

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

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| **Code assigned:** | **2021.015B** |  |
| **Short title:** Create one new family (*Casjensviridae*) including 20 new genera and four existing genera (*Caudoviricetes*) | | |
|  | | |

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

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| Caudoviricetes Study Group, Bacterial Viruses Subcommittee |

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

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

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

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| Casjensviridae | Sherwood R. Casjens | Y |
|  |  |  |
|  |  |  |

**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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| --- |
| 2021.015B.R.Casjensviridae |

**Abstract**

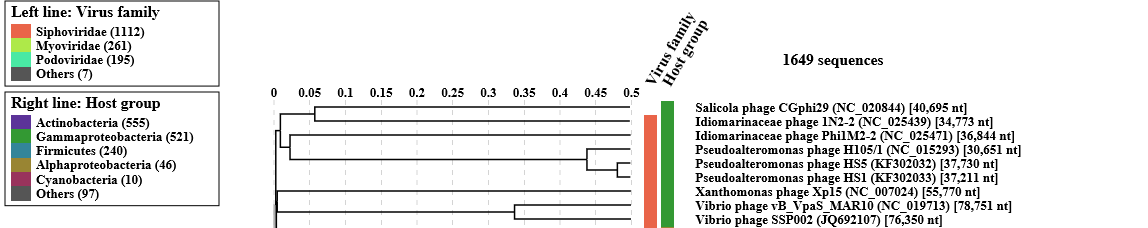
|  |
| --- |
| Salmonella phage Chi is a flagellotropic, lytic siphovirus. ICTV currently recognizes four genera of Chi-like phages *Chivirus, Nazgulvirus, Ahduovirus* and *Sanovirus*. We have structured a new family named *Casjensviridae* in honour of Sherwood Casjens. All the data i.e. genomic (VIRIDIC), proteomic (ViPTree, CoreGenes5.0) and phylogenetic (phylogeny.fr), coupled with the comments of several authors lead us to conclude that the Chi-like phages form a cohesive group which are united at the family level. The general properties of the phages which belong to this family are that their genomes are, on average, 59.3 kb; they have an average mol%G+C content of 57.1 (range: 46.9-63.3); and, they encode approximated 75 proteins. Ten (13%) protein homologs were discovered using CoreGenes 5.0 (<https://coregenes.ngrok.io/>). These included: DNA helicase, small & large terminase subunits, portal protein, head-tail joining protein, prohead protease, major capsid protein, major tail protein, and tail tapemeasure protein. |

**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 – 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:** Not applicable to this proposal. 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.  **Family demarcation criteria: -** The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (VipTree, GRAViTy, vConTACT2). Members of the family share a significant number of orthologous genes (more than 10% of the genome).  (Taken from: Turner D et al. [9] ) | |

**Genera 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]. Some new phages not in the original tree are marked with a **red stars**.

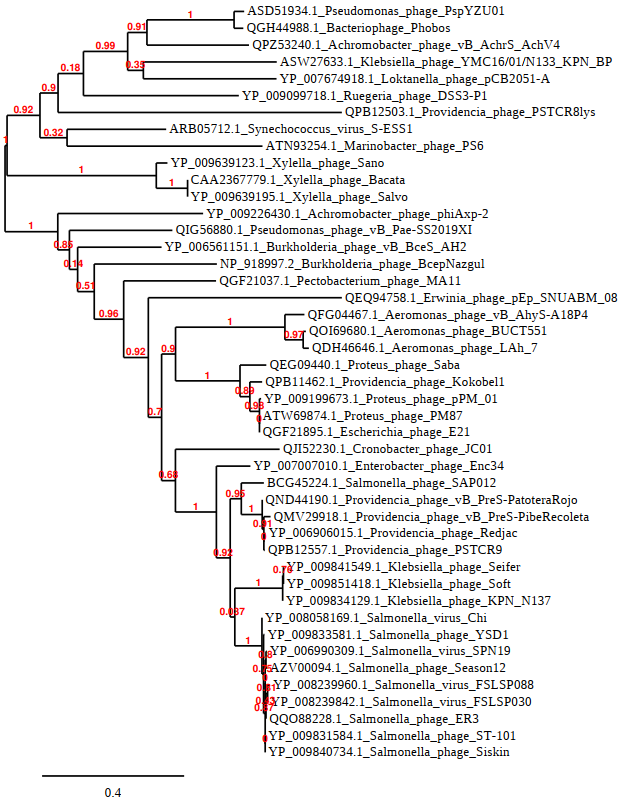
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**CoreGenes5.0 analysis:** The Bidirectional Best Hit (E value 1e-05) was employed at <https://coregenes.ngrok.io/> too assess the conserved proteins in members of this family. It was not applied to phages with underannotated genomes. Ten (13%) homologs were identified which included the portal, major tail protein, capsid, capsid maturation protease, small and large terminase subunits, and DNA helicase.

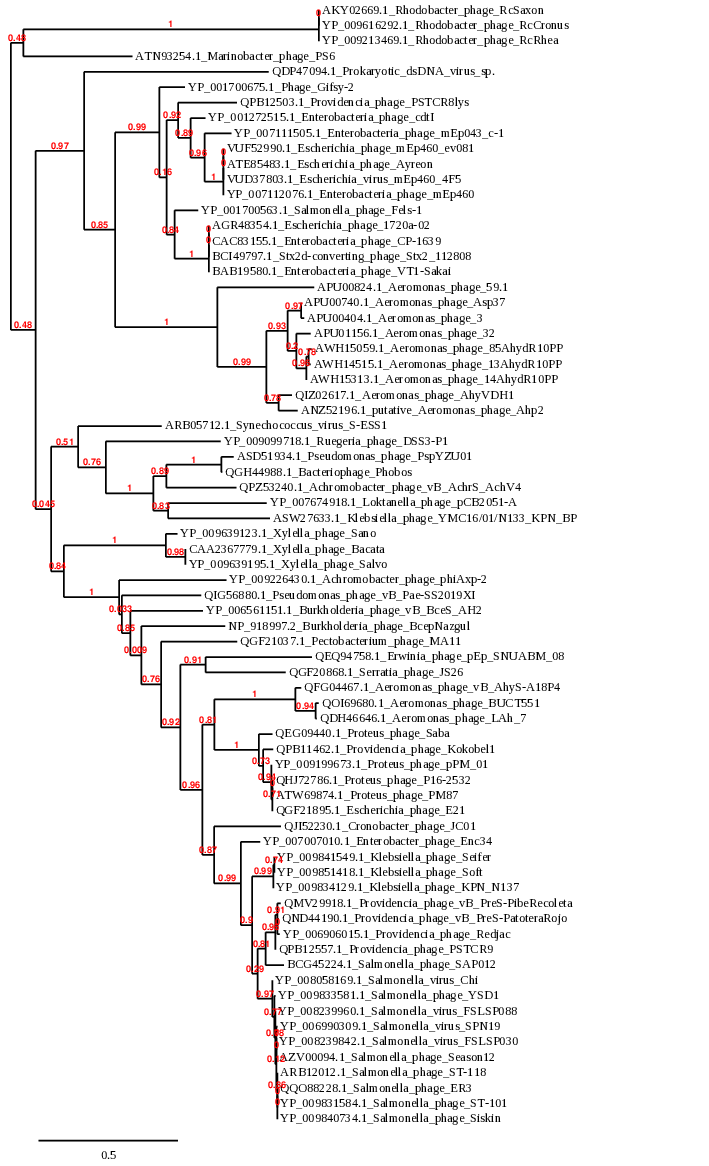
**VIRIDIC heat maps:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. It was run with only the species identified in this study and the heatmap is appended to this proposal.

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of these 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." A. unrooted; B. rooted

1. **UNROOTED**



1. **ROOTED**

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**Proposals:**

1. **To create a new genus *Broinstvirus* with a single species**
2. **To create a new genus *Sessunavirus* with a single species**
3. **To create a new genus *Salvovirus* with two (2) species**
4. **To create a new genus *Gediminasvirus* with a single species**
5. **To create a new genus *Seodaemunguvirus* with a single species**
6. **To create a new genus *Phobosvirus* with two (2) species**
7. **To create a new genus *Cenphatechvirus* with a single species**
8. **To create a new genus *Kokobelvirus* with a single species**
9. **To create a new genus *Lavrentievavirus* with three (3) species**
10. **To create a new genus *Sharonstreetvirus* with three (3) species**
11. **To transfer the genus *Yonseivirus* with three (3) species to this family**
12. **To create a new genus *Jacunavirus* with a single species**
13. **To add 3 new species to the genus *Chivirus***
14. **To create a new genus *Zhonglingvirus* with a single species**
15. **To create a new genus *Redjacvirus* with three (3) species**
16. **To create a new genus *Gwanakrovirus* with a single species**
17. **To create a new genus *Dunedinvirus* with a single species**
18. **To create a new genus *Fengtaivirus* with a single species**
19. **To create a new genus *Maxdohrnvirus* with a single species**
20. **To create a new genus *Newforgelanevirus* with a single species**
21. **To create a new genus *Enchivirus* with a single species**
22. **To create a new family *Casjensviridae* for these and three existing genera.**

**Proposal 1: To create a new genus *Broinstvirus* with a single species**

**Source of the name of this taxon:** This taxon is named in honour of The Eli and Edythe L. Broad Institute of MIT and Harvard

**History:** Loktanella phage pCB2051-A was isolated from the Norwegian Sea on Loktanella sp. CB2051

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Loktanella phage pCB2051-A | [NC\_020853.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_020853.1) | [HQ632859.1](https://www.ncbi.nlm.nih.gov/nuccore/HQ632859.1) | 56.96 | 55.0 | [76](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/3878/455849%7CLoktanella%20phage%20pCB2051-A/viral%20segment%20Unknown/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 2: To create a new genus *Sessunavirus* with a single species**

**Source of the name of this taxon:** The name of this taxon is directly derived from the name of the first isolate of this type, Synechococcus virus S-ESS1

**History:** This phage was isolated by the School of Resource and Environmental Engineering, Hubei University of Technology, China using a Synechococcus strain as the host bacterium.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Synechococcus virus S-ESS1 |  | [KY249644.1](https://www.ncbi.nlm.nih.gov/nuccore/KY249644.1) | 60.36 | 60.9 | [52](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63377/465998%7CSynechococcus%20virus%20S-ESS1/viral%20segment/) (\*\*\*) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**(\*\*\*) Underannotated**

**Proposal 3. To create a new genus Salvovirus with two (2) species**

**Source of the name of this taxon:** This taxon is named after the first isolate of it type, Xylella phage Salvo

**History:** The genus Sanovirus was created through Taxonomy Proposal 2018.097B but even at that time the DNA sequence relatedness between Sano and Silva was considered problematic.

**Specific Reference:** Ahern SJ, Das M, Bhowmick TS, Young R, Gonzalez CF. Characterization of novel virulent broad-host-range phages of Xylella fastidiosa and Xanthomonas. J Bacteriol. 2014 Jan;196(2):459-71. doi: 10.1128/JB.01080-13. Epub 2013 Nov 8. PMID: 24214944; PMCID: PMC3911242.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Xylella phage Salvo | [NC\_042345.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_042345.1) | [KF626668.1](https://www.ncbi.nlm.nih.gov/nuccore/KF626668.1) | 55.6 | 63.0 | [72](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62674/465297%7CXylella%20phage%20Salvo/viral%20segment/) | 100 | 100 |
| Xylella phage Bacata |  | LR743524.1 | 56.2 | 62.9 | 68 | 87.5 | 83.3 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 4. To create a new genus *Gediminasvirus* with a single species**

**Source of the name of this taxon:** This taxon is named after Grand Duke Gediminas (c. 1275–1341) who founded Vilnius were in Molecular Microbiology and Biotechnology, Vilnius University Life Sciences Center, Lithuania the first phage of its type was isolated in 2020.

**History:** None

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Achromobacter phage vB\_AchrS\_AchV4 | [MW269554.1](https://www.ncbi.nlm.nih.gov/nuccore/MW269554.1) | 59.49 | 62.8 | [82](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97698/1533123%7CAchromobacter%20phage%20vB_AchrS_AchV4/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 5. To create a new genus *Seodaemunguvirus* with a single species**

**Source of the name of this taxon:** The name derives from the district in which one finds the Yonsei University College of Medicine

**History:** Klebsiella phage YMC16/01/N133\_KPN\_BP was isolated in the Department of Laboratory Medicine, Yonsei University College of Medicine, Seoul, Republic of Korea in 2017.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Klebsiella phage YMC16/01/N133\_KPN\_BP | [MF476925.1](https://www.ncbi.nlm.nih.gov/nuccore/MF476925.1) | 58.39 | 58.9 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63841/466461%7CKlebsiella%20phage%20YMC16~2F01~2FN133_KPN_BP/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 6. To create a new genus *Phobosvirus* with two (2) species**

**Source of the name of this taxon:** This taxon is named directly after Bacteriophage Phobos.

**History:** Phage Phobos was isolated in Mexico, while PspYZU01 was isolated in China. The latter was isolated for biocontrol of fish and shrimp spoilage by Pseudomonas during chilled storage.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Bacteriophage Phobos | [MN478374.1](https://www.ncbi.nlm.nih.gov/nuccore/MN478374.1) | 56.73 | 63.3 | [63](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85455/742683%7CBacteriophage%20Phobos/viral%20segment/) | 100 | 100 |
| Pseudomonas\_phage\_PspYZU01 | [KY971609.1](https://www.ncbi.nlm.nih.gov/nuccore/KY971609.1) | 58.28 | 63.1 | [67](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/70065/382042%7CPseudomonas%20phage%20PspYZU01/viral%20segment/) | 81.1 | 96.8 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 7. To create a new genus *Cenphatecvirus* with a single species**

**Source of the name of this taxon:** The taxon name derives from the Center for Phage Technology where the first isolate of its type, Proteus phage Saba, was isolated.

**History:** Lytic phage Saba was isolated from wastewater in College Station, TX using Proteus mirabilis strain ATCC 29906 as the host bacterium.The authors noted its relation to Salmonella phage Chi.

**Specific Reference:** Nguyen J, Harb L, Moreland R, Liu M, Gill JJ, Ramsey J. Complete Genome Sequence of Proteus mirabilis Siphophage Saba. Microbiol Resour Announc. 2019 Oct 10;8(41):e01094-19. doi: 10.1128/MRA.01094-19. PMID: 31601673; PMCID: PMC6787330.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Proteus phage Saba | [MN062188.1](https://www.ncbi.nlm.nih.gov/nuccore/MN062188.1) | 60.06 | 48.8 | [76](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83778/672169%7CProteus%20phage%20Saba/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 8. To create a new genus *Kokobelvirus* with a single species**

**Source of the name of this taxon:** The name of this taxon derives directly from the name of the first phage of its type, Providencia phage Kokobel1.

**History:** This phage was isolated in the Institute of Dental Sciences and School of

Dental Medicine, Hebrew University, Hadassah Campus, Jerusalem, Israel from sewage using Providencia stuartii as the host bacterium.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Providencia phage Kokobel1 | [MW145139.1](https://www.ncbi.nlm.nih.gov/nuccore/MW145139.1) | 59.84 | 48.9 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96747/1493972%7CProvidencia%20phage%20Kokobel1/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 9. To create a new genus *Lavrentievavirus* with three (3) species**

**Source of the name of this taxon:** This taxon is named after the street address (Lavrentieva Ave. 8) of the Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia where Proteus phage PM87 was isolated.

**History:** These lytic phages were isolated in Malaysia (Proteus phage pPM\_01), China (Escherichia phage E21) and Russia (remainder).

**Specific Reference:** Morozova V, Kozlova Y, Shedko E, Babkin I, Kurilshikov A, Bokovaya O, Bardashova A, Yunusova A, Tikunov A, Tupikin A, Ushakova T, Ryabchikova E, Tikunova N. Isolation and characterization of a group of new Proteus bacteriophages. Arch Virol. 2018 Aug;163(8):2189-2197. doi: 10.1007/s00705-018-3853-3. Epub 2018 May 2. PMID: 29721709.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Proteus phage PM87 |  | [MG030346.1](https://www.ncbi.nlm.nih.gov/nuccore/MG030346.1) | 59.13 | 46.7 | [57](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68266/369413%7CProteus%20phage%20PM87/viral%20segment/) | 100 | 100 |
| Proteus phage pPM\_01 | [NC\_028812.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028812.1) | [KP063118.1](https://www.ncbi.nlm.nih.gov/nuccore/KP063118.1) | 58.55 | 46.9 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42566/462137%7CProteus%20phage%20pPM_01/viral%20segment%20Unknown/) | 94.2 | 91.2 |
| Escherichia phage E21 |  | [MN604053.1](https://www.ncbi.nlm.nih.gov/nuccore/MN604053.1) | 58.54 | 46.9 | [64](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85383/740784%7CEscherichia%20phage%20E21/viral%20segment/) | 92.7 | 89.5 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 10. To create a new genus *Sharonstreetvirus* with three (3) species**

**Source of the name of this taxon:** This taxon is named for the address of Pharmacy and Biomedical Sciences, La Trobe University, Bendigo, Victoria, Australia where Aeromonas phage LAh\_7 was isolated.

**History:** Theses lytic siphoviruses were isolated in Australia (Lah\_7) and China (remainder).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Proteins | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Aeromonas phage LAh\_7 | [MK838113.1](https://www.ncbi.nlm.nih.gov/nuccore/MK838113.1) | 61.43 | 62.1 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82451/604114%7CAeromonas%20phage%20LAh_7/viral%20segment/) | 100 | 100 |
| Aeromonas phage BUCT551 | [MT952005.1](https://www.ncbi.nlm.nih.gov/nuccore/MT952005.1) | 61.38 | 61.7 | [74](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/95858/1473039%7CAeromonas%20phage%20BUCT551/viral%20segment/) | 77.1 | 84.0 |
| Aeromonas phage vB\_AhyS-A18P4 | [MN317029.1](https://www.ncbi.nlm.nih.gov/nuccore/MN317029.1) | 60.98 | 62.0 | [73](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84873/708430%7CAeromonas%20phage%20vB_AhyS-A18P4/viral%20segment/) | 71.3 | 84.0 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 11. To transfer the genus *Yonseivirus* with three (3) species to this family**

**History:** Approved TaxoProp 2020.184B.R.Yonseivirus

**Proposal 12. To create a new genus *Jacunavirus* with a single species**

**Source of the name of this taxon:** The name of this taxon derives from Cronobacter phage JC01.

**History:** This lytic phage was isolated from sewage against Cronobacter sakazakii

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Cronobacter phage JC01 |  | [MT330372.1](https://www.ncbi.nlm.nih.gov/nuccore/MT330372.1) | 61.74 | 58.5 | [76](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/91503/895962%7CCronobacter%20phage%20JC01/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 13. To add 3 new species to the genus *Chivirus***

**Source of the name of this taxon:** The *Chilikevirus* genus was established through Taxonomy Proposal 2013.039a.

**History:** Salmonella phage Chi was sequenced by groups in Korea and USA, the latter providing the most accurate data revealing that there is a 12 bp 5' GCTCTGCGCACC overhang placed at the left end of the whole genome sequence. The Proposal (2013.039a) used JX094499 as the type species of the *Chilikevirus* genus.Lytic phage KFS-SE1 & BSPM4 was isolated in Korea, phage 118970\_sal1 in Italy; phages YSD1 & ER24 in the UK, Serratia phage KpYy\_1\_41 in China, phages 35 & 37 in India, Siskin in USA; ST-101 in Thailand; and, phage BP12C against Salmonella enterica Hadar in Canada.

**Specific Reference:** Karpe YA, Kanade GD, Pingale KD, Arankalle VA, Banerjee K. Genomic characterization of Salmonella bacteriophages isolated from India. Virus Genes. 2016 Feb;52(1):117-26. doi: 10.1007/s11262-015-1269-7. Epub 2016 Jan 12. PMID: 26757942. **[phage 35, 37]**

O'Leary C, Xie Y, Kongari R, Gill JJ, Liu M. Complete Genome Sequence of Salmonella enterica Serovar Typhimurium Siphophage Siskin. Microbiol Resour Announc. 2019 May 2;8(18):e00188-19. doi: 10.1128/MRA.00188-19. PMID: 31048394; PMCID: PMC6498227. **[Siskin]**

Phothaworn P, Dunne M, Supokaivanich R, Ong C, Lim J, Taharnklaew R, Vesaratchavest M, Khumthong R, Pringsulaka O, Ajawatanawong P, Klumpp J, Brown N, Imam M, Clokie MRJ, Galyov EE, Korbsrisate S. Characterization of Flagellotropic, Chi-Like Salmonella Phages Isolated from Thai Poultry Farms. Viruses. 2019 Jun 5;11(6):520. doi: 10.3390/v11060520. PMID: 31195709; PMCID: PMC6631126. **[Siskin]**

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage Chi | NC\_025442.1 | KM458633.1 | 59.58 | 56.5 | 75 | 100 | 100 |
| Serratia phage KpYy 1 41 |  | [MN871450.1](https://www.ncbi.nlm.nih.gov/nuccore/MN871450.1) | 54.42 | 56.9 | NA | 89.0 | ND |
| Salmonella phage ER24 |  | [MW355479.1](https://www.ncbi.nlm.nih.gov/nuccore/MW355479.1) | 60.44 | 56.6 | [74](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/98102/1546918%7CSalmonella%20phage%20ER24/viral%20segment/) | 92.5 | 93.3 |
| Salmonella phage SeWh-1 |  | [MH791395.1](https://www.ncbi.nlm.nih.gov/nuccore/MH791395.1) | 59.88 | 56.6 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75890/446548%7CSalmonella%20phage%20SeWh-1/viral%20segment/) | 82.3 | 89.3 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 14. To create a new genus *Zhonglingvirus* with a single species**

**Source of the name of this taxon:** This taxon was named after the street address (No. 50 Zhongling Street) of the Jiangsu Academy of Agricultural Science, Food Safety and Nutrition; Nanjing, Jinagsu, China where this phage was sequenced.

**History:** Salmonella phage SAP012 was isolated in Iran.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Salmonella phage SAP012 |  | [LC553736.1](https://www.ncbi.nlm.nih.gov/nuccore/LC553736.1) | 59.62 | 54.1 | [72](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92118/910324%7CSalmonella%20phage%20SAP012/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 15. To create a new genus *Redjacvirus* with three (3) species**

**Source of the name of this taxon:** This taxon is named directly after the first phage of its type Providencia phage Redjac.

**History:** Phage Redjac was isolated in Afghanistan using *Providencia stuartii* isolate MRSN 2154 as the host bacterium. The other two species were isolated in Australia and their genomes possess a 5’ 11 nt cos overhang.

**Specific Reference:** Onmus-Leone F, Hang J, Clifford RJ, Yang Y, Riley MC, Kuschner RA, Waterman PE, Lesho EP. Enhanced de novo assembly of high throughput pyrosequencing data using whole genome mapping. PLoS One. 2013 Apr 17;8(4):e61762. doi: 10.1371/journal.pone.0061762. PMID: 23613926; PMCID: PMC3629165.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Providencia\_phage\_  Redjac | [NC\_018832.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_018832.1) | [JX296113.1](https://www.ncbi.nlm.nih.gov/nuccore/JX296113.1) | 58.1 | 49.5 | [41](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/15267/459732%7CProvidencia%20phage%20Redjac/viral%20segment%20Unknown/) (\*\*\*) | 100 | 100 |
| Providencia\_phage\_  vB\_PreS-PibeRecoleta |  | [MT675124.1](https://www.ncbi.nlm.nih.gov/nuccore/MT675124.1) | 60.73 | 49.3 | [73](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/93843/972065%7CProvidencia%20phage%20vB_PreS-PibeRecoleta/viral%20segment/) | 83.8 | 100 |
| Providencia\_phage\_  vB\_PreS-Stilesk |  | [MT675125.1](https://www.ncbi.nlm.nih.gov/nuccore/MT675125.1) | 60.92 | 49.5 | [73](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/93844/972066%7CProvidencia%20phage%20vB_PreS-Stilesk/viral%20segment/) | 80.7 | 97.6 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**(\*\*\*) Underannotated**

**Proposal 16. To create a new genus *Dunedinvirus* with a single species**

**Source of the name of this taxon:** Named after the city (Dunedin, New Zealand) in which at the University of Otago the first isolate of its type was isolated

**History:** No details available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Serratia phage JS26 |  | [MN505213.1](https://www.ncbi.nlm.nih.gov/nuccore/MN505213.1) | 63.97 | 57.0 | [84](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85364/740765%7CSerratia%20phage%20JS26/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 17. To create a new genus *Gwanakrovirus* with a single species**

**Source of the name of this taxon:** This genus is named after the street address (Gwanak-ro 1) where at the Lab of Aquatic Biomedicine, College of Veterinary Science, Seoul National University, the first phage of its type was isolated.

**History:** Erwinia phage pEp\_SNUABM\_08 was isolated in 2018 in South Korea using Erwinia pyrifoliae as the host bacterium.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Erwinia phage pEp\_SNUABM\_08 | [MN184886.1](https://www.ncbi.nlm.nih.gov/nuccore/MN184886.1) | 62.72 | 57.2 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84625/697035%7CErwinia%20phage%20pEp_SNUABM_08/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 18. To create a new genus *Fengtaivirus* with a single species**

**Source of the name of this taxon:** This taxon is named after the district in Beijing, China where in the Department of Infectious Disease Control, Institute of Disease Control and Prevention, the first phage of its type was isolated.

**History:** isolated on *Achromobacter xylosoxidans*

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Achromobacter phage phiAxp-2 | [NC\_029106.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_029106.1) | [KT321316.2](https://www.ncbi.nlm.nih.gov/nuccore/KT321316.2) | 62.22 | 60.1 | [86](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42937/462207%7CAchromobacter%20phage%20phiAxp-2/viral%20segment%20Unknown/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 19. To create a new genus *Maxdohrnvirus* with a single species**

**Source of the name of this taxon:** This taxon is named after the street address (Max-Dohrn Str. 8-10) where in the Biological Safety, German Federal Institute for Risk Assessment the first phage of its type was isolated.

**History:** This phage was isolated in 2019 on Pseudomonas aeruginosa.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Pseudomonas phage vB\_Pae-SS2019XI |  | [MN536026.1](https://www.ncbi.nlm.nih.gov/nuccore/MN536026.1) | 57.57 | 60.1 | [83](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/87876/811636%7CPseudomonas%20phage%20vB_Pae-SS2019XI/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 20. To create a new genus *Newforgelanevirus* with a single species**

**Source of the name of this taxon:** This taxon is named after the address (Newforge Lane) where in the Sustainable Agri-Food Sciences Division, Agri-Food and Biosciences Institute (Belfast BT9, United Kingdom) the first phage of its type was isolated.

**History:** φMA12 phages was isolated from potato wastewater samples on Pectobacterium carotovorum. EM revealed a head 58.7 × 48.7nm and a non-contractile tail 227.9nm. The authors noted its relationship to Chi.

**Specific Reference:** Zaczek-Moczydłowska MA, Young GK, Trudgett J, Fleming CC, Campbell K, O'Hanlon R. Genomic Characterization, Formulation and Efficacy in Planta of a Siphoviridae and Podoviridae Protection Cocktail against the Bacterial Plant Pathogens Pectobacterium spp. Viruses. 2020 Jan 28;12(2):150. doi: 10.3390/v12020150. PMID: 32012814; PMCID: PMC7077305.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Pectobacterium phage MA12 |  | [MN692199.1](https://www.ncbi.nlm.nih.gov/nuccore/MN692199.1) | 58.57 | 54.5 | [38](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86878/758875%7CPectobacterium%20phage%20MA12/viral%20segment/)(\*\*\*) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**(\*\*\*) Underannotated**

**Proposal 21. To create a new genus *Enchivirus* with a single species**

**Source of the name of this taxon:** The name is derived from the name of the first isolate with “chi” included.

**History:** Phage Enc34 was isolated in Riga, Latvia on Enterobacter cancerogenus

**Specific Reference:** Kazaks A, Dislers A, Lipowsky G, Nikolajeva V, Tars K. Complete genome sequence of the Enterobacter cancerogenus bacteriophage Enc34. J Virol. 2012 Oct;86(20):11403-4. doi: 10.1128/JVI.01954-12. PMID: 22997422; PMCID: PMC3457185.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Enterobacter phage Enc34 | [NC\_019524.2](https://www.ncbi.nlm.nih.gov/nuccore/NC_019524.2) | [JQ340774.2](https://www.ncbi.nlm.nih.gov/nuccore/JQ340774.2) | 60.5 | 51.1 | [80](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/15519/884984%7CEnterobacter%20phage%20Enc34/viral%20segment%20Unknown/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Proposal 22. To create a new family Casjensviridae for the above genera and three existing genera.**

**Source of the name of this taxon:** This taxon is named in honour of Sherwood R Casjens (b. 1945, George, Iowa) who obtained his B.S. at Michigan State University in 1967 and his PhD in 1972 working in the laboratory of Dale Kaiser at Stanford University on the molecular genetics of bacteriophage lambda head morphogenesis. While at Stanford he was the first to unequivocally identify the gene that encodes the lambda major capsid protein, identified the first “capsid decoration protein” and showed that it (gpD) resides on the outside of the phage head, discovered the first morphogenetic cleavage of a phage tail protein (lambda tape measure protein), helped solidify the idea that procapsids are assembled first which then package DNA for phage lambda, and was the first to find that a protein required for lambda virion assembly (the large terminase subunit) is not a component of the completed virion. His post-doctoral studies were with Jonathan King at Massachusetts Institute of Technology, where he discovered scaffolding protein and its catalytic role in phage capsid assembly (now known to be general features of the assembly of large dsDNA viruses). He also was the first to show that scaffolding protein resides within the interior of the capsid shell. During this period he also wrote the first ever review of virus assembly for Annual Reviews of Biochemistry. He joined the University of Utah School of Medicine in 1974, where he rose to the rank of Professor in the Pathology Department and remained for the rest of his career. His phage work in Utah focused largely on understanding the mechanisms of phage P22 scaffolding protein action and headful DNA packaging. His important work on DNA packaging included the first detailed characterization of a packaging recognition site (pac) and showing that the small terminase subunit is responsible for this recognition, as well as the discovery that portal protein is responsible for sensing when the phage head is full of DNA during the packaging process. This work also led, in collaboration with Dr. Jack Johnson, to one of the very first asymmetric (without icosahedral averaging) three-dimensional cryo-electron microscopic reconstructions of a tailed phage virion, the of P22. This was the first time such a structure allowed the determination of the position of every structural protein unit in the virion, including those in the tail. He is active in the phage research community and organized several international meetings on this topic and wrote a number of more recent insightful reviews in this field. He is currently Professor Emeritus and continues to work on three rather different areas: (1) the genetic control of the assembly of and DNA injection by virus particles, (2) modular evolution of bacteriophage genomes, and (3) genome structure and diversity of the Lyme disease causing bacteria, Borrelia burgdorferi. He is responsible for the sequencing of the Salmonella phage Chi genome and the isolation and the sequencing of phage Utah, a close relative of Chi.

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**(from: https://medicine.utah.edu/faculty/mddetail.php?facultyID=u0030530)**

**Rationale:** All the data i.e. genomic (VIRIDIC), proteomic (ViPTree, CoreGenes5.0) and phylogenetic (phylogeny.fr), coupled with the comments of several authors lead us to conclude that the Chi-like phages form a cohesive group which are united at the family level.

**References:**

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