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# ICTV Virus Taxonomy Profile: *Finnlakeviridae*

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## Abstract

*Finnlakeviridae* is a family of icosahedral, internal membrane-containing bacterial viruses with circular, single-stranded DNA genomes. The family includes the genus, *Finnlakevirus*, with the species, *Flavobacterium virus FLiP*. *Flavobacterium* phage FLiP was isolated with its Gram-negative host bacterium from a boreal freshwater habitat in Central Finland in 2010. It is the first described single-stranded DNA virus with an internal membrane and shares minimal sequence similarity with other known viruses. The virion organization (pseudo  $T=21$  *dextro*) and major capsid protein fold (double- $\beta$ -barrel) resemble those of Pseudoalteromonas phage PM2 (family *Corticoviridae*), which has a double-stranded DNA genome. A similar major capsid protein fold is also found in other double-stranded DNA viruses in the kingdom *Bamfordvirae*. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) report on the family *Finnlakeviridae*, which is available at [ictv.global/report/finnlakeviridae](http://ictv.global/report/finnlakeviridae).

**Table 1.** Characteristics of members of the family *Finnlakeviridae*

Typical member:	<b>Flavobacterium phage FLiP (MF361639), species <i>Flavobacterium virus FLiP</i>, genus <i>Finnlakevirus</i></b>
Virion	Icosahedral, internal membrane-containing virions, approximately 59 nm in diameter. Spikes protrude from the virion surface
Genome	9.2 kb of circular, single-stranded DNA
Replication	Possibly rolling circle replication
Translation	By the host translation machinery
Host range	Gram-negative bacteria from the genus <i>Flavobacterium</i>
Taxonomy	The genus <i>Finnlakevirus</i> includes the species <i>Flavobacterium virus FLiP</i>

## VIRION

The virion of *Flavobacterium* phage FLiP consists of an icosahedral protein shell and an internal membrane, uniquely combined with a circular ssDNA genome [1] (Table 1, Fig. 1). The diameter of the virion is about 59 nm (vertex-to-vertex). Pentameric spike complexes protrude about 12 nm from the protein shell surface at the fivefold vertices. The inner surface of the icosahedral protein capsid is covered by a lipid bilayer membrane (5 nm thick), enclosing the single-stranded DNA genome. The major

capsid proteins (MCPs) forming the outer protein shell follow a pseudo  $T=21$  *dextro* icosahedral capsid organization, previously described only for the marine double-stranded DNA *Pseudoalteromonas* phage PM2 [2]. The *Flavobacterium* phage FLiP MCPs consist of two  $\beta$ -barrels with jellyroll topology and arrange into trimers to form pseudo-hexameric molecules [1]. A similar major capsid protein fold has also been described for members of the kingdom *Bamfordvirae* [3], such as *Enterobacteria* phage PRD1 (family *Tectiviridae*) [4].

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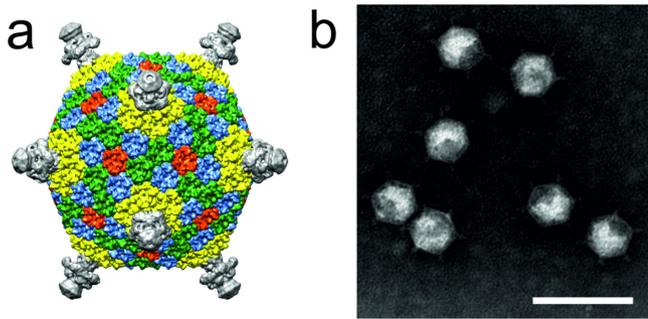
**Abbreviations:** CDS, coding sequence; MCP, major capsid protein;  $T$ , triangulation number.

†These authors contributed equally to this work

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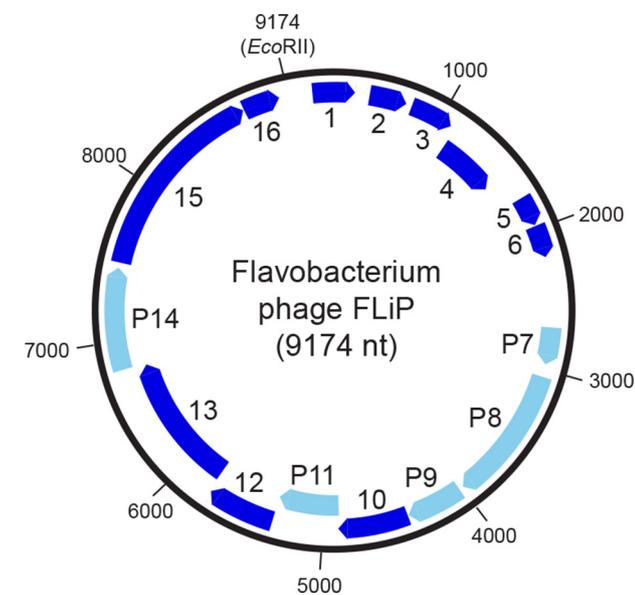
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**Fig. 1.** Flavobacterium phage FLiP virion structure. (a) Cryo-electron microscopic reconstruction [1]. (b) virions negatively-stained with 2% phosphotungstic acid (pH 8.5) and visualized under transmission electron microscopy. Scale bar represents 100 nm.

## GENOME

Virions contain a single copy of a circular single-stranded DNA of 9174 nucleotides with a GC content of 34% [1]. 16 predicted coding sequences (CDS), all in the same orientation (Fig. 2), show limited similarity with other known sequences. Five CDSs have been shown to encode structural proteins (CDS7–9, 11, 14). There are sequence similarities between CDS14 and several lytic transglycosylases and between CDS15 and rolling circle replication proteins [1, 5].



**Fig. 2.** Genome organization of Flavobacterium phage FLiP. Arrows show the direction of transcription of predicted CDSs, with light blue indicating those encoding the structural proteins P7–9, P11 and P14. The unique *EcoRII* restriction site is at nucleotide position 1.

## REPLICATION

Flavobacterium phage FLiP is a virulent virus that induces host-cell lysis at the end of the viral reproduction cycle [1]. CDS14 is predicted to encode a virion-associated lytic protein likely assisting in the penetration of the host peptidoglycan layer during entry. Flvobacterium phage FLiP does not encode any identifiable DNA or RNA polymerase. However, the sequence resemblance of CDS15 to rolling circle replication proteins suggests a replication mechanism typical of single-stranded DNA viruses [1, 5]. The absence of a putative packaging ATPase implies that a viral-encoded ATPase is not required for the encapsidation of the genome [5].

## TAXONOMY

Current taxonomy: [ictv.global/report/finnlakeviridae](http://ictv.global/report/finnlakeviridae). The family *Finnlakeviridae* contains the genus *Finnlakevirus* with the species *Flavobacterium virus FLiP*. Based on phylogenetic analysis of MCP sequences, Flvobacterium phage FLiP forms its own group among the tailless prokaryotic DNA viruses and proviruses with double- $\beta$ -barrel MCPs [5].

## RESOURCES

Current ICTV Report on the family *Finnlakeviridae*: [ictv.global/report/finnlakeviridae](http://ictv.global/report/finnlakeviridae)

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### Conflicts of interest

The authors declare that there are no conflicts of interest.

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