveevirus 4LV2017* | 33,540 | 50.4% | 0 | 48 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 8:** To create a new genus, *Kapieceevirus*, and to reassign *Felsduovirus ST512KPC3phi132* to it.  **Background/History:** This species was originally assigned to the genus *Felsduovirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** The name is derived from the species *Kapieceevirus* *ST512****KPC****3phi132.*  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | MK422449 | NC\_049452 | *Kapieceevirus ST512KPC3phi132* | 32,302 | 51.9% | 0 | 48 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 9:** To create a new genus, *Gegavirus*, and to reassign *Felsduovirus ST15OXA48phi141* to it.  **Background/History:** This species was originally assigned to the genus *Felsduovirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** The last four residues of *Gegavirus ST15OXA48phi141’s* exemplar genome’s major capsid protein are G-E-G-A.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | MK433578 | NC\_049454 | *Gegavirus ST15OXA48phi141* | 33,839 | 52.7% | 1 | 56 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 10:** To create a new genus, *Gegevirus*, and to reassign *Felsduovirus ST437OXA245phi41* to it.  **Background/History:** This species was originally assigned to the genus *Felsduovirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** The last four residues of the major capsid protein are G-E-G-E for all publicly available genomes belonging to *Gegevirus ST437OXA245phi41*.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | MK416011 | NC\_049448 | *Gegevirus ST437OXA245phi41* | 39,642 | 52.8% | 2 | 63 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 11:** To create a new genus, *Arsyunavirus*, and to reassign *Aresaunavirus RSY1* to it.  **Background/History:** This species was originally assigned to the genus *Aresaunavirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** *Arsyunavirus* is derived from the species name *RSY1.*  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | AB981169 | NC\_025115 | *Arsyunavirus RSY1* | 40,002 | 64.8% | 0 | 58 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 12:** To create a new genus, *Aptresvirus*, and to reassign *Kisquinquevirus AP3* to it and create a new species, *Apetresvirus Mana*.  **Background/History:** This species was originally assigned to the genus *Kisquinquevirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity. The exemplar of species *Apetresvirus Mana* was deposited to GenBank on November 15, 2020.  **Source of name of this taxon:** The name of the genus ‘*Aptresvirus’* is derived from the species *AP3.* The species name *‘Mana’* is derived from the name of the exemplar, ‘Burkholderia phage Mana’  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | KP966108 | NC\_047752 | *Aptresvirus AP3* | 36,499 | 64.4% | 1 | 58 | | MT701591 | N/A | *Apetresvirus Mana* | 38,038 | 64.3% | 0 | 65 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 13:** To create a new genus, *Kayeltresvirus*, and to reassign *Tigrvirus KL3* to it.  **Background/History:** This species was originally assigned to the genus *Tigrvirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** ‘*Kayeltresvirus’* is derived from the species name *KL3.*  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | GU911304 | NC\_015266 | *Kayeltresvirus KL3* | 40,555 | 63.2% | 0 | 57 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 14:** To create a new genus, *Duodecimduovirus*, and to reassign *Tigrvirus phiE122* to it.  **Background/History:** This species was originally assigned to the genus *Tigrvirus* when the genus demarcation criterion was set to 50% nucleotide identity over the length of the genome. This species is getting reassigned to a new genus because this criterion is now set to 70% nucleotide identity.  **Source of name of this taxon:** *Duodecimduovirus* is derived from the species name ‘*phiE****122***’***.***  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | CP000624 | NC\_009236 | *Duodecimduovirus phiE122* | 36,690 | 64.6% | ND | 50 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 15:** To create a new genus *Maltschvirus* and new species *Maltschvirus Maltsch*  **Background/History:** The exemplar of*Maltschvirus Maltsch* is an uncultured phage genome assembly uploaded to GenBank on January 12th, 2021.  **Source of name of this taxon:** The exemplar of*Maltschvirus Maltsch* was extracted from a sample collected from Maltsch river in the Czech Republic.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | LR797314 | N/A | *Maltschvirus Maltsch* | 36,306 | 42.1% | 0 | 49 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 16:** To create a new genus *Bracchivirus* and new species *Bracchivirus U2F1.*  **Background/History:** The exemplar of*Bracchivirus U2F1* is an uncultured phage genome assembly uploaded to GenBank on Feburary 27th, 2018.  **Source of name of this taxon:** The species name ‘*U2F1*’ comes from the genbank entry name of the exemplar genome (Uncultured Caudovirales phage clone 2F\_1), with ‘U’ standing for ‘uncultured’. *Bracchivirus* is named for the origin of the *Bracchivirus* *U2F1* exemplar, which was collected from the skin of a human forearm.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | MF417929 | N/A | *Bracchivirus U2F1* | 32,618 | 39.2% | 0 | 53 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 17:** To create a new genus, *Plazymidvirus,* and to create 3 new species, *Plazymidvirus* *ZM401, Plazymidvirus* *ZM41*, and *Plazymidvirus* *ZM36.*  **Background/History:** All GenBank sequences belonging to*Plazymidvirus* have been deposited as bacterial plasmids. However, these sequences are the correct size to belong to *Peduoviridae*, have all *Peduoviridae* core genes, and have many other phage genes suggesting that they are plasmid prophages.  **Source of name of this taxon:** The species names *Plazymidvirus* *ZM401, Plazymidvirus* *ZM41*, and *Plazymidvirus* *ZM36* are derived from the GenBank entry of their exemplar genome: *Zymomonas mobilis* ZM4 plasmid pZZM401*, Zymomonas mobilis* plasmid pZM41, and *Zymomonas mobilis* strain ZM4 substr. 2032 plasmid pZM36, respectively. The genus name *Plazymidvirus* is derived from ‘plasmid’ and ‘Zymomonas’. [14]  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | CP001881 | NC\_013784 | *Plazymidvirus ZM401* | 37,066 | 42.4% | 0 | 69 | | CP023686 | N/A | *Plazymidvirus ZM41* | 40,858 | 43.9% | 0 | 72 | | CP023718 | N/A | *Plazymidvirus ZM36* | 36,494 | 43.1% | 0 | 64 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Reference:** Yang S, Vera JM, Grass J, Savvakis G, Moskvin OV, Yang Y, McIlwain SJ, Lyu Y, Zinonos I, Hebert AS, Coon JJ, Bates DM, Sato TK, Brown SD, Himmel ME, Zhang M, Landick R, Pappas KM, Zhang Y (2018) Complete genome sequence and the expression pattern of plasmids of the model ethanologen Zymomonas mobilis ZM4 and its xylose-utilizing derivatives 8b and 2032. Biotechnol Biofuels 11:125  **Proposal 18:** To create a new genus, *Sanguivirus*, and to create a new species *Sanguivirus H5569V* to it.  **Background/History:** The exemplar sequence for *Sanguivirus H5569V* was deposited to GenBank as a plasmid of *Haematospirillum jordaniae* strainH5569. However, this sequence is the correct size to belong to *Peduoviridae*, has all *Peduoviridae* core genes, and has other phage genes suggesting that it is a plasmid prophage.  **Source of name of this taxon:** The exemplar of *Sanguivirus H5569V* was isolated from a human blood sample (sanguis). ‘*H5569V’* is derived from the host strain (H5569), with ‘V’ indicating it is a virus.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | CP014526 | N/A | *Sanguivirus H5569V* | 32,967 | 57.2% | 0 | 69 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 19:** To create a new genus *Valbvirus*, and to assign species *Valbvirus ValB1MD2*.  **Background/History:** The exemplar genome for species *Valbvirus ValB1MD2* was deposited to GenBank on August 3, 2020.  **Source of name of this taxon:** The genus name ‘*Valbvirus’* is derived from the species name ‘*ValB1MD2’.* The species *Valbvirus ValB1MD2* is derived from the name of the exemplar GenBank entry (Vibrio phage ValB1MD-2).  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | MT662115 | N/A | *Valbvirus ValB1MD2* | 36,616 | 43.2% | 0 | 55 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 20:** To create a new genus*, Yulgyerivirus*, and a new species, *Yulgyerivirus* *E16KP0115V.*  **Background/History:** The exemplar sequence for *Yulgyerivirus* *E16KP0115V* was deposited to GenBank as a plasmid of *Klebsiella pneumoniae* strain *E16KP0115*. However, this sequence is the correct size to belong to *Peduoviridae*, has all *Peduoviridae* core genes, and has other phage genes suggesting that it is a plasmid prophage.  **Source of name of this taxon:** The exemplar for *Yulgyerivirus* *E16KP0115V* was isolated fromYulgye-ri, South Korea. The species name, ‘*E16KP0115V’,* is derived from its exemplar’s host strain.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | CP052639 | N/A | *Yulgyerivirus E16KP0115V* | 32,368 | 56.3% | 0 | 52 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 21:** To create a new genus*, Finvirus*, and a new species, *Finvirus* *FIN13.*  **Background/History:** The exemplar sequence for *Finvirus* *FIN13* was deposited to GenBank as a plasmid of *Arsenophonus nasoniae* strain *FIN*. However, this sequence is the correct size to belong to *Peduoviridae*, has all *Peduoviridae* core genes, and has other phage genes suggesting that it is a plasmid prophage.  **Source of name of this taxon:** The species and genus name are derived from name of the GenBank entry for *Finvirus* *FIN13*’sexemplar*, Arsenophonus nasoniae* strain FIN plasmid pArsFIN13.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | CP038625 | N/A | *Finvirus FIN13* | 33,626 | 45.9% | 0 | 66 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 22:** To create two new species in the genus *Citexvirus*, *Citexvirus PS75V and Citexvirus* *BR319A.*  **Background/History:** The exemplar of species *Citexvirus PS75V* was deposited to GenBank on October 20, 2020 as contig of a Pseudomonas aeruginosa assembly. The exemplar of species *Citexvirus* *BR319A* was deposited to GenBank on April 4th, 2019 as a partial genome.  **Source of name of this taxon:** The species name ‘*Citexvirus PS75V’* is derived from the exemplar’s host strain, *PS75*. The species name ‘*Citexvirus* *BR319A’* is derived from the name of its exemplar’s GenBank entry, ‘Pseudomonas phage vB\_Pae\_BR319a’.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | NZ\_KK213166 | N/A | *Citexvirus PS75V* | 37,788 | 62.3% | 1 | 58 | | MK511066 | N/A | *Citexvirus BR319A* | 35,343 | 62.4% | 0 | 53 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 23:** To create a new genus*, Mersinvirus*, and a new species, *Mersinvirus* *YA0848V*.  **Background/History:** The exemplar of species *Mersinvirus* *YA0848V* was deposited to GenBank on December 26, 2020 as contig of a bacterial assembly.  **Source of name of this taxon:** The exemplar sequence of *Mersinvirus* *YA0848V* is from a sample originating from Mersin, Turkey.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | NZ\_JAEILC010000038 | N/A | *Mersinvirus YA0848V* | 35,647 | 62.6% | 0 | 58 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 24:** To create a new species in the genus *Kisquattuordecimvirus*, *Kisquattuordecimvirus FLC5.*  **Background/History:** The exemplar of species *Kisquattuordecimvirus FLC5* was deposited to GenBank on September 3rd, 2020.  **Source of name of this taxon:** The species name *‘FLC5’* is derived from the name of the exemplar, ‘Burkholderia phage FLC5’.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | LC528882 | N/A | *Kisquattuordecimvirus FLC5* | 32,090 | 61.8% | 0 | 52 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 25:** To create a new species in the genus *Tigrvirus, Tigrvirus phiE094.*  **Background/History:** The exemplar of species *Tigrvirus phiE094* was deposited to GenBank on March 24, 2021.  **Source of name of this taxon:** The species name *‘phiE094’* is derived from the name of the exemplar, ‘Burkholderia phage phiE094’.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | MW072790 | N/A | *Tigrvirus phiE094* | 37,727 | 64.5% | 1 | 57 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 26:** To create two new species in the genus *Felsduovirus, Felsduovirus IN60.*  **Background/History:** The exemplar of species *Felsduovirus IN60* was deposited to GenBank on August 28, 2018 as contig of a *Salmonella enterica* assembly.  **Source of name of this taxon:** The species ‘*IN60’* is derived from its exemplar’s isolate name alias.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | QUVN01000024 | N/A | *Felsduovirus IN60* | 34,704 | 52.1% | 2 | 58 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry  **Proposal 27:** To create four new species in the genus *Peduovirus: Peduovirus* *STYP1*  *Peduovirus YPM22, Peduovirus YPM50, and Peduovirus YPM46.*  **Background/History:** The exemplars of *Peduovirus YPM22, Peduovirus YPM50, and Peduovirus YPM46* were deposited to GenBank on June 3rd, 2020. The exemplar for *Peduovirus* *STYP1* was deposited to GenBank on December 13, 2016. It is currently classified by NCBI taxonomy as *Salmonella*, despite it being described as a prophage by the GenBank Entry.  **Source of name of this taxon:** The names for all four species are derived by the names of their respective exemplar sequences.  **Genome Summary Table:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Exemplar  Genbank Accession | Exemplar  RefSeq  Accession | Species Name | Genome Length | GC Content | Number of tRNAs\* | Number of ORFs\*\* | | KX833211 | N/A | *Peduovirus STYP1* | 28,946 | 53.0% | 0 | 45 | | MT374855 | N/A | *Peduovirus YPM22* | 31,809 | 51.5% | 0 | 51 | | MT374858 | N/A | *Peduovirus YPM50* | 31,096 | 52.1% | 0 | 50 | | MT374857 | N/A | *Peduovirus YPM46* | 32,336 | 51.7% | 0 | 50 |   *\* Determined using tRNAscan-SE*  *\*\* Determined using PHANOTATE* or GenBank entry | |

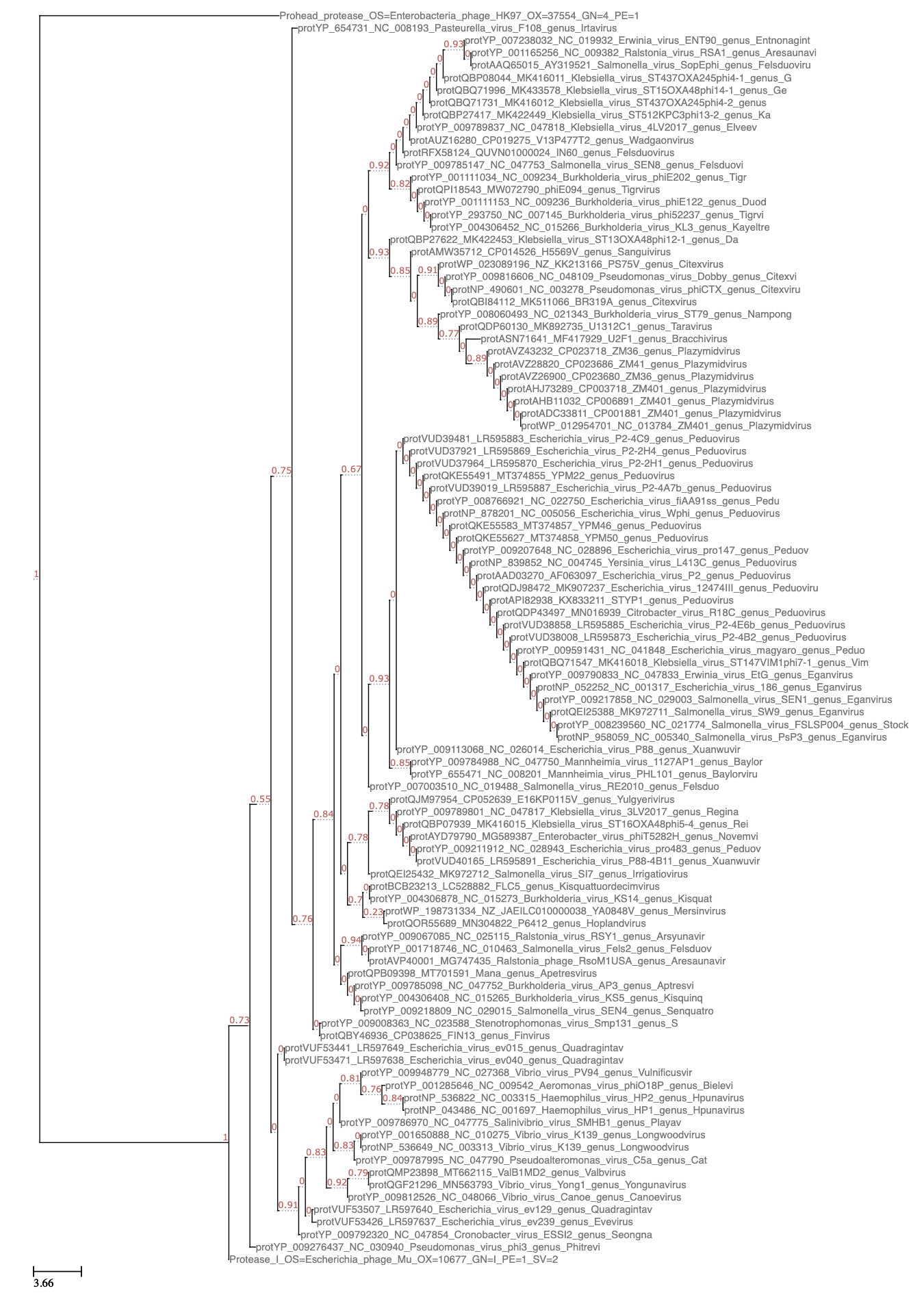
**Supporting evidence**



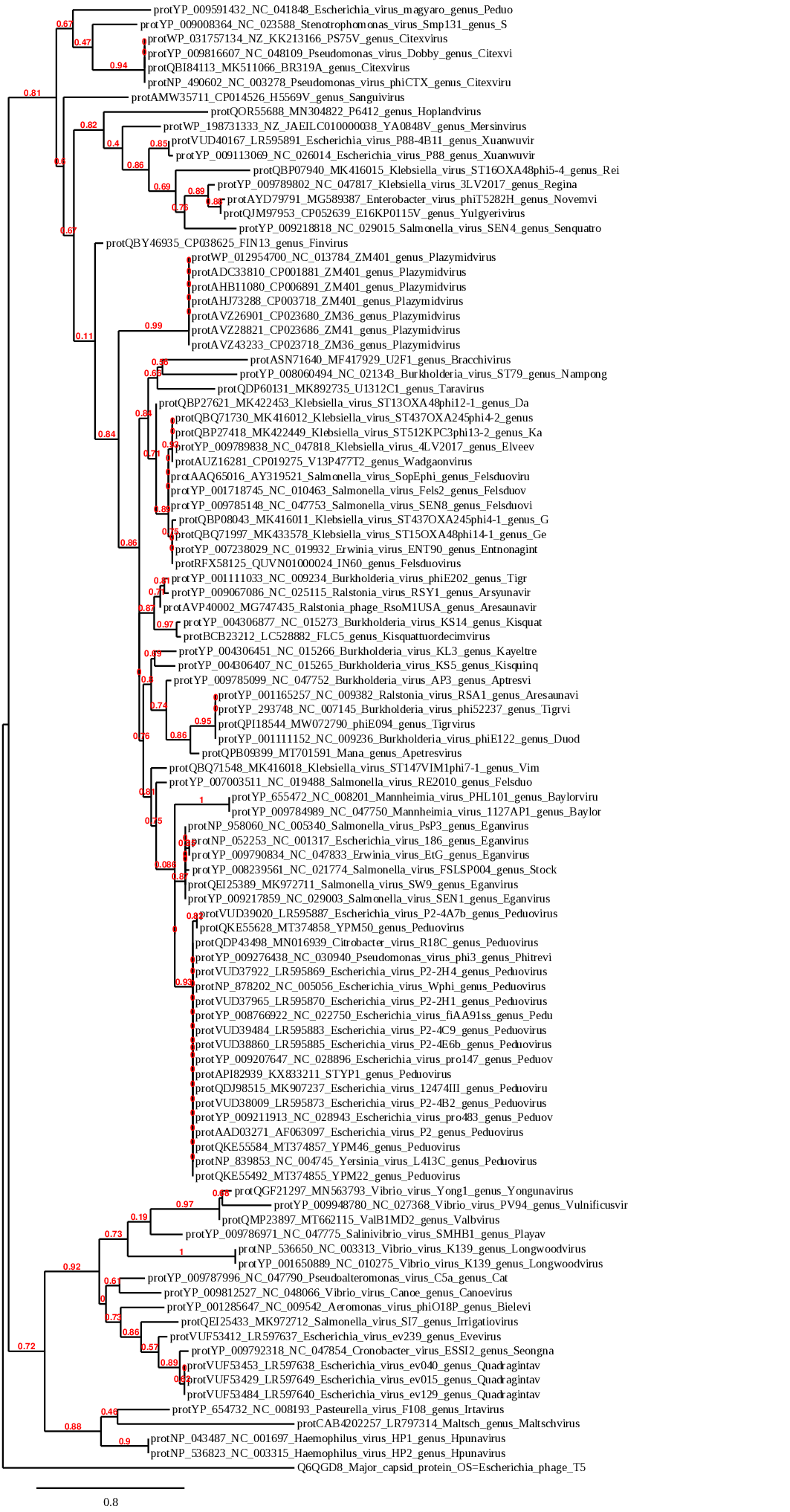
*Figure 1. Peduoviridae large terminase subunit phylogeny created with 'one-click mode' on Phylogeny.fr. The large terminase of Enterobacteria phage P21 is used as an outgroup. Outgroup determined with HHpred. Tree visualized with ETE 3.*

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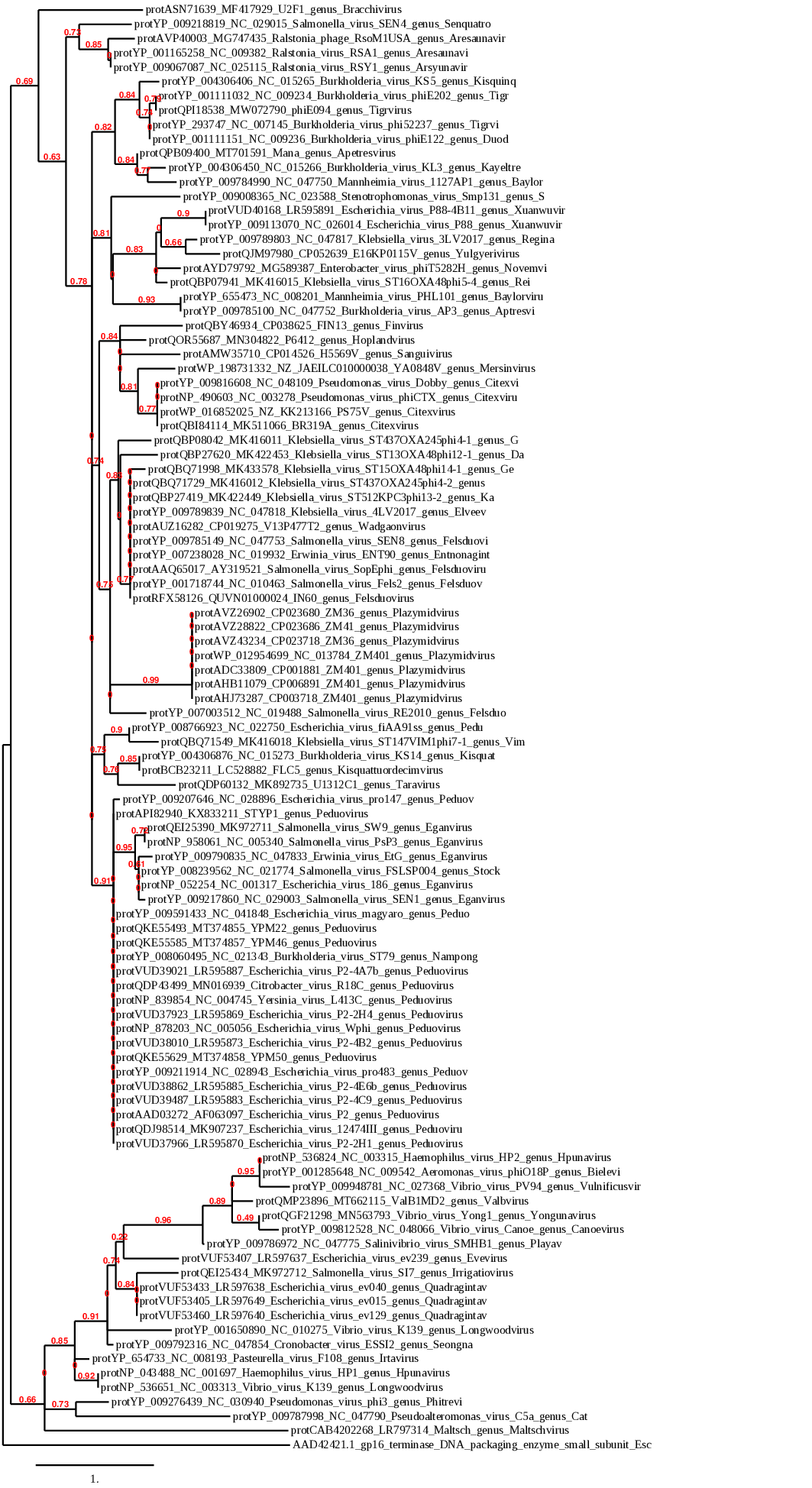
*Figure 2. Peduoviridae portal protein phylogeny created with 'one-click mode' on Phylogeny.fr. Portal proteins from Enterobacteria phage HK97, Bacillus phage SP01, and Vibrio phage VHML are used as an outgroup. Outgroup determined with PSI-BLAST and HHpred.*



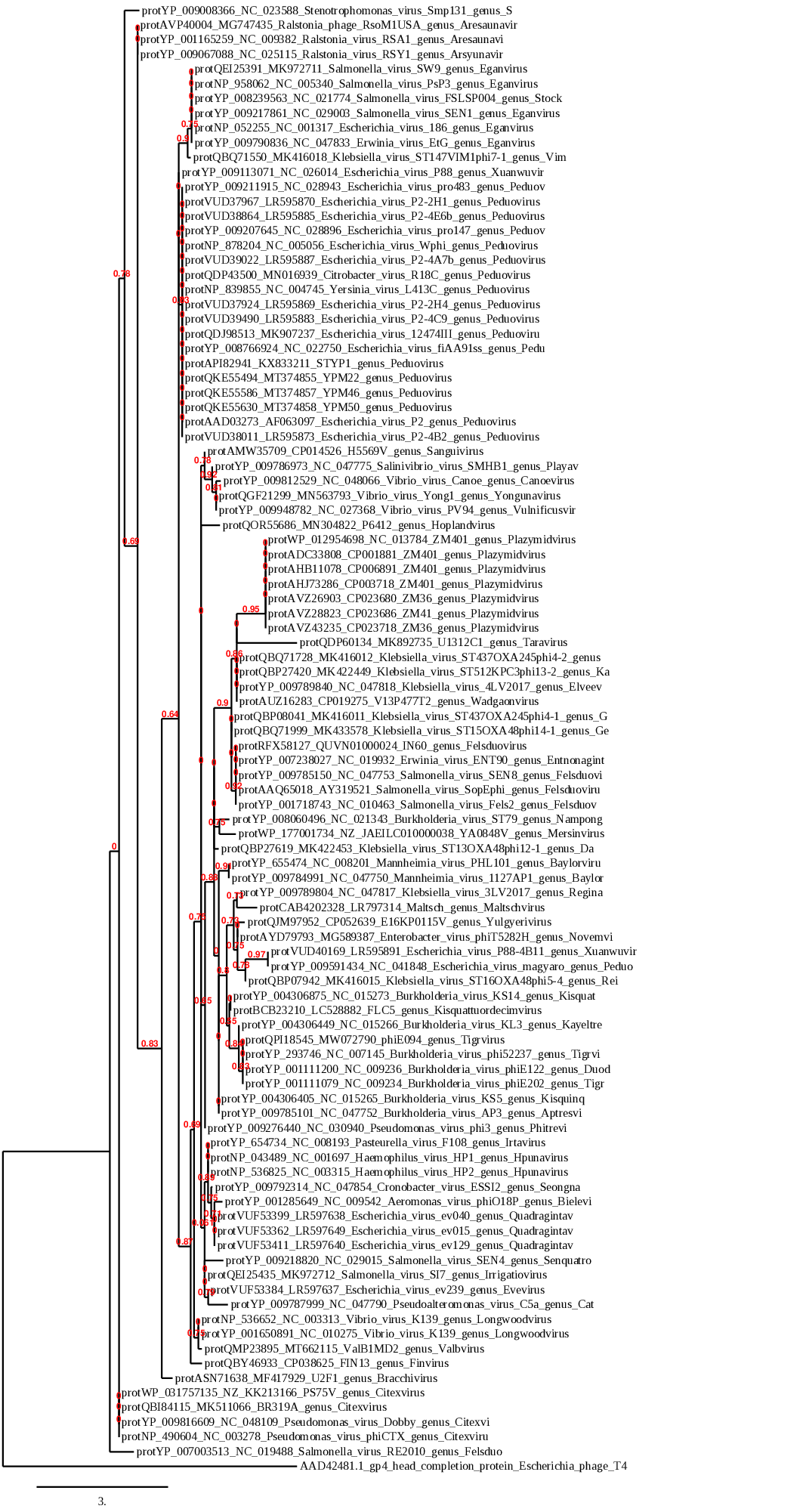
*Figure 3. Peduoviridae capsid scaffolding protein phylogeny created with 'one-click mode' on Phylogeny.fr. Proteases from Enterobacteria phage HK97 and Escherichia phage Mu are used as an outgroup. Outgroup determined with HHpred. Tree visualized with ETE 3.*

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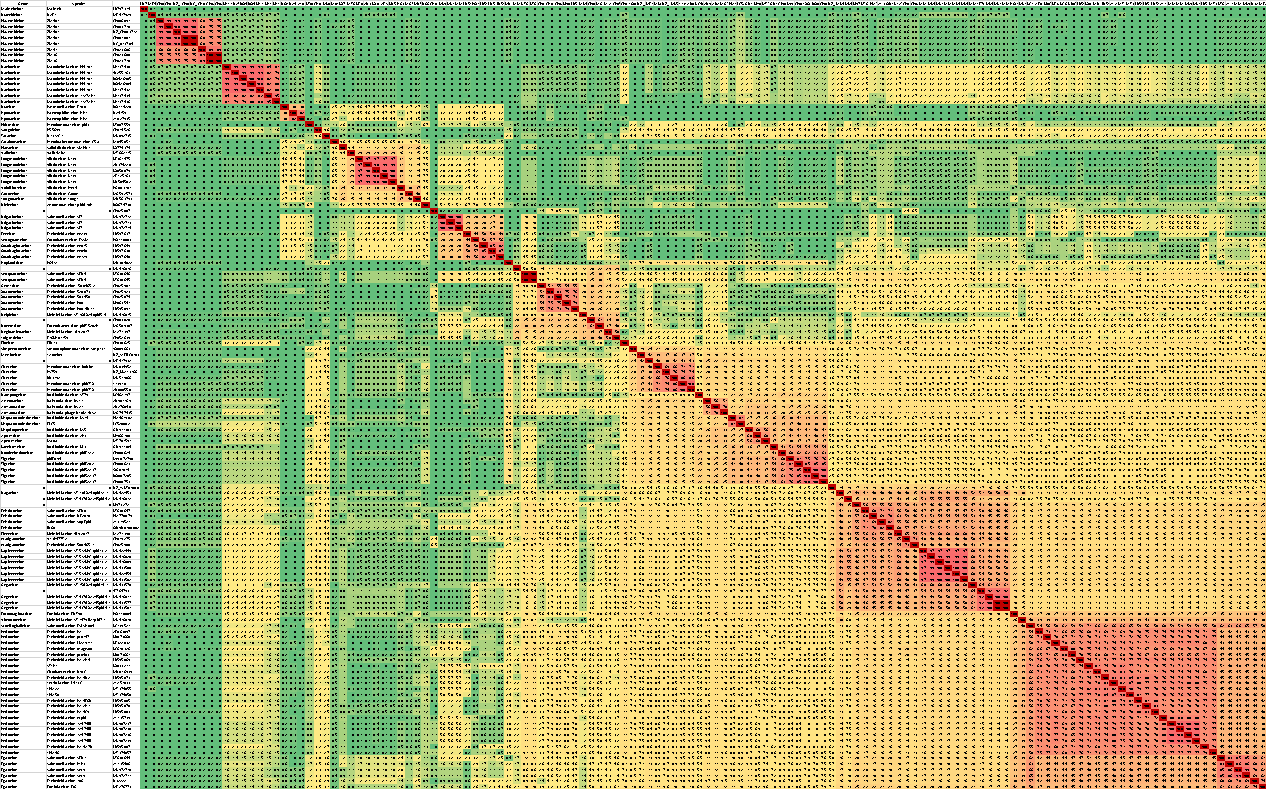
*Figure 4. Peduoviridae major capsid protein phylogeny created with 'one-click mode' on Phylogeny.fr. The major capsid protein of Escherichia phage T5 is used as an outgroup. Outgroup determined with HHpred.*

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*Figure 5. Peduoviridae small terminase subunit phylogeny created with 'one-click mode' on Phylogeny.fr. The small terminase of Escherichia phage T4 is used as an outgroup*

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*Figure 6. Peduoviridae capsid completion/stabilization protein phylogeny created with 'one-click mode' on Phylogeny.fr. The head completion protein of Escherichia phage T4 is used as an outgroup*

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*Figure 7. Pairwise genome identities determined using BLASTn. Values which are rounded to 100 are distinguished from identical genomes by the color of the cell. Cells for identical genomes use a deeper shade of red.*

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