



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	2016.069a-wB	(to be completed by ICTV officers)			
Short title: To create thirty eight (38) new species within existing genera in the Caudovirales. (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 11 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input type="checkbox"/>	5 <input type="checkbox"/> 10 <input type="checkbox"/>

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

ICTV Bacterial and Archaeal Viruses Subcommittee

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: July 2016
Date of this revision (if different to above): January 2017

ICTV-EC comments and response of the proposer:

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MODULE 2: NEW SPECIES

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	2016.069a-wB	(assigned by ICTV officers)	
To create 38 new species within:			
Genus:	Variable (Listed below)	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ (new) ” after its proposed name. • If no genus is specified, enter “ unassigned ” in the genus box.	
Subfamily:	Variable (Listed below)		
Family:	Variable (Listed below)		
Order:	Caudovirales		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)	
See table below			

ICTV code ¹	Family	Subfamily	Genus	Species	Exemplar Accession Number	RefSeq No.	Exemplar Isolate	% DNA Sequence identity to type virus
2016.069aB	<i>Myoviridae</i>	<i>Eucampyvirinae</i>	<i>Cp8virus</i>	<i>Campylobacter virus CP30A</i>	JX569801	NC_018861	Campylobacter phage CP30A	93
2016.069bB	<i>Myoviridae</i>	<i>Spounavirinae</i>	<i>Silviavirus</i>	<i>Staphylococcus virus Stau2</i>	KP881332	None	Staphylococcus phage Stau2	86
2016.069cB	<i>Myoviridae</i>	<i>Spounavirinae</i>	<i>Spo1virus</i>	<i>Bacillus virus Camphawk</i>	KF669649	None	Bacillus phage CampHawk	93
2016.069dB	<i>Myoviridae</i>	<i>Spounavirinae</i>	<i>Kayvirus</i>	<i>Staphylococcus virus S25-4</i>	AB853331	NC_022918	Staphylococcus phage S25-4	89
	<i>Myoviridae</i>	<i>Spounavirinae</i>	<i>Kayvirus</i>	<i>Staphylococcus virus Rodi</i>	KP027446	NC_028765	Staphylococcus phage phiPLA-RODI	85
2016.069eB	<i>Myoviridae</i>	<i>Spounavirinae</i>	<i>Bc431virus</i>	<i>Bacillus virus Deepblue</i>	KU577463		Bacillus phage Deep Blue	77
	<i>Myoviridae</i>	<i>Spounavirinae</i>	<i>Bc431virus</i>	<i>Bacillus virus BM15</i>	KT995480		Bacillus phage BM15	77
2016.069fB	<i>Myoviridae</i>		<i>Cr3virus</i>	<i>Cronobacter virus PBES02</i>	KT353109	NC_028672	Cronobacter phage PBES 02	89
	<i>Myoviridae</i>		<i>Cr3virus</i>	<i>Pectobacterium virus phiTE</i>	JQ015307	NC_020201	Pectobacterium phage phiTE	65
2016.069gB	<i>Myoviridae</i>	<i>Tevenvirinae</i>	<i>Rb49virus</i>	<i>Escherichia virus JSE</i>	EU863408	NC_012740	Escherichia phage JSE	92
2016.069hB	<i>Myoviridae</i>	<i>Tevenvirinae</i>	<i>Js98virus</i>	<i>Escherichia virus QL01</i>	KT176190	None	Escherichia phage QL01	86
2016.069iB	<i>Myoviridae</i>		<i>B4virus</i>	<i>Bacillus virus AvesoBmore</i>	KT307976	None	Bacillus phage AvesoBmore	73
2016.069kB	<i>Myoviridae</i>		<i>Muvirus</i>	<i>Shigella virus SfMu</i>	KP010268	None	Shigella phage SfMu	90
2016.069lB	<i>Myoviridae</i>		<i>T4virus</i>	<i>Escherichia virus HY01</i>	KF925357	None	Escherichia phage HY01	85
2016.069mB	<i>Podoviridae</i>		<i>Phieco32virus</i>	<i>Escherichia virus 172-1</i>	KP308307	None	Escherichia phage 172-1	83
2016.069nB	<i>Podoviridae</i>		<i>Kp34virus</i>	<i>Klebsiella virus KpV475</i>	KX211991	None	Klebsiella phage KpV475	83
	<i>Podoviridae</i>		<i>Kp34virus</i>	<i>Klebsiella virus KpV71</i>	KU666550	None	Klebsiella phage KpV71	77
	<i>Podoviridae</i>		<i>Kp34virus</i>	<i>Klebsiella virus KpV41</i>	KT964103	NC_028670	Klebsiella phage KpV41	79
	<i>Podoviridae</i>		<i>Kp34virus</i>	<i>Klebsiella virus Kp2</i>	KT367886	None	Klebsiella phage Kp2	79
2016.069oB	<i>Siphoviridae</i>		<i>C5virus</i>	<i>Lactobacillus virus phiLdb</i>	KF188410	NC_022762	Lactobacillus phage phiLdb	84

¹ 2016.069jB has been omitted

	<i>Siphoviridae</i>		<i>C5virus</i>	<i>Lactobacillus virus Ld17</i>	KJ564037	NC_025420	Lactobacillus phage Ld17	85
	<i>Siphoviridae</i>		<i>C5virus</i>	<i>Lactobacillus virus Ld25A</i>	KJ564036	NC_025415	Lactobacillus phage Ld25A	84
	<i>Siphoviridae</i>		<i>C5virus</i>	<i>Lactobacillus virus Ld3</i>	KJ564038	NC_025421	Lactobacillus phage Ld3	90
2016.069pB	<i>Siphoviridae</i>		<i>Hk578virus</i>	<i>Escherichia virus EK99P1</i>	KM233151	None	Escherichia phage EK99P-1	79
	<i>Siphoviridae</i>		<i>Hk578virus</i>	<i>Escherichia virus YD2008s</i>	KM896878	None	Escherichia phage YD-2008.s	78
2016.069qB	<i>Siphoviridae</i>	<i>Guernseyvirinae</i>	<i>Jerseyvirus</i>	<i>Salmonella virus f18SE</i>	KR270151	None	Salmonella phage f18SE	71
2016.069rB	<i>Siphoviridae</i>	<i>Tunavirinae</i>	<i>Kp36virus</i>	<i>Klebsiella virus KLPN1</i>	KR262148	NC_028760	Klebsiella phage KLPN1	83
	<i>Siphoviridae</i>	<i>Tunavirinae</i>	<i>Kp36virus</i>	<i>Klebsiella virus PKP126</i>	KR269719	None	Klebsiella phage PKP126	79
	<i>Siphoviridae</i>	<i>Tunavirinae</i>	<i>Kp36virus</i>	<i>Klebsiella virus Sushi</i>	KT001920	None	Klebsiella phage Sushi	84
2016.069sB	<i>Siphoviridae</i>	<i>Tunavirinae</i>	<i>Rogue1virus</i>	<i>Escherichia virus C119</i>	KT825490	None	Escherichia phage C119	87
2016.069tB	<i>Siphoviridae</i>		<i>Sitaravirus</i>	<i>Paenibacillus virus Willow</i>	KT361650	None	Paenibacillus phage Willow	74
2016.069uB	<i>Siphoviridae</i>	<i>Tunavirinae</i>	<i>T1virus</i>	<i>Escherichia virus JMPW2</i>	KU194205	None	Escherichia phage JMPW2	88
	<i>Siphoviridae</i>	<i>Tunavirinae</i>	<i>T1virus</i>	<i>Escherichia virus JMPW1</i>	KU194206	None	Escherichia phage JMPW1	86
2016.069vB	<i>Siphoviridae</i>		<i>T5virus</i>	<i>Salmonella virus 118970sal2</i>	KX017521	None	Salmonella phage 118970_sal2	68
	<i>Siphoviridae</i>		<i>T5virus</i>	<i>Escherichia virus slur09</i>	LN887948	None	Escherichia phage slur09	81
2016.069wB	<i>Siphoviridae</i>		<i>Yuavirus</i>	<i>Pseudomonas virus LKO4</i>	KC758116	None	Pseudomonas phage LKO4	87
	<i>Siphoviridae</i>		<i>Yuavirus</i>	<i>Pseudomonas virus PAE1</i>	KT734862	NC_028980	Pseudomonas phage PAE1	83
	<i>Siphoviridae</i>		<i>Yuavirus</i>	<i>Pseudomonas virus MP1412</i>	JX131330	NC_018282	Pseudomonas phage MP1412	86

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
 - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria.**
 - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 11

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm. In line with TaxoProp 2015.046B these phages fulfill all the requirements for belonging to their respective genera. Without this fast-

track “in-filling” procedure an additional 23 TaxoProps would be submitted.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

