

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

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| **Code assigned:** | ***2023.003M*** |  |
| **Short title:** Create one new species in the genus *Ledantevirus,* one new species in the genus *Lostrhavirus*, three new species in the genus *Tupavirus*, one new species in the genus *Almendravirus* and two new species in the genus *Sigmavirus*, in the subfamily *Alpharhabdovirinae* (*Mononegavirales*: *Rhabdoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Rhabdoviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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| Minor text corrections; completed. |

**ICTV Study Group votes on proposal**

|  |  |  |  |
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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Rhabdoviridae* SG | 13 | 0 | 1 |

**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| N/A | N/A | N/A |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 23, 2023 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2023.003M.N.v1.Alpharhabdovirinae\_8nsp.xlsx |

**Abstract**

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| In the subfamily *Alpharhabdovirinae,* we propose the creation of one new species in the genus *Ledantevirus*, one new species in the genus *Lostrhavirus*,three new species in the genus *Tupavirus*, one new species in the genus *Almendravirus* andtwo new species in the genus *Sigmavirus.* Shanxi arboretum virus (SxABTV; proposed genus *Almendravirus*) was isolated in cell culture from mosquitoes collected in China, and sequenced. All other viruses to be assigned to new species were detected by metagenomic sequencing of tissues or whole organisms and have not yet been isolated. The proposed new species meet the demarcation criteria established for each genus. |

**Text of proposal**

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| |  | | --- | | 1. **Create one new species in the genus *Ledantevirus***   Tongren rhabd tick virus 2 (TrRTV2; sample TIGMIC 2) was detected by metagenomic sequencing of hard ticks (*Haemaphysalis* sp.) collected from swine in Guizhou Province, China, in 2019. We propose TrRTV2 be assigned to the new species *Ledantevirus* *tongren.*  Genome organization  The near-complete genome sequence of TrRTV2 (10,900 nt) is available, lacking only extreme 3' and 5' termini. The genome organization of TrRTV2 is similar to those of most ledanteviruses in phylogroups A and C (**Figure 1**). It contains only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) and very short intergenic sequences.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, TrRTV2 clusters with the ledanteviruses in a distinct and well-supported monophyletic clade (**Figure 4**). By this analysis, it falls within a sub-clade that also includes Longquan Niviventer coninga ledantevirus 1 (LNcoLV1; species *Ledantevirus longquan*).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that TrRTV2 is most closely related to LNcoLV1, sharing 85.8% identity in L, 92.7% identity in N and 80.2% identity G (**Tables 1-3**).  Ecology  Ledanteviruses have been reported in a range of mammals and arthropod vectors. Barur virus (species *Ledantevirus barur*) was previously isolated from hard ticks from India and Yongjia tick virus 2 (species *Ledantevirus yongjia*) was detected in ticks from China by metagenomic sequencing. Nishimuro virus (species *Ledantevirus nishimuro*) was isolated from a wild boar from Japan. Each of these viruses falls with TrRTV2 in phylogroup A **(Figure 1)**.  Species demarcation criteria  According to current criteria, viruses assigned to different species within the genus *Ledantevirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 7% in L; B) minimum amino acid sequence divergence of 15% in G; C) significant differences in genome organisation as evidenced by numbers and locations of ORFs; D) can be distinguished in neutralisation tests; and E) occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors.  TrRTV2 meets criteria A and B. The genome organisation of TrRTV2 is similar to those of ledanteviruses from the same phylogroup (criterion C). Neutralization tests have not been conducted as there are currently no isolates of these viruses (criterion D). Other viruses in phylogroup A have been detected in either swine or hard ticks (criterion E).   1. **Create one new species in the genus *Lostrhavirus***   Alxa tick rhabdovirus (ATRV; strain ZQ16-17) was detected by metagenomic sequencing of hard ticks (*Hyalomma* sp.) collected from herbivore livestock in Xinjiang and Inner Mongolia Autonomous Regions, China, in 2016.  We propose to assign ATRV to the new species *Lostravirus alxa*.  Genome organization  The near-complete genome sequence (11,477 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini. The ATRV genome is similar in organisation to that of other lostrhaviruses, containing only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) (**Figure 2**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, ATRV clusters with the two other known lostrhaviruses in a distinct and well-supported monophyletic clade and is most closely related to Xinjiang tick rhabdovirus (XjTRV; species *Lostrhavirus hyalomma*) (**Figure 4**).  Amino acid sequence identities  ATRV is most closely related to XjTRV in amino acid sequence. The identity in pair-wise alignments (p-distances) is 67.2% in the N proteins, 59.4% in the G proteins and 72.8% in the L proteins **(Tables 4-6).**  Ecology  Lostrhaviruses have been isolated from hard ticks (Ixodidae) of different genera. Like ATRV, XjTRV was isolated from hyalomma ticks (*Hyalomma asiaticum*) in north-western China. Lone star tick rhabdovirus (LSTRV; species *Lostrhavirus lonestar*) was isolated from lone star ticks (*Amblyomma americanum)* in the USA.    Species demarcation criteria  Viruses assigned to different species within the genus *Lostrhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N; B) minimum amino acid sequence divergence of 10% in L; C) minimum amino acid sequence divergence of 15% in G; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  ATRV meets demarcation criteria A, B and C. ATRV has a similar genome organization to LSTRV (criterion D). Neutralisation tests (criterion E) have not been conducted as no virus isolate is currently available. ATRV and XjTRV appear to share similar ecology with each virus being detected in tricks of the genus *Hyalomma* from the same region of northern China (criterion F).     1. **Create three new species in the genus *Tupavirus***   Tupavirus SB8301 (TUPVSB) was detected organ tissue of African marsh rats (*Dasymys incomtus*) collected in Kenya in 1971 and 1975. We propose that TUPVSB be assigned to the new species *Tupavirus incomtus.*  Bat tupavirus BS1 (BtTVBS1; sample RsBS01) was detected by whole organism metagenomic sequencing in lesser brown horseshoe bats (*Rhinolophus stheno*) collected in Yunnan Province, China, in 2015. We propose that BtTVBS21 be assigned to the new species *Tupavirus stheno.*  Bat tupavirus BS2 (BtTVBS2; sample AsBS02) was detected by whole organism metagenomic sequencing in Stoliczka's trident bats (*Aselliscus stoliczkanus*) collected in Yunnan Province, China, in 2017. We propose that BtTVBS2 be assigned to the new species *Tupavirus stoliczkanus.*  Genome organization  The near-complete genome sequences of TUPVSB (11,468 nt) and BtTVBS1 (12,187 nt) are available, lacking only extreme 3' and 5' termini (**Figure 2**). The published genome sequence of BtTVBS2 (11,805 nt) appears to be complete but is extended by two additional nucleotides at the 5’ end and a sequence of 143 nt at the 3’ end that each appears to be extraneous. The genome organisations of the three new viruses are similar to those of several other tupaviruses. Each contains the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*), an alternative ORF in the *P* gene, a gene encoding a small protein between the *M* gene and *G* gene, and a gene encoding a small protein between the *G* gene and *L* gene. In BtTVBS1, there are two genes encoding small proteins between the *G* gene and *L* gene.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, TUPVSB, BtTVBS1 and BtTVBS2 cluster with the tupaviruses in a distinct and well-supported monophyletic clade (**Figure 4**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that BtTVBS1 and BtTVBS2 are most closely related to Wufeng Rhinolophus pearsonii tupavirus 1 (WfRpeTV1; species *Tupavirus pearsonii*) and that TUPVSB is most closely related to Klamath virus (KLAV; species *Tupavirus kmamath*). Maximum sequence identity between all three viruses and all other tupaviruses was estimated to be 75.5% in L (BtTVBS1 and WfRpeTV1), 85.6% identity in N (BtTVBS1 and WfRpeTV1) and 75.2% identity in G (BtTVBS1 or BtTVBS2 and WfRpeTV1) (**Tables 7-9**).  Ecology  Tupaviruses have been isolated from various mammals and birds. KLAV was isolated from a vole (*Microtus montanus*)in the USA; TUPVSB was detected in a rodent of different species (*Dasymys incomtus*) in Kenya*.* BtTVBS1 and BtTVBS2 were isolated from chiroptid bats of two different species (*Rhinolophus stheno* and *Aselliscus stoliczkanus*, respectively) in China; two other tupaviruses (WfRpeTV1 and Wenzhou Rhinilophus langier tick virus 1 [WzMlaTV1; species *Tupavirus laniger*]) have been reported previously from chiroptid bats of two other species (*Rhinolophus pearsonii* and *Myotis laniger*, respectively) in China.  Species demarcation criteria  Viruses assigned to different species within the genus *Tupavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 5% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in serological tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  All proposed members of the genus meet demarcation criteria A, B and C. Their genome organisations are similar to those of other tupaviruses but both TUPVSB and BtTVBS1 have unique additional long ORFs; the genome organization of BtTVBS2 is very similar to that of WfRpeTV1 (criterion D). Neutralisation tests have not been conducted as there are currently no isolates of these viruses (criterion E). Although the viruses have been detected only by metagenomic sequencing, their natural ecology is consistent with other tupaviruses and suggests that they each occupy distinctive ecological niches (criterion F).   1. **Create one new species in the genus *Almendravirus***   Shanxi arboretum virus (SxABTV; strain 1916-1) was isolated from a pool of mosquitoes (*Armigeres subalbatus*) collected in Shanxi Province, China, 2019 [3]. The virus caused cytopathic effect in mosquito cells (C6/36) in which rod-shaped particles (300 nm x 70 nm) were observed in the cytoplasm.  We propose to assign SxABTV to the new species *Almendravirus shanxi*.  Genome organization  The near-complete genome sequence of SxABTV (11,480 nt) has been determined, lacking only extreme 3' and 5' termini (**Figure 2**). Like those of other almendraviruses, the genome contains the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) and an additional gene between the *G* gene and *L* gene encoding a small protein with the predicted structure of a class I viroporin.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, SxABTV clusters within the almendravirus clade (**Figure 4**) and is most closely related to Arboretum virus (ABTV; species *Almendravirus arboretum*)*.*  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicated that SxABTV is most closely related to ABTV with which it shares 90.6% identity in the L protein, 84.2% identity in the G protein and 94.0% identity in the N protein (**Tables 10–12**).  Ecology  Almendraviruses have been exclusively detected in or isolated from mosquitoes in China and the Americas. The isolation of SxABTV represents the first report of an almendravirus from mosquitoes of the genus *Armigeres* which occur in Asia and Australia, although the specific host was not established for Xiangshan rhabdo-like virus 1 (XsRLV-1; species *Almendravirus xianshan*) which was detected in China.  Species demarcation criteria  Viruses assigned to different species within the genus *Almendravirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 5% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  Although marginal, the proposed new member of the genus meets demarcation criteria A C, and is slightly below the demarcation point for criterion B (L protein divergence 9.4%). The genome organization is similar to those of other almendraviruses (criterion D). Neutralisation tests have not been conducted to date (criterion E). As the virus has been isolated from mosquitoes and replicates in mosquito cells, the natural mosquito host/vector has been established and is distinct from other almendraviruses for which the mosquito host/vector is known. The new member appears therefore to also meet demarcation criterion F.   1. **Create two new species in the genus *Sigmavirus***   Jopcycgri virus 1 (JPCGV1; strain NCg19) was detected by metagenomic sequencing of bat flies (*Cyclopodia greeffi*) collected in Nigeria, in 2020 [1]. We propose to assign JPCGV1 to the new species *Sigmavirus jopcycgri.*  Bactrocera tryoni rhabdovirus 1 (BtyrRV1; strain d) was detected by metagenomic sequencing of fruit flies (*Bactrocera tryoni*) collected in Australia, in 2018 [2]. We propose to assign BtyrRV1 to the new species *Sigmavirus tryoni.*  Genome organizations  The near-complete genome sequences of JPCGV1 (11,131 nt) and BtyrRV1 (11,181 nt) are available, lacking only extreme 3' and 5' termini (**Figure 3**). Each contains only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*), lacking the *X* gene between the *P* and *M* genes that is characteristic of most reported sigmaviruses. However, the absence of the *X* gene has been observed previously in several other sigmaviruses (**Figure 3**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, JPCGV1 and BtyrRV1 cluster together within the sigmavirus clade (**Figure 4**) on a branch that also includes Shayang fly virus 2 (SyFV2; species *Sigmavirus shayang*), Wuhan fly virus 2 (WhFV2; species *Sigmavirus domestica*), Yushu rhabdovirus (YsRV; species *Sigmavirus yushu*), Wuhan house fly virus 1 (WhHFV1; species *Sigmavirus wuhan*), Hubei diptera virus 9 (HbDV9; species *Sigmavirus hubei*), Hubei dipteran rhabdovirus 10 (HbDV10; species *Sigmavirus myga*) and Apis rhabdovirus 3 (ApRV3; species *Sigmavirus sichuan*).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicated that JPCGV1 and BtyrRV1 are most closely related to each other with 68.3% identity in the L protein, 44.1% identity in the G protein and 59.3% identity in the N protein (**Tables 13–15**).  Ecology  Most sigmaviruses identified to date infect flies (Diptera), other than ApRV3 which appears to infect bees. The natural host of YsRV is not known but is most likely to be an insect that has been devoured by birds. The detection of JPCGV1 and BtyrRV1 in dipteran flies is consistent with the ecology of most other sigmaviruses.  Species demarcation criteria  Viruses assigned to different species within the genus *Sigmavirus*have one or both of the following characteristics: A) minimum amino acid sequence divergence of 10% in L; and B) occupy different ecological niches as evidenced by differences in hosts.  The proposed members of the genus meet demarcation criterion A. As the viruses have been detected only by metagenomic sequencing, their natural ecology is uncertain but bat flies of the genus *Cyclopodia* (JPCGV1) and fruit flies of the genus *Bactrocera* (BtyrRV1) appear to represent novel hosts (criterion B). | |

**Supporting evidence**

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**Figure 1.** Schematic representation of (-) ssRNA ledantevirus genomes shown in reverse polarity. N, P, M, G and L represent ORFs encoding the structural proteins. Viruses in phylogroup B feature an ORF encoding a small protein following the *G* gene (red). An alternative ORF occurs in the *M* gene of Fukuoka virus (blue). The virus representing proposed new species is listed in red text.

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**Figure 2.** Schematic representation of (-) ssRNA lostrhavirus, tupavirus and almendravirus genomes shown in reverse polarity. N, P, M, G and L represent open reading frames (ORFs) encoding the structural proteins. Additional ORFs in tupaviruses and almendraviruses are coloured to indicate those which encode homologous proteins. The ORF following the *G* gene in all almendraviruses (yellow) encodes proteins with the structural properties of viroporins. The functions of other encoded proteins are not known. Viruses representing proposed new species are listed in red text.



**Figure 3.** Schematic representation of (-) ssRNA sigmavirus genomes shown in reverse polarity. N, P, M, G and L represent ORFs encoding the structural proteins. Homologous genes (*X*) that occur following the *P* gene of most sigmaviruses are shown in light blue. Viruses representing proposed new species are listed in red text.

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**Figure 4.** The evolutionary history was inferred from a MAFFT alignment of complete L protein sequences of 207 rhabdoviruses that are currently assigned or are proposed to be assigned to species in the subfamily *Alpharhabdovirinae* as well as 8 viruses to be assigned to new species in the genera *Ledantevirus*, *Sigmavirus*, *Tupavirus*, *Lostrhavirus* and *Almendravirus*. Phylogenetically informative sites were selected from the alignment using Trim Al resulting in 1642 positions in the final dataset. The tree was inferred in MEGAX by using the Maximum Likelihood method based on the best-fit Le and Gascuel model with gamma distribution of evolutionary rates and invariable sites. The tree with the highest log likelihood (-365703.14) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Several genera have been condensed together into single branches. Bootstrap values (100 iterations) are shown for each node.

**Table 1.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ledantevirus G protein sequences.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BARV | FUKV | NISV | NKOV | LqNcoLV1 | TrRTV2 | YjTV2 | KEUV | LDV | VAPV | KCV | MEBV | TYBV | KYAV | BUGV | WLFV5 | OITAV | WzRpuLV1 | KRV | FKRV | KOLEV |
| BARV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FUKV | 84.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NISV | 77.9 | 78.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NKOV | 47.1 | 46.8 | 49.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LqNcoLV1 | 40.8 | 41.4 | 41.6 | 43.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| TrRTV2 | 40.8 | 40.4 | 42.4 | 42.6 | 80.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YjTV2 | 38.3 | 40.7 | 39.0 | 40.2 | 42.0 | 40.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KEUV | 30.6 | 31.5 | 31.8 | 32.6 | 34.1 | 33.6 | 34.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LDV | 30.9 | 31.6 | 31.1 | 31.5 | 33.1 | 32.5 | 33.6 | 69.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VAPV | 33.6 | 33.6 | 33.0 | 34.7 | 31.6 | 32.2 | 36.2 | 57.0 | 58.2 |  |  |  |  |  |  |  |  |  |  |  |  |
| KCV | 33.8 | 34.8 | 33.5 | 33.0 | 32.3 | 33.5 | 36.2 | 48.5 | 49.1 | 51.4 |  |  |  |  |  |  |  |  |  |  |  |
| MEBV | 28.2 | 28.7 | 29.2 | 29.0 | 28.1 | 28.9 | 30.9 | 29.7 | 30.6 | 31.6 | 32.2 |  |  |  |  |  |  |  |  |  |  |
| TYBV | 29.8 | 31.9 | 30.0 | 30.8 | 28.1 | 28.5 | 29.8 | 30.8 | 30.2 | 32.8 | 29.9 | 64.4 |  |  |  |  |  |  |  |  |  |
| KYAV | 30.5 | 30.1 | 30.2 | 30.2 | 27.0 | 27.4 | 29.6 | 30.7 | 29.9 | 31.2 | 31.0 | 47.0 | 47.0 |  |  |  |  |  |  |  |  |
| BUGV | 29.9 | 31.4 | 30.5 | 31.0 | 28.7 | 29.5 | 30.0 | 30.8 | 30.1 | 32.9 | 32.1 | 45.8 | 47.4 | 70.0 |  |  |  |  |  |  |  |
| WLFV5 | 29.8 | 29.8 | 29.9 | 32.8 | 29.8 | 29.6 | 29.7 | 29.5 | 29.4 | 30.7 | 29.9 | 43.6 | 44.5 | 43.2 | 41.7 |  |  |  |  |  |  |
| OITAV | 25.9 | 25.7 | 26.5 | 27.7 | 27.7 | 26.6 | 28.3 | 26.4 | 24.5 | 26.8 | 25.5 | 30.0 | 31.9 | 30.6 | 29.8 | 29.5 |  |  |  |  |  |
| WzRpuLV1 | 27.8 | 28.0 | 28.4 | 26.4 | 26.2 | 25.8 | 27.4 | 26.5 | 26.6 | 25.2 | 25.6 | 30.4 | 31.9 | 31.0 | 30.2 | 28.7 | 58.0 |  |  |  |  |
| KRV | 25.0 | 25.4 | 24.5 | 23.8 | 22.4 | 21.6 | 25.4 | 24.4 | 24.9 | 24.6 | 27.0 | 26.8 | 26.4 | 28.7 | 27.9 | 25.0 | 32.4 | 34.3 |  |  |  |
| FKRV | 24.9 | 23.8 | 24.6 | 26.5 | 27.5 | 26.6 | 27.2 | 26.6 | 27.5 | 27.2 | 24.8 | 31.3 | 32.4 | 30.3 | 30.3 | 28.7 | 43.3 | 41.4 | 32.4 |  |  |
| KOLEV | 26.8 | 27.0 | 26.5 | 28.0 | 27.1 | 27.5 | 28.1 | 27.3 | 28.0 | 26.1 | 26.6 | 29.9 | 31.6 | 33.0 | 31.2 | 32.2 | 39.1 | 40.8 | 33.2 | 50.7 |  |

**Table 2.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of lednatevirus L protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BARV | FUKV | NISV | NKOV | LqNcoLV1 | TrRTV2 | YjTV2 | KEUV | LDV | VAPV | KCV | MEBV | TYBV | KYAV | BUGV | WLFV5 | OITAV | WzRpuLV1 | KRV | FKRV | KOLEV |
| BARV | 100. |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FUKV | 92.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NISV | 87.6 | 89.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NKOV | 61.4 | 61.8 | 61.1 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LqNcoLV1 | 55.4 | 55.1 | 55.6 | 56.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| TrRTV2 | 55.8 | 55.7 | 56.0 | 55.5 | 85.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YjTV2 | 54.1 | 54.0 | 54.2 | 54.3 | 53.8 | 53.4 | 100. |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KEUV | 50.5 | 51.2 | 51.0 | 51.1 | 49.2 | 49.2 | 50.2 | 10.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LDV | 50.0 | 50.2 | 49.9 | 50.4 | 49.1 | 49.0 | 50.2 | 80.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VAPV | 50.8 | 50.6 | 50.9 | 50.9 | 49.7 | 50.0 | 49.1 | 69.9 | 69.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| KCV | 50.2 | 50.7 | 50.9 | 51.1 | 49.8 | 49.8 | 50.5 | 62.9 | 62.8 | 63.1 | 100. |  |  |  |  |  |  |  |  |  |  |
| MEBV | 48.9 | 49.0 | 49.1 | 49.1 | 48.6 | 48.2 | 47.4 | 49.1 | 48.7 | 49.8 | 49.0 |  |  |  |  |  |  |  |  |  |  |
| TYBV | 49.1 | 49.2 | 49.0 | 49.5 | 48.3 | 48.2 | 48.2 | 48.9 | 48.6 | 50.0 | 48.3 | 75.5 | 10.0 |  |  |  |  |  |  |  |  |
| KYAV | 49.0 | 48.8 | 48.7 | 48.2 | 48.0 | 47.9 | 48.3 | 48.4 | 47.7 | 48.9 | 48.4 | 63.8 | 63.1 |  |  |  |  |  |  |  |  |
| BUGV | 46.7 | 47.0 | 46.9 | 47.5 | 47.7 | 47.8 | 47.2 | 47.8 | 47.4 | 47.8 | 47.6 | 62.8 | 62.0 | 71.6 |  |  |  |  |  |  |  |
| WLFV5 | 47.8 | 47.9 | 48.1 | 47.8 | 47.7 | 47.6 | 46.7 | 49.1 | 49.0 | 50.1 | 48.5 | 61.6 | 61.1 | 59.1 | 57.0 |  |  |  |  |  |  |
| OITAV | 48.0 | 48.1 | 47.8 | 48.1 | 46.9 | 46.7 | 46.9 | 47.7 | 47.8 | 50.0 | 48.7 | 54.9 | 54.9 | 53.6 | 52.6 | 55.8 | 100.0 |  |  |  |  |
| WzRpuLV1 | 47.2 | 47.8 | 47.7 | 47.1 | 46.8 | 46.8 | 47.1 | 48.7 | 48.2 | 49.7 | 48.0 | 54.9 | 55.1 | 54.2 | 52.9 | 56.3 | 74.1 |  |  |  |  |
| KRV | 47.7 | 47.5 | 46.9 | 47.1 | 46.4 | 46.4 | 48.2 | 49.1 | 49.1 | 50.1 | 48.6 | 55.7 | 55.4 | 54.8 | 53.6 | 55.3 | 63.2 | 63.2 | 100. |  |  |
| FKRV | 47.8 | 47.6 | 47.8 | 47.0 | 46.6 | 46.4 | 46.7 | 47.8 | 47.1 | 48.7 | 48.4 | 54.9 | 53.6 | 53.1 | 52.3 | 53.8 | 62.2 | 62.8 | 61.6 |  |  |
| KOLEV | 47.4 | 48.0 | 47.6 | 48.3 | 47.2 | 46.9 | 47.8 | 49.4 | 48.5 | 49.6 | 49.2 | 55.1 | 54.7 | 54.7 | 53.4 | 54.3 | 62.2 | 63.0 | 62.6 | 75.3 | 100.0 |

**Table 3.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of lednatevirus N protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BARV | FUKV | NISV | NKOV | LqNcoLV1 | TrRTV2 | YjTV2 | KEUV | LDV | VAPV | KCV | MEBV | TYBV | KYAV | BUGV | WLFV5 | OITAV | WzRpuLV1 | KRV | FKRV | KOLEV |
| BARV | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FUKV | 96.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NISV | 94.1 | 95.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NKOV | 76.2 | 77.2 | 75.5 | 100. |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LqNcoLV1 | 52.5 | 53.0 | 52.3 | 52.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| TrRTV2 | 52.5 | 52.7 | 52.0 | 52.5 | 92.7 | 100. |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YjTV2 | 52.7 | 53.0 | 52.7 | 53.4 | 47.6 | 47.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KEUV | 39.4 | 39.4 | 38.9 | 40.1 | 40.4 | 39.7 | 38.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LDV | 39.1 | 39.1 | 38.4 | 39.6 | 41.1 | 39.7 | 38.8 | 80.7 | 100. |  |  |  |  |  |  |  |  |  |  |  |  |
| VAPV | 42.7 | 42.0 | 41.8 | 43.9 | 40.1 | 39.2 | 38.1 | 62.5 | 63.9 |  |  |  |  |  |  |  |  |  |  |  |  |
| KCV | 39.9 | 40.4 | 39.0 | 40.4 | 38.1 | 37.6 | 39.1 | 46.9 | 47.9 | 47.9 |  |  |  |  |  |  |  |  |  |  |  |
| MEBV | 41.4 | 41.0 | 40.7 | 40.2 | 42.5 | 42.3 | 39.4 | 41.4 | 40.7 | 37.1 | 37.7 | 10.0 |  |  |  |  |  |  |  |  |  |
| TYBV | 41.0 | 40.5 | 40.0 | 39.5 | 42.0 | 41.3 | 38.2 | 41.9 | 40.0 | 37.9 | 37.4 | 87.1 |  |  |  |  |  |  |  |  |  |
| KYAV | 39.8 | 40.0 | 39.3 | 39.5 | 40.4 | 39.4 | 38.2 | 41.2 | 38.8 | 36.9 | 35.8 | 75.2 | 77.3 | 100.0 |  |  |  |  |  |  |  |
| BUGV | 39.5 | 40.0 | 39.0 | 40.7 | 39.0 | 38.0 | 37.1 | 38.6 | 37.1 | 37.6 | 37.0 | 74.7 | 75.9 | 85.2 |  |  |  |  |  |  |  |
| WLFV5 | 38.1 | 37.9 | 38.1 | 38.8 | 39.2 | 38.5 | 36.1 | 39.8 | 38.8 | 38.3 | 37.0 | 72.6 | 72.6 | 67.4 | 69.3 |  |  |  |  |  |  |
| OITAV | 37.9 | 37.6 | 37.1 | 37.9 | 42.0 | 40.9 | 36.1 | 39.2 | 39.4 | 35.6 | 38.8 | 55.0 | 55.0 | 51.5 | 53.2 | 52.2 | 100.0 |  |  |  |  |
| WzRpuLV1 | 37.9 | 37.4 | 36.4 | 37.9 | 41.8 | 40.9 | 37.8 | 39.2 | 39.4 | 37.1 | 37.4 | 54.1 | 54.8 | 52.2 | 50.6 | 51.1 | 71.2 |  |  |  |  |
| KRV | 41.7 | 41.0 | 40.0 | 42.1 | 40.4 | 39.9 | 38.7 | 39.5 | 39.3 | 35.5 | 38.2 | 60.2 | 61.4 | 57.6 | 56.0 | 58.3 | 58.3 | 53.6 | 100. |  |  |
| FKRV | 40.2 | 40.0 | 40.2 | 40.2 | 39.0 | 38.2 | 40.9 | 36.7 | 37.1 | 35.0 | 36.7 | 60.4 | 60.0 | 58.1 | 57.8 | 56.7 | 56.4 | 55.0 | 60.0 |  |  |
| KOLEV | 39.9 | 39.9 | 40.1 | 40.1 | 42.4 | 41.0 | 39.8 | 38.7 | 39.9 | 37.5 | 38.7 | 62.4 | 61.3 | 60.1 | 58.2 | 62.4 | 57.7 | 55.6 | 63.4 | 73.7 | 100. |

**Table 4.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of lostrhavirus G protein sequences.

|  |  |  |  |
| --- | --- | --- | --- |
|  | LSTRV | XjTRV | ATRV |
| LSTRV |  |  |  |
| XjTRV | 41.1 |  |  |
| ATRV | 41.5 | 59.4 |  |

**Table 5.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of lostrhavirus L protein sequences.

|  |  |  |  |
| --- | --- | --- | --- |
|  | LSTRV | XjTRV | ATRV |
| LSTRV |  |  |  |
| XjTRV | 58.1 |  |  |
| ATRV | 57.5 | 72.8 |  |

**Table 6.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of lostrhavirus N protein sequences.

|  |  |  |  |
| --- | --- | --- | --- |
|  | LSTRV | XjTRV | ATRV |
| LSTRV |  |  |  |
| XjTRV | 40.0 |  |  |
| ATRV | 38.6 | 67.2 |  |

**Table 7.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of tupavirus G protein sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | DURV | KLAV | TUPVSB | TUPV | WzMlaTV1 | BtTVBS2 | WfRpeTV1 | BtTVBS1 |
| DURV |  |  |  |  |  |  |  |  |
| KLAV | 19.0 |  |  |  |  |  |  |  |
| TUPVSB | 23.0 | 51.0 |  |  |  |  |  |  |
| TUPV | 25.5 | 28.1 | 26.6 |  |  |  |  |  |
| WzMlaTV1 | 24.9 | 25.6 | 28.2 | 40.3 |  |  |  |  |
| BtTVBS2 | 27.1 | 30.4 | 29.3 | 40.6 | 51.6 |  |  |  |
| WfRpeTV1 | 26.9 | 29.4 | 30.4 | 41.9 | 50.9 | 75.2 |  |  |
| BtTVBS1 | 25.7 | 29.2 | 29.1 | 40.9 | 51.6 | 67.5 | 75.2 |  |

**Table 8.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of tupavirus L protein sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | DURV | KLAV | TUPVSB | TUPV | WzMlaTV1 | BtTVBS2 | WfRpeTV1 | BtTVBS1 |
| DURV |  |  |  |  |  |  |  |  |
| KLAV | 52.6 |  |  |  |  |  |  |  |
| TUPVSB | 52.1 | 68.9 |  |  |  |  |  |  |
| TUPV | 52.6 | 56.5 | 56.1 |  |  |  |  |  |
| WzMlaTV1 | 53.5 | 59.0 | 57.3 | 61.7 |  |  |  |  |
| BtTVBS2 | 54.5 | 58.1 | 57.0 | 62.4 | 63.6 |  |  |  |
| WfRpeTV1 | 53.9 | 57.8 | 57.3 | 62.8 | 63.6 | 72.5 |  |  |
| BtTVBS1 | 53.1 | 59.3 | 57.7 | 62.0 | 63.3 | 71.3 | 75.5 |  |

**Table 9.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of tupavirus N protein sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | DURV | KLAV | TUPVSB | TUPV | WzMlaTV1 | BtTVBS2 | WfRpeTV1 | BtTVBS1 |
| DURV |  |  |  |  |  |  |  |  |
| KLAV | 47.1 |  |  |  |  |  |  |  |
| TUPVSB | 48.3 | 71.4 |  |  |  |  |  |  |
| TUPV | 57.1 | 55.1 | 55.3 |  |  |  |  |  |
| WzMlaTV1 | 53.6 | 52.1 | 53.0 | 70.2 |  |  |  |  |
| BtTVBS2 | 55.5 | 51.6 | 53.0 | 68.1 | 67.2 |  |  |  |
| WfRpeTV1 | 55.2 | 52.6 | 55.3 | 67.2 | 66.7 | 81.4 |  |  |
| BtTVBS1 | 53.8 | 52.1 | 56.0 | 67.7 | 66.5 | 80.9 | 85.6 |  |

**Table 10.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of almendravirus G protein sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | ABTV | SxABTV | PTAMV | CBV | MRV | BALV | RCHV | XsRLV1 |
| ABTV | 10.0 |  |  |  |  |  |  |  |
| SxABTV | 84.2 |  |  |  |  |  |  |  |
| PTAMV | 37.0 | 36.2 |  |  |  |  |  |  |
| CBV | 20.7 | 21.4 | 21.9 | 1000 |  |  |  |  |
| MRV | 22.9 | 22.4 | 22.0 | 36.9 |  |  |  |  |
| BALV | 19.7 | 19.7 | 22.8 | 22.3 | 23.0 | 1000 |  |  |
| RCHV | 25.6 | 24.7 | 24.3 | 25.5 | 24.4 | 24.7 |  |  |
| XsRLV1 | 23.3 | 23.7 | 24.3 | 25.7 | 25.3 | 26.6 | 37.8 | 100. |

**Table 11.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of almendravirus L protein sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | ABTV | SxABTV | PTAMV | CBV | MRV | BALV | RCHV | XsRLV1 |
| ABTV | 100. |  |  |  |  |  |  |  |
| SxABTV | 90.6 |  |  |  |  |  |  |  |
| PTAMV | 63.9 | 64.1 |  |  |  |  |  |  |
| CBV | 41.8 | 41.5 | 42.5 | 1000 |  |  |  |  |
| MRV | 41.5 | 41.2 | 41.6 | 58.3 |  |  |  |  |
| BALV | 44.1 | 44.5 | 45.3 | 44.4 | 43.9 | 10.0 |  |  |
| RCHV | 46.0 | 45.7 | 46.0 | 45.4 | 45.1 | 54.3 |  |  |
| XsRLV1 | 45.7 | 45.8 | 46.8 | 44.8 | 44.6 | 52.5 | 62.9 | 100.0 |

**Table 12.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of almendravirus N protein sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | ABTV | SxABTV | PTAMV | CBV | MRV | BALV | RCHV | XsRLV1 |
| ABTV | 100.0 |  |  |  |  |  |  |  |
| SxABTV | 94.0 |  |  |  |  |  |  |  |
| PTAMV | 61.4 | 60.7 |  |  |  |  |  |  |
| CBV | 24.2 | 24.6 | 23.5 | 10.0 |  |  |  |  |
| MRV | 25.1 | 24.9 | 23.0 | 34.7 |  |  |  |  |
| BALV | 25.9 | 25.9 | 25.9 | 26.4 | 28.6 | 1000 |  |  |
| RCHV | 23.3 | 22.6 | 24.5 | 25.5 | 27.5 | 32.5 |  |  |
| XsRLV1 | 24.5 | 24.1 | 22.7 | 27.9 | 27.8 | 33.5 | 57.7 | 10.0 |

**Table 13.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of sigmavirus G protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SyFV2 | WhFV2 | YsRV | HbDV10 | WhHFV1 | HbDV9 | ApRV3 | JPCGV1 | BtyrRV1 | DObsSV | DImmSV | DAnaSV | DStuSV | DAffSV | CCapSV | HbDRV1 | DMelSV | ADMSV | WhLFV9 | WhLFV10 |
| SyFV2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 67.9 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YsRV | 58.4 | 59.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 36.1 | 35.8 | 37.1 | 100. |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 26.9 | 23.9 | 27.3 | 26.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 26.7 | 26.3 | 28.0 | 28.2 | 22.0 | 10.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ApRV3 | 31.0 | 29.3 | 30.9 | 30.4 | 26.4 | 27.2 | 10.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JPCGV1 | 23.7 | 22.9 | 25.9 | 24.1 | 21.6 | 24.0 | 22.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BtyrRV1 | 23.3 | 22.9 | 23.2 | 23.6 | 21.2 | 22.2 | 19.0 | 44.1 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 20.0 | 21.8 | 22.7 | 19.9 | 22.6 | 18.9 | 19.7 | 21.4 | 20.9 | 100.0 |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 20.8 | 20.8 | 21.5 | 20.9 | 24.1 | 19.5 | 20.5 | 20.6 | 21.0 | 36.2 |  |  |  |  |  |  |  |  |  |  |
| DAnaSV | 23.0 | 22.0 | 21.1 | 24.5 | 22.7 | 20.3 | 20.8 | 23.5 | 22.4 | 20.2 | 19.4 | 100.0 |  |  |  |  |  |  |  |  |
| DStuSV | 25.0 | 25.5 | 25.8 | 24.0 | 23.3 | 22.1 | 21.7 | 22.5 | 19.2 | 21.0 | 20.3 | 19.2 |  |  |  |  |  |  |  |  |
| DAffSV | 23.3 | 26.0 | 25.2 | 24.7 | 23.3 | 21.9 | 21.6 | 19.4 | 18.6 | 20.3 | 18.1 | 20.5 | 46.2 |  |  |  |  |  |  |  |
| CCapSV | 21.2 | 22.3 | 21.7 | 23.0 | 22.8 | 20.6 | 21.5 | 22.4 | 20.9 | 20.4 | 21.3 | 22.1 | 20.4 | 19.1 | 100. |  |  |  |  |  |
| HbDRV1 | 20.4 | 21.2 | 21.7 | 22.6 | 24.1 | 23.7 | 20.1 | 25.4 | 25.0 | 21.8 | 19.6 | 23.4 | 19.9 | 20.4 | 25.1 |  |  |  |  |  |
| DMelSV | 20.7 | 21.2 | 22.4 | 23.8 | 22.5 | 21.3 | 22.1 | 26.0 | 25.2 | 21.3 | 20.2 | 23.1 | 23.0 | 24.0 | 26.6 | 27.1 | 100.0 |  |  |  |
| ADMSV | 22.1 | 21.3 | 20.2 | 22.5 | 19.0 | 18.8 | 21.2 | 23.2 | 23.7 | 18.0 | 18.7 | 20.6 | 18.3 | 18.8 | 20.7 | 22.2 | 20.5 |  |  |  |
| WhLFV9 | 19.3 | 19.9 | 20.6 | 18.1 | 23.1 | 21.2 | 21.2 | 20.8 | 22.9 | 20.3 | 20.2 | 22.0 | 19.1 | 17.9 | 24.2 | 24.2 | 22.5 | 19.9 |  |  |
| WhLFV10 | 20.1 | 19.9 | 21.6 | 20.7 | 21.0 | 23.0 | 20.7 | 22.5 | 20.8 | 19.8 | 21.2 | 20.2 | 20.9 | 19.1 | 23.5 | 23.1 | 23.6 | 22.1 | 35.1 | 0.0 |

**Table 14.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of sigmavirus L protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SyFV2 | WhFV2 | YsRV | HbDV10 | WhHFV1 | HbDV9 | ApRV3 | JPCGV1 | BtyrRV1 | DObsSV | DImmSV | DAnaSV | DStuSV | DAffSV | CCapSV | HbDRV1 | DMelSV | ADMSV | WhLFV9 | WhLFV10 |
| SyFV2 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 82.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YsRV | 74.0 | 73.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 53.1 | 52.6 | 52.4 | 100. |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 50.9 | 51.2 | 50.0 | 52.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 50.4 | 50.3 | 51.3 | 52.5 | 51.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ApRV3 | 48.6 | 49.2 | 47.8 | 48.8 | 46.4 | 46.0 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JPCGV1 | 46.9 | 46.1 | 46.9 | 46.5 | 45.3 | 47.2 | 43.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BtyrRV1 | 47.6 | 47.4 | 47.0 | 46.8 | 45.7 | 47.4 | 43.7 | 68.3 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 43.2 | 43.3 | 43.5 | 42.4 | 41.5 | 44.1 | 41.5 | 43.2 | 43.7 |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 42.5 | 42.1 | 41.9 | 41.8 | 42.7 | 43.4 | 41.4 | 43.0 | 43.6 | 55.1 | 100.0 |  |  |  |  |  |  |  |  |  |
| DAnaSV | 43.9 | 43.9 | 43.0 | 45.4 | 42.6 | 43.7 | 41.7 | 43.9 | 43.0 | 41.3 | 41.9 |  |  |  |  |  |  |  |  |  |
| DStuSV | 41.9 | 42.3 | 42.5 | 43.7 | 41.8 | 42.7 | 39.8 | 42.3 | 42.4 | 41.1 | 39.8 | 41.3 |  |  |  |  |  |  |  |  |
| DAffSV | 41.4 | 41.9 | 41.7 | 43.7 | 41.7 | 41.8 | 40.2 | 41.7 | 42.2 | 40.7 | 39.0 | 41.0 | 60.3 | 100.0 |  |  |  |  |  |  |
| CCapSV | 43.8 | 43.6 | 43.3 | 44.8 | 43.9 | 43.3 | 41.0 | 44.2 | 43.6 | 40.8 | 41.4 | 42.1 | 40.8 | 40.5 |  |  |  |  |  |  |
| HbDRV1 | 43.0 | 42.9 | 42.3 | 43.2 | 42.1 | 42.3 | 41.2 | 43.4 | 42.7 | 40.8 | 41.3 | 41.5 | 40.7 | 39.7 | 47.6 | 100.0 |  |  |  |  |
| DMelSV | 42.5 | 42.1 | 42.5 | 43.0 | 41.3 | 42.8 | 40.6 | 43.7 | 41.7 | 41.1 | 41.0 | 40.9 | 40.6 | 39.1 | 48.1 | 48.9 |  |  |  |  |
| ADMSV | 43.5 | 42.7 | 44.0 | 42.8 | 43.0 | 42.7 | 40.3 | 43.5 | 43.1 | 41.4 | 41.4 | 39.8 | 40.1 | 38.4 | 50.6 | 50.0 | 50.1 |  |  |  |
| WhLFV9 | 42.5 | 41.6 | 41.8 | 42.4 | 42.1 | 41.8 | 39.9 | 43.5 | 43.5 | 40.8 | 40.6 | 41.1 | 40.8 | 40.1 | 49.8 | 50.8 | 51.2 | 52.0 | 1000 |  |
| WhLFV10 | 42.6 | 42.5 | 41.9 | 42.5 | 42.5 | 42.3 | 39.7 | 43.5 | 43.3 | 41.3 | 40.5 | 41.7 | 40.5 | 39.7 | 49.5 | 50.4 | 50.9 | 51.7 | 67.6 |  |

**Table 15.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of sigmavirus N protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SyFV2 | WhFV2 | YsRV | HbDV10 | WhHFV1 | HbDV9 | ApRV3 | JPCGV1 | BtyrRV1 | DObsSV | DImmSV | DAnaSV | DStuSV | DAffSV | CCapSV | HbDRV1 | DMelSV | ADMSV | WhLFV9 | WhLFV10 |
| SyFV2 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 83.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YsRV | 65.5 | 65.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 34.6 | 34.4 | 33.8 | 100. |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 28.5 | 28.0 | 28.5 | 27.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 31.0 | 30.1 | 30.8 | 28.1 | 27.9 | 1000 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ApRV3 | 24.9 | 24.4 | 24.2 | 24.2 | 22.9 | 27.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JPCGV1 | 28.8 | 29.5 | 29.3 | 28.3 | 26.1 | 28.6 | 25.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BtyrRV1 | 29.1 | 27.9 | 30.8 | 27.9 | 23.6 | 27.8 | 23.6 | 59.3 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 19.9 | 20.5 | 21.7 | 19.1 | 18.5 | 20.9 | 17.4 | 21.6 | 24.1 |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 21.5 | 21.8 | 22.0 | 20.3 | 20.0 | 22.8 | 20.0 | 24.9 | 24.2 | 43.5 |  |  |  |  |  |  |  |  |  |  |
| DAnaSV | 27.0 | 26.5 | 26.0 | 24.1 | 23.2 | 21.9 | 18.3 | 26.7 | 24.9 | 22.9 | 21.7 | 100.0 |  |  |  |  |  |  |  |  |
| DStuSV | 26.6 | 27.5 | 26.4 | 25.5 | 23.2 | 23.5 | 23.1 | 25.9 | 23.9 | 20.6 | 19.9 | 23.3 |  |  |  |  |  |  |  |  |
| DAffSV | 27.0 | 27.7 | 28.4 | 25.6 | 23.9 | 24.4 | 25.9 | 25.8 | 24.7 | 23.4 | 19.8 | 23.1 | 43.3 | 100. |  |  |  |  |  |  |
| CCapSV | 22.3 | 22.3 | 20.9 | 21.1 | 19.1 | 23.7 | 19.9 | 22.6 | 22.8 | 21.2 | 22.0 | 19.4 | 20.8 | 21.0 |  |  |  |  |  |  |
| HbDRV1 | 19.7 | 19.0 | 20.7 | 19.9 | 21.1 | 18.5 | 20.0 | 19.7 | 19.7 | 18.5 | 16.4 | 19.3 | 18.3 | 20.8 | 24.1 |  |  |  |  |  |
| DMelSV | 22.6 | 21.2 | 24.2 | 22.1 | 23.6 | 21.8 | 23.4 | 21.3 | 21.5 | 21.8 | 19.6 | 19.6 | 20.8 | 20.0 | 30.3 | 24.9 | 100.0 |  |  |  |
| ADMSV | 23.8 | 23.8 | 23.6 | 22.6 | 24.9 | 20.5 | 22.6 | 22.4 | 21.1 | 20.0 | 20.0 | 20.0 | 22.5 | 21.1 | 29.4 | 25.1 | 29.6 |  |  |  |
| WhLFV9 | 24.2 | 24.5 | 23.8 | 21.8 | 22.0 | 20.9 | 19.3 | 24.8 | 24.9 | 20.4 | 19.2 | 21.9 | 22.9 | 21.7 | 27.9 | 21.3 | 33.9 | 27.3 | 100.0 |  |
| WhLFV10 | 22.6 | 23.5 | 22.8 | 20.2 | 22.0 | 23.4 | 21.6 | 25.5 | 25.2 | 21.1 | 19.4 | 19.4 | 20.6 | 22.4 | 27.4 | 24.5 | 34.5 | 29.7 | 50.0 | 100.0 |

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