

## **SUPPLEMENTARY INFORMATION**

### **Title**

Revisiting the genetic diversity of emerging hantaviruses circulating in Europe using a pan-viral resequencing microarray

### **Authors**

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## SUPPLEMENT 1

### List of hantavirus sequences tiled on the 3rd generation resequencing microarray (PathogenID v3.0).

The number of the sequence is referred to the position on the pan-viral chip (total number: 838 sequences). Sequences are named as in the NCBI database (Description and Accession number) or according to laboratory nomenclature, for the sequences experimentally obtained at the laboratory. The size of hantavirus sequences tiled on the microarray is in most cases 425 nucleotides (nt), except for the sequence >seq234 (251 nt), and sequences from position >seq238 to >seq243 (303 nt). Complementary information is found in Table 1.

#### >seq222Puumalavirus\_RNA\_for\_nucleocapsid\_protein\_CG1444\_AJ277075

ACTGGTATAACAATTGGAGTGTATGTTATAGGCTTCACACTTCCTATTATCCTGAAGGCTCTATATAT  
GTTGTCAACACGTGGGAGACAAACTGTGAAAGAAAACAAAGGGACTCGTATCCGTTTTAAAGATG  
ACACTTCCTTCGAGGACATTAATGGTATCAGGAGACCGAAGCACCTATATGTTCCATGCCTACTG  
CTCAATCAACTATGAAGGCTGAAGAAGTACCCCTGGGCGATTTAGAACCATAGTATGCGGTCTAT  
TTCCGACTCAAATCAAGTACGCAACATAATGAGCCCTGTAATGGGAGTCATTGGTTTTCTTTTT  
TGTC AAGGACTGGGCAGATCGGATTAGGGAATTCATGGAAAAAGAGTGCCCTTTTATCAAACCAG  
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#### >seq223Puumalavirus\_CG13891\_RNA\_nucleocapsid\_protein\_gene\_U22423

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TCCCAACTCAAATCAAGTGCCTAACATAATGAGTCTGTAAATGGGAGTAATTGGCTTCTCTTTTT  
CGTTAAAGACTGGGCAGATCGGATTAGAGAATCTATGGAAAAAGAGTGCCCTTTCTAAAACCAG  
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#### >seq224Puumalavirus\_Bavaria\_CG9/04\_AY954722\_nucleocapsid\_protein

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TTCCA ACTCAGATTCAAGTACGTAATATAATGAGTCTGTGATGGGAGTCATCGGTTTTTCTTTCTT  
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#### >seq225Puumalavirus\_Sotkamo\_NC\_005224

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TTCCCACTCAGATCCAGGTTTCGTAACATCATGAGTCCAGTTATGGGGGTCATTGGTTTTTCTTTCTT  
TGTGAAGGATTGGTCTGAGAGAATCAGAGAGTTCATGGAAAAAGAGTGCCCATTCATAAAGCCTG  
AAGTAAAACCAGGCACACCAGCACAGGAG

#### >seq226Puumalavirus\_Puu/Kazan\_Z84204

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#### >seq227Puumalavirus\_Umea/hu\_AY526219

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TGTTAAGGACTGGCCAGACAGGATAAGAGAGTTTATGGAAAAGGAATGCCCATTTATAAAGCCAG  
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**>seq228 Puumalavirus\_PUU/Ernstbrunn/Cg641/1995\_AJ888752**

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CCCAGTCAACAATGAAGGCAGAAAAGCTTACTCCAGGTAGGTTTCGGACAATTGTGTGTGGTCTTT  
TCCCAACTCAGATTCAGGTGCGCAACATTATGAGTCCCTGTAATGGGGGTTATAGGATTCTCTTTTT  
TGTAAGGATTGGTCAGAGAGGGTAAGAGATTTTATGGAGAAAGAATGCCCTTTTATAAACCAG  
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**>seq229 Puumalavirus\_Berkel\_L36943**

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**>seq230 Puumalavirus\_Couvin/59Cg/97\_AJ277034**

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TGTCAAGGACTGGGCAGATCGGATTAGGGAGTTCATGGAAAAAGAGTGCCCTTTTATCAAACCAG  
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**>seq231 Puumalavirus\_Pallasjarvi/63Cg/98\_AJ314598**

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CCCAGTCAACCATGAAGGCAGAAGAACTCACACCAGGTAGATTTTCGTACAATAGTATGTGGTCTAT  
TTCCAACTCAGATTCAAAGTCCGTAACATCAGTCCAGTAATGGGGGTTATTGGGTTTTCATTTTT  
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**>seq232 Puumalavirus\_Munga/Mg16/05\_GQ339487**

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ACACCTCATTGGAAGACATCAATGGCATTAGGAGACCAAAGCACTTATATGTGTCTATGCCACAG  
CACAGTCAACAATGAAAGCAGAAGAGTTAACACCAGGTCGATTCCGGACAATAGTATGTGGCCTA  
TTCCCTACCCAGATTCAAGTACGTAATATAATGAGTCCAGTTATGGGGGTCATTGGCTTTTCTTTCT  
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**>seq233 Puumalavirus\_PUU/Mignovillard/CgY02/2005\_AM695638**

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TTCCAACTCAAATCAAGTGCGAAACATAATGAGTCCCTGTGATGGGAGTCATCGGGTTTTCATTTTT  
TGTTAAGGATTGGACAGATCGGATTAGGGAATTTATGGAAAAAGGAATGCCCTTTTATAAACCAG  
GATGAAACCGGGAACACCAGCCCAAGAA

**>seq234 Puumalavirus\_strainFrance/Perpignan1999\_nucleocapsid\_protein\_gene\_partial**

ATGAGTGACTTGACAGACATTCAGGAAGATATAACCCGCCATGAGCAACAACCTTGTGTGCCAGA  
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**>seq235 Puumala\_Fusong90006\_EF488806**

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>seq236Puumala\_CH-214\_Franche\_Comb

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>seq238Puumala\_167-2Charleville-Mezieres

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>seq240Puumala\_178-2Charleville-Mezieres

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>seq241Puumala\_180-78Charleville-Mezieres

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>seq242Puumala\_RU-11Ruminy-Troyes

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>seq243Puumala\_OR-52\_Orleans

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>seq244Pulmonary\_syndrome\_hantavirus\_ConvictCreek107\_L33683

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**>seq245DobravaBelgrade\_L41916**

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**>seq246Dobrava\_Esl/81Aa/01\_AY533120**

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**>seq247Saarema\_virus\_AJ616854**

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**>seq248Kenkemevirus\_MSB148794\_GQ306148**

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**>seq249Hantaan\_M14626\_reference**

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**>seq252Hantaan\_AA2499\_AF427320**

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**>seq253Hantaan\_CGHu1\_EU092218**

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**>seq254Hantaan\_Q32\_AB027097**

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**>seq255Hantavirus\_Z37\_AF187082**

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CCCAATCCAGCATGAAAGCTGAAGAGATAACACCTGGAAGATTCCGCACAGCAGTATGCGGGCTA  
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**>seq256Hantavirus\_Nc167\_AB027523**

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**>seq257Hantavirus\_L99\_AF488708**

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GTTAACAACAAGAGGCAGGCAGACTTCAAAGGACAACAAGGGGATGAGGATCAGATTCAAGGAT  
GACAGCTCATATGAGGATGTCAATGGAATCAGAAAACCCAAGCATCTGTATGTGTCAATGCCAAA  
CGCCCAATCCAGCATGAAGGCTGAAGAGATAACACCTGGAAGATTCCGCACACTGCAGTATGTGGGC  
TATATCCTGCACAGATAAAGGCAAGGAACATGGTGAGCCCTGTCATGAGTGTAGTTGGGTTTTTGG  
CACTGGCAAAGATTGGACATCTAGAATTGAAGAATGGCTTGGTGCACCCTGCAAGTTTATGGCGG  
AATCTCCAATTGCTGGGAGTTTATCTGGGAAT

**>seq258Seoul\_8039\_NC005236**

ATTGGCTGACTATAATTGTCTATCTAACATCATTGTTGGTCCCGATCATCTTGAAGGCACTGTACAT  
GTTAACAACAAGAGGTAGGCAGACTTCAAAGGACAACAAGGGGATGAGGATCAGATTCAAGGAT  
GACAGCTCATATGAGGATGTCAATGGGATCAGAAAAGCCTAAACATCTGTATGTGTCAATGCCAAA  
GCCCAATCCAGTATGAAGGCTGAAGAGATAACACCAGGAAGATTCCGCACACTGCAGTATGTGGGCT  
ATATCCTGCACAGATAAAGGCAAGGAATATGGTAAGCCCTGTCATGAGTGTAGTTGGGTTTTTGGC  
ACTAGCAAAGACTGGACATCTAGAATTGAAGAATGGCTTGGCGCACCTGCAAGTTTATGGCAG  
AGTCTCCTATTGCTGGGAGTTTATCTGGGAAT

**>seq259Asamavirus\_N10\_EU929072**

ATTGGATTTTCGATTATCACATATCTGATAGCATTGTGGATGTTATTCTTCTTAAAGGCCTTTATATG  
CTAACTACCAGAGGTAGACAAACAATTAAGGACAACAAGGGACAAGAATTAGGCTTAAAGATGA  
CTCATCTTATATTGAAGTCAATGGGATCCGAAAACCTAAGCACTTATATATTTCCCTCCCTAATGCA  
CAGTCAAGTATGAGAGCAGAGGAATTAACCTCCAGGTAGGTACCGGACAGTGATTGTGGATTGTAT  
CCAGCACAAATAAAAAGCAAAGAGTATGATTAGCCCTGTAATGGGAGTTATTGGATTCCCGAAATTG  
TCTAAAGACTGGGATAAACGAATTAATGATTTTTTAAAGAAGATTGTCCATTTCTTCGACCTGTAG  
CTTTCCAGCCCTTTTCTTTGACAGAT

**>seq260Novavirus\_MSB95703\_FJ539178**

ACTGGGTTGCAATTTGTACTTACATTTTAGGATTTGGTGCTACAATTCTTCTCAAAGCACTTTATAT  
GTTAACTACACGTGGCAGACAGACCATTAAGAGCATAAAGGGTAATCGGGTTCGATTTTCGTGATGA  
TTCATCATTTATTGAGAAAAGGTGGTGTAAAGTCCCAAAGCATCTTTATGTTTCACTTCCAACAGCT  
CAATCTGCAATAAAGGCAGAGAAGAACTACTCCAGGGAGATTCAGGACCATTGTTTGTGGATTATAC  
CCCTCGAGGCAAAGTGCAGCGGGCTGATAAGTCTGTTATGGGAGTGATAGGCTTTCAATATATG  
GCACAGAATTGGAGTGAAATGATTCATAAGTTCATGCATATGAGGTGCCATTTCATTGAAGCCCT  
AGCCTACAGTTGATTCTGCTCTCTTA

**>seq261ProspectHill\_M34011**

ATTGGCTTAAGATTGGCAGCTACATCATAGAATTTGCACTACCTATCATCTTGAAAGCCTTGCAAT  
GTTGTCAACTAGAGGGAGGCAAACCTGTAAGAGAGAATAAGGGGACAAGGATCAGGTTCAAAGAT  
GATAGTTCCTATGAAGATGTGAATGGCATTAGACGCCCAAAGCACCTTTATGTGTCTATGCCAACA  
GCCAGTCAACAATGAAAGCTGAGGAATTAACACCAGGGAGATTCAGGACAATTGTTTGTGGACT  
ATTTCTGCACAGATCATGGCAAGAAATATCATCAGTCTGTAATGGGTGTGATCGGATTTGCATTT  
TTTGTAAGGATTGGGCTGACAAAGTAAAGGCATTTCTTGACCAGAAATGTCCATTCTCAAAGGCT  
GAGCCACGTCTGGACAGCCTGCCGGTGAA

**>seq262Soochong\_SC-1\_AY675349\_mRNA**

ACTGGCTGAGCATTGTTGTTTATCTTACATCCTTTGTGGTTCGGATACTCCTGAAAGCCCTTTACAT  
GCTGACAACAAGGGGAAGACAGACAATAAGGACAATAAAGGGACAAGAATCCGATTCAAAGAT  
GACAGCTCTTTGAAGATGTGAATGGAATTCGGAAGCCGAAACATCTCTATGTGTCTTTACCTAAT  
GCACAGTCTAGTATGAAGGCAGAAGAGATAACACCTGGAAGGTACAGGACAGCAATCTGTGGATT  
ATACCTGCTCAGATTAAGCCAGACAGATGGTAAGCCAGTCATGAGTGTAATTGGATTCTTTCG  
CTTGCTAAAGACTGGGGTGATAGGATTGAGCAGTGGCTAAGTGAACCTGTAAGCTCCTCCCAGA  
CACAGCAGCAGTAAGCCTCCATGGTGGTCTT

**>seq263Tula\_Sennickerode\_Sen05/204\_EU439950**

ATTGGTTTTTCGATTGGGCAATACATCATTGGGTTTGCCTACTGGCTATTGTCTTAAAGGCATTGTACAT  
GTTGTCAACTCGTGGAAGGCAGACAATTAAGAGAGAACAAGGCCTAGAAATTAGGTTAAGGATG  
ACAGTCTGTTTTGAAGAAATTAACGGGATAAGGGGACCAAAGCATTATATGTCTCAATGCCAACTG  
CCAATCCACCATGAAAGCTGATGAGTTAACACCAGGCAGGTTTAGGACAATTGTGTGTGGATTAT  
TCCCTGCTCAGATAATGCACAGGAATATAATAAGTCTGTCATGGGTGTGATTGGATTCTCCTTCTT  
TGTCAGGACTGGCCGGACAAGATTGAAGAATTTCTCATAAAACCTTGCCCATTCCTAAAGAAACA  
AGGTGGCCCAACAAGGATGAAGACTTT

**>seq264Tula\_Kosice144/Ma/95\_Y13979**

ACTGGTCTCCATTGGACAATACATTATAGGGTTTGCCTAGCAATAGTCCTAAAGGCATTATACA  
TGTTATCAACAAGAGGAAGGCAGACAATTAAGGAAAACAAGGGGACTAGAATCAGGTTCAAAGAT  
GACAGTTCCTTTGAGGAGATCAATGGCATAACGGCGTCTAAGCACCTCTATGTGTCAATGCCTACT  
GCACAGTCCACTATGAAAGCTGATGAGTTAACACCAGGTAGGTTTAGAACAATTGTTTGTGGACTT  
TTCCCGGCTCAAATCATGCACAGAAATATCATAAGTCCAGTCATGGGTGTTATTGGGTTTTTCATTCT  
TTGTGAAAGACTGGCCTGAGAAGATCGAAGAATTTTAATTAAGCCTTGTCTTTTTTAAAGAAAC  
AAGGTGCACCTGGGAAAGAGGAAGACTTT

**>seq265Tula/Moravia/5293Ma/94\_Z48574**

ATTGGTTTTCTATCGGCCAGTACATTACAGGCTTTGCACTTGAATAATCTTGAAGGCATTGTATAT  
GCTGTCAACTAGAGGGAGGCAAACAATCAAGGAAAATAAGGGGACAAGAATCCGGTTCAAAGGAT  
GACAGTCTATATGAAGAGATCAATGGCATTAGACGCCCGAAACATCTGTATGTGTCTATGCCAACA  
GCCAGTCTACTATGAAAGCCGATGAATTGACACCAGGTAGGTTTAGAACAATTGTTTGTGGACTC  
TTTCTGCTCAAATATGCACAGAAACATCATAAGTCTGTCATGGGTGTGATTGGATTTCTTTTTT  
CGTTAAAGATTGGCCTGAAAAGATTGAGGAGTTCCTTATTAACCTTGCCCATTCCTGAAGAAAAG  
TGGTCTAGTAAGGAAGAGGATTTTCTT

**>seq266Tula/MG23/Omsk/AF442621**

ACTGGTTTTCTATCGGTACGTACATAATGGGATTTGCACTTGAATCGTGCTTAAAGGCCTTGTACAT  
GTTGTGACACGCGGGAGACAAACCATCAAGGAAAATAAAGGGACAAGAATTAAGTTTAAAGATG  
ACAGTTCAATTGAGGAGATTAACGGGATAAGACGTCCAAAACACCTGTATGTCTCAATGCCAACTG  
CACAGTCCACAATGAAAGCAGATGAGTTAACACCAGGAAGATTTAGGACAATTGTCTGTGGCCTCT

TCCCTGCCAAATAATGCATAGAAACATCATCAGTCCAGTAATGGGTGTAATAGGATTCTCTTTCTT  
TGTC AAAGATTGGCCAGATAAGATTGAGGAGTTCCTTATTA AACCATGTCCCTTCTGAAAAACA  
AGTTCCACCAAAGAAGAATTTCTT

**>seq267Thottapalayam\_AY526097**

ATTGGGGAAAGATATTCGAATACATTTTGACCCTTACACAGGTTCTTCTCCTTAAAGGCCTCTACAT  
CTTGACCACCCGAGGAAGACAGACTAGTAAAGACAACAAAGGTA TAGAATCAAGCTTAAGGATG  
ACTCATGCATGGAGGACCGAATGGGATAAAACAACACAAGTACCTTTACATATCCCTTCCAACAA  
GCCAATCTTCCATCCAAGATGATGAACTCACACCTGGACGTTTTAGGACAATGATCTCAGGACTCT  
TGCCAAATGAGATAAAGGCAAAAAAGCTGATGAGCCCTGTAATGGGTGTCATTGGTTTTCAACATT  
TAGCTGAGGCTTGGCCAGGTGCAATGGAAAAGATGTTGAGTGACCAGTGTAATATATGACCAAG  
GATAAAGCAAACCCATCAAATAGCACTAAT

**>seq268Andes\_Chile-9717869\_AF291702**

ATTGGAAGGCTATAGGAGCATACTTTAGGGTTTTGCAATTCCGATCATCTTAAAGGCCTTATACA  
TGCTGTCAACCCGTGGGAGACAACTGTGAAAGACAACAAAGGGACCAGGATAAGGTTAAGGAT  
GATTCTTCCTTTGAAGAAGTCAATGGGATACGTAAACCAAAACACCTTTACGTCTCAATGCCAACT  
GCACAGTCCACTATGAAGGCTGAAGAAATCACGCCAGGACGATTTAGGACAATTGCTTGTGGCCTT  
TTTCCAGCACAGGTCAAAGCCCGAAATATAATAAGTCTGTAAATGGGAGTAATTGGATTGGCTTC  
TTTGTAAGGATTGGATGGATCGGATAGAAGAGTTTCTGGCTGCAGAGTGCCATTCTTACCTAAG  
CCAAAGGTCGCCTCAGAAGCCTTCATGTCT

**>seq269Andes\_NK104619\_EU241691**

ACTGGAAAGCAATAGGAGCATATATCCTAGGATTTGCAATCCCAATCATCTTAAAGCCCTATACA  
TGCTGTCAACTCGTGGGAGACAACTGTGAAGGACAACAAGGGGACCCGGATAAGATTCAAGGAT  
GATTCTCCTTTGAAGAGGTGAACGGGATACGCAAACCAAAACATCTTTATGTCTCAATGCCAACT  
GCACAATCCACAATGAAAGCTGAAGAGATCACACCAGGGCGGTTTCAGGACAATTGCTTGTGGCCT  
TTTTCCAGCACAGGTCAAAGCTAGGAACATAATAAGCCCTGTAATGGGTGTAATTGGGTTGGTTT  
CTTTGTGAAAGACTGGATGGACCGGATAGAAGAATTCTGGCTGCAGAGTGCCATTCTTGCCTAA  
GCCAAAGGTAGCTTCTGAATCCTTTATGTCT

**>seq270SinNombre\_NMR11\_L37904**

ATTGGAATCCATCGGACTCTACATTTCTAAGTTTTCGCATTACCGATTATTCTTAAAGCCTTGTACAT  
GTTATCTACTAGGGGCCGTCAAACAATCAAAGAAAACAAGGGAACAAGAATTCGATTCAAGGATG  
ATTCATCTTATGAAGAAGTCAATGGGATACGTAAGCCAAGACATCTGTATGTTTCTATGCCAACTG  
CCCAGTCTACAATGAAAGCAGATGAGATTACTCCCAGGAGGTTCCGTACAATTGCTTGTGGATTAT  
TCCCAGCCCAAGTCAAAGCAAGGAATATTATCAGTCTGTATGGGTGTGATTGGCTTTAGTTTTTT  
TGTGAAAGATTGAGTGGAAAGGATTGATGACTTCTGGCTGCACGTTGCCATTCTGCCTGAGCA  
GAAAGACCCTAGATGCTGCATTGGCA

**>seq271NewYorkhantavirus\_nucleocapsid\_U09488**

ATTGGAAGCTATTGGAATGTATATCTTGAGCTTTGCAATACCAATCATCTTAAAGGCCCTCTATAT  
GTTATCAACCAGAGGTCGTCAAACAGTTAAGGAAAATAAGGGGACAAGAATCAGGTTCAAGGATG  
ACTCATCTTATGAAGAAGTCAACGGAATCAGAAAGCCAAGACATTTATATGTATCAATGCCTACAG  
CCCAATCCACAATGAAGGCAGATGAGATCACTCCAGGGCGTTTCCGCACGATTGCATGTGGATTGT  
TCCCTGCACAAGTGAAGGCTAGGAATATTATCAGTCCAGTCATGGGTGTGATAGGATTTAACTTTTT  
TGTTAAGGACTGGATGGACAGGATTGATGATTTTCTAGCTGAGCGGTGCCATTCTACCTGAGCC  
AAGAGACCCTAAGGATGCTGCATTAGGA

**>seq272Choclovirus\_segmentS\_DQ285046**

ATTGGAGGTCAATTGGTGCTTATATCCTCGGATTTGCACTACCAATCATCTTGAAGGCCCTCTACAT  
GTTATCCACAAGAGGGAGGCAGACTGTGAAAGAAAACAAGGCACCAGGATCAGATTTAAAGATG  
ATTCATCCTTGAAGAGGTAATGGGATAAGAAAGCCTAAACATCTTTATGTGTCGATGCCCACTG  
CACAGTCAACAATGAAGGCTGATGAAATAACACCTGGAAGGTTCCGGACAATTGCATGTGGCCTTT  
TCCCAGCTCAAGTCAAAGCCAGGAATATAATTAGCCCAGTAATGGGTGTCATCGGTTTTGGTTTTTT  
TGTAAGGATTGGATGGATCGTATTGATAATTTCTTATCTGCTGAGTGCCATTTTGCAGAAGCCA  
AAGTTCCATCTGAGGCATTTACAACC

**>seq273LagunaNegra\_AF005727**

ATTGGAAGGCTATTGGAGCCTATATTCTAGGATTTGTAATACCAATTATCCTAAAGGCATTATATAT  
GCTTTCAACAAGAGGGAGGCAGACTGTTAAAGAGAACAAGGGACCAGGATTTCGATTCAAGGATG  
ATTCATCATTTGAAGAAGTCAATGGCATCCGAAAACCTAAACACTTGTATGTGTCAATGCCTACTG  
CACAATCTACAATGAAGGCAGATGAGATAACACCGGGGAGGTTTTAGGACAATTGCATGTGGCTTA  
TTTTCTGCTCAAATCAAAGCTCGGAACATTATAAGTCCAGTCATGGGTGTCATTGGCTTTGGTCACT  
TTGTGAAGGACTGGATGGAAAGGATTGACAACCTTTCTAGGAGAAGATTGCCCATTTCTTCAAAGG  
CTAGGGTTCAATCAGAGGCATTCATGTCA

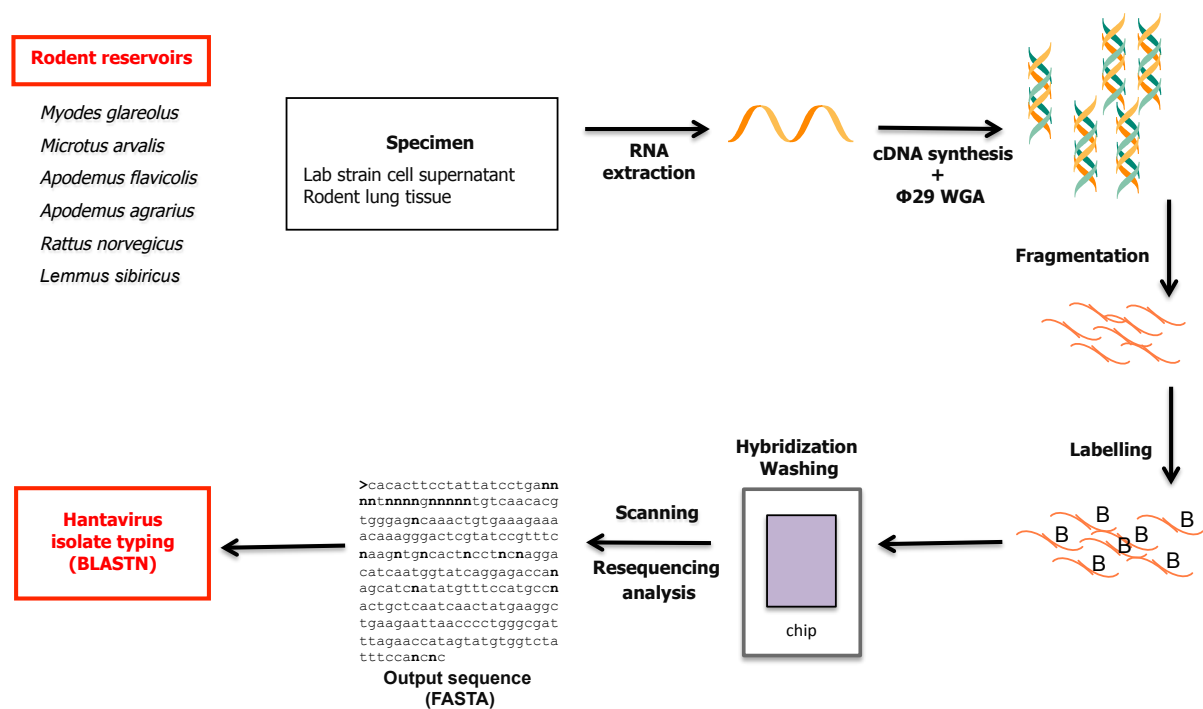


## SUPPLEMENT 2

### Hantavirus resequencing from animal reservoirs in Europe.

Flowchart of the experimental procedure for European hantavirus detection and genetic characterization using PathogenID v3.0 resequencing pan-viral chip.

Plasmids used for the preliminary assay were not subjected to the Retro-Transcription step. However they were processed by WGA (Whole Genome Amplification) as well as the cDNAs from extracted RNAs.









Identity: 85%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.

**>seq232:Hanta\_Puumala\_Plasmid\_1\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```
nnnnngtgnatgttnnngggttcacacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnngggncagactgtnaan  
naannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntntntcattgaagacatcaatggcatanggagaccaaagcatnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnncaactatgaaagcagannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnngagtcaggtatggnggtcattntntntnnannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (138/401): 34.4%**

**(B)**

Max score: 68.0

Total score: 68.0

Query coverage: 9%

E value: 2e-07

Identity: 97%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- GU808825.1: Puumala virus strain Kuhmo/X11 nucleocapsid protein (N) mRNA, complete cds.
- GU808824.1: Puumala virus strain Kuhmo/X5 nucleocapsid protein (N) mRNA, complete cds.
- AJ314597.1: Puumala virus mRNA for nucleocapsid protein (N gene), strain Pallasjarvi/63Cg/98.
- AJ238789.1: Puumala virus RNA for nucleocapsid protein, strain Kolodozero.
- AJ238788.1: Puumala virus RNA for nucleocapsid protein, strain Karhumaki.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq233:Hanta\_Puumala\_Plasmid\_1\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```
tnnnnnnnnnnnnnnnnngctttacacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
aaaataagggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaagcagannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (79/401): 19.7%**

**(B)**

Max score: 64.4

Total score: 64.4

Query coverage: 8%

E value: 3e-06

Identity: 100%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- AJ238790.1: Puumala virus RNA for nucleocapsid protein, strain Gomselga.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq234:Hanta\_Puumala\_Plasmid\_1\_13-02-2013\_(VirIDv3r520827) Start=12 End=238**

```
acagntnnnnnnnnngntataaccgcatgnanngnnnnnnnnnnggtccagacaaaacntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
tgaccagatgacgtaataannacanacngcaagccnggaacaacagtggtcagcacngaggacaaactgnannnnnnnnnnnnnnnnnnnn  
gatggcagatgctgngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (141/227): 62.1%**

**(B)**

Max score: 129

Total score: 129

Query coverage: 47%

E value: 4e-26

Identity: 83%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.



attggagtgatgtgntagggttnacacttctatcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacgcgtgggagacagactgnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncannnancnatgncanannnnnnnnnnngngnnnnnnnnnn  
nctatgccnncngcccagtnancnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnn

**(A) CR (96/279): 34.4%**

**(B)**

Max score: 59.0

Total score: 59.0

Query coverage: 12%

E value: 8e-05

Identity: 94%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq240:Hanta\_Puumala\_Plasmid\_1\_13-02-2013\_(VirIDv3r520827) Start=12 End=290**

attggagtgatgtggnnggggttnaacttctatcannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacgcgtgggagacagnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
atgcctnnnnccngtcaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnn

**(A) CR (107/279): 38.3%**

**(B)**

Max score: 51.8

Total score: 98.2

Query coverage: 33%

E value: 0.012

Identity: 75%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq241:Hanta\_Puumala\_Plasmid\_1\_13-02-2013\_(VirIDv3r520827) Start=12 End=290**

attggagtgatgtggnnggntnacacttctatcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnacgcgtgggagagagnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nncnctatgcttncnnncngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (75/279): 26.9%**

**(B)**

no BLASTN identification

**>seq242:Hanta\_Puumala\_Plasmid\_1\_13-02-2013\_(VirIDv3r520827) Start=12 End=290**

nnnnnnnnnnnnnnnnnnnnnttannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
ggaaaatanggggacgctatnngggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnaactatgaaagcagnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (86/279): 30.8%**

**(B)**

Max score: 69.8

Total score: 69.8

Query coverage: 15%

E value: 5e-08

Identity: 93%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- AJ238790.1: Puumala virus RNA for nucleocapsid protein, strain Gomselga.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.





**(A) CR (107/401): 26.7%**

**(B)**

Max score: 44.6

Total score: 44.6

Query coverage: 14%

E value: 2.7

Identity: 72%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq225:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```
ttggagtgtatgtgatagggtcacacttctatcatccttaaagctttatatacatgctctcaacgcgtggngacagactgtaaagggaaaataagggga  
cacgtataaggtttaaggatgatacatcattgaagacatcaatggcataaggagaccaaagcatttatatgtttctatgccnactgccagtcactat  
gaaagcagaagaactcacaccaggcagatttcgacaatagatgtggcttttcccactcagatccagggtcgnaacatcatgagtcagttatgg  
nggtcattggttttcattctttgtgaaggattggctgagagaatcagagagttcatggaaaaagagtgccattcataaagcctgaagnaaaccng  
gcaca
```

**(A) CR (395/401): 98.5%**

**(B)**

Max score: 702

Total score: 702

Query coverage: 100%

E value: 0.0

Identity: 99%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.

**>seq226:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```
ttnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
ngnnnnnnnnnnngggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnggcataagnaaacnnagnnntnnn  
nnnnntntgtcactgcccagtcnannatgaaagcngangaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnngtaacatcatgagtcagttatnnnnnnnncattnnannntncannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnggnnnnnnataaagcctgaannnnnnnnanncnca
```

**(A) CR (128/401): 31.9%**

**(B)**

Max score: 46.4

Total score: 46.4

Query coverage: 8%

E value: 0.78

Identity: 86%

- KT885052.1: Puumala virus strain CG1820/POR segment S, complete sequence.
- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- GQ339478.1: Puumala virus strain Jockfall/Mg12/05 segment S, complete sequence.
- EU652442.1: Puumala virus isolate Tyumen/223\_Myod\_gl/06 nucleocapsid protein (N) gene, partial cds.
- EU652436.1: Puumala virus isolate Tyumen/198\_Myod\_gl/06 nucleocapsid protein (N) gene, partial cds.
- EU652434.1: Puumala virus isolate Tyumen/195\_Myod\_gl/06 nucleocapsid protein (N) gene, partial cds.
- EU652432.1: Puumala virus isolate Tyumen/185\_Myod\_gl/06 nucleocapsid protein (N) gene, partial cds.
- EU652431.1: Puumala virus isolate Tyumen/181\_Myod\_gl/06 nucleocapsid protein (N) gene, partial cds.
- EU652428.1: Puumala virus isolate Tyumen/170\_Myod\_gl/06 nucleocapsid protein (N) gene, partial cds.



E value: 2e-08  
Identity: 73%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq229:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

nnggnngnnnnnnnncncttncacttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnggnnnnnnnnnnn  
nnnnnnnnnnnggnccngntncgattaaggatgatacatcattnnnanacatnnntngcannngntnannnnngnnncnnnnnnngn  
tnnnnnnnnnnnncngnncannnnnnnannnnnnnagcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnggtcnnncnc  
tcagannnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
annanngttcatggaaaagagtgccannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncnnncnca

**(A) CR (112/401): 27.9%**

**(B)**

Max score: 44.6  
Total score: 44.6  
Query coverage: 7%  
E value: 2.7  
Identity: 88%

- AB675463.1: Hokkaido virus Small gene for nucleocapsid protein, complete cds, isolate: Kitahiyama128S/2008.
- AB675478.1: Hokkaido virus Small gene for nucleocapsid protein, complete cds, isolate: ShariP5-3S/2010.
- AB675477.1: Hokkaido virus Small gene for nucleocapsid protein, complete cds, isolate: Shari6-10S/2010.
- AB675475.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Abashiri22S/1994.
- AB675472.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Nakagawa73S/2004.
- AB675471.1: Hokkaido virus Small gene for nucleocapsid protein, complete cds, isolate: Nakagawa49S/2004.
- AB675470.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Nakagawa13S/2004.
- AB675468.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Tobetsu84S/2010.
- AB675467.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Tobetsu60S/2010 .
- AB675466.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Tobetsu57S/2004 .
- AB675465.1: Hokkaido virus Small gene for nucleocapsid protein, complete cds, isolate: Tobetsu27S/2004.
- AB675464.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Tobetsu89S/2000.
- AB675462.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Kitahiyama124S/2008.
- AB675461.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Kitahiyama96S/2008.
- AB675460.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Kitahiyama85S/2008.
- AB675459.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Kitahiyama77S/2008.
- AB675458.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Kitahiyama63S/2008.
- AB675457.1: Hokkaido virus Small gene for nucleocapsid protein, partial cds, isolate: Kitahiyama57S/2008.





Query coverage: 12%

E value: 0.001

Identity: 82%

- HQ697348.1: Tula virus isolate GER/109/Arv nucleocapsid protein gene, partial cds.
- FJ495098.1 : Tula virus strain TULV/Sestrze/Mag98\_02 segment S nucleocapsid protein gene, partial cds.
- EU337015.1: Puumala virus isolate plasma-1 nucleocapsid protein gene, partial cds.
- EU337014.1: Puumala virus isolate saliva-1 nucleocapsid protein gene, partial cds.

(Note) Simultaneous detection of PUUV, TULV, HTNV (at lower values).

**>seq236:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```

tnnnanngnnnnnnnnnngcctnngcacttnnnnnannnnnnnnnnnnnnnnnnnnnnnncnnnacgcgtgggagacagactgtaagga
aaataagggnnnnnnggattcgatttaaggatgatnnnnnnnnnnnnnnnnnnnnnnnnngngaccanngnntnnnnnnnnnnnt
nnnnnnnnnnnnncnngnctancannnaagcnnnnnnnnnnnnnnnnnnnnnnnnnnnnncnnnantagtagtgggtctttcccnnnnnnn
nnnnnnnnnnnnnnncnnnnnnnnnnnnncnnnnnnnnngggnnnnnnnnnnnncnnnnngnnnnnnnnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaccnnn

```

**(A) CR (124/401): 30.9%**

**(B)**

Max score: 80.6

Total score: 80.6

Query coverage: 14%

E value: 4e-11

Identity: 88%

- KY365007.1: Puumala orthohantavirus isolate Septmoncel-Alsace\_2015\_Camp5 nucleoprotein gene, complete cds.
- KY364999.1: Puumala orthohantavirus isolate MontsousVaudrey-Jura\_2014\_NCHA14 nucleoprotein gene, complete cds.
- KY364998.1: Puumala orthohantavirus isolate ChauxdesCrottenay\_Jura\_2014\_NCHA71 nucleoprotein gene, complete cds.
- KY364997.1: Puumala orthohantavirus isolate ChauxdesCrottenay-Jura\_2014\_CI11 nucleoprotein gene, complete cds.
- KT247596.2: Puumala virus isolate PUUV/Jura/Mg2/2010 segment S nucleoprotein gene, complete cds.
- KT247597.1: Puumala virus isolate PUUV/Jura/Mg214/2010 segment S nucleoprotein gene, complete cds .
- AM695638.1: Puumala virus S gene for nucleocapsid protein, strain PUU/Mignovillard/CgY02/2005, genomic RNA.

**>seq237:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```

tggagtgtatgtgntagggttnacacttcctatcnnnnnnnnnnnnngnnnnnnnncnnncaacgcgtgggagacagactgcannnnnnnnn
nnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncnnnnnnnaatggcatanggagaccaaagcnnntttttctatgcc
tctgccngtcaannnnnnnannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnccnnnnnnnnnnnnnnngtcattgntttnnnnnnnnnnnnnnncnnnnngncnnnnnnnnnnnnnnngtcatg
gaaaaagagtncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncnnnnnnnnnnncnnn

```

**(A) CR (164/401): 40.9%**

**(B)**

Max score: 71.6

Total score: 127

Query coverage: 22%

E value: 2e-08

Identity: 85%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.



Max score: 69.8  
Total score: 69.8  
Query coverage: 15%  
E value: 5e-08  
Identity: 93%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- AJ238790.1: Puumala virus RNA for nucleocapsid protein, strain Gomselga.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq243:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=290**

```
attggagngnnnnngnnnnngcttgcactnnnnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngggaggcaaacnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnngnnnnnntttangnnnnnacannatnngaagncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
ntnntgtcactgccagctcaactannnnannngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnanngnntnnnnnc
```

(A) CR (98/279): 35.1%

(B)

No BLASTN identification

**>seq244:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnncngnncgattgaagatnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnngnctatgccannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncgnnaagtctctgcatgggtgtgattgattnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

(A) CR (66/401): 16.4%

(B)

Max score: 50.0  
Total score: 50.0  
Query coverage: 6%  
E value: 0.064  
Identity: 100%

- KU139579.1: Tula virus isolate 10\_1188\_Magr nucleocapsid protein gene, partial cds.
- KU139578.1: Tula virus isolate 10\_0932\_Marv nucleocapsid protein gene, partial cds.
- KU139577.1: Tula virus isolate 10\_0908\_Marv nucleocapsid protein gene, partial cds.
- KU139576.1: Tula virus isolate 10\_0905\_Marv nucleocapsid protein gene, partial cds.
- KU139575.1: Tula virus isolate 12\_1121\_Marv nucleocapsid protein gene, partial cds.
- KU139574.1: Tula virus isolate 12\_1068\_Marv nucleocapsid protein gene, partial cds.
- KU139573.1: Tula virus isolate 10\_1533\_Marv nucleocapsid protein gene, partial cds.
- KU139572.1: Tula virus isolate 12\_526\_Magr nucleocapsid protein gene, partial cds.
- KU139571.1: Tula virus isolate 12\_0492\_Magr nucleocapsid protein gene, partial cds.
- KU139570.1: Tula virus isolate 08\_0545\_Marv nucleocapsid protein gene, partial cds.
- KU139569.1: Tula virus isolate 08\_0362\_Marv nucleocapsid protein gene, partial cds.
- KU139568.1: Tula virus isolate 08\_0356\_Marv nucleocapsid protein gene, partial cds.
- KU139567.1: Tula virus isolate 08\_0352\_Marv nucleocapsid protein gene, partial cds.
- KU139566.1: Tula virus isolate 08\_0350\_Marv nucleocapsid protein gene, partial cds.
- KU139565.1: Tula virus isolate 08\_0538\_Marv nucleocapsid protein gene, partial cds.
- KU139564.1: Tula virus isolate 08\_0534\_Marv nucleocapsid protein gene, partial cds.
- KU139548.1: Tula virus isolate 10\_1625\_Marv nucleocapsid protein gene, partial cds.
- KU139546.1: Tula virus isolate 07\_0081\_Magr nucleocapsid protein gene, partial cds.
- KU139545.1: Tula virus isolate 08\_0894\_Marv nucleocapsid protein gene, partial cds.
- KU139544.1: Tula virus isolate 08\_0849\_Marv nucleocapsid protein gene, partial cds.
- KU139543.1: Tula virus isolate 08\_0848\_Marv nucleocapsid protein gene, partial cds.
- KU139542.1: Tula virus isolate 08\_0802\_Marv nucleocapsid protein gene, partial cds.



- KU139541.1: Tula virus isolate 08\_0789\_Marv nucleocapsid protein gene, partial cd
- KU139540.1: Tula virus isolate 11\_1433\_Marv nucleocapsid protein gene, partial cds.
- KU139539.1: Tula virus isolate 11\_1429\_Marv nucleocapsid protein gene, partial cds.
- KU139536.1: Tula virus isolate 11\_1373\_Marv nucleocapsid protein gene, partial cds.
- HQ697347.1: Tula virus isolate GER/09/2155/Arv nucleocapsid protein gene, partial cds.
- GU300137.1: Tula virus strain dpz06-29 nucleocapsid protein gene, partial cds.
- GU300135.1: Tula virus strain dpz06-1 nucleocapsid protein gene, partial cds.
- EU439952.1: Tula virus strain Sennickerode Sen05/222 nucleocapsid protein gene, partial cds.
- EU439951.1: Tula virus strain Sennickerode Sen05/205 nucleocapsid protein gene, complete cds.
- EU439950.1: Tula virus strain Sennickerode Sen05/204 nucleocapsid protein gene, complete cds.
- EU439949.1: Tula virus strain Sennickerode Sen05/175 nucleocapsid protein gene, complete cds.
- EU439948.1: Tula virus strain Sennickerode Sen05/174 nucleocapsid protein gene, partial cds.
- EU439946.1: Tula virus strain Sennickerode Sen05/121 nucleocapsid protein gene, partial cds.
- AJ223600.1: Tula virus genomic RNA for nucleocapsid protein, (strain Tula/Koziky/5247Ma/94).
- Y13984.1: Tula virus partial genomic RNA for nucleocapsid protein, strain (Tula/D540/Ma/95).
- U95304.1: Tula virus O20 nucleocapsid protein gene, partial cds.
- U95303.1: Tula virus O52 nucleocapsid protein gene, partial cds.
- U95302.1: Tula virus O24 nucleocapsid protein gene, partial cds.
- Z69991.1: Tula virus genomic RNA for nucleocapsid protein, strain (Tula/Moravia/5302v/95).
- Z49915.1: Tula virus segment S, strain Tula/Moravia/5302Ma/94, genomic RNA.
- Z48741.1: Tula virus segment S, strain Tula/Moravia/5294Ma/94, genomic RNA.
- Z48574.1: Tula virus segment S, strain Tula/Moravia/5293Ma/94, genomic RNA.
- Z48573.1: Tula virus segment S, strain Tula/Moravia/5286Ma/94, genomic RNA.

**>seq245:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

nnnnnnnnnnnnnnnnnnnnnnncngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnngnnnnnnngn  
 nnnnnnnnnnnnnnnnnnnnnnattcgattgaaggatganagctcanannnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncnnnnnnnggcagaagagattacnctgannnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (68/401): 16.9%**

**(B)**

No BLASTN identification.

**>seq246:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

nnnnnnnnnnnnnnnnnnnnnnncgncgccgnncnnngnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnngcnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnttaaggatgatagctcgttcgaggatnntnncggtntccggaaccaaacaannnnnnnn  
 nnnnnnnnnnnngnacagncangcntnncnnnnnnnagngcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (104/401): 25.9%**

**(B)**

Max score: 77.0

Total score: 77.0

Query coverage: 12%

E value: 5e-10

Identity: 90%

- KX601186.1: Hantaan hantavirus isolate SNHRC-HTN-128 nucleocapsid protein gene, partial cds.
- KU207190.1: Hantaan virus isolate Aa04-722 segment S nucleocapsid protein gene, complete cds.
- KP970573.1: Hantaan virus isolate JS2 segment S, complete sequence.
- KP970572.1: Hantaan virus isolate JS1 segment S, complete sequence.
- EF208934.1: Hantavirus CJAA1109 nucleocapsid protein gene, partial cds.
- EF208933.1: Hantavirus CJAA716 nonfunctional nucleocapsid protein gene, partial sequence.

- EF208932.1: Hantavirus CJAa594 nucleocapsid protein gene, partial cds.
- AF288659.1: Hantavirus S85-46 nucleocapsid protein mRNA, complete cds.
- AF288294.1: Hantavirus LR1 segment S S protein mRNA, complete cds.
- U37768.1: Hantaan virus S segment nucleocapsid protein mRNA, complete cds.
- D25533.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- D25530.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- M14626.1: Hantaan virus S segment encoding nucleocapsid protein.

>seq247:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412

nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnatatgntntcaacnngggggcnnncnnncn  
nnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncgaaacaaaacnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nennnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (106/401): 26.4%

(B)

No BLASTN identification

>seq248:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412

nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngncaacanggggggagncnnntnncn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
acnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (66/401): 16.4%

(B)

No BLASTN identification

>seq249:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412

tcacgncctatctacatcttctgtcgtcccgcactctctgaaagctctgnatgttgacaacangnnnnnaggcaactaccaaggataataaggga  
ccggattcgatgtaggatgatgctcgttcgaggatgttaacggatgccgnaacaaaacatctttacgtgtccttgccaaangcngncaagc  
atgaaggcagaagagattacacctggtagatataaacagcagctctgtgggctctacctgcacagattnnggcnccggcagngancagcagc  
tatgagtgaattgggttttagcattagcaaaggactggagtgatcgatcaacaatggtaattgaaccttgcaagctctccagatacagcagca  
gttagcctc

(A) CR (382/401): 95.3%

(B)

Max score: 655

Total score: 655

Query coverage: 100%

E value: 0.0

Identity: 95%

- KP970573.1: Hantaan virus isolate JS2 segment S, complete sequence.
- KP970572.1: Hantaan virus isolate JS1 segment S, complete sequence.
- AF288659.1: Hantavirus S85-46 nucleocapsid protein mRNA, complete cds.
- U37768.1: Hantaan virus S segment nucleocapsid protein mRNA, complete cds.
- D25533.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- D25530.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- M14626.1: Hantaan virus S segment encoding nucleocapsid protein.

>seq250:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412

nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnactagnnggncnnnnnnnnnnnnnnnnnnnn  
nataatnnnnnggaccgnttcgatttaaggatganagcnnnnnnncaggatgttaacggtnccggaaaccaaagcnnnttatatgntnnnnnn  
nnaatgcacagcaagcatgaaggcagaagagcctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnctgtgggctctacctgcacagatgagc



- KP970573.1: Hantaan virus isolate JS2 segment S, complete sequence.
- KP970572.1: Hantaan virus isolate JS1 segment S, complete sequence.
- AF288659.1: Hantavirus S85-46 nucleocapsid protein mRNA, complete cds.
- U37768.1: Hantaan virus S segment nucleocapsid protein mRNA, complete cds.
- D25533.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- D25530.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- M14626.1: Hantaan virus S segment encoding nucleocapsid protein.

>seq253:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412

nnnnnnnnnnnnnnnnnnnnnnnctccgatactctgaaagctctgtatattgtgncaacaagggggnnnnnnnnncaccaaggataat  
 anagggaccgggattcgatttnnggatgntagctcgntcagaggnntnaanngcnnnnnnnnnnnnnnnnnnngnnngnnnnnnnnnn  
 nnatgcacagtcaagcatgaaggcagaagagattacacctggtagatagancnngggnnnnnnnnnnnnnntcncncagattaangcnc  
 ngnnnnnnnnnnnnccngtcagggtggtgattgntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntnn  
 ntntnnacagctctccagntacagcancagttagctc

(A) CR (231/401): 57.6%

(B)

Max score: 176

Total score: 224

Query coverage: 59%

E value: 6e-40

Identity: 74%

- KP970573.1: Hantaan virus isolate JS2 segment S, complete sequence
- KP970572.1: Hantaan virus isolate JS1 segment S, complete sequence.
- AF288659.1: Hantavirus S85-46 nucleocapsid protein mRNA, complete cds.
- AF288294.1: Hantavirus LR1 segment S S protein mRNA, complete cds.
- U37768.1: Hantaan virus S segment nucleocapsid protein mRNA, complete cds.
- D25533.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- D25530.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- M14626.1: Hantaan virus S segment encoding nucleocapsid protein.

>seq254:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412

nnnnnnnnnnnnnnnnnnnnnnnctccgatactctgannnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnggaccgggattcgatttaaggatgacagctcnnncnaggatgtaaacgntnncnnnnnnnnnnnnnnantgtcnngctcct  
 gccaaangcangtcaagcatgaaggcagaagagattacncnggnagnnttntnngnagcngctgnnnnnnnnntcnnnnnnnnnnnn  
 nnnnnnnnnnnnnngnnnnnnnnnnntgggtgtgattnnnnnnnnnnngngngnnnnnnnnnnnnnnntcgnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (175/401): 43.6%

(B)

Max score: 116

Total score: 116

Query coverage: 32%

E value: 5e-22

Identity: 75%

- KP970573.1: Hantaan virus isolate JS2 segment S, complete sequence.
- KP970572.1: Hantaan virus isolate JS1 segment S, complete sequence.
- EF208934.1: Hantavirus CJAa1 109 nucleocapsid protein gene, partial cds.
- AF288659.1: Hantavirus S85-46 nucleocapsid protein mRNA, complete cds.
- U37768.1: Hantaan virus S segment nucleocapsid protein mRNA, complete cds.
- D25533.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- D25530.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- M14626.1: Hantaan virus S segment encoding nucleocapsid protein.

>seq255:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412



**>seq257:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**  
ncnnnnnnnnnnnnnnnnnnnnnnncnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncngcagacttcan  
nnnnngnnnnnnnnnnnnnnnnnnnnntnnggatgacagctcatnnnnanncnnnnnnnnnnnnnnnnnnnnnnntctgtatg  
tgtctatgccnngnnnnnnancnncatgaaggcagaagagattacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncccncc  
acagattannnnnnnnnnnnnnnnngggnnnnnnngnnnnnnnnnnnnnnnnnnnnnnngnnnnnggnngnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (104/401): 25.9%**  
**(B)**

No BLASTN identification.

**>seq258:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**  
ncnnnnnnnnnnnnnancatcngcnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncagacttcannn  
nnnnncanggnnnnnnnnnnnnnnnnnnnnntnnggatgacagctcatnnnnanncnnnnnnnnnnnnnnnnnnngnacatctgtatgt  
ctatgcnnngnnnnnnnnnnnnnnnnnnnggcagaagagntnnnnnnnnnnngannntnngnnnnnnnnnnnnnnnnnnnnccnccnca  
nagattnnnnnnnnnnnnnnnggtaannncnnnnnnngnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (110/401): 27.4%**  
**(B)**

No BLASTN identification.

**>seq259:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnn  
cnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnatgcacagtaancnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (25/401): 6.2%**  
**(B)**

No BLASTN identification.

**>seq260:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnncnnnnnnnc  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
cnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngagcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (29/401): 7.2%**  
**(B)**

No BLASTN identification.

**>seq261:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnccannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
gtgtctatgccacagcccagtcactatgannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (122/401): 30.4%**  
**(B)**

Max score: 59.0  
Total score: 101  
Query coverage: 20%  
E value: 1e-04  
Identity: 78%

- Z48574.1: Tula virus segment S, strain Tula/Moravia/5293Ma/94, genomic RNA.
- Z48573.1: Tula virus segment S, strain Tula/Moravia/5286Ma/94, genomic RNA.

(Note) Simultaneous detection of TULV and PUUV (at lower values).

>seq262:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412

```
ncnnnnncnnncttaccatccttgnccnncngntactctgannnnnnnnnnnnnnnnnnnnncaacaagggnnnnnnnngnnnnnnnnnt  
nnnnnggggacaagaatcngntncgnnnnnnngnnnanannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnngtcangcatgaaggcagaagagattacnnnnnnnnnnnnnnnnnnnnnggnnnnnnnnnnnnnnnnnnnnnnn  
annnnnnnnnnnnnnngatggtaagcnnnnntatgagtgtgattgntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

(A) CR (151/401): 37.6%

(B)

Max score: 46.4

Total score: 46.4

Query coverage: 6%

E value: 0.78

Identity: 96%

- MF141838.1: Hantaan orthohantavirus isolate AYW118/2015 nucleocapsid protein gene, partial cds.
- MF141833.1: Hantaan orthohantavirus isolate AYW76/2014 nucleocapsid protein gene, partial cds.
- MF141832.1: Hantaan orthohantavirus isolate AWY69/2014 nucleocapsid protein gene, partial cds.
- MF141831.1: Hantaan orthohantavirus isolate AWY68/2014 nucleocapsid protein gene, partial cds.
- MF141830.1: Hantaan orthohantavirus isolate AWY66/2014 nucleocapsid protein gene, partial cds.
- MF141829.1: Hantaan orthohantavirus isolate SG40/2012 nucleocapsid protein gene, partial cds.
- KY807172.1: Hantaan orthohantavirus isolate GAN19/2011 nucleocapsid protein gene, complete cds.
- KY807168.1: Hantaan orthohantavirus isolate GAN13/2011 nucleocapsid protein gene, complete cds.
- KY807167.1: Hantaan orthohantavirus isolate GAN21/2011 nucleocapsid protein gene, complete cds.
- KP970573.1: Hantaan virus isolate JS2 segment S, complete sequence.
- KP970572.1: Hantaan virus isolate JS1 segment S, complete sequence.
- JQ665908.1: Hantaan virus strain WuhanHu16 nucleocapsid gene, partial cds.
- EF208934.1: Hantavirus CJAa1109 nucleocapsid protein gene, partial cds.
- EF208932.1: Hantavirus CJAa594 nucleocapsid protein gene, partial cds.
- DQ658415.1: Hantaan virus strain N8 nucleocapsid protein gene, complete cds.
- AF288659.1: Hantavirus S85-46 nucleocapsid protein mRNA, complete cds.
- AF288294.1: Hantavirus LR1 segment S S protein mRNA, complete cds.
- U71282.1: Hantaan virus nucleocapsid protein gene, partial cds.
- U37768.1: Hantaan virus S segment nucleocapsid protein mRNA, complete cds.
- D25533.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- D25530.1: Hantaan virus gene for nucleocapsid protein, complete cds.
- M14626.1: Hantaan virus S segment encoding nucleocapsid protein.

>seq263:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412

```
nnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nntnnnnntanagnnnnngntnnnatgaaanccnangaannngnanncaggtagattnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

(A) CR (130/401): 32.4%

**(B)**

Max score: 50.0

Total score: 50.0

Query coverage: 6%

E value: 0.064

Identity: 100%

- KU139579.1: Tula virus isolate 10\_1188\_Magr nucleocapsid protein gene, partial cds.
- KU139578.1: Tula virus isolate 10\_0932\_Marv nucleocapsid protein gene, partial cds.
- KU139577.1: Tula virus isolate 10\_0908\_Marv nucleocapsid protein gene, partial cds.
- KU139576.1: Tula virus isolate 10\_0905\_Marv nucleocapsid protein gene, partial cds.
- KU139575.1: Tula virus isolate 12\_1121\_Marv nucleocapsid protein gene, partial cds.
- KU139574.1: Tula virus isolate 12\_1068\_Marv nucleocapsid protein gene, partial cds.
- KU139573.1: Tula virus isolate 10\_1533\_Marv nucleocapsid protein gene, partial cds.
- KU139572.1: Tula virus isolate 12\_526\_Magr nucleocapsid protein gene, partial cds.
- KU139571.1: Tula virus isolate 12\_0492\_Magr nucleocapsid protein gene, partial cds.
- KU139570.1: Tula virus isolate 08\_0545\_Marv nucleocapsid protein gene, partial cds.
- KU139569.1: Tula virus isolate 08\_0362\_Marv nucleocapsid protein gene, partial cds.
- KU139568.1: Tula virus isolate 08\_0356\_Marv nucleocapsid protein gene, partial cds.
- KU139567.1: Tula virus isolate 08\_0352\_Marv nucleocapsid protein gene, partial cds.
- KU139566.1: Tula virus isolate 08\_0350\_Marv nucleocapsid protein gene, partial cds.
- KU139565.1: Tula virus isolate 08\_0538\_Marv nucleocapsid protein gene, partial cds.
- KU139564.1: Tula virus isolate 08\_0534\_Marv nucleocapsid protein gene, partial cds.
- KU139548.1: Tula virus isolate 10\_1625\_Marv nucleocapsid protein gene, partial cds.
- KU139546.1: Tula virus isolate 07\_0081\_Magr nucleocapsid protein gene, partial cds.
- KU139545.1: Tula virus isolate 08\_0894\_Marv nucleocapsid protein gene, partial cds.
- KU139544.1: Tula virus isolate 08\_0849\_Marv nucleocapsid protein gene, partial cds.
- KU139543.1: Tula virus isolate 08\_0848\_Marv nucleocapsid protein gene, partial cds.
- KU139542.1: Tula virus isolate 08\_0802\_Marv nucleocapsid protein gene, partial cds.
- KU139541.1: Tula virus isolate 08\_0789\_Marv nucleocapsid protein gene, partial cds.
- KU139540.1: Tula virus isolate 11\_1433\_Marv nucleocapsid protein gene, partial cds.
- KU139539.1: Tula virus isolate 11\_1429\_Marv nucleocapsid protein gene, partial cds.
- KU139536.1: Tula virus isolate 11\_1373\_Marv nucleocapsid protein gene, partial cds.
- HQ697347.1: Tula virus isolate GER/09/2155/Arv nucleocapsid protein gene, partial cds.
- GU300137.1: Tula virus strain dpz06-29 nucleocapsid protein gene, partial cds.
- GU300135.1: Tula virus strain dpz06-1 nucleocapsid protein gene, partial cds.
- EU439952.1: Tula virus strain Sennickerode Sen05/222 nucleocapsid protein gene, partial cds.
- EU439951.1: Tula virus strain Sennickerode Sen05/205 nucleocapsid protein gene, complete cds.
- EU439950.1: Tula virus strain Sennickerode Sen05/204 nucleocapsid protein gene, complete cds.
- EU439949.1: Tula virus strain Sennickerode Sen05/175 nucleocapsid protein gene, complete cds.
- EU439948.1: Tula virus strain Sennickerode Sen05/174 nucleocapsid protein gene, partial cds.
- EU439946.1: Tula virus strain Sennickerode Sen05/121 nucleocapsid protein gene, partial cds.
- AJ223600.1: Tula virus genomic RNA for nucleocapsid protein, (strain Tula/Koziky/5247Ma/94).
- Y13984.1: Tula virus partial genomic RNA for nucleocapsid protein, strain (Tula/D540/Ma/95).
- U95304.1: Tula virus O20 nucleocapsid protein gene, partial cds.
- U95303.1: Tula virus O52 nucleocapsid protein gene, partial cds.
- U95302.1: Tula virus O24 nucleocapsid protein gene, partial cds.
- Z69991.1: Tula virus genomic RNA for nucleocapsid protein, strain (Tula/Moravia/5302v/95).
- Z49915.1: Tula virus segment S, strain Tula/Moravia/5302Ma/94, genomic RNA.
- Z48741.1: Tula virus segment S, strain Tula/Moravia/5294Ma/94, genomic RNA.
- Z48574.1: Tula virus segment S, strain Tula/Moravia/5293Ma/94, genomic RNA.
- Z48573.1: Tula virus segment S, strain Tula/Moravia/5286Ma/94, genomic RNA.







- M34011.1: Prospect Hill virus (PHV) S genomic segment encoding N protein, complete cds.  
**(Note)** Simultaneous detection of TULV and PUUV (at lower values).

**>seq271:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncnnnngnnnnnnnn  
cnnngaaaataaggggacaagaatccngntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngcnnnnnnnnnn  
nnnnntntnnnnnancnngnnngnnnnnggcnagnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnctgtcatgggtgtgattggnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (68/401): 16.9%**

**(B)**

Max score: 42.8

Total score: 42.8

Query coverage: 5%

E value: 9.5

Identity: 100%

- Y13984.1: Tula virus partial genomic RNA for nucleocapsid protein, strain (Tula/D540/Ma/95).
- Z69991.1: Tula virus genomic RNA for nucleocapsid protein, strain (Tula/Moravia/5302v/95).
- Z49915.1: Tula virus segment S, strain Tula/Moravia/5302Ma/94, genomic RNA.
- Z48741.1: Tula virus segment S, strain Tula/Moravia/5294Ma/94, genomic RNA.
- Z48574.1: Tula virus segment S, strain Tula/Moravia/5293Ma/94, genomic RNA.
- Z48573.1: Tula virus segment S, strain Tula/Moravia/5286Ma/94, genomic RNA.

**>seq272:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnacnannnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
cngnncnnnnntnnnnnnnangcccngtcangntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnt  
tttgnnnnnnnnnnnnngnnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnngnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (38/401): 9.5%**

**(B)**

No BLASTN identification.

**>seq273:Hantavirus\_Puumala\_2\_13-02-2013\_(VirIDv3r520827) Start=12 End=412**

```
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnngnnaactagngnnnacnannnnnn  
nnnnnnnnnnnnnnnaccggattcgatttaagnnnnntacatcattnaagncatcaannnnnnnnngnnnnnnnnnnnnnnnnnnnnnnntgn  
ntctntnnnnnnnnnnnnnnnnnnnnnnnagaagannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (84/401): 20.9%**

**(B)**

No BLASTN identification.

## SUPPLEMENT 4

### Validation of PathogenID v3.0 resequencing microarray using plasmids coding orthohantavirus N proteins: comparison between hybridization results obtained with PUUV Sotkamo alone and in a pool with TULV and HTNV.

Plasmid containing the S segment of Puumala virus (PUUV, strain Sotkamo 2009), were hybridized on the PathogenID v3.0 resequencing microarray separately or in pool with Tula virus (TULV, strain Moravia) and Hantaan virus (HTNV, strain 76/118) to compare the efficiency of hybridization.

For each PUUV sequence tiled on the microarray (seq222 - seq243), a comparative analysis is presented with PUUV alone or PUUV mixed with TULV and HTNV. This comparison includes Call Rate and BLASTN results detailed in Supplement 3.

Complementary informations are found in Table 2 and Figure 2.

PUUV sequence on the chip (position)	Call Rate PUUV (%)	Call Rate PUUV+TULV+HTNV (%)	BLASTN identification PUUV	BLASTN identification PUUV+TULV+HTNV
seq222	23.9	28.4	yes: Sotkamo	yes: Sotkamo
seq223	23.7	38.1	no	yes: Sotkamo
seq224	18.9	26.7	no	yes: Sotkamo
seq225	97.7	98.5	yes: Sotkamo	yes: Sotkamo
seq226	26.2	31.9	no	yes: Sotkamo + others <sup>°</sup>
seq227	39.6	42.9	yes: Sotkamo	yes: Sotkamo
seq228	22.7	33.9	yes: Sotkamo + others <sup>°</sup> Finland	yes: Sotkamo
seq229	19.4	27.9	no	yes: others <sup>°</sup>
seq230	33.9	38.6	yes: Sotkamo	yes: Sotkamo
seq231	75.0	78.0	yes: Sotkamo	yes: Sotkamo
seq232	34.4	44.9	yes: Sotkamo + others <sup>°</sup> Finland	yes: Sotkamo
seq233	19.7	27.4	yes: Sotkamo + others <sup>°</sup>	yes: others <sup>°</sup>
seq234	62.1	64.3	yes: Sotkamo	yes: Sotkamo
seq235	7.0	25.2	no	yes: PUUV+ TULV, HTNV
seq236	19.9	30.9	yes: Sotkamo + others <sup>°</sup>	yes: others <sup>°</sup>
seq237	35.2	40.9	yes: Sotkamo	yes: Sotkamo
seq238	24.7	27.2	no	no
seq239	34.4	41.9	yes: Sotkamo	yes: Sotkamo
seq240	38.3	46.6	yes: Sotkamo	yes: Sotkamo
seq241	26.9	32.2	no	no
seq242	30.8	35.8	yes: Sotkamo + others <sup>°</sup>	yes: Sotkamo + others <sup>°</sup>
seq243	25.1	35.1	no	no

<sup>°</sup> others: PUUV geographical isolates other than Sotkamo.

## SUPPLEMENT 5

### Detection and genetic characterization of hantavirus species endemic in Europe using the PathogenID v3.0 resequencing microarray: Call Rate and BLASTN analysis

Ampified cDNAs of RNA extracts from European rodents infected with hantaviruses or from hantavirus laboratory strains were hybridized on the PathogenID v3.0 resequencing microarray.

After hybridization of the samples to each hantavirus sequence tiled on the array (seq222 - seq273) the following parameters are indicated (A) the Call Rate (CR: % of determined/total number of nucleotides) of the output sequence; (B) the raw results when BLASTN analysis allowed virus/variant identification including: Max score, Total score, Query coverage, E value, Identity. When the same score was obtained for different sequences (multiple BLASTN identical results), all data are presented with corresponding accession number(s).

Complementary informations are found in Tables 3-7.

#### Species: Puumala orthohantavirus (PUUV)

#### Origin: France

#### PUUV 87 Ardennes

>seq222:1-09-04-2013\_(VirIDv3r520827) Start=12 End=412

```
ttggagtgtatgatttaggctncacacttctatctgtnnnntnnnnnnngntgtcancacgtggnagncaaactgtgaaagnaancnaag
ggctcgtatccgttncnnngnncacttctcgcaggnccnnngggnnnagnannnnnnnnnnnnnnngttccatgccnctgc
tcaatcaactatgaagcnnnnnnnnnnnnnnngggcgatttagaacannnnnnngtnnnnnnnnnnnnnancncaaattcaagnacgcaa
canaatgagccctgtnatngagnnnnnnnnnnnnnnnntncaagnnnnngcagancggattaggaattcatggnaaanntn
ncntttatcaaacagangnagncagncnncn
```

(A) CR (263/401): 65.6%

(B)

Max score: 226

Total score: 226

Query coverage: 98%

E value: 4e-55

Identity: 66%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

>seq223:1-09-04-2013\_(VirIDv3r520827) Start=12 End=412

```
ntntnnnnngntnnnnncnnncncnctctattatctgtnnnntnnnnnnnnngtgcancacgtggnagncaaactgtgaaagnann
nnnnnncnngannnnnnncncaagntgnnnnngnnnnnnnnnnnnnnnnnncgcagnnnnnnnnnnnnnnnnnngttccat
gccnctgctcaancaantnnngnnnnnnnnnnnnnnnnnnngggcgatttagaacatagntgtggtcnnntnnanctnnnnnnn
nnnnnnnnnnnnnnnnnntgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnggcagatcggnnnnnnnnnnn
nngngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (144/401): 35.9%**

**(B)**

Max score: 44.6

Total score: 89.1

Query coverage: 14%

E value: 2.5

Identity: 90%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.

**>seq230:1-09-04-2013\_(VirIDv3r520827) Start=12 End=412**

```
ttggagtgtatggtataggttcacacttctattatcctgaagccttatatatgtgtcaacacnnggnnnnnnnnnnnnnnaannnnnnnnnnnn  
nntcgnatccgttcaaagntgncacttctctcgaggacatcaatgggtatcaggnnncnncnncntcnnntgtttccangccnctgctcaatc  
aactatgaaggctgaagnannnnncctgggcgattagaaccanngtntgtgtctattccaactcaaattcaagnacgcaacanaatgagccc  
tgnnatgggagnnnnnnnnntnnnnntttgncaaggnnnngcagatcgntnnggnannnnnnnggnnaannngtgnnttttatcaaa  
ccagangngnngncagncn
```

**(A) CR (296/401): 73.8%**

**(B)**

Max score: 351

Total score: 351

Query coverage: 98%

E value: 1e-92

Identity: 74%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

**>seq237:1-09-04-2013\_(VirIDv3r520827) Start=12 End=412**

```
tggagtgtatggtataggttcacacttctattatcctgaagccttatatangttgtcancacnnggnnnnnnnnnnnnnnaagnanncn  
gnnnnnnnccgttncnannntgncacttctctcgaggacatcaatgggnncngnnnnnnnnnnncntcnnnttttccatgccnctgctca  
atcaactatganggctgaannannnacnctgggcgattagaaccanagtntgtgtcnaattccaactcaaattcaagnncgcaacanantgan  
ccctggnatgngagnnnnnnnntnnnnntttgncaaggnnnngcagntcggnnnnnnnnnnnnnggnnaaanngtgncntttat  
caaaccagnggnagnncannncn
```

**(A) CR (272/401): 67.8%**

**(B)**

Max score: 268

Total score: 268

Query coverage: 98%

E value: 1e-67

Identity: 69%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

**>seq238:1-09-04-2013\_(VirIDv3r520827) Start=12 End=290**

```
atnnnngnntggnnnnggcncncttctattatcctganggctnnnnnnnnntgtcancacgtggnagncannnnnnnnnnnnnn  
nnnnannngctcgnatccgttcaaagnnnnnnnnngnnnnnnngncannantggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

nnnccnctgctcaatcaactatgaaggcngnnnnnnnnnnnnntgnnnnntngancnngnntgtggtcnattccaactcaaattcaagnacgaac

**(A) CR (147/279): 52.7%**

**(B)**

Max score: 62.6

Total score: 108

Query coverage: 55%

E value: 6e-06

Identity: 68%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.
- AJ277034.1: Puumala virus RNA for nucleocapsid protein (N gene), strain Couvin/59Cg/97.
- AJ277033.1: Puumala virus RNA for nucleocapsid protein (N gene), strain Momignies/55Cg/96.
- AJ277032.1: Puumala virus RNA for nucleocapsid protein (N gene), strain Momignies/47Cg/96.

**>seq239:1-09-04-2013\_(VirIDv3r520827) Start=12 End=290**

attggngtgtatgtataggtcncacacttctattatcctgaaggctttatntatgtgtcancacnnggnnnnnnnnnnnnaagnnnnnnnnngnctcgatccgtttcaaaagntgncacttctctcaggacatcaatggtatcagnnnnnnnnnnnnnnnnnnnttccatgcennctgctcaatcaactatgaaggctgnagaattaacnctgggcgatttagaacanagntgtggtcnattccaactcaaattcaagnacgaac

**(A) CR (219/279): 78.5%**

**(B)**

Max score: 288

Total score: 288

Query coverage: 100%

E value: 9e-74

Identity: 78%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

**>seq240:1-09-04-2013\_(VirIDv3r520827) Start=12 End=290**

attggngtgtatgtataggtcncacacttctattatcctgnnnnntngnngnnnnntgtcancacgtgggnagncaaactgtgnnagnaanaaaaggactcgtatccgttncnnnnnnncnnnnncnaggnatcaatggatcaggannccnngcnnnnntgttccatgcennctgctcaatcaactatgaaggctgaaganntaacnctgggcgatttagaacatagtagtggtctattcnannncnanntcaagnacgaac

**(A) CR (216/279): 77.4%**

**(B)**

Max score: 268

Total score: 268

Query coverage: 100%

E value: 8e-68

Identity: 77%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.





- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

**>seq229:Lung29\_pure\_21-02-2013\_(VirIDv3r520827) Start=12 End=412**

```

nnncnnngnnnnnnnnnnncnnccnnnnntnnnnnnnnnnngnnnnntnnnnntatgtgtcaacacnngggngnnnnnnnnngggn
nnnnnnnnnnccggnnnnnnnnnngnnnnnnnnnggngnnnnnnnnnnannccnnnnccnnnnnnnnnnnnnnnnnnnnnn
gnnnnnnnnnccctnctgctcaatcaactatgaaggcngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnngngtntnnnnnnnn
nnnnnnnnccnnnnccnnnnnnnnngnnnnnccgntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnggncnnngcnnnn
nnnnntnngnnngcatggnaaaagagtgcenntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnggncnnnnnnnn

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**(A) CR (106/401): 26.4%**

**(B)**

Max score: 44.6

Total score: 44.6

Query coverage: 6%

E value: 2.7

Identity: 96%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KU670634.1: Puumala hantavirus isolate KS11/2387 nucleocapsid protein gene, partial cds.
- KU670633.1: Puumala hantavirus isolate KS11/2384 nucleocapsid protein gene, partial cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.
- DQ322681.1: Puumala virus strain Cologne Mu05/273 nucleocapsid protein (N) gene, partial cds.
- DQ322679.1: Puumala virus strain Cologne Mu05/270 nucleocapsid protein (N) gene, partial cds.
- DQ322678.1: Puumala virus strain Cologne Mu05/269 nucleocapsid protein (N) gene, partial cds.
- DQ322676.1: Puumala virus strain Cologne Mu05/262 nucleocapsid protein (N) gene, partial cds.
- DQ322675.1: Puumala virus strain Cologne Mu05/258 nucleocapsid protein (N) gene, partial cds.
- DQ322672.1: Puumala virus strain Cologne Mu05/244 nucleocapsid protein (N) gene, partial cds.
- DQ322670.1: Puumala virus strain Cologne Mu05/242 nucleocapsid protein (N) gene, partial cds.
- DQ322669.1: Puumala virus strain Cologne Mu05/241 nucleocapsid protein (N) gene, partial cds.
- EU004036.1: Puumala virus strain Kob13/05 nucleocapsid protein (N) mRNA, partial cds.
- DQ408276.1: Puumala virus strain Cologne Mu05/162 nucleocapsid (N) gene, partial cds.
- DQ408275.1: Puumala virus strain Cologne Mu05/161 nucleocapsid (N) gene, partial cds.
- DQ408274.1: Puumala virus strain Cologne Mu05/286 nucleocapsid (N) gene, partial cds.
- DQ408273.1: Puumala virus strain Cologne Mu05/285 nucleocapsid (N) gene, partial cds.
- DQ408271.1: Puumala virus strain Cologne Mu05/281 nucleocapsid (N) gene, partial cds.
- DQ408268.1: Puumala virus strain Cologne Mu05/274 nucleocapsid (N) gene, partial cds.
- AJ277076.1: Puumala virus RNA for nucleocapsid protein (n gene), strain CG14445.
- AJ277075.1: Puumala virus RNA for nucleocapsid protein (n gene), strain CG14444.
- AJ277034.1: Puumala virus RNA for nucleocapsid protein (N gene), strain Couvin/59Cg/97.
- AJ277033.1: Puumala virus RNA for nucleocapsid protein (N gene), strain Momignies/55Cg/96.
- AJ277032.1: Puumala virus RNA for nucleocapsid protein (N gene), strain Momignies/47Cg/96.
- AJ277031.1: Puumala virus RNA for nucleocapsid protein (N gene), strain Montbliart/23Cg/96.
- AJ238788.1: Puumala virus RNA for nucleocapsid protein, strain Karhumaki.
- AJ238779.1: Puumala virus mRNA for nucleocapsid protein.

**>seq230:Lung29\_pure\_21-02-2013\_(VirIDv3r520827) Start=12 End=412**



attggannngnangtnnnnggctncncncttctattatcctgaaggctntanntntgttgcaacacgtgggagacaaacnnngnnnnnnnnnn  
nagnnctcgtatccgtttcaaagntnncnnngnnnnncngnacancaatggngncnnnnnnnnnnnnnnnnngnnnnnnnnntnncntgccn  
nctgctcaatcaactatgaaggctgaagannaannncngnncgntttagaacannngtatgtggtcnaattccaanncaantcaagnacgcaa  
c

**(A) CR (190/279): 68.1%**

**(B)**

Max score: 156

Total score: 156

Query coverage: 100%

E value: 4e-34

Identity: 66%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

**>seq239:Lung29\_pure\_21-02-2013\_(VirIDv3r520827) Start=12 End=290**

attggagtgtatgtataggcttcacacttctattatcctgaaggctttatatgttgcaacacntgggnagnnnnnnnngaaagnaaacanagn  
gnctcgtatccgtttcaaagatgacacttctcctcaggacatcaatggatcaggannnnnnngnnnnnnntgtttccatgccnactgctcaatca  
actatgaaggctgaagaattaacnctgggcgatttagaacatagtatgtggtctattccaactcaaattcaagtacgcaac

**(A) CR (248/279): 88.9%**

**(B)**

Max score: 392

Total score: 392

Query coverage: 100%

E value: 3e-105

Identity: 89%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

**>seq240:Lung29\_pure\_21-02-2013\_(VirIDv3r520827) Start=12 End=290**

attggagtgtatgtataggcttcacacttctattatcctgannnnnnnnngnnnnntgtcaacacgtgggagncaaactgtgaaagaaaacaaag  
ggactcgtatccgtttcnaagntgncactnctncnaggacatcaatggatcaggagaccanagcatcnatattgtttccatgccnactgctcaatca  
actatgaaggctgaagaattaaccctgggcgatttagaacatagtatgtggtctattccancncaaattcaagtacgcaac

**(A) CR (254/279): 91.0%**

**(B)**

Max score: 408

Total score: 408

Query coverage: 100%

E value: 4e-110

Identity: 91%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

>seq241:Lung29\_pure\_21-02-2013\_(VirIDv3r520827) Start=12 End=290

attggagtgtatgtatagnnnnncnnncntncnnttatcctgaagcctttatatatgttgcaacacgtgggagncaaaactgtgaaagaaaacaagg  
gactcgtatccgtttcaagntgacacttccttcgaggacatcaatggatcaggannnnnnnnnnnnnnnnnttccatgccnactgctcaatc  
aactangaaggcngnngnnnaannnctgggcgatttagaacatagtagtggtctatttccaactcaaatcaagtaacanc

(A) CR (235/279): 84.2%

(B)

Max score: 345

Total score: 345

Query coverage: 99%

E value: 4e-91

Identity: 84%

- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.

**Origin: Germany**

**PUUV Mu557 Gilserberg/10**

>seq223:19\_16-09-2014\_(VirIDv3r520827) Start=12 End=412

ttngtgntnnnnnnanngggtncncnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnncgngcgnctntgggagacaaacnnnnnnn  
nnnnnnnnnnncnncgannnnnnnnnnngnncnncnnttncattgngnnnnncntnncngcaggangcnnnnncnnnnnnnnnn  
nnnnnnnnnagetgctcaatcaaccatgaaagctgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnngnctatttccaacnc  
nnnnnngnntnncgnnataatgagtcctgtgntggnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnngcnnnnnnnnnnnn  
nnnnnnngnngnnnnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (134/401): 33.4%

(B)

Max score: 44.6

Total score: 44.6

Query coverage: 5%

E value: 2.5

Identity: 100%

- MF687747.1: Tula orthohantavirus strain Tul/NL/Ma89-Twente/2007 nucleocapsid protein gene, partial cds.
- MF687746.1: Tula orthohantavirus strain Tul/NL/Ma135-Fr-A&W/2015 nucleocapsid protein gene, partial cds.
- MF687745.1: Tula orthohantavirus strain Tul/NL/Ma3-Fr-Nes/2015 nucleocapsid protein gene, partial cds.
- MF687744.1: Tula orthohantavirus strain Tul/NL/Ma1964-Fr-Feyte/2015 nucleocapsid protein gene, partial cds.
- MF687743.1: Tula orthohantavirus strain Tul/NL/Ma117-Fr-A&W/2015 nucleocapsid protein gene, partial cds.
- MF687742.1: Tula orthohantavirus strain Tul/NL/Ma75-Fr-A&W/2015 nucleocapsid protein gene, partial cds.
- MF687741.1: Tula orthohantavirus strain Tul/NL/Ma126-Fr-A&W/2015 nucleocapsid protein gene, partial cds.
- KU670641.1: Puumala hantavirus isolate Mu07/116 nucleocapsid protein gene, partial cds.
- KU670632.1: Puumala hantavirus isolate KS11/1342 nucleocapsid protein gene, partial cds.
- KU139600.1: Tula virus isolate 08\_0277\_Marv nucleocapsid protein gene, partial cds.
- KU139599.1: Tula virus isolate 08\_0260\_Marv nucleocapsid protein gene, partial cds.

- KU139598.1: Tula virus isolate 08\_1033\_Marv nucleocapsid protein gene, partial cds.
- KU139597.1: Tula virus isolate 10\_0215\_Marv nucleocapsid protein gene, partial cds.
- KU139558.1: Tula virus isolate D34\_Gato\_Marv nucleocapsid protein gene, partial cds.
- KU139553.1: Tula virus isolate 09\_1477\_Marv nucleocapsid protein gene, partial cds.
- KU139531.1: Tula virus isolate 10\_0029\_Marv nucleocapsid protein gene, partial cds.
- KU139529.1: Tula virus isolate 09\_2375\_Marv nucleocapsid protein gene, partial cds.
- KU139528.1: Tula virus isolate 09\_2324\_Marv nucleocapsid protein gene, partial cds.
- **JN696368.1: Puumala virus strain Mu557Gilsberg/10 nucleocapsid protein (N) gene, partial cds.**
- JN696333.1: Puumala virus strain H347Melsungen/10 nucleocapsid protein (N) gene, partial cds.
- GU300143.1: Puumala virus strain Sen05/176 nucleocapsid protein gene, partial cds.
- GU300140.1: Puumala virus strain Sen05/120 nucleocapsid protein gene, partial cds.
- GU300138.1: Puumala virus strain Sen05/107 nucleocapsid protein gene, partial cds.
- EF409820.1: Tula virus strain Brandenburg Mu95/1335 nucleocapsid protein (N) gene, partial cds.
- EF409819.1: Tula virus strain Brandenburg Mu95/1272 nucleocapsid protein (N) gene, partial cds.
- EF409818.1: Tula virus strain Brandenburg Mu95/1049 nucleocapsid protein (N) gene, partial cds.
- EF409817.1: Tula virus strain Brandenburg Mu05/520 nucleocapsid protein (N) gene, partial cds.

**>seq230:19\_16-09-2014\_(VirIDv3r520827) Start=12 End=412**

ttggngntngnnnnnnnncnncnnnnnnnccccnnnnnnnnngnnnnngnnnnngngncntnnnnnnnnannnnnnn  
 nnnnnnnnccccnnncacnnnnnnnnnnncnnncnnnnngnnnnngntggagatcaatggatcaggangcnnnnncnnnnnnnn  
 nnnnnnnnnnactgctcaatnaaccnngnnancnnnnnnncngnnnnnnnnnnngnnnnnnnnnnngtggctatttccaaact  
 caaatcaggntcgcancanaatgagtcntngnntnnnnngnnnnnnnnnnngnnnnnnnnnnnannnnnnnn  
 nnnnnntnngnnnnnnncnnnnngnnnnngnnnnnnnnngnnnnnnnnngnnnnnnnn

**(A) CR (137/401): 34.2%**

**(B)**

Max score: 77.0

Total score: 121

Query coverage: 18%

E value: 4e-10

Identity: 92%

- JN696368.1: Puumala virus strain Mu557Gilsberg/10 nucleocapsid protein (N) gene, partial cds.

**>seq233:19\_16-09-2014\_(VirIDv3r520827) Start=12 End=412**

nnnnatntnnnnnnnnngggtcnnnnnnnnnnnnnnnnnnnnnttatacatgtatcaaccntggngncaaannnnngnnnnnn  
 nnnnnnnnnnnngtattcgatttaaggncgaccttctgaggacannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnngctnnnnnnnnngnnnnnnnnnnngnnnnnnnnnnngngnnnnntctatttccaaactcaaan  
 ncngnnnnncnnnaanaatgagtcctgtgatggnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngn  
 tnatggaanannngncnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (142/401): 35.4%**

**(B)**

Max score: 62.6

Total score: 153

Query coverage: 29%

E value: 9e-06

Identity: 97%

- JN696368.1: Puumala virus strain Mu557Gilsberg/10 nucleocapsid protein (N) gene, partial cds.

**>seq234:19\_16-09-2014\_(VirIDv3r520827) Start=12 End=238**

ncagacattcagnggatataaccgccannaancgncnnnnngnttgctngacaaaagctcaaggatgnagnnnnnnnnnngnnanng  
gaccagatgacgttaacaaaacanacnncannnnnncaacaancagnnngngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnng  
nnnnngnnnnnnnnngnncnnnnnaaagatggatacnnnnnnnnctga

**(A) CR (123/227): 54.2%**

**(B)**

Max score: 80.6

Total score: 80.6

Query coverage: 51%

E value: 2e-11

Identity: 70%

- Select seq KU314905.1: Puumala virus strain PUUV/NL/Mg591/2008 nucleocapsid protein gene, complete cds.
- Select seq DQ094844.1: Puumala virus strain Heidelberg/hu nucleocapsid protein (NP) gene, partial cds.

**>seq236:19\_16-09-2014\_(VirIDv3r520827) Start=12 End=412**

nnnnnnnnngnnnnnnnnncnnnnnnnnnnnnnnnnngncnnnnntatacatgtatcaaccntggnnnncaaacnnnnnnnn  
nnnnnnnnncnnnnngtattcgatttaaggncgacacttcattgaggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnancnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
aannncngnnnnnnnnnnnnntgagtcctgtgatggnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnngnnnnnnnnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnngnnn

**(A) CR (115/401): 28.7%**

**(B)**

Max score: 57.2

Total score: 57.2

Query coverage: 8%

E value: 4e-04

Identity: 97%

- JN696368.1: Puumala virus strain Mu557Gilsberg/10 nucleocapsid protein (N) gene, partial cds.

**>seq237:19\_16-09-2014\_(VirIDv3r520827) Start=12 End=412**

tggngntngnnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnccnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnagctgctcaatnaaccnngnnnancnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
caaattcagntcgcannanaatgagtcctgngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (130/401): 32.4%**

**(B)**

Max score: 73.4

Total score: 73.4

Query coverage: 11%

E value: 5e-09

Identity: 92%

- JN696368.1: Puumala virus strain Mu557Gilsberg/10 nucleocapsid protein (N) gene, partial cds.

**>seq238:19\_16-09-2014\_(VirIDv3r520827) Start=12 End=290**

attggagntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
gngnnnnnnnnccnncnncnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nngannnnnnncanctgctcaatnaaccnngnnnancnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
ctcaaattcagntcgcann

**(A) CR (115/279): 41.2%**

**(B)**

Max score: 57.2

Total score: 57.2

Query coverage: 11%







- KR047195.1: Puumala virus strain astrup\_07\_005 nucleocapsid protein gene, partial cds.
- KJ994776.1: Puumala virus isolate Mu/07/1219 segment S, complete sequence.
- JN696365.1: Puumala virus strain Mu3072Bramsche/10 nucleocapsid protein (N) gene, partial cds.
- **JN696364.1: Puumala virus strain Mu2232Bramsche/09 nucleocapsid protein (N) gene, partial cds.**
- JN696358.1: Puumala virus strain Mu362Osnabrueck/05 nucleocapsid protein (N) gene, complete cds.
- JN696355.1: Puumala virus strain Mu727Astrup/07 nucleocapsid protein (N) gene, partial cds.
- JN696337.1: Puumala virus strain H362Melle/10 nucleocapsid protein (N) gene, partial cds.
- JN696336.1: Puumala virus strain H368Bad\_Iburg/10 nucleocapsid protein (N) gene, partial cds.
- JN696335.1: Puumala virus strain H358Ostercappeln/10 nucleocapsid protein (N) gene, partial cds.
- JN696332.1: Puumala virus strain H389Gramberg/10 nucleocapsid protein (N) gene, partial cds.
- JN696323.1: Puumala virus strain H156Ostercappeln/10 nucleocapsid protein (N) gene, partial cds.

>seq229:20\_16-09-2014\_(VirIDv3r520827) Start=12 End=412

nnnnngntnnnnnnnngctnnnnncntnnncnnnnnnncnnnnnnngnnnnnnnnancannnnnnangnnnnnnnnnnngn  
 nnnnnnnnnnnnnngangtattcggttaaggatgatacttcattnnnnnnnnnnnnncnnnnnnnnnnnnnnnnccnnnnnnngt  
 ccatgccaactgencaatcaacnngaaggctgaagnnnnngnanncngnnnnannnnnnnnnnnnnnnnnnnnnnntnnntccanctcag  
 nntnnnnnggnnnnncnnnnngngcnnngngntgggggttataggctnnnnanncnnntgtcaaggattngcagatcggnntnnnnannng  
 nnnngnnnnncnangncnnnnnnngcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (159/401): 39.7%

(B)

Max score: 55.4  
 Total score: 158  
 Query coverage: 28%  
 E value: 0.001  
 Identity: 89%

- KU670640.1: Puumala hantavirus isolate KS10/3078 nucleocapsid protein gene, partial cds.
- KU670639.1: Puumala hantavirus isolate KS14/778 nucleocapsid protein gene, partial cds.
- KU670638.1: Puumala hantavirus isolate KS14/766 nucleocapsid protein gene, partial cds.
- KU670637.1: Puumala hantavirus isolate KS14/873 nucleocapsid protein gene, partial cds.
- KU670636.1: Puumala hantavirus isolate KS14/833 nucleocapsid protein gene, partial cds.
- KU670635.1: Puumala hantavirus isolate KS14/715 nucleocapsid protein gene, partial cds.

>seq233:20\_16-09-2014\_(VirIDv3r520827) Start=12 End=412

nnnganntnnnnnnnncggctnnncncntnnnnnnnnnnncnnnnnnnnnnncnnnnnnntatcaacacgtgggagacagactgnnnaa  
 nnnnnnnnnnncggnnnnnnnnngnnnnngncngntactnnannnnngngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nngnnnnnnnnnnnnnnnnnnnnnnnnnnnnngcnnnnnnnnngnnngnnncnnnnngnnnnnnntnnnnnnnnnnnnnnnnnnnn  
 nnnnnnncagnttcaagtcgaaacataatgagcncctgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntgggcagntcgg  
 nnnnnannngnnnnngnnnnnanaangnnnnnttantnnnnnnnnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (114/401): 28.4%

(B)

Max score: 50.0  
 Total score: 94.5  
 Query coverage: 13%  
 E value: 0.064  
 Identity: 94%

- KU670640.1: Puumala hantavirus isolate KS10/3078 nucleocapsid protein gene, partial cds.
- KU670639.1: Puumala hantavirus isolate KS14/778 nucleocapsid protein gene, partial cds.

>seq234:20\_16-09-2014\_(VirIDv3r520827) Start=12 End=238

nnnnnnnnnaanngnanataaccngccatgaacnnnnnnnnngnnnnncnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnngcagtg  
 ngatggnccngatgacgttnacangntnnnnnnannccnnnnnnnaannagtgnnagcattgnnnnacaaactgcagacannnnnn  
 nnnnnnnngnnnnnnnnngngnnnnnnnnncnnaacngnnnnncnnannnnncnna

(A) CR (93/227): 41.0%

(B)

Max score: 48.2

Total score: 48.2

Query coverage: 39%

E value: 0.12

Identity: 64%

- KJ994776.1: Puumala virus isolate Mu/07/1219 segment S, complete sequence.
- JN696358.1: Puumala virus strain Mu362Osnabrueck/05 nucleocapsid protein (N) gene, complete cds.

>seq242:20\_16-09-2014\_(VirIDv3r520827) Start=12 End=290

nnnnnannnnnnnnnnnnnnncnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntatcaacacgtgggagncagnnngngn  
nannaanaaaaggacagctattcggtttnggngntnnnnnnnnnnngntnnnnnnnnnnngnnnnngnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnncnncnnnnnnncnnnnngnggcnnnnnnnnnnngngngntnnncnagaactannnnnnnnnnnnnnnn  
nnnnncagntncnnnnngnnanan

(A) CR (85/279): 30.5%

(B)

Max score: 60.8

Total score: 60.8

Query coverage: 20%

E value: 2e-05

Identity: 80%

- KU670640.1: Puumala hantavirus isolate KS10/3078 nucleocapsid protein gene, partial cds.
- KR047313.1: Puumala virus strain varus\_12\_032 nucleocapsid protein gene, partial cds.
- KR047309.1: Puumala virus strain varus\_10\_026 nucleocapsid protein gene, partial cds.
- KR047308.1: Puumala virus strain tower\_07\_001 nucleocapsid protein gene, partial cds.
- JN696365.1: Puumala virus strain Mu3072Bramsche/10 nucleocapsid protein (N) gene, partial cds.
- **JN696364.1: Puumala virus strain Mu2232Bramsche/09 nucleocapsid protein (N) gene, partial cds.**
- JN696339.1: Puumala virus strain H372Bissendorf/10 nucleocapsid protein (N) gene, partial cds.
- JN696338.1: Puumala virus strain H363Bissendorf/10 nucleocapsid protein (N) gene, partial cds.
- JN696336.1: Puumala virus strain H368Bad\_Iburg/10 nucleocapsid protein (N) gene, partial cds.
- JN696334.1: Puumala virus strain H357Bissendorf/10 nucleocapsid protein (N) gene, partial cds.
- JN696322.1: Puumala virus strain H137Bissendorf/10 nucleocapsid protein (N) gene, partial cds.

>seq243:20\_16-09-2014\_(VirIDv3r520827) Start=12 End=290

attgganntnnnnnnncnncnncnncncttncnncnncnncnaaggcncnnnnnnnnnnnnncnnnnnnnnnnnnnnnnnnnnn  
nnnnnnncnnncngagnnnnnnngnttngnnnnnnnnnnnnnnnnnnnnnggngngngngnnnnnnnnnnnnnnnnngn  
nnnnnnncntgccancngntnnaactatgaaggctgaagngntgnnnnnnnnnnntncgnnnnnnnnnnngnnnnnnnnnnnnn  
cnnnnnnnnnnntnnnnnnnagnc

(A) CR (84/279): 30.1%

(B)

Max score: 44.6

Total score: 44.6

Query coverage: 13%

E value: 1.7

Identity: 82%

- KU670640.1: Puumala hantavirus isolate KS10/3078 nucleocapsid protein gene, partial cds.
- KU670639.1: Puumala hantavirus isolate KS14/778 nucleocapsid protein gene, partial cds.
- KU670638.1: Puumala hantavirus isolate KS14/766 nucleocapsid protein gene, partial cds.
- KU670637.1: Puumala hantavirus isolate KS14/873 nucleocapsid protein gene, partial cds.
- KU670636.1: Puumala hantavirus isolate KS14/833 nucleocapsid protein gene, partial cds.
- KU670635.1: Puumala hantavirus isolate KS14/715 nucleocapsid protein gene, partial cds.

- KR047313.1: Puumala virus strain varus\_12\_032 nucleocapsid protein gene, partial cds.
- KR047309.1: Puumala virus strain varus\_10\_026 nucleocapsid protein gene, partial cds.
- KR047308.1: Puumala virus strain tower\_07\_001 nucleocapsid protein gene, partial cds.
- KR047300.1: Puumala virus strain schle\_12\_148 nucleocapsid protein gene, partial cds.
- KR047294.1: Puumala virus strain schle\_12\_141 nucleocapsid protein gene, partial cds.
- KR047284.1: Puumala virus strain schle\_11\_124 nucleocapsid protein gene, partial cds.
- KR047281.1: Puumala virus strain schle\_11\_110 nucleocapsid protein gene, partial cds.
- KR047259.1: Puumala virus strain schle\_08\_059 nucleocapsid protein gene, partial cds.
- KR047257.1: Puumala virus strain schle\_08\_053 nucleocapsid protein gene, partial cds.
- KR047252.1: Puumala virus strain schle\_05\_015 nucleocapsid protein gene, partial cds.
- KR047246.1: Puumala virus strain eller\_10\_029 nucleocapsid protein gene, partial cds.
- KR047245.1: Puumala virus strain eller\_10\_028 nucleocapsid protein gene, partial cds.
- KR047244.1: Puumala virus strain eller\_08\_025 nucleocapsid protein gene, partial cds.
- KR047228.1: Puumala virus strain astrup\_12\_067 nucleocapsid protein gene, partial cds.
- KR047225.1: Puumala virus strain astrup\_11\_062 nucleocapsid protein gene, partial cds.
- KR047207.1: Puumala virus strain astrup\_09\_042 nucleocapsid protein gene, partial cds.
- KR047202.1: Puumala virus strain astrup\_08\_033 nucleocapsid protein gene, partial cds.
- KR047199.1: Puumala virus strain astrup\_07\_017 nucleocapsid protein gene, partial cds.
- KR047195.1: Puumala virus strain astrup\_07\_005 nucleocapsid protein gene, partial cds.
- KJ994776.1: Puumala virus isolate Mu/07/1219 segment S, complete sequence.
- JN696365.1: Puumala virus strain Mu3072Bramsche/10 nucleocapsid protein (N) gene, partial cds.
- **JN696364.1: Puumala virus strain Mu2232Bramsche/09 nucleocapsid protein (N) gene, partial cds.**
- JN696358.1: Puumala virus strain Mu362Osnabrueck/05 nucleocapsid protein (N) gene, complete cds.
- JN696355.1: Puumala virus strain Mu727Astrup/07 nucleocapsid protein (N) gene, partial cds.
- JN696340.1: Puumala virus strain H373Osnabrueck/10 nucleocapsid protein (N) gene, partial cds.
- JN696339.1: Puumala virus strain H372Bissendorf/10 nucleocapsid protein (N) gene, partial cds.
- JN696338.1: Puumala virus strain H363Bissendorf/10 nucleocapsid protein (N) gene, partial cds.
- JN696337.1: Puumala virus strain H362Melle/10 nucleocapsid protein (N) gene, partial cds.
- JN696336.1: Puumala virus strain H368Bad\_Iburg/10 nucleocapsid protein (N) gene, partial cds.
- JN696335.1: Puumala virus strain H358Ostercappeln/10 nucleocapsid protein (N) gene, partial cds.
- JN696334.1: Puumala virus strain H357Bissendorf/10 nucleocapsid protein (N) gene, partial cds.
- JN696332.1: Puumala virus strain H389Gramberg/10 nucleocapsid protein (N) gene, partial cds.
- JN696323.1: Puumala virus strain H156Ostercappeln/10 nucleocapsid protein (N) gene, partial cds.
- JN696322.1: Puumala virus strain H137Bissendorf/10 nucleocapsid protein (N) gene, partial cds.
- JN696321.1: Puumala virus strain H126Muenster/10 nucleocapsid protein (N) gene, partial cds.
- JN696317.1: Puumala virus strain H400Samern/10 nucleocapsid protein (N) gene, partial cds.

**PUUV Mu978 Weissach/10**

>seq222:21\_16-09-2014\_(VirIDv3r520827) Start=12 End=412

```
gngngngnggnnnnccgnannncactctctatntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngncntgggagacaaactgtganggn
aaacaaagggactcgtatccggtttaagatgncactntttcaggacattaatggcnggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncnnc
cgncgtcctcaatcnacnngnnnnncngnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncagatt
caagnacgcaatnnnnnnannnnnggnnttncnnnnnnnnnnnnnnnnnnngnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnggggan
ngnnnnnnnnnnnnntnnnnnttcacannnnnnnnnnnnngncannncnn
```

(A) CR (170/401): 42.4%

(B)

Max score: 129

Total score: 129

Query coverage: 20%

E value: 8e-26

Identity: 94%

- KU670631.1: Puumala hantavirus isolate Mu10/1001 nucleocapsid protein gene, partial cds.
- **JN696370.1: Puumala virus strain Mu978Weissach/10 nucleocapsid protein (N) gene, partial cds.**
- JN696360.1 : Puumala virus strain Mu1054Heimerdingen2/10 nucleocapsid protein (N) gene, partial cds.
- EU085562.1: Puumala virus strain Weissach31 nucleocapsid protein gene, partial cds.
- EU085558.1: Puumala virus strain Hemmingen13 nucleocapsid protein gene, partial cds.
- EU085559.1: Puumala virus strain Weissach20 nucleocapsid protein gene, partial cds.

**>seq224:21\_16-09-2014\_(VirIDv3r520827) Start=12 End=412**

```
ttggggttnnnnnnnnnncnnnnnnnnnnntnnnnngnnnnnnnnnnntgttatcaacccgtgggagncaannnnngnnngna  
aaacaaaggactcgtatccgggttaaagatgncngngnnnnnnggacattaatggtnnnnnannnnccaaagcattgtatgtccatgngn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnngggttcagnnnnnnnnntngtnnnnnnnnnncngncncagattcaa  
gtacgcaatatantngtntgncnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (195/401): 48.6%**

**(B)**

Max score: 123

Total score: 172

Query coverage: 40%

E value: 4e-24

Identity: 78%

- KU670631.1: Puumala hantavirus isolate Mu10/1001 nucleocapsid protein gene, partial cds.
- **JN696370.1: Puumala virus strain Mu978Weissach/10 nucleocapsid protein (N) gene, partial cds.**
- JN696360.1: Puumala virus strain Mu1054Heimerdingen2/10 nucleocapsid protein (N) gene, partial cds.

**>seq234:21\_16-09-2014\_(VirIDv3r520827) Start=12 End=238**

```
acagacattcagnggatataacngccatgaacannnnnnngtggcagncaaangetcaaggatgnagnnnnnnnnnnnnnnnnnnnn  
accagatgacgttaacaaaaancanacnncangnaaggcaacngcagtggnagctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nangcnnnnnnnnngnnnnnnnnnaaagatggannnnnaannngcna
```

**(A) CR (135/227): 59.5%**

**(B)**

Max score: 132

Total score: 132

Query coverage: 64%

E value: 4e-27

Identity: 75%

- DQ094844.1: Puumala virus strain Heidelberg/hu nucleocapsid protein (NP) gene, partial cds.

**>seq240:21\_16-09-2014\_(VirIDv3r520827) Start=12 End=290**

```
ngnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngngcngtgggagacaaactgtgngg  
naaacaaggactcgtatccgggttaaagatgncnctntnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nngcngctgtcaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
cagattcaagtacgcaat
```

**(A) CR (127/279): 45.5%**

**(B)**

Max score: 89.7

Total score: 89.7

Query coverage: 21%

E value: 4e-14

Identity: 92%

- KU670631.1: Puumala hantavirus isolate Mu10/1001 nucleocapsid protein gene, partial cds.
- **JN696370.1: Puumala virus strain Mu978Weissach/10 nucleocapsid protein (N) gene, partial cds.**
- JN696360.1: Puumala virus strain Mu1054Heimerdingen2/10 nucleocapsid protein (N) gene, partial cds.
- EU085562.1: Puumala virus strain Weissach31 nucleocapsid protein gene, partial cds.
- EU085558.1: Puumala virus strain Hemmingen13 nucleocapsid protein gene, partial cds.
- EU085559.1: Puumala virus strain Weissach20 nucleocapsid protein gene, partial cds.

>seq241:21\_16-09-2014\_(VirIDv3r520827) Start=12 End=290

ngnngngnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngncnnngggagacaaactgtg  
 nnggnaaacaagggactcgtatcnggtttaaagnnnncactntttcgagnncantnnnnncnggnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnncgncgtctcaatcaaccannnnnnncngnnnnnnngnannnnnnnnnnnnnnnnnnnnnnnnngngnnnnnnnnnnng  
 nnnngnttcaagtacgcaat

(A) CR (112/279): 40.1%

(B)

Max score: 87.8

Total score: 87.8

Query coverage: 23%

E value: 2e-13

Identity: 86%

- KU670631.1: Puumala hantavirus isolate Mu10/1001 nucleocapsid protein gene, partial cds.
- **JN696370.1: Puumala virus strain Mu978Weissach/10 nucleocapsid protein (N) gene, partial cds.**
- JN696360.1: Puumala virus strain Mu1054Heimerdingen2/10 nucleocapsid protein (N) gene, partial cds.
- EU085562.1: Puumala virus strain Weissach31 nucleocapsid protein gene, partial cds.
- EU085558.1: Puumala virus strain Hemmingen13 nucleocapsid protein gene, partial cds.
- EU085559.1: Puumala virus strain Weissach20 nucleocapsid protein gene, partial cds.

>seq242:21\_16-09-2014\_(VirIDv3r520827) Start=12 End=290

nntgggnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngncntgtatcaaccggtggagacaaactgngnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 ggnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
 ggnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (110/279): 39.4%

(B)

Max score: 75.2

Total score: 75.2

Query coverage: 40%

E value: 1e-09

Identity: 69%

- KU670631.1: Puumala hantavirus isolate Mu10/1001 nucleocapsid protein gene, partial cds.
- **JN696370.1: Puumala virus strain Mu978Weissach/10 nucleocapsid protein (N) gene, partial cds.**
- JN696360.1: Puumala virus strain Mu1054Heimerdingen2/10 nucleocapsid protein (N) gene, partial cds.
- EU085562.1: Puumala virus strain Weissach31 nucleocapsid protein gene, partial cds.
- EU085558.1: Puumala virus strain Hemmingen13 nucleocapsid protein gene, partial cds.
- EU085559.1: Puumala virus strain Weissach20 nucleocapsid protein gene, partial cds.

**Origin: Finland**

**PUUV laboratory strain Sotkamo**

**>seq222:PUUV\_Finland\_cells\_(VirIDv3r520827) Start=12 End=412**

ttggagtgtatgtgntnggggttcacacttctnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnngggannnnngnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnntctatgncngcnnccccgnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnancnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (96/401): 23.9%**

**(B)**

Max score: 51.8  
Total score: 51.8  
Query coverage: 7%  
E value: 0.017  
Identity: 94%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq225:PUUV\_Finland\_cells\_(VirIDv3r520827) Start=12 End=412**

ttggagtgtatgtgatagggttcacacttctatcatccttaaagctttatacatgctctcaacgcnnnnagacagactgtaaaggaaaataagggga  
cacgtataaggttaaggatgatacatcattgaagacatcaatggcataaggagaccaaagcatttatatgttctatgccnactgccagtcacnnt  
gaaagcagaagaactcacacnngcagattcgcacaatagatgtggtcttttccactcagatccaggttcgnaacatcatgagtcagttatgn  
nggtcattggttttctttgtgaaagattggtctgagagaatcagagagttcatggaaaaagagtgccattcataaagcctgaagnaaaccng  
gcaca

**(A) CR (387/401): 96.5%**

**(B)**

Max score: 673  
Total score: 673  
Query coverage: 100%  
E value: 0.0  
Identity: 97%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq227:PUUV\_Finland\_cells\_(VirIDv3r520827) Start=12 End=412**

ttggagtgtatgtgannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (116/401): 28.9%**

**(B)**

Max score: 51.8  
Total score: 51.8  
Query coverage: 6%  
E value: 0.017  
Identity: 100%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq228:PUUV\_Finland\_cells\_(VirIDv3r520827) Start=12 End=412**



Max score: 50.0  
Total score: 50.0  
Query coverage: 7%  
E value: 0.064  
Identity: 94%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq231:PUUV\_Finland\_cells\_(VirIDv3r520827) Start=12 End=412**

nnnnnnngnnnnnnnnnnngnncnnnnnagntnncgnnnnnnnagcttntnnnnnnncncnnnnangnnngggngacagactgtaaag  
gaaaaaagggnacacgtataagggttaaggatgatacatcattggaagacatcaatggcataaggngaccaaaagcatttatatgtttctatgcctact  
gccagtaactangnnancagaagaactcacaccaggcagatttcgcncaatagtagtggcctntnncnnnnnnnnncgntngtaac  
atcatgagtccagttatgnnnnnncnnnnntnnnnnnnncnnnnngnnnnnattggctgagagaatcagagagttcatggaaaaagagtgccca  
ttcnnaaagcnnnnntnngnngnnnnnnga

**(A) CR (281/401): 70.1%**

**(B)**

Max score: 361  
Total score: 361  
Query coverage: 78%  
E value: 8e-96  
Identity: 82%

- HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.

**>seq232:PUUV\_Finland\_cells\_(VirIDv3r520827) Start=12 End=412**

nnggnntgngngnnnnnnngnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnagacngnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
ntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (110/401): 27.4%**

**(B)**

Max score: 68.0  
Total score: 68.0  
Query coverage: 10%  
E value: 2e-07  
Identity: 93%

- **HE801633.1: Puumala virus N and Ns genes, segment S, genomic RNA, strain Sotkamo 2009.**
- AJ314597.1: Puumala virus mRNA for nucleocapsid protein (N gene), strain Pallasjarvi/63Cg/98.
- AJ238789.1: Puumala virus RNA for nucleocapsid protein, strain Kolodozero.
- AJ238788.1: Puumala virus RNA for nucleocapsid protein, strain Karhumaki.
- X61035.1: Puumala virus genomic RNA for nucleocapsid protein.

**>seq233:PUUV\_Finland\_cells\_(VirIDv3r520827) Start=12 End=412**

nnnnannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
aggaaaataannnnngnnnnnnnnnnnnngnnnnnnntnagnnnnnnncaannnnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (62/401): 15.5%**

**(B)**

Max score: 51.8  
Total score: 51.8  
Query coverage: 7%  
E value: 0.018









- KY364995.1: Puumala orthohantavirus isolate Ardennes\_2011\_87 nucleoprotein gene, complete cds.
- KT247596.2: Puumala virus isolate PUUV/Jura/Mg2/2010 segment S nucleoprotein gene, complete cds.
- KU314905.1: Puumala virus strain PUUV/NL/Mg591/2008 nucleocapsid protein gene, complete cds.
- KU314901.1: Puumala virus strain PUUV/NL/Mg1439/2011 nucleocapsid protein gene, complete cds.
- KU314900.1: Puumala virus strain PUUV/NL/Mg1012/2010 nucleocapsid protein gene, complete cds.
- KU314899.1: Puumala virus strain PUUV/NL/Mg753/2009 nucleocapsid protein gene, complete cds.
- KU314898.1: Puumala virus strain PUUV/NL/Mg343/2008 nucleocapsid protein gene, complete cds.
- KU314897.1: Puumala virus strain PUUV/NL/Mg25/2007 nucleocapsid protein gene, complete cds.
- KU314896.1: Puumala virus strain PUUV/NL/Mg31/2007 nucleocapsid protein gene, complete cds.
- KT247597.1: Puumala virus isolate PUUV/Jura/Mg214/2010 segment S nucleoprotein gene, complete cds.
- KT247595.1: Puumala virus isolate PUUV/Orleans/Mg29/2010 segment S nucleoprotein gene, complete cds.
- KT247594.1: Puumala virus isolate PUUV/Orleans/Mg23/2010 segment S nucleoprotein gene, complete cds.
- KT247593.1: Puumala virus isolate PUUV/Ardennes/Mg75/2011 segment S nucleoprotein gene, complete cds.
- KT247592.1: Puumala virus isolate PUUV/Ardennes/Mg156/2011 segment S nucleoprotein gene, complete cds.
- JQ319163.2: Puumala virus strain PUUV/Konnevesi/Mg\_M94A/2005 segment S, complete sequence.
- **JQ319162.2: Puumala virus strain PUUV/Konnevesi/Mg\_O78A/2005 segment S, complete sequence.**
- JQ319161.2: Puumala virus strain PUUV/Konnevesi/Mg\_O57A/2005 segment S, complete sequence.
- JQ319171.1: Puumala virus strain PUUV/Konnevesi/Mg\_M114B/2005 segment S, complete sequence.
- JQ319167.1: Puumala virus strain PUUV/Konnevesi/Mg\_O15B/2005 segment S, complete sequence.
- JN831943.1: Puumala virus strain PUUV/Pieksamaki/Mg7/2008 segment S, complete sequence.
- JN696373.1: Puumala virus strain MuEb10Karlstadt/10 nucleocapsid protein (N) gene, complete cds.
- JN696372.1: Puumala virus strain MuEb4Karlstadt/10 nucleocapsid protein (N) gene, complete cds.
- JN696371.1: Puumala virus strain MuEb6Karlstadt/10 nucleocapsid protein (N) gene, complete cds.
- GQ339479.1: Puumala virus strain Moskosel/Mg17/05 segment S, complete sequence.
- AM695638.1: Puumala virus S gene for nucleocapsid protein, strain PUU/Mignovillard/CgY02/2005, genomic RNA.
- EF488806.1: Puumala virus isolate Fusong 900-06 nucleocapsid gene, complete cds.
- EF488804.1: Puumala virus isolate Fusong 114-05 nucleocapsid gene, complete cds.
- EF488803.1: Puumala virus isolate Fusong 199-05 nucleocapsid gene, complete cds.
- EF442091.1: Puumala-like virus isolate Fusong-Cr-275 segment S nucleocapsid protein gene, complete cds.





Total score: 44.6  
Query coverage: 7%  
E value: 2.7  
Identity: 90%

- KF776902.1: Puumala virus isolate HtSi\_293\_p2010 nucleocapsid protein gene, partial cds.
- KF776901.1: Puumala virus isolate HtSi\_283\_p2009 nucleocapsid protein gene, partial cds.
- KF776898.1: Puumala virus isolate HtSi\_254\_p2008 nucleocapsid protein gene, partial cds.
- KF776891.1: Puumala virus isolate HtSi\_199\_p2005 nucleocapsid protein gene, partial cds.
- KF776885.1: Puumala virus isolate HtSi\_1071\_a1999 nucleocapsid protein gene, partial cds.
- KF776880.1: Puumala virus isolate HtSi\_1068\_a1998 nucleocapsid protein gene, partial cds.
- KF776879.1: Puumala virus isolate HtSi\_1063\_a1999 nucleocapsid protein gene, partial cds.
- KF776873.1: Puumala virus isolate HtSi\_1069\_a1999 nucleocapsid protein gene, partial cds.
- KF776868.1: Puumala virus isolate HtSi\_483\_p2012 nucleocapsid protein gene, partial cds.
- KF776855.1: Puumala virus isolate HtSi\_335\_p2012 nucleocapsid protein gene, partial cds.
- JF499663.1: Puumala virus strain PUUcroMP nucleocapsid protein gene, partial cds.
- JF499661.1: Puumala virus strain PUUcro97rd nucleocapsid protein gene, partial cds.
- JF499660.1: Puumala virus strain PUUcro62ps nucleocapsid protein gene, partial cds.
- JF499659.1: Puumala virus strain PUUcro39vd nucleocapsid protein gene, partial cds.
- FN377822.1: Puumala virus N gene for nucleocapsid protein, strain PUUV/Mg23/HungaryTR17/00.
- AJ314600.1: Puumala virus mRNA for nucleocapsid protein (N gene), strain Balkan-1.
- AJ888738.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Pat7.
- AJ888734.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Cg4.
- AJ888733.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Cg3.

**>seq228:PUUV\_Slovenia-8098\_03-05-2013\_(VirIDv3r520827) Start=12 End=412**

```
ttggagttatntcantgntcncnnnnnnnnnnnnnnnnnnnnnnnnnnntnnntatcaacacgaggaagncngnnnnnnnnnnna
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
cagncaccagncaacaatgaaggcagangnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
gncgcaatnttangagtctgngntgggggtataggattctntnttncntaaaggattggtcagagagngnnnnnnnnnnnnnnnnnnnn
atgccctttataannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (224/401): 55.9%**

**(B)**

Max score: 167  
Total score: 167  
Query coverage: 67%  
E value: 3e-37  
Identity: 67%

- KF776902.1: Puumala virus isolate HtSi\_293\_p2010 nucleocapsid protein gene, partial cds.

**>seq231:PUUV\_Slovenia-8098\_03-05-2013\_(VirIDv3r520827) Start=12 End=412**

```
ttggannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nnnnncagncagncagncagncagncagncagncagncagncagncagncagncagncagncagncagncagncagncagncagncagnc
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
```

**(A) CR (113/401): 28.2%**

**(B)**

Max score: 73.4  
Total score: 73.4  
Query coverage: 14%  
E value: 6e-09  
Identity: 84%

- KF776903.1: Puumala virus isolate HtSi\_339\_p2012 nucleocapsid protein gene, partial cds.





Max score: 48.2  
Total score: 48.2  
Query coverage: 7%  
E value: 0.22  
Identity: 91%

- KF776902.1: Puumala virus isolate HtSi\_293\_p2010 nucleocapsid protein gene, partial cds.
- KF776901.1: Puumala virus isolate HtSi\_283\_p2009 nucleocapsid protein gene, partial cds.
- KF776900.1: Puumala virus isolate HtSi\_269\_p2008 nucleocapsid protein gene, partial cds.
- KF776899.1: Puumala virus isolate HtSi\_262\_p2008 nucleocapsid protein gene, partial cds.
- KF776898.1: Puumala virus isolate HtSi\_254\_p2008 nucleocapsid protein gene, partial cds.
- KF776896.1: Puumala virus isolate HtSi\_250\_p2008 nucleocapsid protein gene, partial cds.
- KF776895.1: Puumala virus isolate HtSi\_248\_p2008 nucleocapsid protein gene, partial cds.
- KF776892.1: Puumala virus isolate HtSi\_235\_p2007 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776891.1: Puumala virus isolate HtSi\_199\_p2005 nucleocapsid protein gene, partial cds.
- KF776890.1: Puumala virus isolate HtSi\_142\_p2002 nucleocapsid protein gene, partial cds.
- KF776884.1: Puumala virus isolate HtSi\_1079\_a1995 nucleocapsid protein gene, partial cds.
- KF776881.1: Puumala virus isolate HtSi\_1058\_a1995 nucleocapsid protein gene, partial cds.
- KF776880.1: Puumala virus isolate HtSi\_1068\_a1998 nucleocapsid protein gene, partial cds.
- KF776879.1: Puumala virus isolate HtSi\_1063\_a1999 nucleocapsid protein gene, partial cds.
- KF776876.1: Puumala virus isolate HtSi\_363\_p2012 nucleocapsid protein gene, partial cds.
- KF776873.1: Puumala virus isolate HtSi\_1069\_a1999 nucleocapsid protein gene, partial cds.
- KF776871.1: Puumala virus isolate HtSi\_317\_p2012 nucleocapsid protein gene, partial cds.
- KF776869.1: Puumala virus isolate HtSi\_485\_p2012 nucleocapsid protein gene, partial cds.
- KF776866.1: Puumala virus isolate HtSi\_434\_p2012 nucleocapsid protein gene, partial cds.
- KF776864.1: Puumala virus isolate HtSi\_1054\_a1995 nucleocapsid protein gene, partial cds.
- KF776860.1: Puumala virus isolate HtSi\_410\_p2012 nucleocapsid protein gene, partial cds.
- KF776859.1: Puumala virus isolate HtSi\_402\_p2012 nucleocapsid protein gene, partial cds.
- KF776857.1: Puumala virus isolate HtSi\_377\_p2012 nucleocapsid protein gene, partial cds.
- KF776856.1: Puumala virus isolate HtSi\_374\_p2012 nucleocapsid protein gene, partial cds.
- KF776855.1: Puumala virus isolate HtSi\_335\_p2012 nucleocapsid protein gene, partial cds.
- KC676615.1: Puumala virus strain PUUV/Croatia\_Gerovo/Mg982/2008 nucleocapsid protein (N) mRNA, partial cds.
- KC676614.1: Puumala virus strain PUUV/Croatia\_Gerovo/Mg980/2008 nucleocapsid protein (N) mRNA, partial cds.
- KC676612.1: Puumala virus strain PUUV/Croatia\_Gerovo/Mg978/2008 nucleocapsid protein (N) mRNA, partial cds.
- KC676611.1: Puumala virus strain PUUV/Croatia\_Gerovo/Mg955/2008 nucleocapsid protein (N) mRNA, partial cds.
- KC676609.1: Puumala virus strain PUUV/Croatia\_Gerovo/Mg938/2008 nucleocapsid protein (N) mRNA, partial cds.
- JF499661.1: Puumala virus strain PUUcro97rd nucleocapsid protein gene, partial cds
- JF499660.1: Puumala virus strain PUUcro62ps nucleocapsid protein gene, partial cds.
- JF499659.1: Puumala virus strain PUUcro39vd nucleocapsid protein gene, partial cds.
- FN377822.1: Puumala virus N gene for nucleocapsid protein, strain PUUV/Mg23/HungaryTR17/00.
- AJ314601.1: Puumala virus mRNA for nucleocapsid protein (N gene), strain Balkan-2.
- AJ888739.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Pat5.
- AJ888738.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Pat7.
- AJ888736.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Pat3.
- AJ888735.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Pat1.
- AJ888734.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Cg4.

- AJ888731.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Cg1.

**>seq234:PUUV\_Slovenia-8098\_03-05-2013\_(VirIDv3r520827) Start=12 End=238**

ncnnnnnnnnnnnnnnnataaccncnnaannngnnnnntgtgtgccagnngnnncnnnnnnnnnnanngnnnncnnnggna  
atggaccagatgacgtaacannnnntnnncngcaagcaaggcaacaancagtgtcagcattggaggacaaacncgcannnnctnnnnnnn  
nnngncnnnnnnngngcncnnnaaaagatggatacnnancctactga

**(A) CR (133/227): 58.6%**

**(B)**

Max score: 109

Total score: 109

Query coverage: 36%

E value: 4e-20

Identity: 87%

- FN377822.1: Puumala virus N gene for nucleocapsid protein, strain PUUV/Mg23/HungaryTR17/00.
- FN377821.1: Puumala virus N gene for nucleocapsid protein, strain PUUV/Mg9/HungaryTR17/00.
- AJ314601.1: Puumala virus mRNA for nucleocapsid protein (N gene), strain Balkan-2.
- AJ888752.1: Puumala virus mRNA for nucleocapsid protein (N gene), PUU/Ernstbrunn/Cg641/1995.
- AJ888751.1: Puumala virus mRNA for nucleocapsid protein (N gene), PUU/Klippitztoerl/Cg9/1995.

**>seq242:PUUV\_Slovenia-8098\_03-05-2013\_(VirIDv3r520827) Start=12 End=290**

nnnnnnnnnnnnnnnnntgncctncacactcngncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnaacnncnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
cccaactcaaattcagnnnnnnnnnn

**(A) CR (67/279): 24.0%**

**(B)**

Max score: 50.0

Total score: 50.0

Query coverage: 9%

E value: 0.042

Identity: 100%

- KF776902.1: Puumala virus isolate HtSi\_293\_p2010 nucleocapsid protein gene, partial cds.
- KF776901.1: Puumala virus isolate HtSi\_283\_p2009 nucleocapsid protein gene, partial cds.
- KF776898.1: Puumala virus isolate HtSi\_254\_p2008 nucleocapsid protein gene, partial cds.
- KF776885.1: Puumala virus isolate HtSi\_1071\_a1999 nucleocapsid protein gene, partial cds.
- KF776880.1: Puumala virus isolate HtSi\_1068\_a1998 nucleocapsid protein gene, partial cds.
- FN377821.1: Puumala virus N gene for nucleocapsid protein, strain PUUV/Mg9/HungaryTR17/00.
- AJ888734.1: Puumala virus partial mRNA for nucleocapsid protein (N gene), PUU/Slovenia-Cg4.

**Viral species: Dobrava virus (DOBV)**

**Origin: Finland**

**DOBV laboratory strain**

>seq245:3\_08-08-2013\_(VirIDv3r520827) Start=12 End=412

nnntngncgccctgncatcattcgtgnntnnnnntnnnnngnaggctctttacatgcttaccaccagagnncaaacnactnaaanacnataa  
gggnnngnngnnncnatttaaggatgacagcncctttgaaatgtgaatgggannannaagccanancacctgttcttgaatgccnaatgcac  
nactnagcnnngngcagntgagattncaccaggctcggntcnggctgcaanttggtgactatannnagnncaggngnnnnnnngnnacn  
nnnnngtctgtgntgagtgtgnttntgntnnnnnnnnnnngnnnnnnnnnngngncngngnntatngcnnngnctnccgtgcaa  
gctactatctgagccatcnccaacnctntg

**(A) CR (284/401): 70.8%**

**(B)**

Max score: 293

Total score: 293

Query coverage: 97%

E value: 3e-75

Identification: 71%

- AJ410615.1: Dobrava virus complete S segment gene for nucleocapsid protein, strain DOBV/Ano-Poroia/Afl9/1999.

**SAAV laboratory strain**

>seq245:4\_08-08-2013\_(VirIDv3r520827) Start=12 End=412

ttgtgatcngnnnnncnntnnnnnannngnnnnnnncngnggctctttncnnnnnnnnnnncnngcaaacactactaaagac  
aataagggatgagggatcgattaaaggatgacagtnnnnntgngnnngngnnnggannnnnnnnnnnnnnnnnnnnntnttgcgatgc  
nannnnnnnnnnnnnnnnnnnancagatgagattacacctgnnannnnnnnnnnnnnnnnnggntnataccagcccagggttaa  
gcangnnnnngnnngngngncnnnnnnngnnnnnnnnnnntgnnnnnnnnnnnnnnnnngnnntnncngngggggn  
genngnctnntnnnnnnnnntnnncnnnancnnnnnnnnnnnnna

**(A) CR (177/401): 44.1%**

**(B)**

Max score: 95.1

Total score: 137

Query coverage: 19%

E value: 2e-15

Identity: 100%

- AJ009773.1: Dobrava virus S segment gene encoding nucleocapsid protein, strain DOB/Saaremaa/160V), genomic RNA.

>seq247:4\_08-08-2013\_(VirIDv3r520827) Start=12 End=412

nnnnganctattnnnnnnnnncnannncaataactcctgaaggctcttntcgttgacaactagaggaggcanacnnnnnnnnnng  
nnnnnnnnnnnnngnnanntnnnnnnnnngnnnnnnngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
ggnnccnnnncccagtcngcatgaaagcagatgagattacnctnnnnncngnnannngcngtctgtgattatcnnanccnann  
ncnnngnnngnnnnnnnnncncngcngcagtgatgtgattggnncncnannnnnnnnnnnttgacgnaacgggtgaggagtg  
cgnnncnnnnncaagctattatctnaannnnntnnnnnnnnna

**(A) CR (194/401): 48.4%**

**(B)**

Max score: 78.8

Total score: 145

Query coverage: 61%

E value: 1e-10

Identity: 94%



>seq247:2\_14-08-2013\_(VirIDv3r520827) Start=12 End=412

nnnnngnnnnngnnnnngnannctggtnnnnnncngnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnngggagacaaacnacnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
cnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (150/401): 37.4%

(B)

Max score: 60.8

Total score: 103

Query coverage: 14%

E value: 4e-05

Identity: 97%

- KT885043.1: Dobrava-Belgrade virus strain Stamforrad/POR segment S, complete sequence.
- KF776846.1: Dobrava-Belgrade virus isolate HtSi\_301\_p2010 nucleocapsid protein gene, partial cds.
- KF776845.1: Dobrava-Belgrade virus isolate HtSi\_275\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776842.1: Dobrava-Belgrade virus isolate HtSi\_279\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776841.1: Dobrava-Belgrade virus isolate HtSi\_261\_p2008 nucleocapsid protein gene, partial cds.
- KF776839.1: Dobrava-Belgrade virus isolate HtSi\_256\_p2008 nucleocapsid protein gene, partial cds.
- KF776819.1: Dobrava-Belgrade virus isolate HtSi\_1036\_a2001 nucleocapsid protein gene, partial cds.
- KC676594.1: Dobrava-Belgrade virus strain DOBV/Croatia\_Gerovo/Af956/2008 nucleocapsid protein (N) gene, partial cds.
- GU904032.1: Dobrava-Belgrade virus clone B5 nucleocapsid protein (N) gene, complete cds.
- GU904031.1: Dobrava-Belgrade virus clone A36 nucleocapsid protein (N) gene, complete cds.
- GU904029.1: Dobrava-Belgrade virus strain Slo/Af-BER nucleocapsid protein (N) gene, complete cds.
- L41916.1: Dobrava-Belgrade virus segment S, complete sequence.

>seq254:2\_14-08-2013\_(VirIDv3r520827) Start=12 End=412

nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

(A) CR (97/401): 24.2%

(B)

Max score: 69.8

Total score: 69.8

Query coverage: 13%

E value: 7e-08

Identity: 85%

- KY649187.1: Dobrava-Belgrade orthohantavirus isolate S\_2925\_Hu\_BA\_11 nucleoprotein gene, partial cds.
- KY649184.1: Dobrava-Belgrade orthohantavirus isolate S\_3861\_Hu\_CRS\_08 nucleoprotein gene, partial cds.
- KY649180.1: Dobrava-Belgrade orthohantavirus isolate S\_2890\_Hu\_WRS\_10 nucleoprotein gene, partial cds.

- KT315642.1: Dobrava-Belgrade virus isolate Turkey/Igneada/89Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315641.1: Dobrava-Belgrade virus isolate Turkey/Igneada/84Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315640.1: Dobrava-Belgrade virus isolate Turkey/Igneada/57Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315639.1: Dobrava-Belgrade virus isolate Turkey/Igneada/32Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315638.1: Dobrava-Belgrade virus isolate Turkey/Igneada/13Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315636.1: Dobrava-Belgrade virus isolate Turkey/Igneada/03Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT885043.1: Dobrava-Belgrade virus strain Stamforrad/POR segment S, complete sequence.
- KF776849.1: Dobrava-Belgrade virus isolate HtSi\_274\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776848.1: Dobrava-Belgrade virus isolate HtSi\_297\_p2010 nucleocapsid protein gene, partial cds.
- KF776845.1: Dobrava-Belgrade virus isolate HtSi\_275\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776843.1: Dobrava-Belgrade virus isolate HtSi\_268\_p2008 nucleocapsid protein gene, partial cds.
- KF776841.1: Dobrava-Belgrade virus isolate HtSi\_261\_p2008 nucleocapsid protein gene, partial cds.
- KF776838.1: Dobrava-Belgrade virus isolate HtSi\_231\_p2007 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776837.1: Dobrava-Belgrade virus isolate HtSi\_230\_p2007 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776836.1: Dobrava-Belgrade virus isolate HtSi\_215\_p2005 nucleocapsid protein gene, partial cds.
- KF776835.1: Dobrava-Belgrade virus isolate HtSi\_207\_p2005 nucleocapsid protein gene, partial cds.
- KF776834.1: Dobrava-Belgrade virus isolate HtSi\_200\_p2005 nucleocapsid protein gene, partial cds.
- KF776833.1: Dobrava-Belgrade virus isolate HtSi\_129\_p2000 nucleocapsid protein gene, partial cds.
- KF776832.1: Dobrava-Belgrade virus isolate HtSi\_132\_p2000 nucleocapsid protein gene, partial cds.
- KF776831.1: Dobrava-Belgrade virus isolate HtSi\_136\_p2001 nucleocapsid protein gene, partial cds.
- KF776830.1: Dobrava-Belgrade virus isolate HtSi\_193\_p2005 nucleocapsid protein gene, partial cds.
- KF776829.1: Dobrava-Belgrade virus isolate HtSi\_1022\_a2000 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776828.1: Dobrava-Belgrade virus isolate HtSi\_1030\_a1995 nucleocapsid protein gene, partial cds.
- KF776827.1: Dobrava-Belgrade virus isolate HtSi\_1038\_a2002 nucleocapsid protein gene, partial cds.
- KF776826.1: Dobrava-Belgrade virus isolate HtSi\_130\_p2000 nucleocapsid protein gene, partial cds.
- KF776824.1: Dobrava-Belgrade virus isolate HtSi\_1040\_a1999 nucleocapsid protein gene, partial cds.
- KF776823.1: Dobrava-Belgrade virus isolate HtSi\_1043\_a1995 nucleocapsid protein gene, partial cds.

- KF776821.1: Dobrava-Belgrade virus isolate HtSi\_1042\_a2008 nucleocapsid protein gene, partial cds.
- KF776820.1: Dobrava-Belgrade virus isolate HtSi\_1037\_a2001 nucleocapsid protein gene, partial cds.
- KF776819.1: Dobrava-Belgrade virus isolate HtSi\_1036\_a2001 nucleocapsid protein gene, partial cds.
- KF776818.1: Dobrava-Belgrade virus isolate HtSi\_1035\_a2002 nucleocapsid protein gene, partial cds.
- KF776817.1: Dobrava-Belgrade virus isolate HtSi\_1034\_a2001 nucleocapsid protein gene, partial cds.
- KF776816.1: Dobrava-Belgrade virus isolate HtSi\_1033\_a2001 nucleocapsid protein gene, partial cds.
- KF776815.1: Dobrava-Belgrade virus isolate HtSi\_1032\_a2001 nucleocapsid protein gene, partial cds.
- KF776813.1: Dobrava-Belgrade virus isolate HtSi\_1029\_a1995 nucleocapsid protein gene, partial cds.
- KF776812.1: Dobrava-Belgrade virus isolate HtSi\_1024\_a2000 nucleocapsid protein gene, partial cds.
- KF776811.1: Dobrava-Belgrade virus isolate HtSi\_1021\_a1995 nucleocapsid protein gene, partial cds.
- KF776810.1: Dobrava-Belgrade virus isolate HtSi\_1020\_a2008 nucleocapsid protein gene, partial cds.
- KF776808.1: Dobrava-Belgrade virus isolate HtSi\_1015\_a1995 nucleocapsid protein gene, partial cds.
- KF776807.1: Dobrava-Belgrade virus isolate HtSi\_1011\_a2007 nucleocapsid protein gene, partial cds.
- KF776805.1: Dobrava-Belgrade virus isolate HtSi\_1009\_a1995 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776804.1: Dobrava-Belgrade virus isolate HtSi\_1008\_a1999 nucleocapsid protein gene, partial cds.
- KF776803.1: Dobrava-Belgrade virus isolate HtSi\_1013\_a2002 nucleocapsid protein gene, partial cds.
- KF776799.1: Dobrava-Belgrade virus isolate HtSi\_1014\_a2002 nucleocapsid protein gene, partial cds.
- KF776797.1: Dobrava-Belgrade virus isolate HtSi\_270\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776796.1: Dobrava-Belgrade virus isolate HtSi\_499\_p2012 nucleocapsid protein gene, partial cds.
- KF776795.1: Dobrava-Belgrade virus isolate HtSi\_492\_p2012 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776794.1: Dobrava-Belgrade virus isolate HtSi\_465\_p2012 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776793.1: Dobrava-Belgrade virus isolate HtSi\_397\_p2012 nucleocapsid protein gene, partial cds.
- KJ154958.1: Dobrava-Belgrade virus strain KOS-1 nucleocapsid protein (N) gene, partial cds.
- KC676600.1: Dobrava-Belgrade virus strain DOBV/Croatia\_Gerovo/Af968/2008 nucleocapsid protein (N) mRNA, complete cds.
- KC676599.1: Dobrava-Belgrade virus strain DOBV/Croatia\_Gerovo/Af967/2008 nucleocapsid protein (N) mRNA, complete cds.
- KC676598.1: Dobrava-Belgrade virus strain DOBV/Croatia\_Gerovo/Af966/2008 nucleocapsid protein (N) mRNA, complete cds.
- KC676597.1: Dobrava-Belgrade virus strain DOBV/Croatia\_Gerovo/Af965/2008 nucleocapsid protein (N) mRNA, complete cds.





- MH427127.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Chalkidiki-398/13 nucleocapsid protein gene, partial cds.
- MH427126.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Lamia-135/13 nucleocapsid protein gene, partial cds.
- MH427125.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Drama-29/09 nucleocapsid protein gene, partial cds.
- MH427123.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Drama-196/07 nucleocapsid protein gene, partial cds.
- MH427122.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Imathia-159/07 nucleocapsid protein gene, partial cds.
- MH427121.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Kozani-116/07 nucleocapsid protein gene, partial cds.
- MH427119.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Larisa-272/06 nucleocapsid protein gene, partial cds.
- MH427118.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Florina-167/06 nucleocapsid protein gene, partial cds.
- MH427117.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Pieria-188/06 nucleocapsid protein gene, partial cds.
- MH427116.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Chalkidiki-177/06 nucleocapsid protein gene, partial cds.
- MH427115.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Pella-246/05 nucleocapsid protein gene, partial cds.
- MH427113.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Ioannina-203/05 nucleocapsid protein gene, partial cds.
- MH427112.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Magnesia-167/05 nucleocapsid protein gene, partial cds.
- MH427111.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Grevena-240/04 nucleocapsid protein gene, partial cds.
- MH427110.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Trikala-102/04 nucleocapsid protein gene, partial cds.
- MH427109.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Fthiotida-75/03 nucleocapsid protein gene, partial cds.
- MH427107.1: Dobrava-Belgrade orthohantavirus isolate DOBV/Magnesia-73/02 nucleocapsid protein gene, partial cds.
- KY649188.1: Dobrava-Belgrade orthohantavirus isolate S\_3528\_Hu\_SRS\_11 nucleoprotein gene, partial cds.
- KY649187.1: Dobrava-Belgrade orthohantavirus isolate S\_2925\_Hu\_BA\_11 nucleoprotein gene, partial cds.
- KY649186.1: Dobrava-Belgrade orthohantavirus isolate S\_5502\_Hu\_ERS\_10 nucleoprotein gene, partial cds.
- KY649185.1: Dobrava-Belgrade orthohantavirus isolate S\_5312\_Hu\_NRS\_10 nucleoprotein gene, partial cds.
- KY649184.1: Dobrava-Belgrade orthohantavirus isolate S\_3861\_Hu\_CRS\_08 nucleoprotein gene, partial cds.
- KY649183.1: Dobrava-Belgrade orthohantavirus isolate S\_3748\_Hu\_CRS\_09 nucleoprotein gene, partial cds.
- KY649182.1: Dobrava-Belgrade orthohantavirus isolate S\_3526\_Hu\_SRS\_11 nucleoprotein gene, partial cds.
- KY649181.1: Dobrava-Belgrade orthohantavirus isolate S\_3431\_Hu\_SRS\_10 nucleoprotein gene, partial cds.
- KY649180.1: Dobrava-Belgrade orthohantavirus isolate S\_2890\_Hu\_WRS\_10 nucleoprotein gene, partial cds.

- KY649179.1: Dobrava-Belgrade orthohantavirus isolate S\_2331\_Hu\_SRS\_10 nucleoprotein gene, partial cds.
- KT971014.1: Dobrava-Belgrade virus strain Geshtenjias/Pogradec/261Af/2007/ALB nucleocapsid protein gene, partial cds.
- KT971013.1: Dobrava-Belgrade virus strain Mollas/Kolonje/243Af/2007/ALB nucleocapsid protein gene, partial cds.
- KT971011.1: Dobrava-Belgrade virus strain Diellas/Korce/201Af/2007/ALB nucleocapsid protein gene, partial cds.
- KT971010.1: Dobrava-Belgrade virus strain Llogora/Vlore/85Af/2006/ALB nucleocapsid protein gene, partial cds.
- KT971009.1: Dobrava-Belgrade virus strain Voskopoje/Korce/65Af/2006/ALB nucleocapsid protein gene, partial cds.
- KT971008.1: Dobrava-Belgrade virus strain TogeZ/Librazhd/54Af/2006/ALB nucleocapsid protein gene, partial cds.
- KT971007.1: Dobrava-Belgrade virus strain Llasen/Diber/22Af/2006/ALB nucleocapsid protein gene, partial cds.
- KT971006.1: Dobrava-Belgrade virus strain Pilafe/Diber/20Af/2006/ALB nucleocapsid protein gene, partial cds.
- KT971005.1: Dobrava-Belgrade virus strain Brezhdan/Diber/19Af/2006/ALB nucleocapsid protein gene, partial cds.
- KT315642.1: Dobrava-Belgrade virus isolate Turkey/Igneada/89Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315641.1: Dobrava-Belgrade virus isolate Turkey/Igneada/84Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315640.1: Dobrava-Belgrade virus isolate Turkey/Igneada/57Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315639.1: Dobrava-Belgrade virus isolate Turkey/Igneada/32Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315638.1: Dobrava-Belgrade virus isolate Turkey/Igneada/13Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315637.1: Dobrava-Belgrade virus isolate Turkey/Igneada/09Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315636.1: Dobrava-Belgrade virus isolate Turkey/Igneada/03Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT315635.1: Dobrava-Belgrade virus isolate Turkey/Igneada/02Af/2009 segment S nucleocapsid protein gene, partial cds.
- KT885043.1: Dobrava-Belgrade virus strain Stamforrad/POR segment S, complete sequence.
- KF776850.1: Dobrava-Belgrade virus isolate HtSi\_286\_p2009 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776849.1: Dobrava-Belgrade virus isolate HtSi\_274\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776848.1: Dobrava-Belgrade virus isolate HtSi\_297\_p2010 nucleocapsid protein gene, partial cds.
- KF776846.1: Dobrava-Belgrade virus isolate HtSi\_301\_p2010 nucleocapsid protein gene, partial cds.
- KF776845.1: Dobrava-Belgrade virus isolate HtSi\_275\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776843.1: Dobrava-Belgrade virus isolate HtSi\_268\_p2008 nucleocapsid protein gene, partial cds.
- KF776842.1: Dobrava-Belgrade virus isolate HtSi\_279\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776841.1: Dobrava-Belgrade virus isolate HtSi\_261\_p2008 nucleocapsid protein gene, partial cds.

- KF776840.1: Dobrava-Belgrade virus isolate HtSi\_239\_p2008 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776839.1: Dobrava-Belgrade virus isolate HtSi\_256\_p2008 nucleocapsid protein gene, partial cds.
- KF776838.1: Dobrava-Belgrade virus isolate HtSi\_231\_p2007 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776837.1: Dobrava-Belgrade virus isolate HtSi\_230\_p2007 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776836.1: Dobrava-Belgrade virus isolate HtSi\_215\_p2005 nucleocapsid protein gene, partial cds.
- KF776835.1: Dobrava-Belgrade virus isolate HtSi\_207\_p2005 nucleocapsid protein gene, partial cds.
- KF776834.1: Dobrava-Belgrade virus isolate HtSi\_200\_p2005 nucleocapsid protein gene, partial cds.
- KF776833.1: Dobrava-Belgrade virus isolate HtSi\_129\_p2000 nucleocapsid protein gene, partial cds.
- KF776832.1: Dobrava-Belgrade virus isolate HtSi\_132\_p2000 nucleocapsid protein gene, partial cds.
- KF776831.1: Dobrava-Belgrade virus isolate HtSi\_136\_p2001 nucleocapsid protein gene, partial cds.
- KF776830.1: Dobrava-Belgrade virus isolate HtSi\_193\_p2005 nucleocapsid protein gene, partial cds.
- KF776829.1: Dobrava-Belgrade virus isolate HtSi\_1022\_a2000 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776828.1: Dobrava-Belgrade virus isolate HtSi\_1030\_a1995 nucleocapsid protein gene, partial cds.
- KF776827.1: Dobrava-Belgrade virus isolate HtSi\_1038\_a2002 nucleocapsid protein gene, partial cds.
- KF776826.1: Dobrava-Belgrade virus isolate HtSi\_130\_p2000 nucleocapsid protein gene, partial cds.
- KF776824.1: Dobrava-Belgrade virus isolate HtSi\_1040\_a1999 nucleocapsid protein gene, partial cds.
- KF776823.1: Dobrava-Belgrade virus isolate HtSi\_1043\_a1995 nucleocapsid protein gene, partial cds.
- KF776821.1: Dobrava-Belgrade virus isolate HtSi\_1042\_a2008 nucleocapsid protein gene, partial cds.
- KF776820.1: Dobrava-Belgrade virus isolate HtSi\_1037\_a2001 nucleocapsid protein gene, partial cds.
- KF776819.1: Dobrava-Belgrade virus isolate HtSi\_1036\_a2001 nucleocapsid protein gene, partial cds.
- KF776818.1: Dobrava-Belgrade virus isolate HtSi\_1035\_a2002 nucleocapsid protein gene, partial cds.
- KF776817.1: Dobrava-Belgrade virus isolate HtSi\_1034\_a2001 nucleocapsid protein gene, partial cds.
- KF776816.1: Dobrava-Belgrade virus isolate HtSi\_1033\_a2001 nucleocapsid protein gene, partial cds.
- KF776815.1: Dobrava-Belgrade virus isolate HtSi\_1032\_a2001 nucleocapsid protein gene, partial cds.
- KF776813.1: Dobrava-Belgrade virus isolate HtSi\_1029\_a1995 nucleocapsid protein gene, partial cds.
- KF776812.1: Dobrava-Belgrade virus isolate HtSi\_1024\_a2000 nucleocapsid protein gene, partial cds.



- KF776802.1: Dobrava-Belgrade virus isolate HtSi\_1090\_a2000 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776801.1: Dobrava-Belgrade virus isolate HtSi\_1092\_a1997 nucleocapsid protein gene, partial cds.
- KF776800.1: Dobrava-Belgrade virus isolate HtSi\_1097\_a1995 nucleocapsid protein gene, partial cds.
- AJ251999.1: Dobrava virus proviral partial gene for nucleocapsid protein, genomic RNA.

**>seq246:3\_14-08-2013\_(VirIDv3r520827) Start=12 End=412**

nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaactcttaaggnccnnnnnnnnnnnnnnnaactagaggagncagactactaagga  
taacanggggaatgaggattcgctnntnaggatgacagctcgttgaagnnnnnnnnnnnnnnnnnnnnnnnnnnnnnancat  
gccantgctcaatccagtatgaaggcagatgaaanccacctgnnnnnnnnnnnnnnnnnnnnngtntgtgnnttannccnnncaanncna  
gcaagaaattggncngctctgtcatgagtgtanntggtttttgccctgcaaagaactggnnnnnannnnngnagagtggtagatnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (248/401): 61.8%**

**(B)**

Max score: 221  
Total score: 221  
Query coverage: 81%  
E value: 2e-53  
Identity: 69%

- KF776882.1: Dobrava-Belgrade virus isolate HtSi\_1012\_a1997 nucleocapsid protein gene, partial cds.
- KF776822.1: Dobrava-Belgrade virus isolate HtSi\_1095\_a1997 nucleocapsid protein gene, partial cds.
- KF776802.1: Dobrava-Belgrade virus isolate HtSi\_1090\_a2000 nonfunctional nucleocapsid protein gene, partial sequence.
- KF776801.1: Dobrava-Belgrade virus isolate HtSi\_1092\_a1997 nucleocapsid protein gene, partial cds.
- KF776800.1: Dobrava-Belgrade virus isolate HtSi\_1097\_a1995 nucleocapsid protein gene, partial cds.

**>seq247:3\_14-08-2013\_(VirIDv3r520827) Start=12 End=412**

nnnnngngcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

**(A) CR (159/401): 39.6%**

**(B)**

Max score: 53.6  
Total score: 99  
Query coverage: 13%  
E value: 0.005  
Identity: 100%

- KF776882.1: Dobrava-Belgrade virus isolate HtSi\_1012\_a1997 nucleocapsid protein gene, partial cds.
- KF776852.1: Dobrava-Belgrade virus isolate HtSi\_1096\_a1995 nucleocapsid protein gene, partial cds.
- KF776822.1: Dobrava-Belgrade virus isolate HtSi\_1095\_a1997 nucleocapsid protein gene, partial cds.
- KF776802.1: Dobrava-Belgrade virus isolate HtSi\_1090\_a2000 nonfunctional nucleocapsid protein gene, partial sequence.

- KF776801.1: Dobrava-Belgrade virus isolate HtSi\_1092\_a1997 nucleocapsid protein gene, partial cds.
- KF776800.1: Dobrava-Belgrade virus isolate HtSi\_1097\_a1995 nucleocapsid protein gene, partial cds.
- FN813291.1: Saaremaa virus partial S segment, strain SAAV/Croatia\_Migalovci/Aa12/2003, genomic RNA.
- FN377826.2: Saaremaa virus partial N gene for nucleocapsid protein, strain SAAV/Aa1/HungaryTR16/00.
- AJ251999.1: Dobrava virus proviral partial gene for nucleocapsid protein, genomic RNA.



**TULV 09\_1000 Cunnersdorf**

**>seq265:24\_16-09-2014\_(VirIDv3r520827) Start=12 End=412**

nnnnnnacnnnnncnnnnnnngnannnnncnnnnnnngnnnnncnnnnnnnnctgncaacngagnnnggcannnnancn  
ngnnngnnnnngnnnacaagnannnggncnnnnngnngncagcncnnnnngaagagatcaangnnncnnnnnnnnnnnnnnnn  
nngnnngnnnnnnnnnnnnnnncncnntgaaagccgngnnnnnnnnngnnnnncnnannncngngnnnnnnntgnggnnnnn  
nnnnngcncngnnnnngcacaganacnncanaagtcctgncntnnnnnnnnnnncnnnnnnngnnnnnnnnnaagattggcngaaa  
agnnnnnnncnnngnnngnncnnnnnnngnnnnnnntngaagnaagtgctcctagtaaggaa

**(A) CR (154/401): 38.4%**

**(B)**

Max score: 42.8  
Total score: 42.8  
Query coverage: 6%  
E value: 9.4  
Identity: 96%

- KU139560.1: Tula virus isolate 09\_1000\_Marv nucleocapsid protein gene, partial cds.
- KU139559.1: Tula virus isolate 09\_0972\_Marv nucleocapsid protein gene, partial cds.
- AJ223601.1: Tula virus genomic RNA for nucleocapsid protein, (strain Tula/Koziky/5276Ma/94).
- Y13984.1: Tula virus partial genomic RNA for nucleocapsid protein, strain (Tula/D540/Ma/95).
- Z69991.1: Tula virus genomic RNA for nucleocapsid protein, strain (Tula/Moravia/5302v/95).
- Z49915.1: Tula virus segment S, strain Tula/Moravia/5302Ma/94, genomic RNA.
- Z48741.1: Tula virus segment S, strain Tula/Moravia/5294Ma/94, genomic RNA.
- Z48574.1: Tula virus segment S, strain Tula/Moravia/5293Ma/94, genomic RNA.
- Z48573.1: Tula virus segment S, strain Tula/Moravia/5286Ma/94, genomic RNA.

**Origin: Finland**

**TULV laboratory strain Moravia**

**>seq234:2\_08-08-2013\_(VirIDv3r520827) Start=12 End=238**

nnnnnnncnnnnncnnnnngncnnnnnnnnnnnancgnnnnnnngntnnnnnnngnnnnnnnnnnnnnnnnnnnnnnncnn  
nnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnnnngngnncnnnnnnnnnnnnngtcagcattggaggacaaacnggcagant  
tcaagnnnnnnngnnnnnnnnnggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnggngngn

**(A) CR (54/227): 23.8%**

**(B)**

Max score: 55.4  
Total score: 55.4  
Query coverage: 14%  
E value: 8e-04  
Identity: 94%

- AF063897.1: Hantavirus Lodz-2 S segment nucleocapsid protein mRNA, complete cds.
- AF063892.1: Hantavirus Lodz-1 S segment nucleocapsid protein mRNA, complete cds.
- AF289821.1: Tula virus isolate D63-98 segment S nucleocapsid protein mRNA, complete cds.
- AF289820.1: Tula virus isolate D17-98 segment S nucleocapsid protein mRNA, complete cds.
- AF289819.1: Tula virus isolate D5-98 segment S nucleocapsid protein mRNA, complete cds.
- AF164094.1: Tula virus S segment nucleocapsid protein mRNA, complete cds.
- Z69991.1: Tula virus genomic RNA for nucleocapsid protein, strain (Tula/Moravia/5302v/95).
- Z49915.1: Tula virus segment S, strain Tula/Moravia/5302Ma/94, genomic RNA.

**>seq244:2\_08-08-2013\_(VirIDv3r520827) Start=12 End=412**

nnnnncnnnnngnnnnnnnnnnnnnnnnnnnnnnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
nncnnnnngnnnnncnnnnnnnnnnngnncnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn







- KU139579.1: Tula virus isolate 10\_1188\_Magr nucleocapsid protein gene, partial cds.
- KU139578.1: Tula virus isolate 10\_0932\_Marv nucleocapsid protein gene, partial cds.
- KU139577.1: Tula virus isolate 10\_0908\_Marv nucleocapsid protein gene, partial cds.
- KU139576.1: Tula virus isolate 10\_0905\_Marv nucleocapsid protein gene, partial cds.
- KU139575.1: Tula virus isolate 12\_1121\_Marv nucleocapsid protein gene, partial cds.
- KU139574.1: Tula virus isolate 12\_1068\_Marv nucleocapsid protein gene, partial cds.
- KU139573.1: Tula virus isolate 10\_1533\_Marv nucleocapsid protein gene, partial cds.
- KU139572.1: Tula virus isolate 12\_526\_Magr nucleocapsid protein gene, partial cds.
- KU139571.1: Tula virus isolate 12\_0492\_Magr nucleocapsid protein gene, partial cds.
- KU139570.1: Tula virus isolate 08\_0545\_Marv nucleocapsid protein gene, partial cds.
- KU139569.1: Tula virus isolate 08\_0362\_Marv nucleocapsid protein gene, partial cds.
- KU139568.1: Tula virus isolate 08\_0356\_Marv nucleocapsid protein gene, partial cds.
- KU139567.1: Tula virus isolate 08\_0352\_Marv nucleocapsid protein gene, partial cds.
- KU139566.1: Tula virus isolate 08\_0350\_Marv nucleocapsid protein gene, partial cds.
- KU139565.1: Tula virus isolate 08\_0538\_Marv nucleocapsid protein gene, partial cds.
- KU139564.1: Tula virus isolate 08\_0534\_Marv nucleocapsid protein gene, partial cds.
- KU139548.1: Tula virus isolate 10\_1625\_Marv nucleocapsid protein gene, partial cds.
- KU139546.1: Tula virus isolate 07\_0081\_Magr nucleocapsid protein gene, partial cds.
- KU139545.1: Tula virus isolate 08\_0894\_Marv nucleocapsid protein gene, partial cds.
- KU139544.1: Tula virus isolate 08\_0849\_Marv nucleocapsid protein gene, partial cds.
- KU139543.1: Tula virus isolate 08\_0848\_Marv nucleocapsid protein gene, partial cds.
- KU139542.1: Tula virus isolate 08\_0802\_Marv nucleocapsid protein gene, partial cds.
- KU139541.1: Tula virus isolate 08\_0789\_Marv nucleocapsid protein gene, partial cds.
- KU139540.1: Tula virus isolate 11\_1433\_Marv nucleocapsid protein gene, partial cds.
- KU139539.1: Tula virus isolate 11\_1429\_Marv nucleocapsid protein gene, partial cds.
- KU139538.1: Tula virus isolate 08\_1045\_Marv nucleocapsid protein gene, partial cds.
- KU139537.1: Tula virus isolate 08\_0639\_Marv nucleocapsid protein gene, partial cds.
- KU139536.1: Tula virus isolate 11\_1373\_Marv nucleocapsid protein gene, partial cds.
- KU139535.1: Tula virus isolate 13\_0784\_Marv nucleocapsid protein gene, partial cds.
- KU139533.1: Tula virus isolate 07\_0862\_Marv nucleocapsid protein gene, partial cds.
- KU139531.1: Tula virus isolate 10\_0029\_Marv nucleocapsid protein gene, partial cds.
- KU139530.1: Tula virus isolate 10\_0023\_Marv nucleocapsid protein gene, partial cds.
- KU139529.1: Tula virus isolate 09\_2375\_Marv nucleocapsid protein gene, partial cds.
- KU139528.1: Tula virus isolate 09\_2324\_Marv nucleocapsid protein gene, partial cds.
- KT885046.1: Sin Nombre virus strain CC107/POR segment S, complete sequence.
- KJ420559.1: Imjin virus segment S nucleoprotein gene, complete cds.
- JQ690282.1: Sin Nombre virus isolate 2 nucleocapsid protein gene, complete cds.
- HQ697347.1: Tula virus isolate GER/09/2155/Arv nucleocapsid protein gene, partial cds.
- HQ697346.1: Tula virus isolate GER/09/815/Arv nucleocapsid protein gene, partial cds.
- HQ697344.1: Tula virus isolate GER/08/712/Arv nucleocapsid protein gene, partial cds.
- GU300137.1: Tula virus strain dpz06-29 nucleocapsid protein gene, partial cds.
- GU300135.1: Tula virus strain dpz06-1 nucleocapsid protein gene, partial cds.
- EU439952.1: Tula virus strain Sennickerode Sen05/222 nucleocapsid protein gene, partial cds.
- EU439951.1: Tula virus strain Sennickerode Sen05/205 nucleocapsid protein gene, complete cds.
- EU439950.1: Tula virus strain Sennickerode Sen05/204 nucleocapsid protein gene, complete cds.
- EU439949.1: Tula virus strain Sennickerode Sen05/175 nucleocapsid protein gene, complete cds.
- EU439948.1: Tula virus strain Sennickerode Sen05/174 nucleocapsid protein gene, partial cds.
- EU439946.1: Tula virus strain Sennickerode Sen05/121 nucleocapsid protein gene, partial cds.
- DQ768143.1: Tula virus strain Brandenburg Mu137/05 nucleocapsid protein (N) gene, partial cds.
- DQ662087.1: Tula virus strain Brandenburg Mu 46/04 nucleocapsid protein (N) gene, partial cds.
- U54575.1: Muleshoe hantavirus nucleocapsid protein (N) and nonstructural protein (NSx) mRNA, complete cds.





**Species: Seoul orthohantavirus (SEOV)**

**Origin: France**

**Seoul Lyon 892 (unknown at the moment of the analysis)**

**>seq255:3\_26-06-2014\_(VirIDv3r520827) Start=12 End=412**

taattgcnnnnnnnnnnnnnnnnnnnngnnnnncatcttgaaggcactgtnnatgntaanaacaagagnaggcagnnttcgnngnncan  
caagnnnnnnnnnnnnnnnnnnngnnnnangatgncagcncnnntgaggnngncancggaaancagaaagnncaancnntngnnngtgcantg  
ccaaatgnnnnngnnnnnnnnnnnggngngaaganntaacacctggaagannnnnnnnnnnnngtgnncnanatcctgcacaganna  
aggcaaggancntggaagccctgcatgagtgtagttgggtttntggcncctggcaaaagactggacatctagaattgaagaanggctnggcn  
nnnnnnngntcatggcngngtcnnnnattgncgggngn

**(A) CR (257/401): 64.0%**

**(B)**

Max score: 235

Total score: 235

Query coverage: 90%

E value: 8e-58

Identity: 68%

- KF387725.1: Seoul virus isolate LYON/Rn/FRA/2013/LYO852 segment S, complete sequence.

**>seq257:3\_26-06-2014\_(VirIDv3r520827) Start=12 End=412**

taattgcnnnnnnnnnnnnnnnnnnnngnnnnnnnnnnngnggcncngtgnntgnnnanannnnnggnaggcnnnnnnnnnn  
nnnnnnnnngnnnnnnnnnnnnngnncangangacagctnnnnngnggangncncgnnnnnnnnnnngnnnnnnnnngnnng  
nnngcannncnngtgnnnnnngcncncangaaggctgaagagannacacctggaannntcngnnnnncngtatgtgngctatctcnc  
acnganaaaggcaaggannngnnangnnnnngcncatgagtgtagttgggtnttnggcacnngnnaanncngggnntctagnattgaaga  
ntggcncnccnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngnnnnnnnnnn

**(A) CR (179/401): 44.6%**

**(B)**

Max score: 127

Total score: 127

Query coverage: 39%

E value: 3e-25

Identity: 72%

- KY807170.1: Seoul orthohantavirus isolate XJ5/2011 nucleocapsid protein gene, complete cds.
- KX064273.1: Seoul hantavirus strain MANTENAY-MONTLIN/Rn/FRA/2015/2015.00179 nucleoprotein (N) gene, complete cds.
- KX064272.1: Seoul hantavirus strain MANTENAY-MONTLIN/Rn/FRA/2015/2015.00173 nucleoprotein (N) gene, complete cds.
- KX064269.1: Seoul hantavirus strain DIJON/Hu/FRA/2014/2014-00056 nucleoprotein (N) gene, partial cds.
- KT897726.1: Seoul virus strain Northeast Baltimore segment S nucleoprotein gene, partial cds.
- KP859512.1: Seoul virus isolate JiangxiXinjianRn-09-2011 nucleocapsid protein gene, complete cds.
- KP859511.1: Seoul virus isolate JiangxiXinjianRn-07-2011 nucleocapsid protein gene, complete cds.
- **KF387725.1: Seoul virus isolate LYON/Rn/FRA/2013/LYO852 segment S, complete sequence.**
- JQ665923.1: Seoul virus strain WuhanRn57 nucleocapsid gene, complete cds.
- JQ665922.1: Seoul virus strain WuhanRn53 nucleocapsid gene, complete cds.
- JQ665921.1: Seoul virus strain WuhanRn25 nucleocapsid gene, complete cds.
- JQ665920.1: Seoul virus strain WuhanRn10 nucleocapsid gene, complete cds.
- JQ665919.1: Seoul virus strain WuhanRf49 nucleocapsid gene, complete cds.
- JQ665918.1: Seoul virus strain WuhanRf33 nucleocapsid gene, complete cds.
- JQ665917.1: Seoul virus strain WuhanRf18 nucleocapsid gene, complete cds.



**(A) CR (212/401): 52.9 %**

**(B)**

Max score: 113

Total score: 161

Query coverage: 58%

E value: 6e-21

Identity: 69%

- KC626089.1: Seoul virus nucleocapsid protein gene, complete cds.  
(*KC626089.1strain="Cherwell"*)

>seq257:S\_UK\_03-10-2013\_(VirIDv3r520827) Start=12 End=412

```
nnnnnnnnncnnnnnnnnntntgtggctcccgatcatctngnngncacnnnnctgtnancaacnnnnggcaggcagnnnnncnagnnc  
annnnngnncnngaggncagnttcaaggatgncagcnnngnngnngnngnngnancannnnnnnnnnnnngngntgtgtca  
angccaaacgnnnnnccagnatganggcngnagagannacacctggaaganccgcacngcngnatgtgngctnttccnncnnnnn  
nnnnnnnnnnnnnnnnngnnngncntgagtgnngnnnnnnncnnngnnnnnggnnnnnnncnggnnttctaagaattgaagant  
ggcnnnccngnnnnnnnnnnnnnggnnnncnnngnnngnnnnnnnt
```

**(A) CR (193/401): 48.1%**

**(B)**

Max score: 91.5

Total score: 91.5

Query coverage: 58%

E value: 2e-14

Identity: 61%

- KC626089.1: Seoul virus nucleocapsid protein gene, complete cds.  
(*KC626089.1strain="Cherwell"*)

>seq258:S\_UK\_03-10-2013\_(VirIDv3r520827) Start=12 End=412

```
ngnnnnnnncnnnnnnnnntntgtggctcccgatcatctgaaggcacngnncangttnnacagcngnngagnncnnncagnttcanaggac  
ancaagntntgaggncagnttcaaggatgncagnnnnnnnnnnnnnnnnngnannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn  
ngccanacgnnnnnnnnnnngnnggctgnagagannncacctnnnagantccgcannngcngtatgtgngctnnnnnnnnnnnn  
nnnnnnnnnnnnnnnnngnngcctgtcatgagtgtnnnnnnnnnncnnnnnnnggnaaaagntggacatctagaattgaagaatgncn  
ngnnngnncnngcaannnnnnnnnnnnngnannnnngnncgntnnnt
```

**(A) CR (207/401): 51.6%**

**(B)**

Max score: 86.0

Total score: 136

Query coverage: 33%

E value: 9e-13

Identity: 74%

- MG764079.1: Seoul orthohantavirus strain SEOV/NL/Rn2147/2016 segment S nucleocapsid protein gene, complete cds.
- MG764078.1: Seoul orthohantavirus strain SEOV/NL/Rn2125/2016 segment S nucleocapsid protein gene, complete cds.
- KX064271.1: Seoul hantavirus strain TURCKHEIM/Rn/FRA/2016/2016.00033 nucleoprotein (N) gene, complete cds.
- KX064270.1: Seoul hantavirus strain TURCKHEIM/Hu/FRA/2016/2016.00044 nucleoprotein (N) gene, complete cds.
- KX079476.1: Seoul hantavirus isolate IR162 nucleocapsid protein gene, complete cds.
- KX079473.1: Seoul hantavirus isolate IR33 nucleocapsid protein gene, complete cds.
- KX079470.1: Seoul hantavirus isolate IR473 nucleocapsid protein gene, complete cds.
- KM948598.1: Seoul virus strain Humber segment S, complete sequence.
- **KC626089.1: Seoul virus nucleocapsid protein gene, complete cds.**
- JX879769.1: Seoul virus strain Humber segment S, complete sequence.





nnnnncnnnnnnnnnnnnnnntcatgagccccgtgntnncnnnnnnnnnnnnnnnftngnnnnngnnnnnnnnnnnnncnnnnng  
nnnnnnngnnnnnnnnngnnnnngnnnctttattaancnngaannngnnnnnnnnnnnn

**(A) CR (118/401): 29.4%**

**(B)**

Max score: 50.0

Total score: 50.0

Query coverage: 11%

E value: 0.064

Identity: 80%

AJ011646.1: Topografov hantavirus S segment gene for N protein.