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:	***2013.002a-gB***	(to be completed by ICTV officers)

Short title: Create the family *Turriviridae*, comprising the new genus, *Alphaturrivirus*, and two new species. (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:

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David Prangishvili david.prangishvili@pasteur.fr

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)	Archaeal Viruses Study Group

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

EC45 Decision: 2013.002a-gB.N.v1.Turriviridae. Presented by DP and DHB. Decision: Uc. Use Genbank accession numbers. Consider better genus name (Alphaturrivirus?) in 2013.002bB. Correct typo in species names on page 3. Move isolate names from species box on page 2.

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

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	***2013.002aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Alphaturrivirus (new)***
Subfamily:	
Family:	***Turriviridae (new)***
Order:	

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:**
Sulfolobus turreted icosahedral virus 1	AY569307.1
Sulfolobus turreted icosahedral virus 2	GU080336.1

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

The two proposed virus species which infect members of the hyperthermophilic archaeal genus *Sulfolobus* (order *Sulfolobales*, Phylum *Crenarchaeota*) share overall virion morphology (turreted icosahedra with an internal membrane layer**)** and protein sequences, gene synteny, and genomic structure. The virions of both viruses are arranged on a pseudo-T=31 icosahedral lattice, which was previously undescribed. The two viruses differ from each other—as well as from other known virus species— by sequences of their genomes and the architecture of their virion turrets (see Module 9, Annex - Figures 1-5).

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.002bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Turriviridae (new)***
Order:	

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	***2013.002cB***	(assigned by ICTV officers)

To name the new genus: *Alphaturrivirus*

Assigning the type species and other species to a new genus

Code	***2013.002dB***	(assigned by ICTV officers)

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

Sulfolobus turreted icosahedral virus 1

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:**

2

Reasons to justify the creation of a new genus:

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

We propose classifying the *Sulfolobus turreted icosahedral virus 1* and *Sulfolobus turreted icosahedral virus 2* as first representatives of a new family because of the unique combination of exceptional morphological and genomic properties of the two viruses. Although the overall morphology of the virions (icosahedral with an internal membrane layer**)** resembles that of bacterial viruses from the families *Tectiviridae* and *Corticoviridae*, the turreted structure of the icosahedral virion is unique and the virion is built on a pseudo-T = 31 icosahedral lattice, which was previously undescribed (see Module 9, Annex-Figures 1, 3, 4 and 5). On the genome level the two viruses share very limited similarities to any known virus (Module 9, Annex-Figure 2). These limited genomic similarities are mainly with other viruses of hyperthermophilic archaea and comprise homologues to a putative DNA-binding protein and a putative transcription regulator of the *Fuselloviridae*. The existence of these few homologues is compatible with horizontal gene transfer, rather than with common ancestry with the viruses from other families of archaeal viruses.

Origin of the new genus name:

From Latin *turris*, for turret

Reasons to justify the choice of type species:

Sulfolobus turreted icosahedral virus 1 was the first member of the genus to be discovered and has been chatacterized in significantly more detail than the other member of the genus - *Sulfolobus turreted icosahedral virus 2.*

Species demarcation criteria in the new genus:

Species demarcation within this genus is based on the differences in the nucleotide sequences of the viral genomes. The two proposed species share less than 75% nucleotide similarity across their aligned genomes and the sequence comparisons reveal several insertions/deletions (see Module 9, Annex – Figure 2).

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	***2013.002eB***	(assigned by ICTV officers)

To create a new family containing the subfamilies and/or genera listed below within the Order: unassigned

If there is no Order, write "**unassigned**" here.

If the Order has yet to be created (in Module 6) please write **"(new)"** after the proposed name.

Code	***2013.002fB***	(assigned by ICTV officers)

To name the new family: *Turriviridae*

assigning subfamilies, genera and unassigned species to a new family

Code		(assigned by ICTV officers)

To assign the following subfamilies (if any) to the new family:

You may list several subfamilies here. For each subfamily, please state whether it is new or existing.

- If the subfamily is new, it must be created in Module 4
- If the subfamily already exists, please complete Module 7 to 'REMOVE' it from its existing family

None

Code	***2013.002gB***	(assigned by ICTV officers)

To assign the following genera to the new family:

You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family
- *Alphaturrivirus*

Alphaturriviris

The new family will also contain any other new species created and assigned to it (Module 3) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):**

None

Reasons to justify the creation of the new family:

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

We propose classifying the *Sulfolobus turreted icosahedral virus 1* and *Sulfolobus turreted icosahedral virus 2* as first representatives of a new family because of the unique combination of exceptional morphological and genomic properties of the two viruses. Although the overall morphology of the virions (icosahedral with an internal membrane layer**)** resembles that of bacterial viruses from the families *Tectiviridae* and *Corticoviridae*, the turreted structure of the icosahedral virion is unique and the virion is built on a pseudo-T = 31 icosahedral lattice, which was previously undescribed (see Module 9, Annex-Figures 1, 3, 4 and 5). On the genome level the two viruses share very limited similarities to any known virus (Module 9, Annex-Figure 2).

These limited genomic similarities are mainly with other viruses of hyperthermophilic archaea and comprise homologues to a putative DNA-binding protein and a putative transcription regulator of the *Fuselloviridae*. The existence of these few homologues is compatible with horizontal gene transfer, rather than with common ancestry with the viruses from other families of archaeal viruses.
Origin of the new family name:
From Latin *turris*, for turret

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Brumfield SK, Ortmann AC, Ruigrok V, Suci P, Douglas T, and Young MJ. 2009. Particle assembly and ultrastructural features associated with replication of the lytic archaeal virus Sulfolobus turreted icosahedral virus. *J Virol* 83: 5964-5970.

Happonen L. Redder P, Peng X, Schleper C, Prangishvili D, and Butcher SJ. 2010. Familial relationships in hyperthermo- and acidophilic archaeal viruses. *J. Virol* 84: 4747-4754.

Khayat R, Fu CY, Ortmann AC, Young MJ, Johnson JE. 2010. The architecture and chemical stability of the archaeal *Sulfolobus* turreted icosahedral virus. *J Virol* 84: 9575-9583.

Maaty WS, Ortmann AC, Dlakić M, Schulstad K, Hilmer JK, Liepold L, Weidenheft B, Khayat R, Douglas T, Young MJ, Bothner B. 2006. Characterization of the archaeal thermophile Sulfolobus turreted icosahedral virus validates an evolutionary link among double-stranded DNA viruses from all domains of life. *J Virol* 80: 7625-7635.

Ortmann AC., Brumfield SK, Walther J, McInnerney K, Brouns SJ, van de Werken HJ, Bothner B, Douglas T, van de Oost J, and Young MJ. 2008. Transcriptome analysis of infection of the archaeon *Sulfolobus solfataricus* with *Sulfolobus* turreted icosahedral virus. *J Virol* 82: 4874-4883.

Rice G, Tang L, Stedman K, Roberto F, Spuhler J, Gillitzer E, Johnson JE, Douglas T, and Young M. 2004. The structure of a thermophilic archaeal virus shows a double-stranded DNA viral capsid type that spans all domains of life. *Proc Natl Acad Sci USA* 101: 7716-7720.

Veesler D, NgTS, Sendamarai AK, Eilers BJ, Lawrence CM, Lok SM, Young MJ, Johnson JE, Fu CY. 2013. *Proc Natl Acad Sci USA* 110: 5504-5509.

Annex:

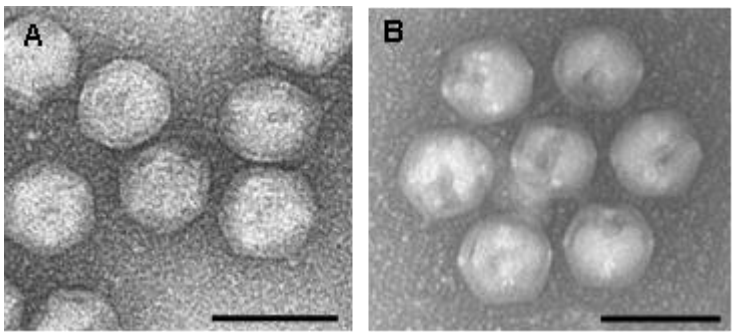

Figure 1. Negative contrast electron micrographs of *(A) Sulfolobus islandicus turreted icosahedral virus 1* and *(B) Sulfolobus islandicus turreted icosahedral virus 2.* Scale bars, 100 nm.

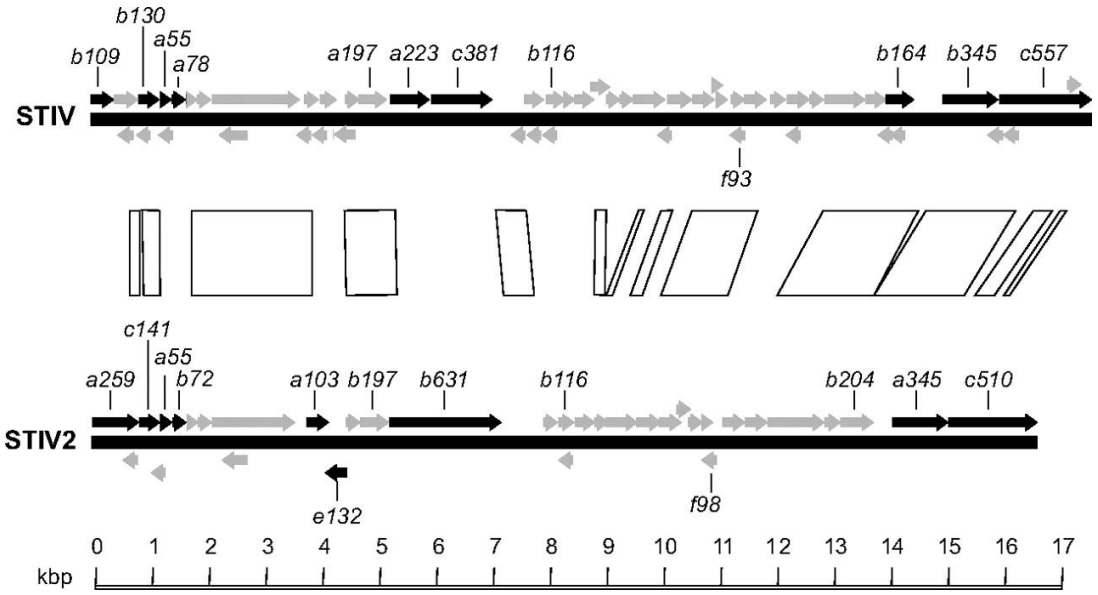

Figure 2. Genome comparison of the *Sulfolobus islandicus turreted icosahedral virus 1* (STIV) and *Sulfolobus islandicus turreted icosahedral virus 2* (STIV2). The genomes are represented by solid black bars, and the predicted ORFs are indicated by arrows showing their relative orientations. Black arrows, structural proteins detected by mass spectrometry. The parallelograms between the two genomes indicate regions of more than 70% nucleotide sequence identity. (Reproduced from Happonen *et al.*, 2010).

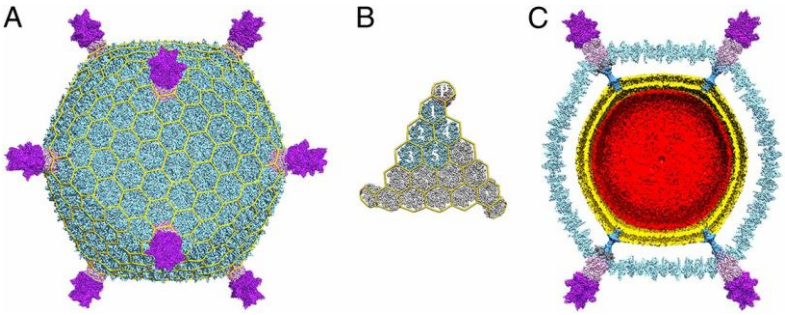

Figure 3. Near-atomic resolution electron cryomicroscopy reconstruction of STIV. (*A*) The overall virus reconstruction is displayed with the different protein components individually colored (B345, light blue; A223, light pink; C381, purple) and with an icosahedral cage overlaid onto it. (*B*) Blow-up view of an icosahedral face with one capsid icosahedral asymmetric unit colored as in *A* and labeled (1–5 for the trimeric B345 capsomers and P for the A223 penton base). (*C*) Cross-section of the reconstruction revealing the presence of the viral membrane (gold) and the internal genome (red). The cement protein (dark gray) has been removed from the two vertex complexes located on the right-hand side to allow a better visibility of the β-pore. (Reproduced from Vessler *et al.*, 2013)

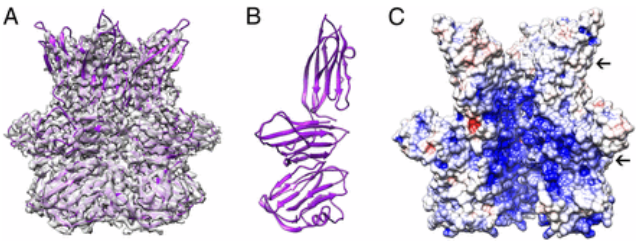

Figure 4. Architecture of the STIV turret. (*A*) The pentameric C381 turret protein X-ray structure is shown fit into the corresponding region of the cryoEM density. (*B*) Each C381 monomer is formed of three layers of jelly-rolls with markedly different orientations. (*C*) The interior of the C381 pentamer exhibits a positive electrostatic surface potential and several constrictions (indicated by black arrows). These characteristics are unfavorable to allow dsDNA genome transit during packaging or infection. Electrostatics calculations were carried out at pH 3.0 and 80 °C, and the result is displayed colored from red (−5 kT/e) to blue (+5 kT/e). One C381 monomer has been removed to allow visualization of the pentamer central cavities. (Reproduced from Vessler *et al.*, 2013).

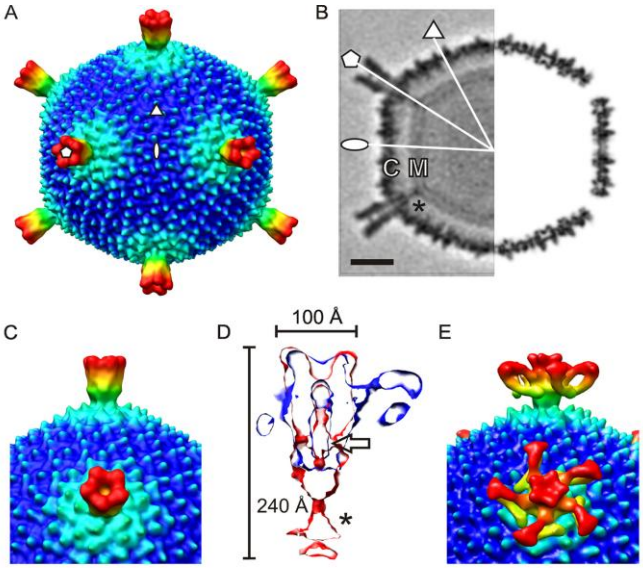

Figure 5. Structure of STIV2 and its turrets. *(A)* A radially depth-cued isosurface representation (at 2 σ above the mean) of the 20-Å-resolution STIV2 reconstruction viewed down a 2-fold symmetry axis. Symmetry axes are indicated by a white ellipse (2-fold), triangle (3-fold), and pentagon (5-fold). *(B)* A 0.44-nm-thick central section through the STIV2 virion (left). The right side shows the capsid protein density generated by fitting the homology-modeled coat protein into the reconstruction. Symmetry axes are indicated as in panel A. The viral capsid *(C)* and the underlying membrane (M) are indicated. Bar, 20 nm. (C) A close-up (at 1 σ above the mean) of the STIV2 turrets. *(D)* Comparison of the central sections of the manually segmented STIV2 (red outline) and STIV (blue outline) turrets. The dimensions are indicated for the STIV2 turret. The open arrow points to the channel in the middle of the turrets through which DNA may travel. *(E)* A close-up (at 1 σ above the mean) of the STIV turrets clearly showing the central barrel and the attached ear-like structures. (Reproduced from Happonen *et al*., 2010).