This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2018.011S*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **2 new species (*Rosavirus B, Rosavirus C*) in the genus *Rosavirus*** | | | |
|  | | | |
| **Author(s):** | | | |
| Roland Zell, Alexander E. Gorbalenya, Tapani Hovi, Andrew M.Q. King, Nick J. Knowles, A. Michael Lindberg, M. Steven Oberste, Ann C. Palmenberg, Gabor Reuter, Peter Simmonds, Tim Skern, Caroline Tapparel, Katja C. Wolthers, Patrick C.Y. Woo | | | |
| **Corresponding author with e-mail address:** | | | |
| Roland Zell ([roland.zell@med.uni-jena.de](mailto:roland.zell@med.uni-jena.de)) | | | |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | ***Picornaviridae* Study Group** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | 15/06/2018 |
| Date of this revision (if different to above): | | |  |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** **2018.011S.N.v1.Rosavirus\_2sp** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**Create 2 new species (*Rosavirus B, Rosavirus C*) in the genus *Rosavirus***

The genus *Rosavirus* presently consists of only 1 species, *Rosavirus A* (host: canyon mouse, *Peromyscus crinitus*). Novel, rosavirus-like picornaviruses have been detected in faecal specimens collected from *Rattus norvegicus* (proposed *Rosavirus B*) and *Rattus rattus, R. andamanensis, Niviventer fulvescens, N. coxingi* (proposed *Rosavirus C*) in Hong Kong. Other rosavirus-like viruses were detected in faecal specimens of an unspecified rodent in China and faecal samples of children in Gambia. Altogether 16 almost complete genomes plus partial sequences are available and suggest the existence of 3 species with at least eight types.

**Relation to other picornaviruses:**

- Genome layout:

5'-UTRIRES-II[1A-1B-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

(compare Fig. 1 of supporting material)

- Rosaviruses have typical hallmarks of picornaviruses:

- 5'-UTR: >500-721 nt; similarity to IRES type II,

- capsid proteins: 1B, 1C, 1D have **rhv** domains with a drug-binding site,

- 2A: **H-box/NC** sequence motif,

- 2Chel: **G**xx**G**x**GKS** motif of helicases,

- 3BVPg: **Y-3** residue, passeriviruses have two putative 3BVPg peptides,

- 3Cpro: **G**x**CG**x14**G**x**H** motif,

- 3Dpol: **KDE**, **PSG**, **YGDD**, **FLKR** motifs

- 3'-UTR: longest known 3'-UTRs of picornaviruses (up to 946 nt).

- Phylogenetic analyses indicate that the novel viruses are related to the rosaviruses

(compare Figs. 2-5 of supporting material).

**Distinguishing features of rosaviruses B and C compared to *Rosavirus A*:**

1. Host specificity: All rosaviruses are associated with rodent hosts.

*Rosavirus A*: canyon mouse

*Rosavirus B*: Norway rat

*Rosavirus C*: house rat, Sikkim rat, chestnut white-bellied rat, Coxing's white-bellied rat.

2. Capsid protein 1D is c. 30 aa longer in rosaviruses B; rosaviruses C have a C-terminal extension of capsid protein 1C (c. 30 aa).

3. **Sequence divergences** (uncorrected p-distances) of all relevant genome regions suggest three species with althogether 8 types:

- P1: within type aa divergence: <0.10

between types aa divergence 0.12-0.25

between species aa divergence 0.43-0.50

divergence to other picornavirus genera: >0.6

- 2Chel: between species aa divergence 0.3-0.5

divergence to other picornavirus genera: >0.6

- 3Cpro: between species aa divergence 0.3-0.5

divergence to other picornavirus genera: >0.6

- 3Dpol: between species aa divergence 0.25-0.35

divergence to other picornavirus genera: >0.45 (compare Tables 1-4)

**Exemplar:**

***Rosavirus B***, rosavirus B1 [RNCW0602091R/Hong Kong/2009], GenBank acc. no. KX783423

***Rosavirus C***, rosavirus C1 [RASK8F/Hong Kong/2008], GenBank acc. no. KX783424

**Species demarcation criteria:**

Based on available sequence data, preliminary species demarcation criteria were defined.

Members of a species of genus *Rosavirus*:

- share a common genome organization,

- share greater than 70% aa identity in the polyprotein,

- share greater than 70% aa identity in the P1,

- share greater than 75% aa identity in the non-structural proteins 2C + 3CD.

| **References:** |
| --- |
| 1. Lau SKP, Woo PCY, Li KSM, Zhang HJ, Fan RYY, Zhang AJX, Chan BCC, Lam CSF, Yip CCY, Yuen MC, Chan KH, Chen ZW, Yuen KY. Identification of novel rosavirus species that infects divers rodent species and causes multisystemic dissemination in mouse model, PLoS Pathog (12(10):e1005911.  2. Du J, Lu L, Liu F, Su H, Dong J, Sun L, Zhu Y, Ren X, Yang F, Guo F, Liu Q, Wu Z, Jing Q. 2016. Distribution and characteristics of rodent picornaviruses in China. Sci Rep 6:34381.  3. Phan TG, Kapusinszky B, Wang C, Rose RK, Lipton HL, Delwart EL. 2011. The fecal viral flora of wild rodents. PLoS Pathog 7(9):E1002218.  4. Lim ES, Cao S, Holtz LR, Antonio M, Stine OC, Wang D. 2014. Discovery of rosavirus 2, a novel variant of a rodent-associated picornavirus, in children from The Gambia. Virology 454-455:25-33. |



**Figure 1:** Schematic depiction of the genome organisation of rosaviruses. The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated by ▼, the 1AB processing site is indicated by a ¶. The names and lengths of the deduced proteins are presented.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Eighty-nine picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/Sakobuvirus/ Sicinivirus/Rosavirus* supergroup were retrieved from GenBank; the newt ampivirus sequence served as outgroup. [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)] Presented are GenBank accession numbers, ***genus*** ***names***, ***species names***, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 3:**  Phylogenetic analysis of picornavirus **2Chel** using Bayesian tree inference (MrBayes 3.2). Eighty-seven picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/Sakobuvirus/ Sicinivirus/Rosavirus* supergroup were retrieved from GenBank; the newt ampivirus sequence served as outgroup. [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)] Presented are GenBank accession numbers, ***genus*** ***names***, ***species names***, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 4:**  Phylogenetic analysis of picornavirus **3Cpro** using Bayesian tree inference (MrBayes 3.2). Eighty-seven picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/Sakobuvirus/ Sicinivirus/Rosavirus* supergroup were retrieved from GenBank; the newt ampivirus sequence served as outgroup. [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)] Presented are GenBank accession numbers, ***genus*** ***names***, ***species names***, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 5:**  Phylogenetic analysis of picornavirus **3Dpol** using Bayesian tree inference (MrBayes 3.2). Eighty-seven picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/Sakobuvirus/ Sicinivirus/Rosavirus* supergroup were retrieved from GenBank; the newt ampivirus sequence served as outgroup. [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)] Presented are GenBank accession numbers, ***genus*** ***names***, ***species names***, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 10,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

**Table 1. Estimates of Evolutionary Divergence between P1 AA Sequences**

[ 1] JF973686, Rosavirus A1 [M-7]

[ 2] KJ158169, Rosavirus A2 [GA7403]

[ 3] KX783421, Rosavirus B1 [RNCW1002091R]

[ 4] KX783422, Rosavirus B1 [RNYL1109081R]

[ 5] KX783423, Rosavirus B1 [RNCW0602091R]

[ 6] KJ950906, Rosavirus B2 [NrRV/NYC-A15]

[ 7] KX783424, Rosavirus C1 [RASK8F]

[ 8] KX783426, Rosavirus C1 [RAWKT4F]

[ 9] KX783427, Rosavirus C1 [NFWKT7F]

[10] KX783433, Rosavirus C1 [RASM14A]

[11] KX783429, Rosavirus C1 [RRTPC2A]

[12] KX783430, Rosavirus C1 [RRTPC4A]

[13] KX783425, Rosavirus C2 [RATLC11A]

[14] KX783428, Rosavirus C2 [NFSM6F]

[15] KX783431, Rosavirus C3 [NCHN06IO]

[16] KX783432, Rosavirus C3 [NCGX12IN]

[17] KX156156, Rosavirus C4 [rodent/RL/PicoV/FJ2015]

[18] JN819202, Cadicivirus A (canine picodicistrovirus) [209]

[19] JN819203, Cadicivirus A (canine picodicistrovirus9 [236]

[20] JN819204, Cadicivirus A (canine picodicistrovirus) [244U]

[21] MF188967, Cadicivirus B (hedgehog dicipivirus9 [hedgehog/H14/2015/HUN]

[22] KU977108, Poecivirus [BCCH-449]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 ]

[ 1]

[ 2] 0.225

[ 3] 0.465 0.479

[ 4] 0.464 0.478 0.021

[ 5] 0.467 0.480 0.042 0.045

[ 6] 0.472 0.494 0.138 0.137 0.132

[ 7] 0.501 0.495 0.443 0.442 0.442 0.457

[ 8] 0.501 0.495 0.442 0.441 0.441 0.456 0.010

[ 9] 0.501 0.495 0.442 0.441 0.441 0.456 0.010 0.000

[10] 0.502 0.496 0.446 0.444 0.444 0.460 0.007 0.015 0.015

[11] 0.503 0.495 0.443 0.442 0.441 0.455 0.062 0.065 0.065 0.065

[12] 0.503 0.495 0.443 0.442 0.441 0.455 0.062 0.065 0.065 0.065 0.000

[13] 0.491 0.494 0.438 0.437 0.436 0.446 0.154 0.156 0.156 0.153 0.158 0.158

[14] 0.491 0.492 0.435 0.432 0.434 0.441 0.156 0.158 0.158 0.157 0.160 0.160 0.026

[15] 0.503 0.494 0.438 0.437 0.435 0.448 0.150 0.152 0.152 0.151 0.151 0.151 0.168 0.168

[16] 0.504 0.494 0.436 0.435 0.432 0.448 0.152 0.154 0.154 0.153 0.151 0.151 0.170 0.170 0.002

[17] 0.498 0.496 0.439 0.438 0.443 0.460 0.122 0.127 0.127 0.125 0.121 0.121 0.192 0.194 0.187 0.189

[18] 0.634 0.626 0.644 0.641 0.640 0.644 0.624 0.624 0.624 0.626 0.616 0.616 0.628 0.629 0.626 0.626 0.622

[19] 0.637 0.629 0.645 0.643 0.642 0.646 0.625 0.625 0.625 0.628 0.618 0.618 0.629 0.630 0.629 0.629 0.624 0.019

[20] 0.634 0.627 0.644 0.642 0.640 0.644 0.624 0.624 0.624 0.627 0.617 0.617 0.629 0.630 0.627 0.627 0.623 0.000 0.019

[21] 0.635 0.617 0.607 0.605 0.603 0.600 0.608 0.607 0.607 0.610 0.609 0.609 0.610 0.611 0.605 0.607 0.616 0.548 0.549 0.547

[22] 0.814 0.823 0.833 0.833 0.833 0.830 0.814 0.817 0.817 0.817 0.820 0.820 0.811 0.814 0.816 0.817 0.818 0.838 0.836 0.838 0.828

\_\_\_ within type comparison, \_\_\_ between types/within species comparison,

\_\_\_ between species/within genus comparison, \_\_\_ between genera comparison

**Table 2. Estimates of Evolutionary Divergence between 2Chel AA Sequences**

[ 1] JF973686, Rosavirus A1 [M-7]

[ 2] KX783421, Rosavirus B1 [RNCW1002091R]

[ 3] KX783422, Rosavirus B1 [RNYL1109081R]

[ 4] KX783423, Rosavirus B1 [RNCW0602091R]

[ 5] KX783424, Rosavirus C1 [RASK8F]

[ 6] KX783426, Rosavirus C1 [RAWKT4F]

[ 7] KX783427, Rosavirus C1 [NFWKT7F]

[ 8] KX783433, Rosavirus C1 [RASM14A]

[ 9] KX783429, Rosavirus C1 [RRTPC2A]

[10] KX783430, Rosavirus C1 [RRTPC4A]

[11] KX783425, Rosavirus C2 [RATLC11A]

[12] KX783428, Rosavirus C2 [NFSM6F]

[13] KX783431, Rosavirus C3 [NCHN06IO]

[14] KX783432, Rosavirus C3 [NCGX12IN]

[15] KX156156, Rosavirus C4 [rodent/RL/PicoV/FJ2015]

[16] JN819202, Cadicivirus A (canine picodicistrovirus) [209]

[17] JN819203, Cadicivirus A (canine picodicistrovirus9 [236]

[18] JN819204, Cadicivirus A (canine picodicistrovirus) [244U]

[19] MF188967, Cadicivirus B (hedgehog dicipivirus9 [hedgehog/H14/2015/HUN]

[20] KU977108, Poecivirus [BCCH-449]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 ]

[ 1]

[ 2] 0.364

[ 3] 0.361 0.009

[ 4] 0.367 0.017 0.009

[ 5] 0.421 0.334 0.334 0.337

[ 6] 0.424 0.337 0.337 0.340 0.009

[ 7] 0.421 0.334 0.334 0.337 0.006 0.003

[ 8] 0.421 0.334 0.334 0.337 0.000 0.009 0.006

[ 9] 0.411 0.335 0.335 0.341 0.090 0.090 0.087 0.090

[10] 0.413 0.338 0.338 0.338 0.090 0.090 0.087 0.090 0.003

[11] 0.421 0.337 0.337 0.340 0.017 0.014 0.012 0.017 0.093 0.093

[12] 0.424 0.337 0.337 0.340 0.009 0.006 0.003 0.009 0.090 0.090 0.014

[13] 0.430 0.360 0.360 0.363 0.093 0.093 0.090 0.093 0.125 0.125 0.084 0.093

[14] 0.430 0.360 0.360 0.363 0.096 0.096 0.093 0.096 0.128 0.128 0.087 0.096 0.006

[15] 0.419 0.338 0.338 0.344 0.090 0.087 0.084 0.090 0.052 0.055 0.084 0.087 0.113 0.119

[16] 0.674 0.653 0.653 0.659 0.663 0.666 0.666 0.663 0.674 0.676 0.663 0.666 0.660 0.660 0.662

[17] 0.672 0.650 0.650 0.656 0.660 0.663 0.663 0.660 0.671 0.674 0.660 0.663 0.657 0.657 0.659 0.011

[18] 0.674 0.650 0.650 0.656 0.663 0.666 0.666 0.663 0.674 0.676 0.663 0.666 0.660 0.660 0.662 0.011 0.011

[19] 0.641 0.604 0.607 0.607 0.628 0.625 0.622 0.628 0.630 0.630 0.619 0.622 0.622 0.622 0.618 0.521 0.518 0.518

[20] 0.682 0.700 0.700 0.700 0.678 0.678 0.678 0.678 0.683 0.683 0.675 0.680 0.675 0.675 0.671 0.716 0.718 0.713 0.717

\_\_\_ within type comparison, \_\_\_ between types/within species comparison,

\_\_\_ between species/within genus comparison, \_\_\_ between genera comparison

**Table 3. Estimates of Evolutionary Divergence between 3Cpro AA Sequences**

[ 1] JF973686, Rosavirus A1 [M-7]

[ 2] KJ158169, Rosavirus A2 [GA7403]

[ 3] KX783421, Rosavirus B1 [RNCW1002091R]

[ 4] KX783422, Rosavirus B1 [RNYL1109081R]

[ 5] KX783423, Rosavirus B1 [RNCW0602091R]

[ 6] KJ950906, Rosavirus B2 [NrRV/NYC-A15]

[ 7] KX783424, Rosavirus C1 [RASK8F]

[ 8] KX783426, Rosavirus C1 [RAWKT4F]

[ 9] KX783427, Rosavirus C1 [NFWKT7F]

[10] KX783433, Rosavirus C1 [RASM14A]

[11] KX783429, Rosavirus C1 [RRTPC2A]

[12] KX783430, Rosavirus C1 [RRTPC4A]

[13] KX783425, Rosavirus C2 [RATLC11A]

[14] KX783428, Rosavirus C2 [NFSM6F]

[15] KX783431, Rosavirus C3 [NCHN06IO]

[16] KX783432, Rosavirus C3 [NCGX12IN]

[17] KX156156, Rosavirus C4 [rodent/RL/PicoV/FJ2015]

[18] JN819202, Cadicivirus A (canine picodicistrovirus) [209]

[19] JN819203, Cadicivirus A (canine picodicistrovirus9 [236]

[20] JN819204, Cadicivirus A (canine picodicistrovirus) [244U]

[21] MF188967, Cadicivirus B (hedgehog dicipivirus9 [hedgehog/H14/2015/HUN]

[22] KU977108, Poecivirus [BCCH-449]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 ]

[ 1]

[ 2] 0.405

[ 3] 0.405 0.005

[ 4] 0.405 0.015 0.020

[ 5] 0.425 0.385 0.385 0.380

[ 6] 0.425 0.380 0.380 0.375 0.010

[ 7] 0.430 0.385 0.385 0.380 0.015 0.005

[ 8] 0.425 0.385 0.385 0.380 0.000 0.010 0.015

[ 9] 0.435 0.370 0.370 0.365 0.115 0.115 0.120 0.115

[10] 0.440 0.375 0.375 0.370 0.120 0.120 0.125 0.120 0.010

[11] 0.430 0.380 0.380 0.375 0.040 0.040 0.045 0.040 0.115 0.120

[12] 0.430 0.390 0.390 0.385 0.010 0.020 0.025 0.010 0.110 0.115 0.050

[13] 0.435 0.390 0.390 0.385 0.090 0.085 0.090 0.090 0.115 0.120 0.080 0.090

[14] 0.440 0.385 0.385 0.380 0.085 0.080 0.085 0.085 0.110 0.115 0.075 0.085 0.005

[15] 0.435 0.380 0.380 0.375 0.115 0.115 0.120 0.115 0.045 0.055 0.115 0.110 0.120 0.115

[16] 0.665 0.678 0.678 0.673 0.598 0.598 0.603 0.598 0.623 0.628 0.593 0.598 0.618 0.613 0.613

[17] 0.665 0.678 0.678 0.673 0.598 0.598 0.603 0.598 0.623 0.628 0.593 0.598 0.618 0.613 0.613 0.000

[18] 0.665 0.678 0.678 0.673 0.598 0.598 0.603 0.598 0.623 0.628 0.593 0.598 0.618 0.613 0.613 0.000 0.000

[19] 0.630 0.663 0.663 0.658 0.643 0.643 0.648 0.643 0.648 0.653 0.643 0.643 0.648 0.648 0.648 0.416 0.416 0.416

[20] 0.713 0.713 0.713 0.707 0.723 0.718 0.723 0.723 0.723 0.729 0.723 0.723 0.713 0.718 0.723 0.726 0.726 0.726 0.700

\_\_\_ within type comparison, \_\_\_ between types/within species comparison,

\_\_\_ between species/within genus comparison, \_\_\_ between genera comparison

**Table 4. Estimates of Evolutionary Divergence between 3Dpol AA Sequences**

[ 1] JF973686, Rosavirus A1 [M-7]

[ 2] KJ158169, Rosavirus A2 [GA7403]

[ 3] KX783421, Rosavirus B1 [RNCW1002091R]

[ 4] KX783422, Rosavirus B1 [RNYL1109081R]

[ 5] KX783423, Rosavirus B1 [RNCW0602091R]

[ 6] KJ950906, Rosavirus B2 [NrRV/NYC-A15]

[ 7] KX783424, Rosavirus C1 [RASK8F]

[ 8] KX783426, Rosavirus C1 [RAWKT4F]

[ 9] KX783427, Rosavirus C1 [NFWKT7F]

[10] KX783433, Rosavirus C1 [RASM14A]

[11] KX783429, Rosavirus C1 [RRTPC2A]

[12] KX783430, Rosavirus C1 [RRTPC4A]

[13] KX783425, Rosavirus C2 [RATLC11A]

[14] KX783428, Rosavirus C2 [NFSM6F]

[15] KX783431, Rosavirus C3 [NCHN06IO]

[16] KX783432, Rosavirus C3 [NCGX12IN]

[17] KX156156, Rosavirus C4 [rodent/RL/PicoV/FJ2015]

[18] JN819202, Cadicivirus A (canine picodicistrovirus) [209]

[19] JN819203, Cadicivirus A (canine picodicistrovirus9 [236]

[20] JN819204, Cadicivirus A (canine picodicistrovirus) [244U]

[21] MF188967, Cadicivirus B (hedgehog dicipivirus9 [hedgehog/H14/2015/HUN]

[22] KU977108, Poecivirus [BCCH-449]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 ]

[ 1]

[ 2] 0.267

[ 3] 0.267 0.008

[ 4] 0.267 0.008 0.004

[ 5] 0.286 0.265 0.263 0.263

[ 6] 0.286 0.263 0.261 0.261 0.031

[ 7] 0.286 0.263 0.261 0.261 0.031 0.000

[ 8] 0.292 0.263 0.261 0.261 0.013 0.038 0.038

[ 9] 0.292 0.277 0.275 0.275 0.103 0.109 0.109 0.105

[10] 0.292 0.277 0.275 0.275 0.103 0.109 0.109 0.105 0.000

[11] 0.273 0.261 0.258 0.258 0.046 0.048 0.048 0.052 0.111 0.111

[12] 0.279 0.261 0.258 0.258 0.019 0.031 0.031 0.025 0.107 0.107 0.052

[13] 0.282 0.254 0.250 0.252 0.113 0.113 0.113 0.119 0.124 0.124 0.101 0.115

[14] 0.279 0.256 0.252 0.254 0.113 0.115 0.115 0.119 0.122 0.122 0.103 0.115 0.008

[15] 0.292 0.267 0.265 0.265 0.122 0.128 0.128 0.124 0.069 0.069 0.122 0.122 0.111 0.107

[16] 0.503 0.530 0.527 0.527 0.524 0.528 0.528 0.531 0.526 0.526 0.533 0.516 0.528 0.526 0.516

[17] 0.501 0.530 0.527 0.527 0.522 0.526 0.526 0.528 0.524 0.524 0.533 0.516 0.526 0.524 0.512 0.015

[18] 0.501 0.530 0.527 0.527 0.526 0.526 0.526 0.533 0.524 0.524 0.533 0.520 0.526 0.524 0.514 0.008 0.010

[19] 0.456 0.457 0.455 0.455 0.460 0.451 0.451 0.458 0.458 0.458 0.454 0.456 0.468 0.468 0.454 0.435 0.431 0.433

[20] 0.579 0.614 0.612 0.612 0.612 0.610 0.610 0.615 0.612 0.612 0.606 0.610 0.602 0.602 0.608 0.650 0.645 0.647 0.622

\_\_\_ within type comparison, \_\_\_ between types/within species comparison,

\_\_\_ between species/within genus comparison, \_\_\_ between genera comparison