

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

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| **Code assigned:** | **2020.028B** |  |
| **Short title:** Create one new genus (*Cbunavirus*) including four new species (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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| Adriaenssens EM, Tolstoy I, Kropinski AM, Wittmann J, Buttimer C, Coffey A | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  Phage.Canada@gmail.com; jow12@dsmz.de; colin.buttimer@mycit.ie;  aidan.coffey@cit.ie |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of Guelph, Canada [AMK]  DSMZ, Germany [JW]  Cork Institute of Technology, Ireland [CB, AC] |

**Corresponding author**

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| Johannes Wittmann |

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

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| *Caudovirales* 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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| --- | --- | --- |
| **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 | June 2020 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

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| We have created a new genus, *Cbunavirus* with four Pectinobacterium phage species. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm | |

**Supporting evidence**

BLASTN and phylogenetic analyses both indicate that the proposed genus *Cbunavirus* is cohesive and distinct from the other genera in the N4-superfamily of viruses (Table 2, Fig.2, Fig. 3). These phages are specific for the phytopathogen *Pectobacterium atrosepticum*.

The genomes of these phages are, on average, 75.6 Kbp in size with DTRs with an average size of 647 bp (49 mol% G+C), encoding between 95 and 102 proteins [Fig. 4]. These phages may also possess tRNA genes, with Pectobacterium phage vB\_PatP\_CB4 found to possess two tRNAs (asparagine & glutamine) [1].

TEM study (Fig 1) indicated that these phages featured a C1 morphotype with isometric capsids (ca. 70 nm) and short non-contractile tails (length: ca. 25 nm) Additionally, a set of (putatively six) short whiskers (length: ca. 25 nm) attached to a collar structure (width: ca. 19 nm) were observed. At their distal ends, the whiskers terminate with elongated globular appendices (ca. 12 nm x 7 nm) [1].

**Source of the name of this taxon:** The name is derived from the designation of the isolated phage of this type, Pectobacterium phage vB\_PatP\_CB1 (CB1).

**History:** Phages CB1 and CB3 are members of the *Podoviridae* family and members of the N4-superfamily of viruses. They were originally isolated from soil from potato fields in Co. Cork, Ireland in 2013 [3]. These phages can infect several *Pectobacterium atrosepticum* strains [3]. Their genomes consist of 76,041 bp and 76,169 respectively, with a terminal redundancy of 647 bp each.

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| vB\_PatP\_CB1 | [KY514264.1](https://www.ncbi.nlm.nih.gov/nuccore/KY514264.1) | 76.04 | 48.7 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68485/369634|Pectobacterium phage vB_PatP_CB1/viral segment/) | 1(\*) | 100 | 100 |
| vB\_PatP\_CB4 | [KY549659.1](https://www.ncbi.nlm.nih.gov/nuccore/KY549659.1) | 76.62 | 48.6 | [100](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68487/369636|Pectobacterium phage vB_PatP_CB4/viral segment/) | 2 | 94.1 | 91.7 |
| Nepra | [MH059638.1](https://www.ncbi.nlm.nih.gov/nuccore/MH059638.1) | 74.51 | 48.7 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/69658/379818|Pectobacterium phage Nepra/viral segment/) | 1 | 92.4 | 86.6 |
| phiA41 | [KY769270.1](https://www.ncbi.nlm.nih.gov/nuccore/KY769270.1) | 75.76 | 48.7 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86568/753337|Pectobacterium phage phiA41/viral segment/) | 1 | 85.1 | 84.5 |
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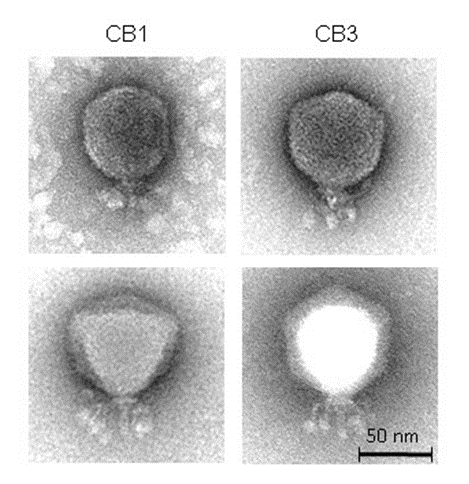
**(\*) Not listed in Replicon Info; determined using tRNAscan-SE at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](http://lowelab.ucsc.edu/tRNAscan-SE/) **[9]**

**(\*\*) Determined using BLASTn at NCBI [5-7]**

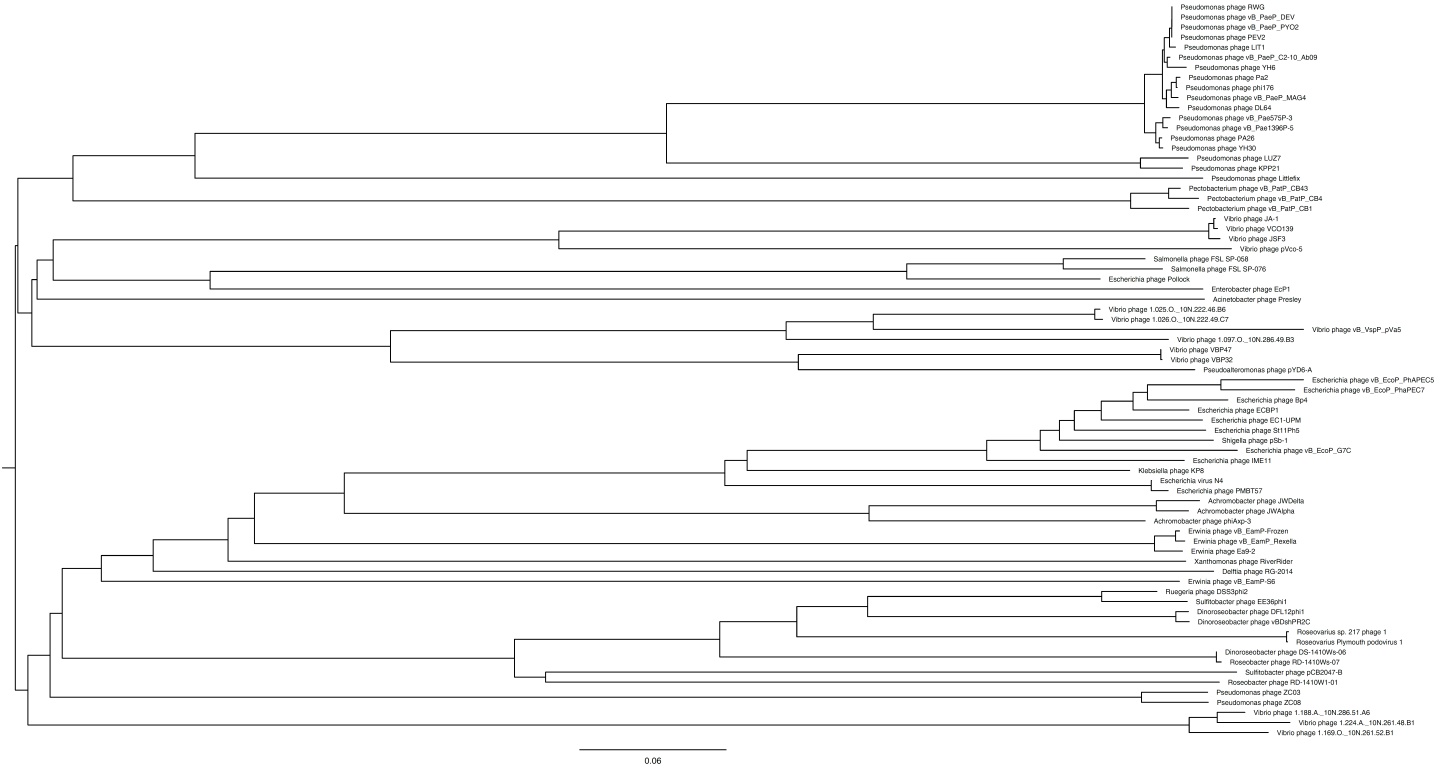
**(\*\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[8]**

**N.B. Pectobacterium phage vB\_PatP\_CB3 [KY514265.1] should be considered a strain of the species *Pectobacterium virus CB4* in this genus**

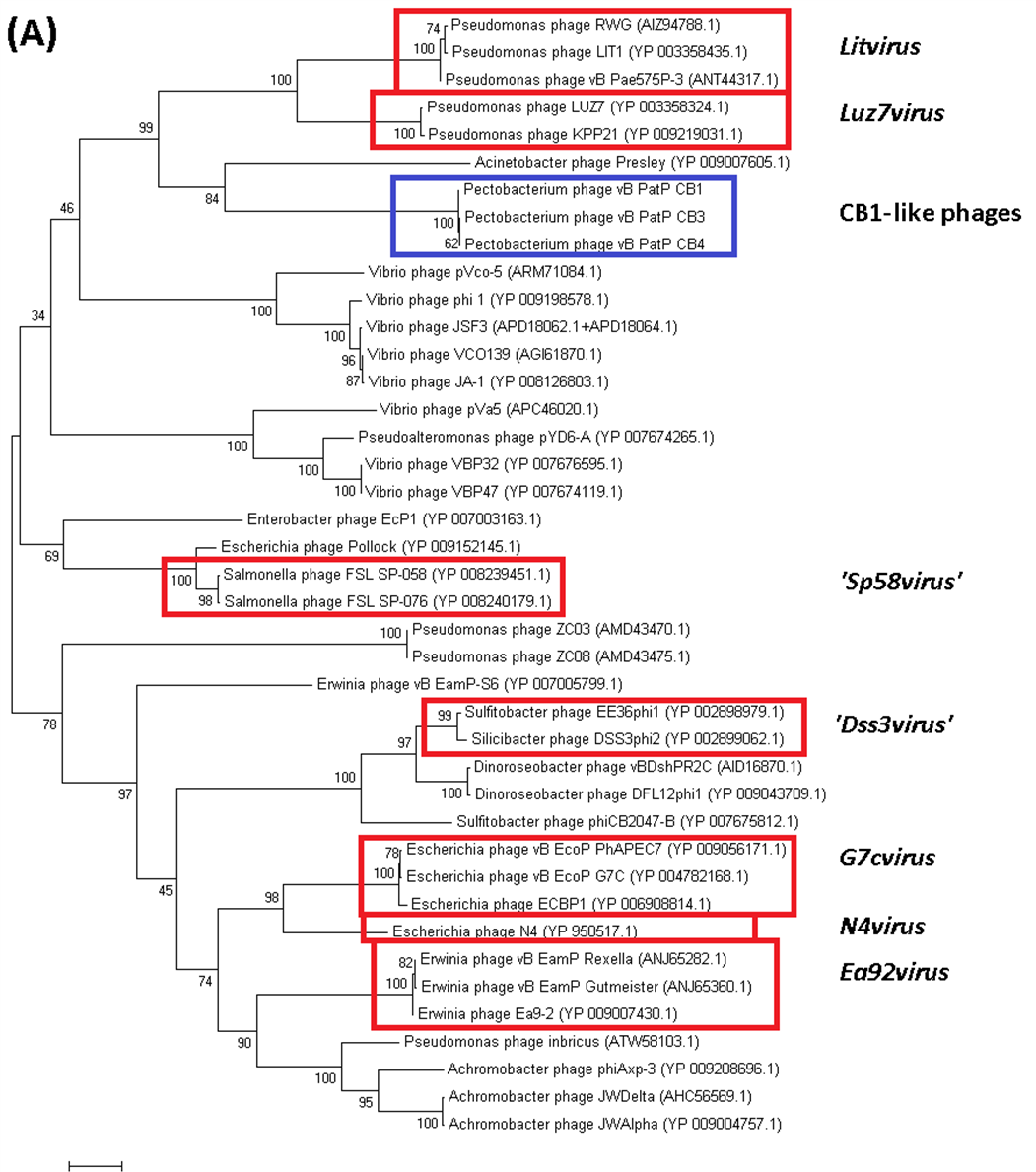
**Electron micrograph:** Fig 1. Transmission electron micrographs of negatively stained Pectobacterium phages vB\_PatP\_CB1 and vB\_PatP\_CB3 using 2% (w/v) uranyl acetate (top) and 1% (w/v) phosphotungstic acid (bottom) [3].

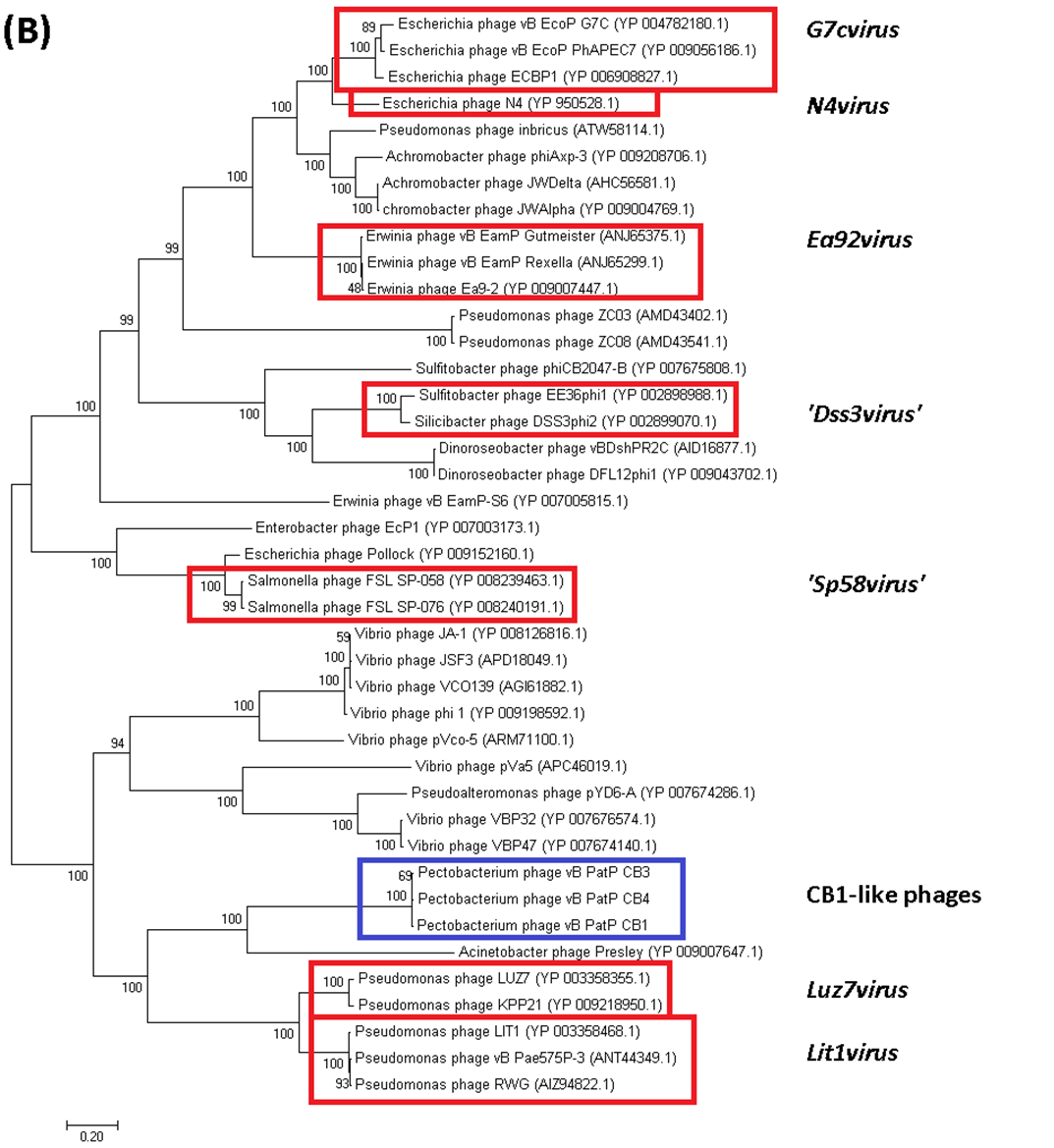


**Phylogeny: Fig 2.** The phylogenetic tree was constructed with VICTOR [2], using whole genomes of Pectobacterium phages CB1, CB3, CB4 and related N4-like phages.

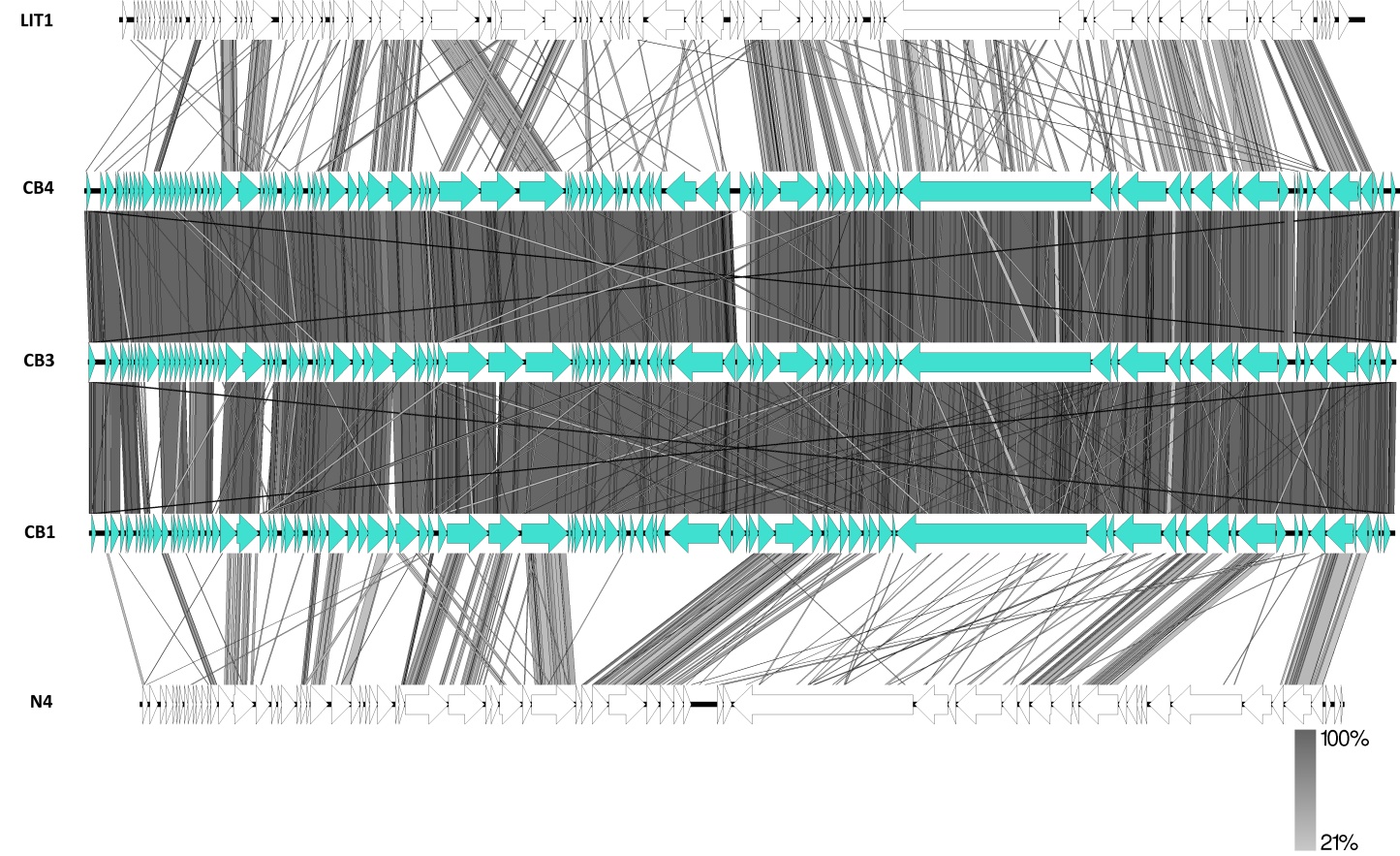


**Fig 3.** Phylogenetic analysis using the (A) DNA polymerase (log likelihood = -16535.57) and (B) vRNA polymerase (log likelihood = -103761.67) protein sequences of *Pectobacterium* phages CB1, CB3 and CB4 and 38 other N4-like phages [1]. Phages belonging to the genera of *G7cvirus*, *Lit1virus*, *Ea92virus*, *Luz7virus* and *N4virus* and proposed genera *Sp58virus* and *Dss3virus* are highlighted. The amino acid sequences were compared using MUSCLE with MEGA7 [3]. The tree was constructed using the maximum likelihood algorithm. The percentages of replicate trees were assessed with the bootstrap test (1000). Currently the genera G7cvirus, Lit1virus, Luz7virus, and N4virus are known as *Gamaleyavirus, Litunavirus, Luzseptimavirus* and *Enquatrovirus*, respectively.



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**Fig 4.** Synteny plot of *Pectobacterium* phages CB1, CB3, CB4 and related phages N4 and LIT1 at the amino acid level. Plot was visualized using EasyFig [4].



**References**

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