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:	***2013.008a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, *Che8likevirus*, within the family *Siphoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

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

Evelien M Adriaenssens, evelien.adriaenssens@gmail.com
Andrew M Kropinski, akropins@uoguelph.ca
Rob Lavigne, rob.lavigne@biw.kuleuven.be

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

Date first submitted to ICTV:	June 2013
Date of this revision (if different to above):	July 2014

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	***2013.008aB***	(assigned by ICTV officers)

To create 28 new species within:

Genus:	***Che8likevirus*** (new)
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Mycobacterium phage Che8	AY129330
Mycobacterium phage PMC	DQ398050
Mycobacterium phage mutaforma13	JN020142
Mycobacterium phage dotproduct	JN859129
Mycobacterium phage gumbie	JN398368
Mycobacterium phage Llij	DQ398045
Mycobacterium phage spartacus	JQ300538
Mycobacterium phage Pacc40	FJ174692
Mycobacterium phage ibhubesi	JF937098
Mycobacterium phage tweety	EF536069
Mycobacterium phage taj	JX121091
Mycobacterium phage wee	HQ728524
Mycobacterium phage dorothy	JX411620
Mycobacterium phage deadp	JN698996
Mycobacterium phage SG4	JN699012
Mycobacterium phage boomer	EU816590
Mycobacterium phage dlane	JF937093
Mycobacterium phage ardmore	GU060500
Mycobacterium phage fruitloop	FJ174690
Mycobacterium phage shilan	JN020143
Mycobacterium phage drago	JN542517
Mycobacterium phage ramsey	FJ174693
Mycobacterium phage rockyhorror	JF704117
Mycobacterium phage mozy	JF937102
Mycobacterium phage shauna1	JN020141
Mycobacterium phage Che9d	AY129336
Mycobacterium phage avani	JQ809702
Mycobacterium phage yoshi	JF704115

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 9

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 EMBOSS Stretcher algorithm.

MODULE 3: NEW GENUS

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2013.008bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.008cB***	(assigned by ICTV officers)

To name the new genus: *Che8likevirus*

Assigning the type species and other species to a new genus

Code	***2013.008dB***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Mycobacterium phage Che8

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

28

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

This genus was originally recognized by the Mycobacteriophage group (www.phagesdb.org) as belonging to cluster F. Phages belonging to this genus share a comparable genome size (56 – 58 kb), a comparable GC content (~61.5%), and defined genome ends with comparable 3' overhangs. Members of this genus also have a comparable morphology, with an isometric head and a long, non-contractile tail (Figure 1).
A ClustalW analysis of the complete genomes of this genus with all other *Mycobacterium* phages belonging to the *Siphoviridae* reveals that this genus is a clearly separate group (Figures 2 and 3). We propose a shared protein content of at least 40% with the type phage, *Mycobacterium phage Che8*. Based on the phylogenetic tree (Figures 2 and 3), two groupings were visible within the genus and we performed a CoreGenes 3.5 analysis [1–3] with all phages to confirm their presence in the same genus (Table 1). The CoreGenes analysis was also performed against the type species of other proposed genera of siphoviruses infecting *Mycobacterium* and the shared protein content was consistently below 40% (data not shown).

Origin of the new genus name:

Mycobacterium phage Che8

Reasons to justify the choice of type species:

The genus *Che8likevirus* is named after one of the first isolated and sequenced phages of this group, *Mycobacterium* phage Che8 [4].

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these 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 EMBOSS Stretcher algorithm.

MODULE 9: APPENDIX: supporting material

additional material in support of this proposal

References:

1. Mahadevan P, King JF, Seto (2009) Data mining pathogen genomes using GeneOrder and CoreGenes and CGUG: gene order, synteny and in silico proteomes. Int J Comput Biol Drug Des 2: 100–114.

2. Mahadevan P, King JF, Seto D (2009) CGUG: in silico proteome and genome parsing tool for the determination of "core" and unique genes in the analysis of genomes up to ca. 1.9 Mb. BMC Res Notes 2: 168. doi:10.1186/1756-0500-2-168.

3. Zafar N, Mazumder R, Seto D (2002) CoreGenes: A computational tool for identifying and cataloging "core" genes in a set of small genomes. BMC Bioinformatics 3: 12. doi:10.1186/1471-2105-3-12.

4. Pedulla ML, Ford ME, Houtz JM, Karthikeyan T, Wadsworth C, et al. (2003) Origins of highly mosaic mycobacteriophage genomes. Cell 113: 171–182.

5. Darling AE, Mau B, Perna NT (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5: e11147. doi:10.1371/journal.pone.0011147.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

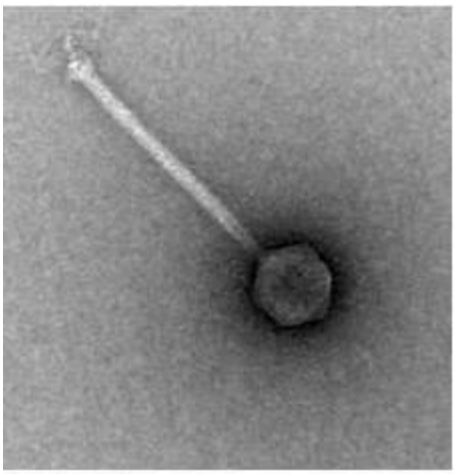

Figure 1: EM picture of phage Che8, the type species of the genus *Che8likevirus* (http://phagesdb.org/media/emPics/Che8.tif).

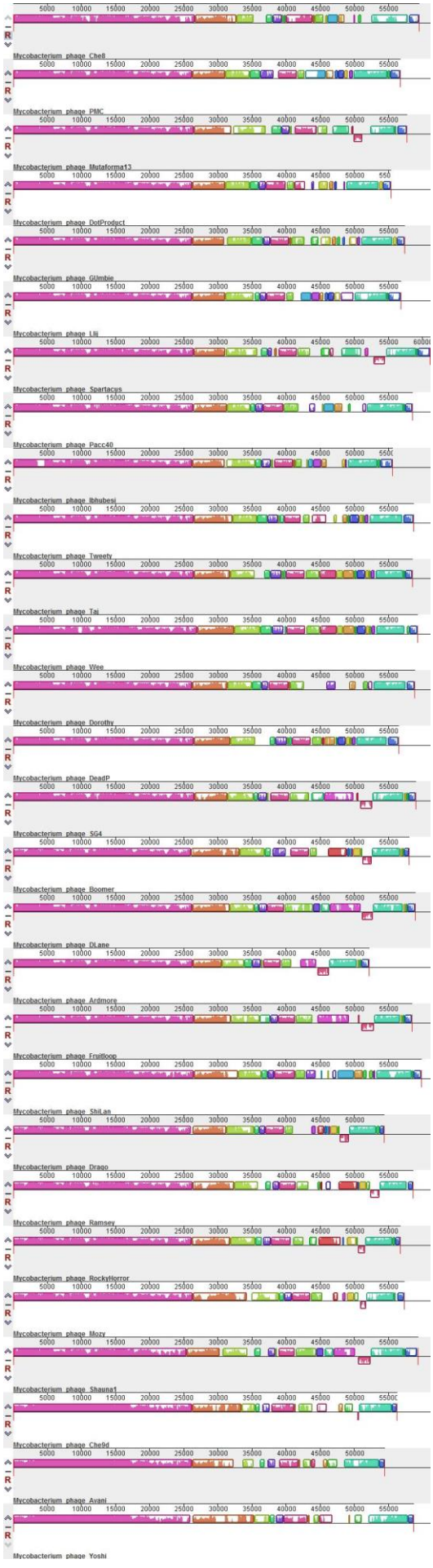
Mycobacterium_phage_Che8
Mycobacterium_phage_PMC
Mycobacterium_phage_Mutaforma13
Mycobacterium_phage_DotProduct
Mycobacterium_phage_GUmbie
Mycobacterium_phage_Lili
Mycobacterium_phage_Spartacus
Mycobacterium_phage_Pacc40
Mycobacterium_phage_Ibhubesi
Mycobacterium_phage_Tweety
Mycobacterium_phage_Tai
Mycobacterium_phage_Wee
Mycobacterium_phage_Dorothy
Mycobacterium_phage_DeadP
Mycobacterium_phage_SG4
Mycobacterium_phage_Boomer
Mycobacterium_phage_DLane
Mycobacterium_phage_Ardmore
Mycobacterium_phage_Fruitloop
Mycobacterium_phage_ShiLan
Mycobacterium_phage_Drago
Mycobacterium_phage_Ramsey
Mycobacterium_phage_RockyHorror
Mycobacterium_phage_Mozy
Mycobacterium_phage_Shauna1
Mycobacterium_phage_Che9d
Mycobacterium_phage_Avani
Mycobacterium_phage_Yoshi

Figure 2: progressiveMauve alignment of the phage genomes belonging to the proposed genus (phages are depicted in the same order as in Table 1) [5]**. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.**

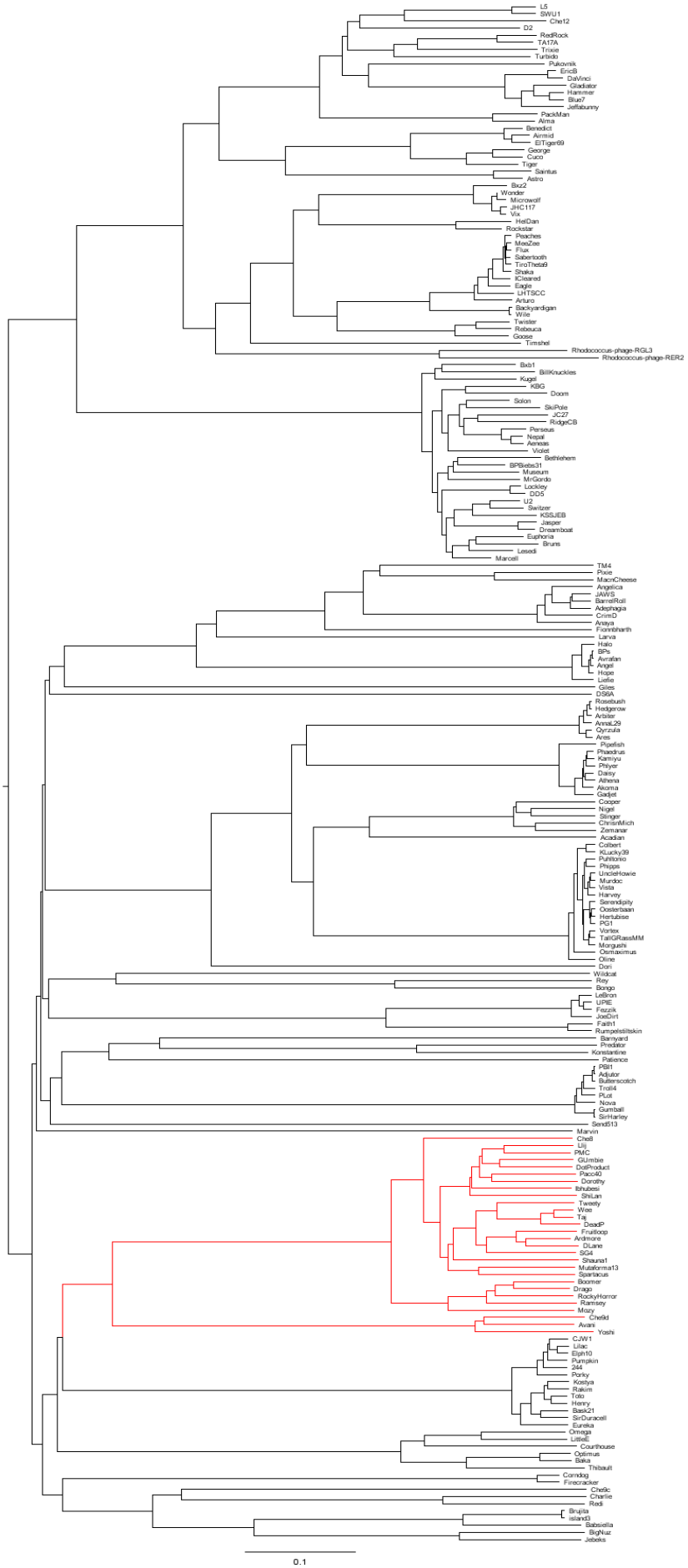
L5
SWU1
Che12
D2
RedRock
TA17A
Trixie
Turbido
Pukovnik
EricB
DaVinci
Gladiator
Hammer
Blue7
Jeffabunny
PackMan
Alma
Benedict
Airmid
ElTiger89
George
Cuco
Tiger
Saintus
Astro
Bxz2
Wonder
Microwolf
JHC117
Vix
HotDan
Rockstar
Peaches
MeeZee
Flux
Saberlooth
TinoTheta9
Sheka
ICleared
Eagle
LHTSCC
Arturo
Backyardigan
Wile
Twister
Rebeuca
Goose
Timshel
Rhodococcus-phage-RGL3
Rhodococcus-phage-RER2
Bxb1
BillKnuckles
Kugel
KBG
Doom
Solon
SkiPole
JC27
RidgeCB
Perseus
Nepal
Aeneas
Violet
BethHeherm
BPBiebs31
Museum
MrGordo
Lockley
DD5
U2
Switzer
KSSJEB
Jasper
Dreamboat
Euphoria
Bruns
Lasedi
Marcell
TM4
Pixie
MacnCheese
Angelica
JAWS
BarrelRoll
Adephagia
CrimD
Araya
Fionnbharth
Larva
Halo
BPs
Averatan
Angel
Hope
Lielie
Giles
DS6A
Rosebush
Hedgerow
Arbiter
Anneal29
Qynzufa
Ares
Pipefish
Phaedrus
Kamiyu
Phlyer
Daisy
Athena
Akoma
Gadjet
Cooper
Nigel
Stinger
ChristenMitch
Zemanar
Acadian
Colbert
KLucky39
Puhltorio
Phipps
UncleHowie
Murdoc
Vista
Harvey
Serendipity
Oosterbaan
Hertubise
PG1
Vortex
TailGRaseMM
Morgushi
Osmaximus
Oline
Dori
Wildcat
Rey
Bongo
LeBron
UPIE
Fezzik
JoeDirt
Faith1
Rumpelstiltskin
Barnyard
Predator
Konstantine
Patience
PBI1
Adjutor
Butterscotch
Trish4
PLot
Nova
Gumball
SirHarley
Send513
Marvin
Che8
Lilj
PMC
GUmbie
DollProduct
Pacc40
Dorothy
Ibhubesi
ShiLan
Tweety
Wee
Taj
DeadP
Fruitloop
Ardmore
DLane
SG4
Shauna1
Mutaforma13
Spartacus
Boomer
Drago
RockyHorror
Ramsey
Mary
Chefld
Avani
Yoshi
CJW1
Lilac
Elph10
Pumpkin
244
Porky
Kostya
Rakim
Toto
Henry
Bask21
SirDuracell
Eureka
Omega
LittleE
Courthouse
Optimus
Baka
Thibault
Corndog
Firecracker
CheSc
Charlie
Redi
Brujita
island3
Babsiella
BigHuz
Jebeks
0.1

Figure 3: ClustalW phylogenetic tree (NJ) of complete genomes of all *Mycobacterium* siphoviruses in the NCBI database in November 2012.

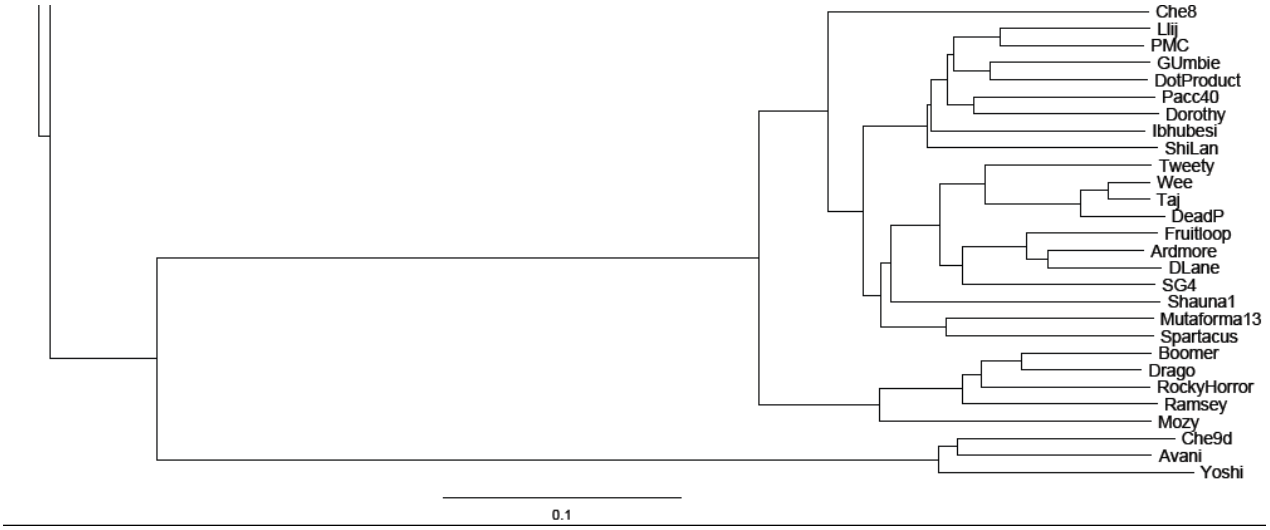

Figure 4: ClustalW phylogenetic tree of complete genomes of the isolates belonging to the genus *Che8likevirus*, excerpt of Figure 2.

Table 1: CoreGenes 3.5 and EMBOSS Stretcher analysis of the members of the proposed genus with the type phage, *Mycobacterium phage Che8*.

Phage name	% proteins in common with Che8	% of shared DNA with Che8
Mycobacterium phage PMC	69,6	74.3
Mycobacterium phage mutaforma13	67,0	72.4
Mycobacterium phage dotproduct	65,2	71.7
Mycobacterium phage gumbie	65,2	72.5
Mycobacterium phage Llij	67,0	72.8
Mycobacterium phage spartacus	67,9	70.3
Mycobacterium phage Pacc40	70,5	72.7
Mycobacterium phage ibhubesi	66,1	73.1
Mycobacterium phage tweety	65,2	72.0
Mycobacterium phage taj	61,6	70.4
Mycobacterium phage wee	60,7	69.4
Mycobacterium phage dorothy	67,0	71.2
Mycobacterium phage deadp	59,8	70.1
Mycobacterium phage SG4	63,4	68.3
Mycobacterium phage boomer	59,8	69.2
Mycobacterium phage dlane	60,7	68.1
Mycobacterium phage ardmore	59,8	68.1
Mycobacterium phage fruitloop	58,0	68.8
Mycobacterium phage shilan	68,8	69.6
Mycobacterium phage drago	59,8	68.0
Mycobacterium phage ramsey	62,5	67.4

Mycobacterium phage rockyhorror	63,4	69.2
Mycobacterium phage mozy	61,6	65.6
Mycobacterium phage shauna1	56,3	64.2
Mycobacterium phage Che9d	47,3	53.4
Mycobacterium phage avani	45,5	55.2
Mycobacterium phage yoshi	42,0	52.7