



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:** **2008.069B** (to be completed by ICTV officers)

**Short title:** create species named Salmonella phage ST64T within the genus "P22-like viruses", family Podoviridae

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

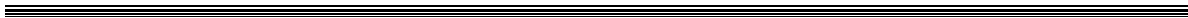
**Modules attached** (please check all that apply):

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"/>						

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



## MODULE 5: NEW SPECIES

Code	<b>2008.069B</b>	(assigned by ICTV officers)
<b>To create new species assigned as follows:</b>		
Genus:	<b>“P22-like viruses”</b>	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:	<b><i>Podoviridae</i></b>	
Order:	<b><i>Caudovirales</i></b>	

### Name(s) of proposed new species:

*Salmonella phage ST64T*

### 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.

ST64T is a serotype-converting temperate bacteriophage. Its genome is 40,679 bp in size with an overall GC content of 47.5% (NC\_004348) and has interspersed DNA homology to P22. Inferred proteins of ST64T which exhibited a high degree of sequence similarity to P22 proteins (>90%) included the functional serotype conversion cassette, integrase, excisionase, Abc1, Abc2, early antitermination (gp24), NinD, NinH, NinZ, packaging (gp3 and gp2), head (with the exception of gp26, gp7, gp20, and gp16), and tail proteins, suggesting differences in host range.

### References:

\*\* Mmolawa PT, Schmieger H, Tucker CP, Heuzenroeder MW. (2003) Genomic structure of the *Salmonella enterica* serovar Typhimurium DT 64 bacteriophage ST64T: evidence for modular genetic architecture. *J Bacteriol.* 185(11):3473-5.

### Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.