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Ferenc Jakab  
University of Pécs | PTE · Szentágotthai Research Centre, National Laboratory of Virology, BSL-4 Laboratory  
Habil MSc, PhD, DSc

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Publications



Publications

Skills and Expertise

Virology Sequencing Genetics RNA DNA Genomics PCR DNA Sequencing Next Generation Sequencing Bioinformatics and C

Affiliations

July 2012 - March 2017

University of Pécs

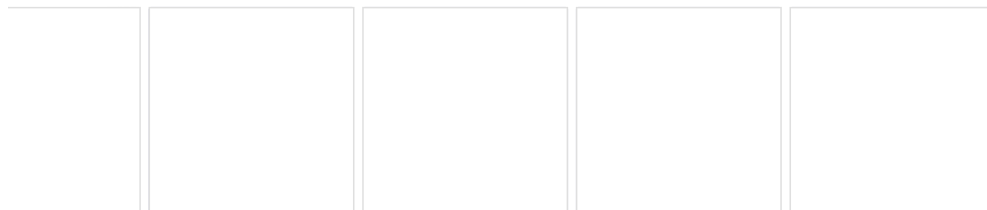
Szentágotthai Research Centre, Virological Research Group · Pécs, Hungary

Position

Professor (Associate)



(255)



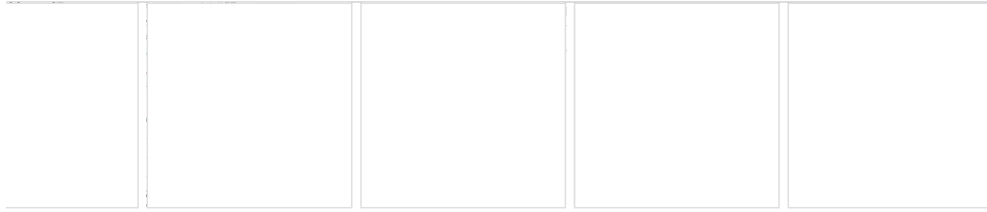
Optimizing targeted mosquito control efforts through mobile West Nile virus detection

Full-text available

23

András Varga · Rubén Bueno Marí · Jose Risueño Iranzo · [...] · Gabor Kemenesi

ound Different mosquito control strategies have been implemented to mitigate or prevent mosquito-  
public health situations. Modern mosquito control largely relies on multiple approaches, including  
l, specific treatments. Given all this, it is becoming increasingly important to supplement these activities  
id and mobile di...



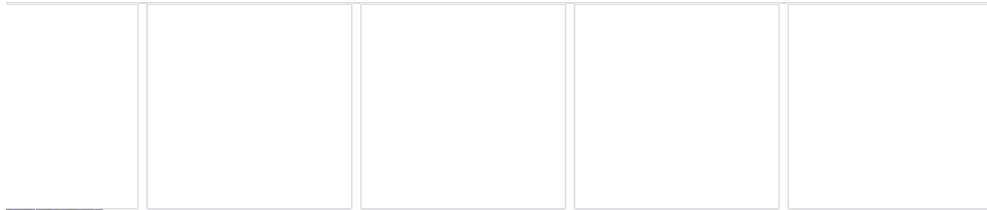
### Genomic similarity of human papillomavirus E4 and polyomaviral VP4 exhibited by genomic analysis of a common kestrel (*Falco tinnunculus*) polyomavirus

[Full-text available](#)

2023

Ó Fehér · Eszter Kaszab · János A Mótyán · [...] · Krisztian Banyai

Polyomaviruses are widely distributed viruses of birds that may induce developmental deformities and internal disorders primarily in nestlings. In this study, polyomavirus sequence was detected in kidney and liver tissues of a common kestrel (*Falco tinnunculus*) that succumbed at a rescue station in Hungary. The amplified nucleotide (nt)...



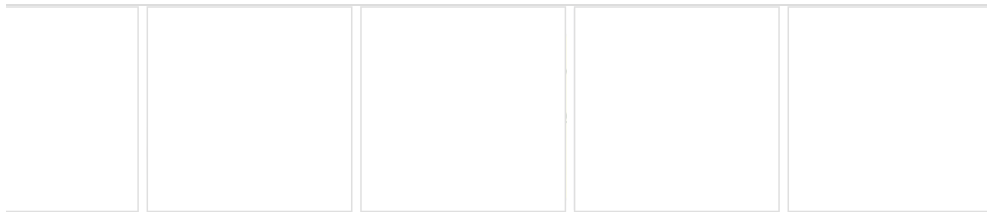
### Phylogenetic analysis and genome characterization of Lloviu virus from Italian Schreibers's bats

[Full-text available](#)

2023

Gábor · Adam J Hume · Ellen Lee Suder · [...] · Gabor Kemenesi

Lloviu virus (LLOV) was the first identified member of Filoviridae family outside the Ebola and Marburg virus genera. A massive die-off of Schreibers's bats (*Miniopterus schreibersii*) in the Iberian Peninsula led to its initial discovery. Recent studies with recombinant and wild-type LLOV isolates confirmed the nature of the vi...



### Mechanisms of circoviral immunosuppression and pathogenesis with a focus on porcine circovirus 2: A review

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2023

Ó Fehér · Ferenc Jakab · Krisztian Banyai

Circoviruses are small, non-enveloped viruses that can cause immunosuppression and pathogenesis in various animals. Pathogens, due to their adverse effects on the immune reaction, aggravate the course of concomitant infectious diseases. Here we summarize mechanisms by which circoviruses, including the most studied porcine circovirus 2, and other mammalian and avian circoviruses, trigger their own replication and confound the host's immune response. A...

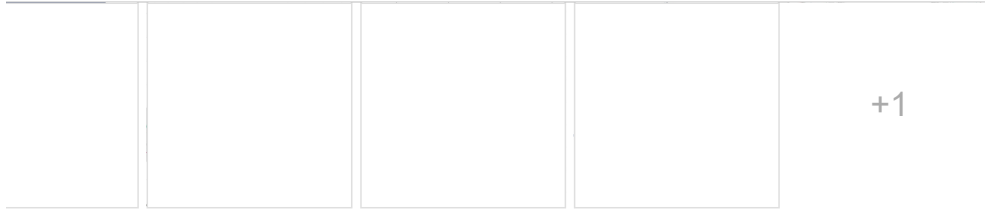
### Importance of equally accessible genomic surveillance in the age of pandemics

[Full-text available](#)

2023

Amr Zeghib · Gabor Kemenesi · Ferenc Jakab

...c epidemiology is now a core component in investigating the spread of a disease during an outbreak  
future preparedness to tackle emerging zoonoses. During the last decades, several viral diseases  
and emphasized the importance of molecular epidemiology in tracking the dispersal route, supporting  
mitigation measures, and ap...



+1

### Temporal Transcriptome Profiling of Monkeypox and Host Cells using Nanopore Sequencing

Full-text available

123

zs Kakuk · Ákos Dörmő · Zsolt Csabai · [...] · Zsolt Boldogkői

...ent human Monkeypox outbreak underlined the importance of studying basic biology of  
...xviruses. However, the transcriptome of its causative agent has not been investigated before neither  
...rt-, nor with long-read sequencing approaches. This Oxford Nanopore long-read RNA-Sequencing  
fills this gap. It will enable the in-dept...



+6

### Development of a novel, entirely herbal-based mouthwash effective against common oral bacteria and CoV-2

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rt Bencze · Viktória Temesfői · Sourav Das · [...] · Tamas Koszegi

...ound Parallel to the growth of the oral healthcare market, there is a constantly increasing demand for  
products as well. Many customers prefer products that contain fewer toxic agents, therefore providing  
environmentally friendly solution with the benefit of smaller risk to the user. Medieval and early modern  
al knowledge mi...



### Herbal-based extracorporeal immuno-affinity virus capture: a feasibility study to address the CoV-2 pandemic

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or Járvás · Dora Szerenyi · Hajnalka Jankovics · [...] · Andras Guttman

...aper, we report on the utilization of micro-technology based tools to fight viral infections. Inspired by  
hemoperfusion and immune-affinity capture systems, a blood virus depletion device has been  
ed that offers highly efficient capture and removal of the targeted virus from the circulation, thus  
sing virus load. Singl...

### Genome and genome characterization of Lloviu virus from Italian Schreibers bent-winged bats

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Gábor · Adam J Hume · Ellen Lee Suder · [...] · Gabor Kemenesi

uevavirus (LLOV) was the first identified member of Filoviridae family outside the Ebola and virus genera. A massive die-off of Schreibers' bent-winged bats ( *Miniopterus schreibersii* ) in the Peninsula in 2002 led to its discovery. Studies with recombinant and wild-type LLOV isolates confirmed ceptibility of human-der...

### Temporal Transcriptome Profiling of Monkeypox and Host Cells using Nanopore Sequencing

Full-text available

22  
zs Kakuk · Akos Domo · Zsolt Csabai · [...] · Zsolt Boldogkői  
ent Monkeypox outbreak showed the importance of studying the basic biology of orthopoxviruses. r, the transcriptome of its causative agent has not been investigated before neither with short-, nor with id sequencing approaches. This Oxford Nanopore long-read RNA-Sequencing dataset fills this gap. ct cDNA and native RNA s...

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### Models Used in Monkeypox Research

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anna Domán · Enikő Fehér · Renáta Kugler · [...] · Krisztian Banyai  
pox is an emerging zoonotic disease with a growing prevalence outside of its endemic area, posing a int threat to public health. Despite the epidemiological and field investigations of monkeypox, little is about its maintenance in natural reservoirs, biological implications or disease management. African are considered p...

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### of Sars-Cov-2 Genetic Material Reduction During a Traditional Wastewater Treatment logy

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lya Adamcsik · Renata Gerencsér-Berta · Borbála Horváth · [...] · Ildiko Galambos  
rmission of Severe Acute Respiratory Syndrome Coronavirus-2 in a community can be monitored by a ater-based epidemiological approach due to fecal shedding. Although sewage surveillance has gained a rable amount of attention over the last 16 months, an indirect issue within the topic is whether ial wastewater treatment t...

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### nthetic teicoplanin derivatives with dual antimicrobial activity against SARS-CoV-2 and sistant bacteria

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Bakai-Bereczki · Vladimir Vimberg · Eszter Lőrincz · [...] · Anikó Borbás






is infected with SARS-CoV-2 risk co-infection with Gram-positive bacteria, which severely affects their  
sis. Antimicrobial drugs with dual antiviral and antibacterial activity would be very useful in this setting.  
h glycopeptide antibiotics are well-known as strong antibacterial drugs, some of them are also active  
RNA vir...

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### Correction: Isolation of infectious Lloviu virus from Schreiber's bats in Hungary

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or Kemenesi ·  Tóth Gábor ·  Martin Mayora Neto · [...] ·  Ferenc Jakab

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### Early Introduction Governed Viral Diversity in the Second Wave of SARS-CoV-2 Epidemic in Hungary

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er Ari ·  Bálint Márk Vásárhelyi ·  Gabor Kemenesi · [...] ·  Balint Kintses

ective evaluation of past waves of the SARS-CoV-2 epidemic is key for designing optimal interventions  
future waves and novel pandemics. Here we report on analysing genome sequences of SARS-CoV-2  
first two waves of the epidemic in 2020 in Hungary, mirroring a suppression and a mitigation strategy,  
vely. Our analysis r...



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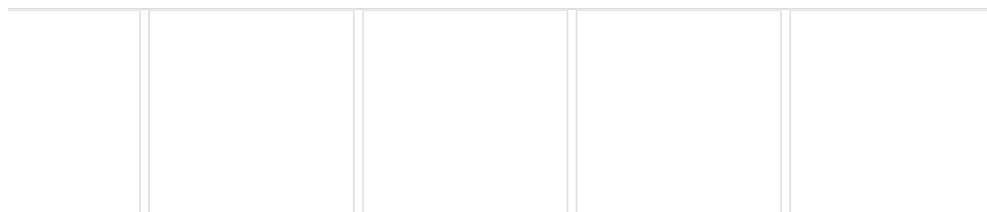
### ADP-rib blocks SARS-CoV-2 virus binding to cells and interleukin-6 release in a model of COVID-19

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rietta Papp ·  Judit Bóvári-Biri ·  Krisztina Banfai-Biri · [...] ·  Peter Bai

virus disease 2019 (COVID-19), caused by SARS-CoV-2 virus, is a major global health challenge, as  
no efficient treatment for the moderate to severe disease. ADP-ribosylation events are involved in  
ng the life cycle of coronaviruses and the inflammatory reactions of the host, hence we assessed the  
sing of registered PAR...




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### Comparison of immune activation of the COVID vaccines: ChAdOx1, BNT162b2, mRNA-1273, BBIBP-CorV and Gam-COVID-Vac from serological human samples in Hungary showed higher protection after cell-based immunization

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er Fodor ·  Isabel Olmos ·  Olga Kuten Pella · [...] ·  Zsombor Lacza

re: To gain insight into the different protective mechanisms of approved vaccines, this study focuses on  
parison of humoral and cellular immune responses of five widely used vaccines including ChAdOx1  
22, AstraZeneca), BNT162b2 (Pfizer), mRNA-1273 (Moderna), BBIBP-CorV (Sinopharm), and Gam-  
Vac (Sputnik V). Materials and...

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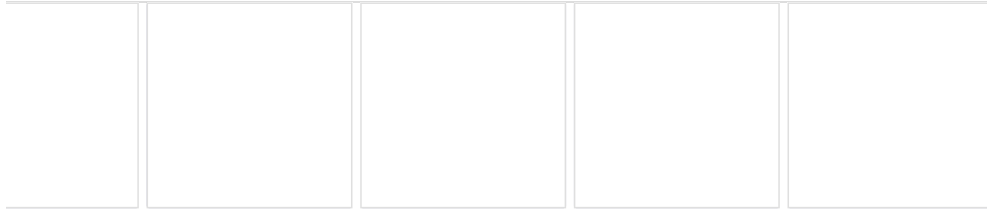
### Particle detection of native SARS-CoV-2 virions by microfluidic resistive pulse sensing

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án Varga · ● Mónika Madai · ● Gábor Kemenesi · [...] · ● Ferenc Jakab

idic resistive pulse sensing (MRPS) was used to determine the size distribution of severe acute  
ory syndrome coronavirus 2 (SARS-CoV-2) based on detecting nearly 30 000 single virions. However,  
structure of SARS-CoV-2 is thoroughly described, but ensemble properties of SARS-CoV-2, e.g., its  
size distribution, are s...



#### **jective Detection and Complete Genomic Sequencing of Canine morbillivirus in Eurasian Otter utra) Using Nanopore Technology**

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ia Lanszki · ● Jozsef Lanszki · ● Tóth Gábor · [...] · ● Gabor Kemenesi

asian otter (*Lutra lutra*) is a piscivorous apex predator in aquatic habitats, and a flagship species of  
ation biology throughout Europe. Despite the wide distribution and ecological relevance of the species,  
a considerable lack of knowledge regarding its virological and veterinary health context, especially in  
Europe....



#### **ion: Recombinant Llovio virus as a tool to study viral replication and host responses**

[Full-text available](#)

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n J Hume · ● Baylee Heiden · ● Judith Olejnik · [...] · ● Elke Mühlberger

rrects the article DOI: 10.1371/journal.ppat.1010268.].



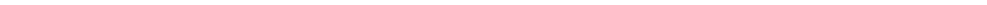
#### **ti-Histamine Azelastine, Identified by Computational Drug Repurposing, Inhibits Infection by ariants of SARS-CoV-2 in Cell Cultures and Reconstituted Human Nasal Tissue**

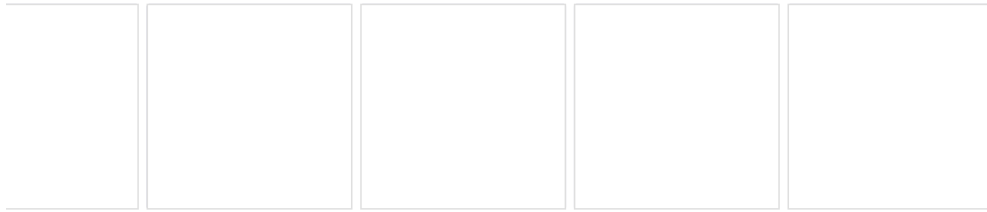
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ert Konrat · ● Henrietta Papp · ● Janine Kimpel · [...] · ● Eszter Nagy

ound and purpose: The COVID-19 pandemic continues to pose challenges, especially with the  
nce of new SARS-CoV-2 variants that are associated with higher infectivity and/or compromised  
on afforded by the current vaccines. There is a high demand for additional preventive and therapeutic  
as effective against this changing v...





### Simple Way to Relate the Effects of SARS-CoV-2-Induced Changes in Transferrin to Severe COVID-Associated Diseases

[Full-text available](#)

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Telek · Zoltán Ujfalusi · Gabor Kemenesi · [...] · Gábor Hild

SARS-CoV-2 infections are responsible for the COVID-19 pandemic. Transferrin has been found to explain the severe diseases associated with impaired iron transport and COVID-19 infection. The effect of SARS-CoV-2 on human whole blood was studied by differential scanning calorimetry. The analysis of the thermal denaturation curves showed that the...



### Methylene Blue Is a Nonspecific Protein–Protein Interaction Inhibitor with Potential for Repurposing as an Antiviral for COVID-19

[Full-text available](#)

122

Jing-Ting Chuang · Henrietta Papp · Anett Kuczmog · [...] · Peter Buchwald

We previously identified methylene blue, a tricyclic phenothiazine dye approved for clinical use for the treatment of methemoglobinemia and for other medical applications as a small-molecule inhibitor of the protein-protein interaction (PPI) between the spike protein of the SARS-CoV-2 coronavirus and ACE2, the first step of the attachment...

### Contribution to: Early Transfusion of Convalescent Plasma Improves the Clinical Outcome in Severe SARS-CoV-2 Infection

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Erőss Fodor · Veronika Müller · Zsolt Dániel Iványi · [...] · Zsombor Lacza

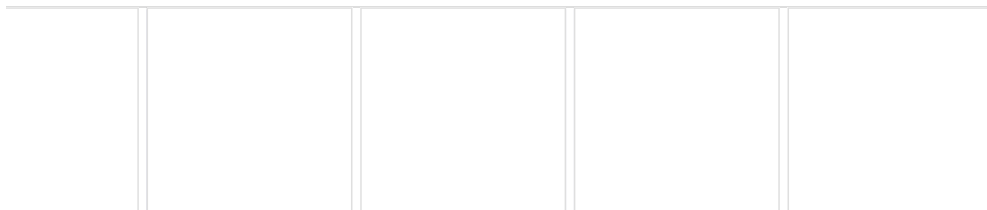
### Antiviral for the treatment of COVID-19 in elderly patients—what do we know after 2 years of COVID-19?

[Full-text available](#)

122

Henrietta Papp · Zsófia Lanszki · György Keseru · Ferenc Jakab

Since the appearance of coronavirus disease 2019 (COVID-19), numerous studies have been conducted to identify effective therapeutics. Favipiravir (FVP) is one of the repurposed drugs which has been authorized in a few countries on an emergency basis to treat COVID-19. Elderly individuals especially 65 years or older are more likely to develop severe illness...



### Antiviral drug repurposing against SARS-CoV-2 reveals plasma membrane cholesterol depletion as a key factor of antiviral drug activity

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ria Barsi · ● Henrietta Papp · ● Alberto Valdeolivas · [...] · ● Bence Szalai

Using SARS-CoV-2 infection-induced gene expression signatures to drug treatment-induced gene expression signatures is a promising bioinformatic tool to repurpose existing drugs against SARS-CoV-2. The hypothesis of signature-based drug repurposing is that drugs with inverse similarity to a disease phenotype can reverse disease phenotype...

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#### Prevalence of infectious Llovium virus from Schreiber's bats in Hungary

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Horváth Klemen · ● Tóth Gábor · ● Martin Mayora Neto · [...] · ● Ferenc Jakab

Llovium viruses can be transmitted to humans by zoonotic spillover events from their natural host and filoviruses have occurred with increasing frequency in the last years. The filovirus Llovium virus (LLOV), was first identified in Schreiber's bats ( *Miniopterus schreibersii* ) in Spain and was subsequently detected in Hungary. Here...

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#### Methylene Blue Is a Nonspecific Protein-Protein Interaction Inhibitor with Potential for Repurposing as a Therapeutic for COVID-19

Full-text available

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Yung-Ting Chuang · ● Henrietta Papp · ● Anett Kuczmog · [...] · ● Peter Buchwald

We previously identified methylene blue, a tricyclic phenothiazine dye approved for clinical use for the treatment of methemoglobinemia and used for other medical applications, as a small-molecule inhibitor of the protein-protein interaction (PPI) between the spike protein of the SARS-CoV-2 coronavirus and ACE2, the first step of the...

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#### Real-time genomic sequencing of canine distemper virus with nanopore technology during an outbreak event

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Anna Lanszki · ● Tóth Gábor · ● Éva Schütz · [...] · ● Gabor Kemenesi

Canine distemper virus (CDV) endangers a wide range of wild animal populations, can cross species barriers and therefore representing a significant conservation and animal health risk around the globe. During spring 2021, according to our current estimates a minimum of 50 red foxes (*Vulpes vulpes*) died of CDV in Hungary, with CDV lesions...

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## Protocol of Resampling: Protocol for the Field-based Detection and Characterization of the European Llovium Cuevavirus (Llovium cuevavirus)

Full-text available

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Gábor · Tamás Görföls · Sandor A. Boldogh · [...] · Gabor Kemenesi

Our main goal was to develop novel sampling protocol and study design for viral discovery and sequencing in bats to support multi-purposal research activities (ie. detection, sequencing, serology, isolation) with minimal conservational effect and disturbance. We tested this method within the framework of Llovium cuevavirus (LLOV) surveillance...

## Objective detection and sequencing of Canine Distemper Virus in road-killed Eurasian otter (Lutra lutra) samples from the last two decades

Preprint Paper

22

Orsolya Lanszki · Jozsef Lanszki · Tóth Gábor · [...] · Gabor Kemenesi

Canine distemper virus (CDV) is a single-stranded negative-sense RNA virus, which belongs to the Morbilliviridae family in the Morbillivirus genus. Based on nucleotide sequence analysis of the hemagglutinin gene, several distinct genotypes are known in different hosts and geographical areas worldwide. A wide range of domestic animals are affected by this virus...

## A possible way to relate the effects of SARS-CoV-2 induced changes in transferrin to severe COVID-19 related diseases

Preprint Full-text available

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Telek · Zoltán Ujfalusi · Gabor Kemenesi · [...] · Gábor Hild

Essentially life-threatening Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) infection is responsible for the coronavirus pandemic in 2019 (COVID-19). The transferrin as an essential component of iron metabolism was suggested to be a link between iron transport associated diseases and COVID-19. The effect of SARS-CoV-2 on...

+1

## Endogenous Llovium virus as a tool to study viral replication and host responses

Full-text available

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John J. Hume · Baylee Heiden · Judith Olejnik · [...] · Elke Mühlberger

Genomic sequencing has revealed the presence of numerous RNA viruses in animal reservoir hosts, many of which are closely related to known human pathogens. Despite their zoonotic potential, most of these viruses remain understudied due to not yet being cultured. While reverse genetic systems can facilitate virus replication, this is often hindered...

## Llovium virus in Europe is an Emerging Disease of Concern

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Tamás Görföls · Tóth Gábor · Sandor A. Boldogh · [...] · Gabor Kemenesi

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### ransfusion of Convalescent Plasma Improves the Clinical Outcome in Severe SARS-CoV2

in

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er Fodor · ● Veronika Müller · ● Zsolt Dániel Iványi · [...] · ● Zsombor Lacza

tionPlasma harvested from convalescent COVID-19 patients (CCP) has been applied as first-line in the early phase of the SARS-CoV2 pandemic through clinical studies using various ls.Methods We present data from a cohort of 267 hospitalized severe COVID-19 patients who received o transfusion-related complications were rep...

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### ete Genomic Sequencing of Canine Distemper Virus With Nanopore Technology During an tic Event

rt [Full-text available](#)

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ia Lanszki · ● Tóth Gábor · ● Éva Schütz · [...] · ● Gabor Kemenesi

distemper virus (CDV) endangers a wide range of wild animal populations and can cross species , representing a significant conservational and animal health risk around the globe. During spring to 2021, according to our current estimates a minimum of 50 wild live red foxes ( Vulpes vulpes ) died of Hungary, with CDV lesi...

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### Apocarotenoids and Their Synthetic Glycopeptide Conjugates Inhibit SARS-CoV-2 Replication

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Bakai-Bereczki · ● Henrietta Papp · ● Anett Kuczmog · [...] · ● Anikó Borbás

tracted global COVID-19 pandemic urges the development of new drugs against the causative agent oV-2. The clinically used glycopeptide antibiotic, teicoplanin, emerged as a potential antiviral, and its was improved with lipophilic modifications. This prompted us to prepare new lipophilic apocarotenoid tes of teicoplanin...

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### ation of sampling points for the detection of SARS-CoV-2 in the sewage system

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re Domokos · ● Viktor Sebestyén · ● Viola Somogyi · [...] · ● János Abonyi

le tool for monitoring the spread of SARS-CoV-2 is to identify potential sampling points in the ater collection system that can be used to monitor the distribution of COVID-19 disease affected within a city. The applicability of the developed methodology is presented through the description of the population equivalent...

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### tational drug repurposing against SARS-CoV-2 reveals plasma membrane cholesterol depletion factor of antiviral drug activity

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ia Barsi · ● Henrietta Papp · ● Alberto Valdeolivas · [...] · ● Bence Szalai

ing SARS-CoV-2 infection-induced gene expression signatures to drug treatment-induced gene expression signatures is a promising bioinformatic tool to repurpose existing drugs against SARS-CoV-2. The hypothesis of signature based drug repurposing is that drugs with inverse similarity to a disease phenotype can reverse disease phenotype...

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#### Major host studies of Lloviu virus: first isolation, sequencing and serology in Schreiber's bats in

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or Kemenesi · Tóth Gábor · Martin Mayora Neto · [...] · Ferenc Jakab

ses are prime examples of emerging human pathogens that are transmitted to humans by zoonotic events. Since their initial discovery, filovirus outbreaks have occurred with increasing frequency and intensity. There is an urgent need to better understand their enzootic ecology and pathogenic potential, given the zoonotic virus species...

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#### Algerian Chapter of SARS-CoV-2 Pandemic: An Evolutionary, Genetic, and Epidemiological

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a Zeghib · Balázs A. Somogyi · Brigitta Zana · [...] · Ferenc Jakab

ore the SARS-CoV-2 pandemic in Algeria, a dataset comprising ninety-five genomes originating from SARS-CoV-2 sampled from Algeria and other countries worldwide, from 24 December 2019, through 4 March 2020, was thoroughly examined. While performing a multi-component analysis regarding the Algerian outbreak, the impact of phylogenetic, phylog...

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#### Reservoir of Lloviu virus as a model to study inaccessible zoonotic viruses

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n J Hume · Baylee Heiden · Judith Olejnik · [...] · Elke Mühlberger

generation sequencing has revealed the presence of many RNA viruses in animal reservoir hosts, including many closely related to known human pathogens. Despite their zoonotic potential, many of these remain understudied due to not yet being cultured. While reverse genetic systems can facilitate virus isolation, this is often hindered by m...

#### COVID-19, vírus, Virologiai Nemzeti Laboratórium

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nc Jakab

oglaló. A fertőző betegségek világméretű fenyegetettsége és terjedése komoly társadalmi, egészségügyi  
t jelent minden nemzet számára. A lokális problémák megoldása mellett minden esetben közös  
és nemzetközi összefogás szükséges. Az elmúlt években hazánkban is egyre nagyobb számban  
, illetve erősödtek meg új fertőző be...

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### ng protein hotspots by optimized fragment pharmacophores

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21  
d Bajusz · ● Warren Wade · ● Grzegorz Satała · [...] · ● György Keseru  
nt-based drug design has introduced a bottom-up process for drug development, with improved  
g of chemical space and increased effectiveness in early drug discovery. Here, we combine the use of  
cophores, the most general concept of representing drug-target interactions with the theory of protein  
s, to develop a design proto...

### ansfusion of convalescent plasma improves the clinical outcome in severe SARS-CoV2

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er Fodor · ● Veronika Muller · ● Zsolt Dániel Iványi · [...] · ● Zsombor Lacza  
harvested from convalescent COVID-19 patients (CCP) has been applied as first-line therapy in the  
ase of the SARS-CoV2 pandemic through clinical studies using various protocols. We present data  
ohort of 267 hospitalized, severe COVID-19 patients who received CCP. No transfusion-related  
ations were reported, indicating...

### ged Infection of Canine Distemper Virus in a Mixed-Breed Dog

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21  
ia Lanszki · ● Brigitta Zana · ● Safia Zeghib · [...] · ● Gabor Kemenesi  
distemper virus (CDV) is a major viral pathogen in domestic dogs, belonging to the Paramyxoviridae  
n the Morbillivirus genus. It is present worldwide, and a wide range of domestic animals and wild  
es are at risk. In the absence of vaccination, dogs have a low chance of survival; however, if and when  
urvives, it can ta...

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### erison of virus neutralization activity and results of 10 different anti-SARS-CoV-2 serological tests ID-19 recovered plasma donors

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ia Szabó · ● Tamás Szabó · ● Kornelia Bodo · [...] · ● Zsombor Lacza  
ical testing is a tool to predict protection against later infection. This potential heavily relies on antibody  
howing acceptable agreement with gold standard virus neutralization tests. The aim of our study was to  
ate diagnostic value of the available serological tests in terms of predicting virus neutralizing activity of

### reness Regarding Hantavirus Detection in Rodent Tissue Samples and Urine



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Ika Madai · Győző Horváth · Robert Herczeg · [...] · Ferenc Jakab

...ual hosts of Orthohantaviruses are rodents, soricomorphs and bats, and it is well known that they may cause serious or even fatal diseases among humans worldwide. The virus is persistent among animals and it is shed via urine, saliva and feces throughout the entirety of their lives. We aim to identify the effectiveness of various detection methods...

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### Effect of An 84-bp Deletion of the Receptor-Binding Domain on the ACE2 Binding Affinity of the SARS-CoV-2 Spike Protein: An In Silico Analysis

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Or Kemesesi · Tóth Gábor · Dávid Bajusz · [...] · Ferenc Jakab

SARS-CoV-2 is a recently emerged, novel human coronavirus responsible for the currently ongoing COVID-19 pandemic. Recombination is a well-known evolutionary strategy of coronaviruses, which may frequently result in significant genetic alterations, such as deletions throughout the genome. In this study we identified a correlation between two genetic...

### Effectiveness Regarding Hantavirus Detection in Rodent Tissue Samples and Urine

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Ika Madai · Győző Horváth · Robert Herczeg · [...] · Ferenc Jakab

...ual hosts regarding Orthohantaviruses are rodents, soricomorphs and bats, and it is well known they cause serious or even fatal diseases among humans worldwide. The virus is persistent among animals and is shed via urine, saliva and feces, throughout the entirety of their lives. We aim to identify the effectiveness regarding hantavirus...

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### Genetic Chapter of SARS-CoV-2 Pandemic: An Evolutionary, Genetic

Full-text available

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Zeghib · Balázs Antal Somogyi · Brigitta Zana · [...] · Ferenc Jakab

...ore the SARS-CoV-2 early pandemic in Algeria, a dataset comprising forty-three genomes originating from SARS-CoV-2 sampled from Algeria and other countries worldwide, from 24 December 2019 through 8 February 2020, of which, were thoroughly examined. While performing a multi-component analysis regarding the early outbreak, the toolkit of phyl...

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### Interfering RNAs Are Highly Effective Inhibitors of Crimean-Congo Hemorrhagic Fever Virus Replication In Vitro

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ri Földes · Mónika Madai · Henrietta Papp · [...] · Ferenc Jakab

1-Congo hemorrhagic fever virus (CCHFV) is one of the prioritized diseases of the World Health Organization, considering its potential to create a public health emergency and, more importantly, the absence of efficacious drugs and/or vaccines for treatment. The highly pathogenic characteristic of CCHFV restricts its use to BSL-4 laboratories...

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### SARS-CoV-2 Introductions Shaped the Early Outbreak in Central Eastern Europe: Comparing Genomic Data to a Worldwide Sequence Data-Matrix

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or Kemenesi · Safia Zeghbib · Balázs Antal Somogyi · [...] · Ferenc Jakab

Acute Respiratory Syndrome Coronavirus 2 is the third highly pathogenic human coronavirus in history. Its emergence in Hubei province, China, during late 2019, the situation evolved to pandemic level. In early 2020, Europe was the second epicenter of the pandemic. To better comprehend the detailed mechanisms of the epidemic e...

### DEVELOPMENT AND OPTIMIZATION OF AN ARTIC-LIKE SEQUENCING PROTOCOL FOR THE ANALYSIS OF HUMAN FILOVIRUS THE LLOVIU CUEVAVIRUS

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Gábor · Balázs Antal Somogyi · Ferenc Jakab · Gabor Kemenesi

Emerging and re-emerging infectious diseases pose an unquestionable challenge to humankind. There is an urgent need to extend our knowledge about these pathogens and develop novel molecular techniques which are capable of rapid and detailed genomic characterisation. These methods should be applicable for real-time monitoring of pathogen evolution, r...

### Magyarországi COVID-járványt meghatározó vírusváltozatok genetikai vizsgálata

[uncovgen.brc.hu/](http://uncovgen.brc.hu/)

arch

20

er Ari · Bálint Márk Vásárhelyi · Gabor Kemenesi · [...] · Balint Kintses

COVID-19 vírus-fertőzés terjedési láncának visszakövetésében és a klinikai fejlesztés alatt álló vakcinajelöltek hosszú távú hatékonyságának előrejelzésében is segíthet az a vírusgenom-kutatási program, amely országos együtműködéssel, szegedi, pécsi, debreceni és budapesti kutatóintézetek és klinikák közreműködésével valósul meg, és bek...

### Detection of Hepatitis E Virus in the Feces of Red Foxes (*Vulpes vulpes*)

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ia Lanszki · Kornélia Kurucz · Safia Zeghbib · [...] · Ferenc Jakab




Hepatitis E virus (HEV) can infect a wide range of animals, showing a relatively strict host specificity; however, its zoonotic potential, natural transmission in the wildlife are less known. Several new HEV-like viruses have been identified in various animal species, including carnivores; however, the phylogenetic relationship among these viruses is...

### Anti-histamine Azelastine, Identified by Computational Drug Repurposing, Inhibits SARS-CoV-2 Infection in Reconstituted Human Nasal Tissue In Vitro

Full-text available

art

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ert Konrat ·  Henrietta Papp ·  Valeria Iren Szijarto · [...] ·  Eszter Nagy

und The COVID-19 pandemic is an enormous threat for healthcare systems and economies worldwide  
ently demands effective preventive and therapeutic strategies. Unlike the development of vaccines and  
igs specifically targeting SARS-CoV-2, repurposing of approved or clinically tested drugs can provide an  
ate solution. Method...

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### tion animals likely do not spread COVID-19 but may get infected themselves

20

a Csiszar ·  Ferenc Jakab ·  Teresa G. Valencak · [...] ·  Zoltan Ungvari

irus disease 2019 (COVID-19) is a highly contagious infectious disease caused by the novel severe  
spiratory syndrome coronavirus 2 (SARS-CoV-2). From the epidemiological data, the picture emerges  
more severe etiopathologies among COVID-19 patients are found in elderly people. The risk of death  
COVID-19 increases expon...

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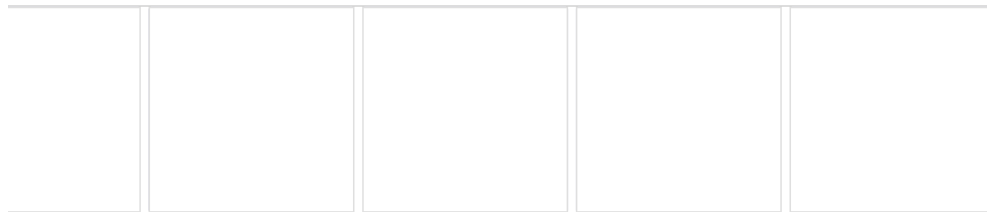
### anin Derivatives Impact on West Nile Virus Pathogenesis

[Full-text available](#)

0

rietta Papp ·  Ilona Bakai-Bereczki ·  Pál Herczegh · [...] ·  Ferenc Jakab

le virus (WNV) is an emerging arbovirus that causes infections worldwide. Clinical manifestations of the  
v vary from asymptomatic to fatal illness when it reaches the central nervous system. To date, vaccine  
ific antiviral treatments are not available. Teicoplanin is already used to treat Gram-positive bacterial  
is. F...



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### g homes and the elderly regarding the COVID-19 pandemic: situation report from Hungary

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or Kemenesi ·  László Kornya ·  Tóth Gábor · [...] ·  Ferenc Jakab

bal impact of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic is  
nt in terms of public health effects and its long-term socio-economic implications. Among all social  
the elderly is by far the most affected age group regarding morbidity and mortality. In multiple countries  
g several continents...

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### nterfering RNAs are highly effective inhibitors regarding Crimean-Congo hemorrhagic fever plication in vitro

1t

20

ri Földes ·  Mónika Madai ·  Henrietta Papp · [...] ·  Ferenc Jakab

r-Congo hemorrhagic fever virus (CCHFV) is one of the prioritized diseases of the World Health  
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research to BSL-4 labo...

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### hls Tygerberg Francie van Zijl Rylaan Drive 25

20

/ W W Csa ·  Daniel R Brooks ·  Eric P Hoberg · [...] ·  Valeria Trivellone

ckholm Paradigm suggests that the capacity for pathogens to be associated with a given host is related  
ccurrence of specific traits possessed by the host that represent required resources for the pathogen.

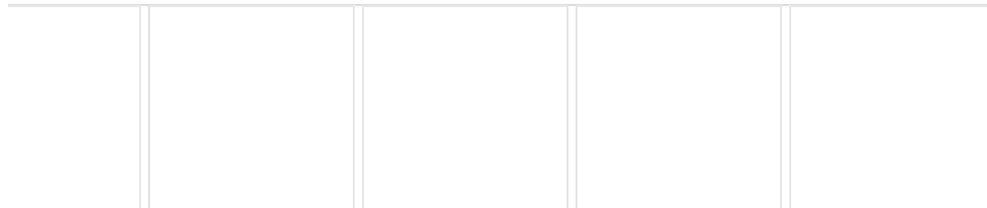
capacity for a pathogen to be associated with more than one host is related to how phylogenetically related those same res...

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### the Pandemic Ends: Making Sure This Never Happens Again

Full-text available

2020  
Daniel R Brooks · Eric P Hoberg · Walter Antonio Boeger · [...] · Valeria Trivellone  
On 30 January 2020, the World Health Organization (WHO) declared a Global Health Emergency of international concern attendant to the emergence and spread of SARS-CoV-2, nearly two months after the reported emergence of human cases in Wuhan, China. In the subsequent two months, global, national and local health personnel and infra...



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### SARS-CoV-2 introductions shaped the early outbreak in Central Eastern Europe: comparing genomic data to a worldwide sequence data-matrix

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2020  
Gábor Kemenesi · Safia Zeghib · Balázs Antal Somogyi · [...] · Ferenc Jakab  
Acute Respiratory Syndrome Coronavirus 2 is the third highly pathogenic human coronavirus in history. Since its emergence in Hubei province, China, during late 2019 the situation evolved to pandemic level. In Central Europe, Europe was the second epicenter of the pandemic. To better comprehend the detailed mechanisms of the epidemic ev...

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### Central African Congo hemorrhagic fever virus infection triggers the upregulation of the Wnt signaling pathway inhibitor genes

2020  
Kriszta Papp · Safia Zeghib · Fanni Földes · [...] · Ferenc Jakab  
Central African Congo hemorrhagic fever virus (CCHFV) is a highly pathogenic agent. Thus far, vaccines and specific therapies are not available against the threat of infection. Our knowledge regarding its pathogenesis is limited, and thus, developing effective antiviral therapies is hampered. Several studies have demonstrated that the CCHF...



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### Approach Investigation Regarding the West Nile Virus Situation in Hungary, 2018

Full-text available

2020  
Kriszta Zana · Károly Erdélyi · Anna Nagy · [...] · Gabor Kemenesi  
West Nile virus is endemic in multiple European countries and responsible for several epidemics throughout the European region. Its evolution into local or even widespread epidemics is driven by multiple factors from genetic diversification of the virus to environmental conditions. The year of 2018 was characterized by an extraordinary increase...

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### West Nile vírus és egyéb szúnyogokkal terjedő flavivírusok hazai relevanciája és a fertőzések megelőzésének lehetőségei

19

Gabor Kemenesi · Brigitta Zana · Ferenc Jakab

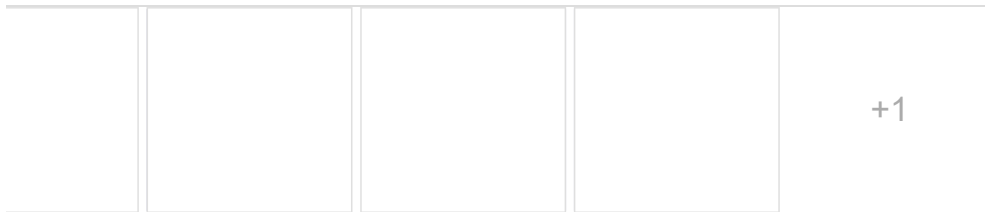
It-nílusi vírus térnyerésére és jelentőségére markáns példát lát-hattunk a 2018-as évben Középkeleten, hiszen minden eddigénél több humán esettel járó európai járványt tapasztalhattunk meg. A cikkben vizsgáljuk azokat a tényezőket, amelyek szerepet játszhattak ebben, valamint megvizsgáljuk a rokon jelentőségét és klinikai rel...

### Local Dynamics of Two Pathogenic Hantaviruses Among Rodents in Hungary

19

Orsi Madai · Viktória Németh · Miklós Oldal · [...] · Ferenc Jakab

Hantaviruses are worldwide pathogens, which often cause serious or even fatal diseases in humans. Hosts are predominantly in the form of rodents and soricomorphs; however, bats are also described as an important reservoir. In Hungary, representatives of two human pathogenic species of the genus Orthohantavirus are present: the Dobrava-Belgrade orth...



### Characterization of a novel picornavirus in Algerian bats: co-evolution analysis of bat-related picornaviruses

Full-text available

19

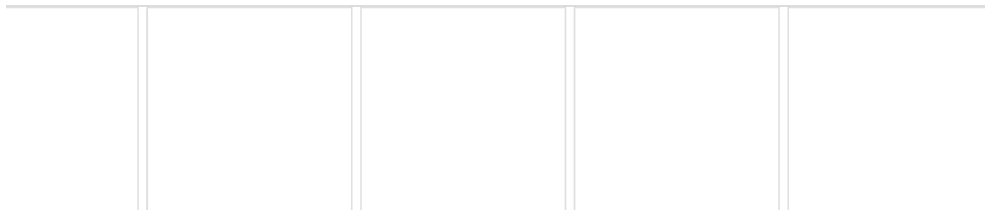
Orsi Zeghib · Robert Herczeg · Gabor Kemenesi · [...] · Ferenc Jakab

Bats are reservoirs of numerous zoonotic viruses. The Picornaviridae family comprises important pathogens that may infect both humans and animals. In this study, a bat-related picornavirus was detected from Algerian *Myotis schreibersii* bats for the first time in the country. Molecular analyses revealed the new virus to be most closely related to the Mischivi...

### Local Identification of a Novel Hantavirus in Malaysian Bronze Tube-Nosed Bats (*Murina aenea*)

19

Brigitta Zana · Gabor Kemenesi · Dóra Buzás · [...] · Ferenc Jakab



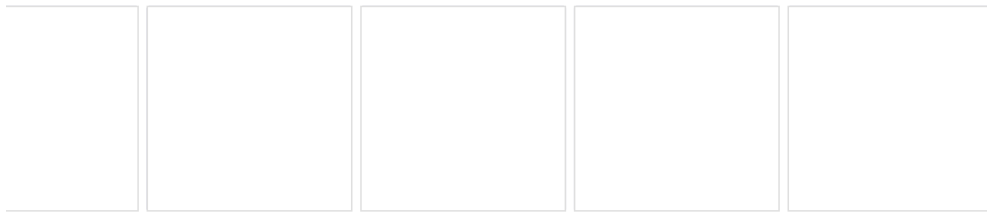
### Local Identification of a Novel Hantavirus in Malaysian Bronze Tube-Nosed Bats (*Murina aenea*)

Full-text available

19

Brigitta Zana · Gabor Kemenesi · Dóra Buzás · [...] · Ferenc Jakab

Over the past ten years, several novel hantaviruses were discovered in shrews, moles, and bats, suggesting the evolution of hantaviruses in many animal taxa other than rodents during their evolution. Interestingly, the phylogenetic analyses of most recent studies have raised the possibility that nonrodents may have served as reservoirs for hantaviruses in terrestrial mammalia...



### Genomic Identification of a Tentatively Novel Hantavirus in Malaysian Bronze Tube-Nosed Bat (*Murina*

Preprint [Full-text available](#)

2019

Zsuzsanna Zana · Gabor Kemenesi · Dóra Buzás · [...] · Ferenc Jakab

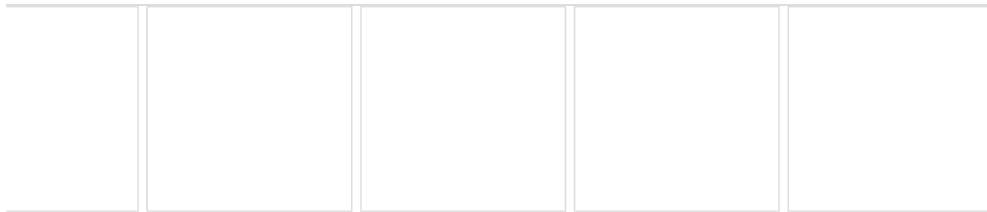
In the last ten years several novel hantaviruses were discovered in shrews, moles and bats, suggesting the spread of hantaviruses in many animal taxa other than rodents during their evolution. Interestingly, the comparative analyses of most recent studies have raised the possibility of non-rodents may have served as the natural mammalian...

### Genomic survey of the Crimean-Congo haemorrhagic fever virus infection among wild rodents in Hungary

2019

Orsi Földes · Mónika Madai · Viktória Németh · [...] · Ferenc Jakab

The Crimean-Congo haemorrhagic fever virus (CCHFV) is a tick-borne pathogen, which causes an increasing number of severe infections in many parts of Africa, Asia and in Europe. The virus is primarily transmitted by ticks. However, the spectrum of natural hosts regarding CCHFV includes a wide variety of domestic and wild animals. Although the presence of...



### Molecular detection of *Apis mellifera* filamentous virus in honey bees (*Apis mellifera*) in Hungary

[Full-text available](#)

2019

Zsuzsanna Zana · Lili Geiger · Anett Kepner · [...] · Ferenc Jakab

Honey bees (*Apis mellifera*) are important pollinators in the ecosystem and also play a crucial economic role in the honey industry. During the last decades, a continuous decay was registered in honey bee populations worldwide, including Hungary. In our study, we used metagenomic approaches and conventional sequencing on healthy and winter-killed...

### Genomic identification of a presumably novel hantavirus in bronze tube-nosed bat (*Murina aenea*) in Hungary

Preprint [Full-text available](#)

2018

Zsuzsanna Zana · Dóra Buzás · Gabor Kemenesi · [...] · Ferenc Jakab

### Significant range expansion of Lloviu virus in Europe: re-emergence in 2016, Hungary

Preprint [Full-text available](#)

2018

Gabor Kemenesi · Sandor A. Boldogh · Tamás Görföl · [...] · Ferenc Jakab

### Genomic survey of zoonotic agents in rodents from an urban environment, Hungary

Preprint [Full-text available](#)

18

Élvia Kurucz · Mónika Madai · Dávid Hederics · [...] · Ferenc Jakab

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### Discovery of a novel hepatitis E virus in Common voles (*Microtus arvalis*) from an urban environment, Hungary: Discovery of a novel hepatitis E virus-specific genotype of Orthohepevirus C

18

Élvia Kurucz · Dávid Hederics · Dominika Bali · [...] · Ferenc Jakab

Hepatitis E virus is a major causative agent of acute hepatitis worldwide. Despite its zoonotic potential, there is little information about the natural chain of hepatitis E virus infection in wildlife, and the potential reservoir species. In this study, we performed a hepatitis E virus survey by heminested RT-PCR on rodent samples from an urban environment (in the city of Pécs, Hungary).

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### Surveillance of nematode (order: Spirurida) in urban habitats, in the city of Pécs (Hungary)

18

Élvia Kurucz · Vivien Kiss · Brigitta Zana · [...] · Gabor Kemenesi

As part of the seasonal mosquito control activities in the city of Pécs (Baranya County, Hungary), a total of 1123 male mosquitoes belonging to 18 species (including the invasive species *Aedes koreicus*) were collected from human-inhabited areas, using CO<sub>2</sub>-baited traps, during two consecutive years. To survey the diversity and prevalence of f...

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### Genetic characterization of Usutu virus from *Culex pipiens* mosquitoes Serbia, 2014

18

Gabor Kemenesi · Dóra Buzás · Brigitta Zana · [...] · Ferenc Jakab

Since its first appearance in Europe, Usutu virus (USUV) diverged to several different genetic lineages. The virus is reported to date from multiple countries across Europe (Hungary, Italy, Switzerland, Spain, Germany, Belgium and Republic and Belgium). Considering the more frequently published impact of the virus on humans it is important to investigate...

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### MOESM1 ESM Supplement

18

Gabor Kemenesi · Kornélia Kurucz · Bianka Dallos · [...] · Ferenc Jakab

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### Prevalence of Lloviu virus in *Miniopterus schreibersii* bats, Hungary, 2016

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18

Gabor Kemenesi · Kornélia Kurucz · Bianka Dallos · [...] · Ferenc Jakab

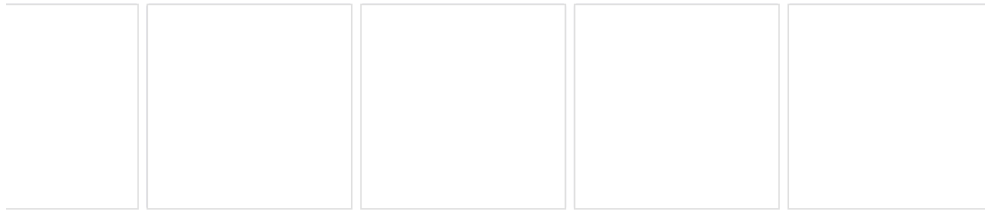
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### Supplementary Material

18

Gabor Kemenesi · Kornélia Kurucz · Bianka Dallos · [...] · Ferenc Jakab

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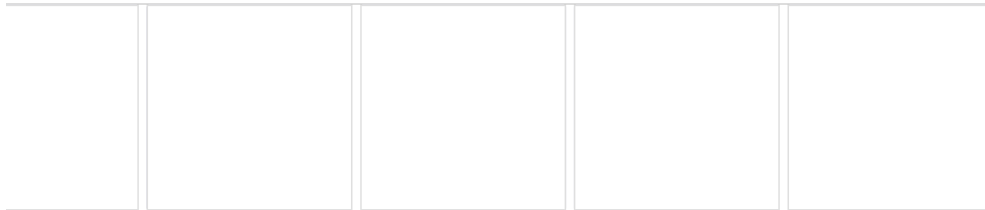
### Genomic analysis and avian malaria screening of mosquitoes collected from human-inhabited areas in Hungary and Serbia

[Full-text available](#)

18

Kornélia Kurucz · Anett Kepner · Bosiljka Krtinić · [...] · Gabor Kemenesi

Vector-borne pathogens have a growing medical importance in several European countries. The emergence and introduction of exotic vector species increases the likelihood that additional vector-borne diseases may appear in regions that have not encountered them previously. In the last few years, different emerging pathogens have been reported in humans, livestock...



### Characterization of replication-associated protein encoding circular DNA viruses in guano samples of Central-European bats

[Full-text available](#)

18

Gabor Kemenesi · Kornélia Kurucz · Brigitta Zana · [...] · Ferenc Jakab

Replication-associated protein encoding single-stranded DNA (CRESS DNA) viruses are increasingly identified worldwide in a variety of samples. Representative members include well-described veterinary pathogens with worldwide distribution, such as porcine circoviruses or beak and feather disease virus. In addition, numerous novel viruses belong to this group...

### Genomic analysis of bat guano samples revealed the presence of viruses potentially carried by honey bees, among others by *Apis mellifera* in Hungary

[Full-text available](#)

18

Brigitta Zana · Gabor Kemenesi · Péter Urbán · [...] · Ferenc Jakab

The dominance of dietary viruses in bat guano samples had been described recently, suggesting a new strategy to survey the prevalence and to detect new viruses of arthropods or even plant-infecting viruses occurring locally in the ecosystem. Here we describe the diversity of viruses belonging to the order Picornavirales in Hungarian insectivorous bats...

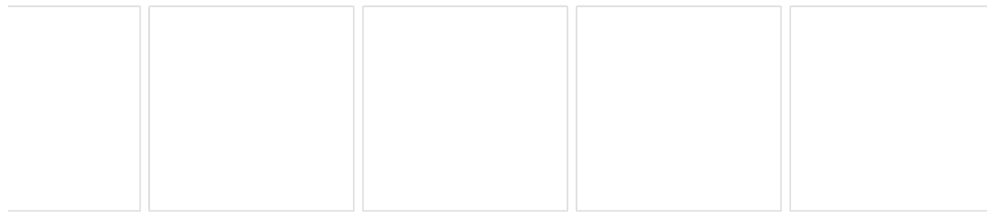
### Survey of Two Widespread Renal Syndrome-Causing Zoonoses: *Leptospira* spp. and *Hantavirus* in Urban Environment, Hungary

18

Kornélia Kurucz · Mónika Madai · Dominika Bali · [...] · Ferenc Jakab

Bats are important reservoir hosts for several zoonotic pathogens that cause significant morbidity and mortality in humans. Among others, leptospirosis is one of the most widespread zoonotic diseases worldwide. The similar clinical manifestation with hantavirus infection in humans. Despite the fact that both pathogens have great epidemiological importance...





### **Ecological preferences of the putative West Nile virus vector *Uranotaenia unguiculata* mosquito with retention of an original larval habitat**

Full-text available

17  
Krisztina Kovács · Gabor Kemenesi · Brigitta Zana · [...] · Ferenc Jakab  
The mosquito species *Uranotaenia unguiculata* has recently been described as a potential vector for a novel lineage of West Nile virus (WNV), but our knowledge about the distribution and ecology of this mosquito is rudimentary. Here, we summarize the literature regarding the ecology and behavior of mosquito *U. unguiculata*, and we provide...

### **Regulation of Toll-like Receptor TLR4 Is Associated with HPV DNA Integration in Penile Intraepithelial Neoplasia**

17  
Zoltán Damásdi · Krisztina Kovács · Nelli Farkas · [...] · Gyula Kovacs  
Background/Aim: Development of penile cancers is attributed to HPV-related carcinogenesis. Our aim was to investigate the association between HPV positivity and TLR4, p16(ink4a) and p53 expression. Materials and methods: HPV presence was detected with virus-specific TaqMan PCR and HPV Genotyping Test in 31 penile cancers. Immunohistochemistry was carried out on tissue microarrays.

### **Identification of a divergent cyclo-like virus in a great roundleaf bat (*Hipposideros armiger*) in Vietnam**

17  
Zoltán Damásdi · Kornélia Kurucz · Brigitta Zana · [...] · Ferenc Jakab  
Members of the viral family Circoviridae are increasingly recognized worldwide. Bats seem to be natural reservoirs or dietary-related dispensers of these viruses. Here, we report a distantly related member of the family Cycloviridae detected in the faeces of a great roundleaf bat (*Hipposideros armiger*). Interestingly, the novel virus shares a Circoviridae-like...

### **Genomic traces of a putative novel insect flavivirus from *Anopheles hyrcanus* mosquito species in Hungary**

17  
Brigitta Zana · Gabor Kemenesi · László Antal · [...] · Ferenc Jakab

### **Identification of a novel rotavirus species in Schreiber's bats, Serbia**

16  
Krisztian Banyai · Gabor Kemenesi · Ivana Budinski · [...] · Ferenc Jakab  
The genus Rotavirus comprises eight species designated A to H and one tentative species, Rotavirus I. In a metagenomic analysis of Schreiber's bats sampled in Serbia in 2014 we obtained sequences likely representing novel rotavirus species. Whole genome sequencing and phylogenetic analysis classified the novel strain into a tentative...

### **Genomic analysis of canine astroviruses reveals genetic heterogeneity and suggests possible inter-species transmission**

16  
Ferenc Mihalov-Kovács · Vito Martella · Gianvito Lanave · [...] · Krisztian Banyai




astrovirus RNA was detected in the stools of 17/63 (26.9%) samples, using either a broadly reactive  
sus RT-PCR for astroviruses or random RT-PCR coupled with massive deep sequencing. The complete  
y complete genome sequence of five canine astroviruses was reconstructed that allowed mapping the  
: organization and to investig...

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### iversity of replication-associated protein encoding circular viruses in guano samples of an bats

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emenesi ·  Brigitta Zana ·  Kornélia Kurucz · [...] ·  Ferenc Jakab

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### gical survey of hantavirus infection among rodents in Hungary

ence Paper

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16




ika Madai ·  Viktória Németh ·  Miklós Oldal · [...] ·  Ferenc Jakab

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### olecular identification of *Dirofilaria* spp. (Onchocercidae) in mosquitoes from Serbia

[Full-text available](#)

16

élia Kurucz ·  Anett Kepner ·  Bosiljka Krtinić · [...] ·  G. Kemenesi

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### ic characterization of West Nile virus strains derived from mosquito samples obtained during erbian outbreak

[Full-text available](#)

16

ttá Zana ·  Gabor Kemenesi ·  Robert Herczeg · [...] ·  Ferenc Jakab

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### n and complete genome characterization of novel reassortant orthoreovirus from common vole us arvalis)

16

ő Fehér ·  Gabor Kemenesi ·  Miklós Oldal · [...] ·  Ferenc Jakab

mammalian orthoreovirus (MRV) strain was isolated from the lung tissue of a common vole (*Microtus*  
with Tula hantavirus infection. Seven segments (L1-L3, M2-M3, S2, and S4) of the Hungarian MRV  
vORV/47Ma/06 revealed a high similarity with an MRV strain detected in bank vole (*Myodes glareolus*)  
any. The M1 and S3 segmen...

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### diversification, homo- and heterologous reassortment and recombination shape the evolution en orthoreoviruses

[Full-text available](#)

16

ia L. Farkas ·  Szilvia Marton ·  Eszter Dandár · [...] ·  Krisztian Banyai

Complete genome sequences of ten field avian orthoreovirus (ARV) strains collected from young birds between 2002 and 2011 in Hungary have been determined in order to explore the genetic diversity and evolutionary mechanisms affecting ARVs in this region. Sequence analyses and phylogenetic calculations of similar geographic distribu...

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## Supplementary Information

16

L. Farkas · Szilvia Marton · Eszter Dandár · [...] · Krisztian Banyai

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