



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned: **2008.038B** (to be completed by ICTV officers)

Short title: create species named Pseudomonas phage F116 to be unassigned in the Podoviridae family

(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):

1	<input type="checkbox"/>	2	<input type="checkbox"/>	3	<input type="checkbox"/>	4	<input type="checkbox"/>	5	<input checked="" type="checkbox"/>
6	<input type="checkbox"/>	7	<input type="checkbox"/>						

Author(s) with e-mail address(es) of the proposer:

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ICTV-EC or Study Group comments and response of the proposer:



MODULE 5: **NEW SPECIES**

Code	2008.038B	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	unassigned	Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)
Subfamily:		
Family:	<i>Podoviridae</i>	
Order:	<i>Caudovirales</i>	

Name(s) of proposed new species:

Pseudomonas phage F116

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

F116 is a temperate, pilus-specific, generalized transducing phage belonging to the Podoviridae virus family. Its genome is linear, ds, TR, and CP DNA with a GC content of 63.2%. The 65 195-bp genome contains 70 putative ORFs, only 16 of which showed sequence similarity to *Pseudomonas* genomic or phage genes ([NC_006552](#)). While the current literature suggests that F116 is a non-integrating phage that maintains itself as a plasmid during the lysogenic life cycle, a putative *int* gene was identified. With the exception of a portal protein, none of the genes involved in capsid and tail morphogenesis could be identified through homology searches.

References:

** Byrne M, Kropinski AM. (2005) The genome of the *Pseudomonas aeruginosa* generalized transducing bacteriophage F116. *Gene*. 14;346:187-94.

Annexes:

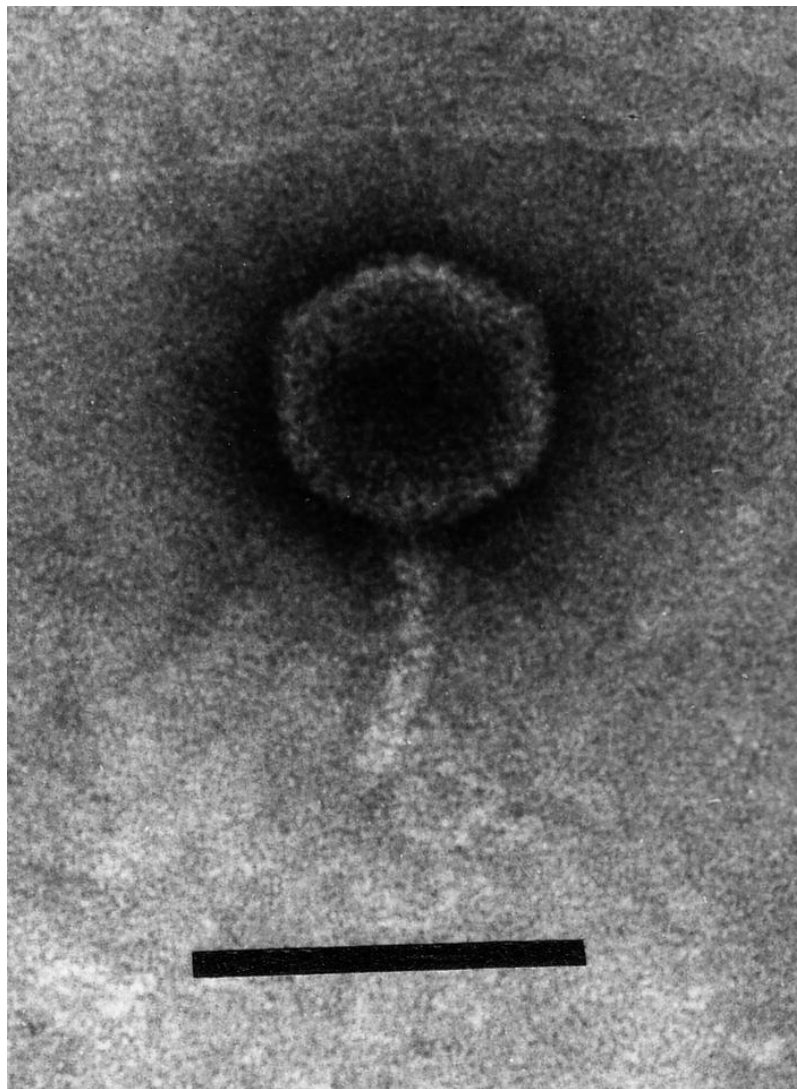


Figure 1: EM image for *Podoviridae* member F116 infecting *Pseudomonas aeruginosa* (uranyl acetate x 297,000)
