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Selected Publications by EVBC Members

[All publications on Pubmed](#)

Thomas Mettenleiter was president of the Friedrich-Loeffler-Institut for 27 years and retired in June 2023. Looking back, he reflects on events around and following the reunification of Germany that changed his career path. (Nat Microbiol: [10.1038/s41564-024-01814-7](https://doi.org/10.1038/s41564-024-01814-7))

Epidemiology and surveillance

Recombination in MERS-related coronaviruses, where viruses swap genetic material, can lead to new variants with altered receptor usage, potentially enabling them to infect new hosts, including humans. **Correspondence to** [10.1016/S0140-6736\(24\)00641-X](https://doi.org/10.1016/S0140-6736(24)00641-X) (Lancet Infect Dis: [10.1016/S1473-3099\(24\)00461-4](https://doi.org/10.1016/S1473-3099(24)00461-4))

The WHO has updated its framework for tracking SARS-CoV-2 variants to account for unpredictable viral evolution, with potential application to other respiratory diseases with pandemic potential. (Nat Med: [10.1038/s41591-024-02949-0](https://doi.org/10.1038/s41591-024-02949-0))

📄📄 This rapid review synthesizes strategies to enhance inclusive pandemic-related crisis communication, revealing that tailored messages and trusted sources significantly improve outreach to underserved populations. (International Journal of Environmental Research and Public Health: [10.3390/ijerph21091216](https://doi.org/10.3390/ijerph21091216))

📄 This study investigates the dynamics of H5N1 clade 2.3.4.4b in calves and cows, revealing that H5N1 can cause severe mammary gland infections in cows, with implications for virus transmission routes among cattle. (Nature: [10.1038/s41586-024-08063-y](https://doi.org/10.1038/s41586-024-08063-y))

📄 This study proposes a new lineage nomenclature for dengue virus genomic surveillance, introducing major and minor lineages to improve tracking and understanding of viral diversity across regions. (PLoS Biol: [10.1371/journal.pbio.3002834](https://doi.org/10.1371/journal.pbio.3002834))

Zoonotic Diseases

📄 This study reports a comprehensive analysis of Borna disease virus 1 (BoDV-1) infections in humans and animals, highlighting new genome sequences and phylogeographic associations that inform zoonotic risk assessment. (Nat Commun: [10.1038/s41467-024-52192-x](https://doi.org/10.1038/s41467-024-52192-x))

📄 This study reveals a significant diversity of viruses in farmed fur animals, including several with zoonotic spillover potential, highlighting fur farming as a potential transmission hub for emerging pathogens. (Nature: [10.1038/s41586-024-07901-3](https://doi.org/10.1038/s41586-024-07901-3))

📄 This study reveals that the Rift Valley fever virus ambisense S segment has a central RNA region that is crucial for transcription and replication, highlighting its functional importance. (Nat Commun: [10.1038/s41467-024-52058-2](https://doi.org/10.1038/s41467-024-52058-2))

Immunology

📄📄 Review discussing the challenges and strategies in rational and structure-driven vaccine design for Arenaviruses, emphasizing the role of computational methods in enhancing pandemic preparedness. (Infect Genet Evol: [10.1016/j.meegid.2024.105626](https://doi.org/10.1016/j.meegid.2024.105626))

📄 Study demonstrating the effectiveness of the AERIAL TempTracker smartphone app for real-time monitoring of respiratory viral infections in cohort studies, providing insights into early life infections and chronic respiratory disease development. (iScience: [10.1016/j.isci.2024.110912](https://doi.org/10.1016/j.isci.2024.110912))

📄 This study investigates the viral infection responses in the non-vascular plant *Marchantia polymorpha*, revealing conserved defense mechanisms and unique features compared to vascular plants. (Nat Commun: [10.1038/s41467-024-52610-0](https://doi.org/10.1038/s41467-024-52610-0))

📄 This study identifies a common set of differentially expressed host cell transcripts in response to infection by distinct negative-sense RNA viruses, revealing a network of proteins that may regulate viral infections and immune responses. (J Virol: [10.1128/jvi.00935-24](https://doi.org/10.1128/jvi.00935-24))

📄 This study identifies diverse RNA viruses associated with parasitic nematodes and demonstrates their ability to elicit antibody responses in vertebrate hosts, indicating potential co-evolutionary dynamics. (Nat Microbiol: [10.1038/s41564-024-01796-6](https://doi.org/10.1038/s41564-024-01796-6))

Viral infection

📄 This study investigates the interactions between plant developmental stages and RNA virus infection in *A. thaliana*, revealing that mature flowering plants, while more susceptible, exhibit greater reproductive fitness compared to earlier stages, highlighting a trade-off between susceptibility and fertility. (J Gen Virol: [10.1099/jgv.0.002023](https://doi.org/10.1099/jgv.0.002023))

📄 This study explores the mechanistic links between viral infections and Alzheimer's disease, highlighting how specific viruses may contribute to AD pathogenesis through integrative systems bioinformatics. (J Infect Dis: [10.1093/infdis/jiae242](https://doi.org/10.1093/infdis/jiae242))

📄 This review examines the potential role of viruses, particularly Hepatitis B and C, in the etiology and exacerbation of intrahepatic cholestasis of pregnancy, a common liver disorder affecting pregnant women. (Rev Obstet Med: [10.1177/1753495X241258385](https://doi.org/10.1177/1753495X241258385))

📄 - open access X - preprints 📄 - reviews, meta analyses 🔧 - tools

EVBC Special Issues

[Special issue list](#)

Our special issue **Virus Bioinformatics 2024** has been closed.

Papers published:

Publications by EVBC members are highlighted ✨.

📄 Evolutionary Insights from Association Rule Mining of Co-Occurring Mutations in Influenza Hemagglutinin and Neuraminidase. [10.3390/v16101515](https://doi.org/10.3390/v16101515)

🌟 CIEVaD: A Lightweight Workflow Collection for the Rapid and On-Demand Deployment of End-to-End Testing for Genomic Variant Detection. [10.3390/v16091444](https://doi.org/10.3390/v16091444)

🌟 Aedes Mosquito Virome in Southwestern Cameroon: Lack of Core Virome, But a Very Rich and Diverse Virome in *Ae. africanus* Compared to Other Aedes Species. [10.3390/v16071172](https://doi.org/10.3390/v16071172)

🌟 Exploring the Complexity of the Human Respiratory Virome through an In Silico Analysis of Shotgun Metagenomic Data Retrieved from Public Repositories. [10.3390/v16060953](https://doi.org/10.3390/v16060953)

📄 Respiratory Syncytial Virus Vaccine Design Using Structure-Based Machine-Learning Models [10.3390/v16060821](https://doi.org/10.3390/v16060821)


🌟 IAVCP (Influenza A Virus Consensus and Phylogeny): Automatic Identification of the Genomic Sequence of the Influenza A Virus from High-Throughput Sequencing Data. [10.3390/v16060873](https://doi.org/10.3390/v16060873)


Selected Publications by EVBC Members (part 2)


 [All publications on Pubmed](#)


Bacteriophages and viromics

This study identifies a family of bacterial immune systems known as Tai, which interfere with phage tail assembly to protect bacterial hosts, highlighting their unique organization and coordinated expression. (Nat Commun: [10.1038/s41467-024-51915-4](#))



 Study describing a novel genus of bacteriophages targeting multiple *Pectobacterium* species, showing potential as biocontrol agents against soft rot and black leg diseases in potatoes. (Virus Research: [10.1016/j.virusres.2024.199435](#))

 This observational study presents a standardized bench-to bedside protocol for optimizing bacteriophage therapy in musculoskeletal infections, emphasizing the importance of a multidisciplinary approach to address antimicrobial resistance. (Front Cell Infect Microbiol: [10.3389/fcimb.2024.1434397](#))


 This research characterizes an archaeal virus that infects the dominant methanogen in the human gut, revealing insights into the dynamics of virus-host interactions and the mechanisms maintaining their stable coexistence. (Nat Commun: [10.1038/s41467-024-51946-x](#))


 This study reveals multiple instances of DNA polymerase swapping in

Caudoviricetes bacteriophages, highlighting the evolutionary significance and adaptive mechanisms behind these genetic exchanges. (Virol J: [10.1186/s12985-024-02482-z](#))

  This review discusses the challenges posed by phage-resistant bacteria and explores innovative strategies, particularly the use of phage cocktails, to enhance the effectiveness of phage therapy against bacterial infections. (Virology: [10.1016/j.virol.2024.110209](#))

Metagenomics


 This study evaluates metagenomics and targeted sequencing approaches for viral diagnosis and surveillance, highlighting the benefits and limitations of each method in clinical settings. (Genome Med: [10.1186/s13073-024-01380-x](#))

 This study presents a comprehensive metagenomic dataset from Lake Mendota, revealing insights into microbial communities and their responses to environmental changes over a twenty-year period. (Sci Data: [10.1038/s41597-024-03826-8](#))

 - [open access](#)  - [preprints](#)  - [reviews, meta analyses](#)  - [tools](#)

Upcoming Events

 [Subscribe to Calendar](#)

We do not endorse any of the listings and do not take any responsibility for the accuracy of the information. EVBC members are involved in events marked .

RECOMB 2025 | Research in Computational Molecular Biology 26 – 29 April 2025 | Seoul, Korea

The conference emphasizes the development and application of mathematical, statistical, and computational methods to solve problems in molecular biology.

Abstract/paper registration deadline: **16 October 2024, AoE**

11h European Seminar in Virology (EuSeV) | Viral Vectors – from Basic Research to Clinical Application

21 – 23 October 2024 | Bertinoro, Italy


The EuSeV conference will focus on discussing the most suitable viral vectors for specific purposes, strategies for optimizing them, and challenges in translating these technologies into clinical applications.

Registration still open.

VEGA (Viral EcoGenomics & Applications) Symposium

12 – 13 November 2024 | Berkeley, USA

How to best capture and characterize uncultivated viruses, understand the role of viruses in natural ecosystems, and functionally explore viral genetic diversity toward innovative biotechnological and industrial applications. **In-person and online registration.**

 **Simon Roux (Organizer)**

viruses *in silico* lecture series

 [Register](#)

This lecture is designed to keep you up to date with the latest developments in virus bioinformatics, especially new tools that might help you in your research.

ViralFlow v1.0—a computational workflow for streamlining viral genomic surveillance

28. October 2024 | 2 pm CET / 10 am BRT

online

Gabriel da Luz Wallau, Bernhard Nocht Institute for Tropical Medicine

Please be aware of the deviating time!

ViralFlow v1.0 is a flexible computational workflow for viral genomic surveillance, adaptable to new viral threats. It now serves as a general-purpose reference-based genome assembler for all viruses with available reference genomes, featuring virus-agnostic modules for characterizing mutations and running on various computational infrastructures, from laptops to HPC environments.



ViralFlow v1.0—a computational workflow for streamlining viral genomic surveillance

28. October 2024 | 2 pm CET

Gabriel da Luz Wallau, Bernhard Nocht Institute for Tropical Medicine

Selected Publications by EVBC Members (part 3)

 [All publications on Pubmed](#)

Evolution

📄 This study explores the evolutionary history of the Flaviviridae family by mapping glycoprotein structures and identifies novel fusion mechanisms associated with various viruses within the family. (Nature: [10.1038/s41586-024-07899-8](#))

📄 Study presenting the first experimental evolution of two Orsay virus strains in *C. elegans*, revealing differences in infectivity and the emergence of minor variants after serial passages. (Infect Genet Evol: [10.1016/j.meegid.2024.105623](#))

📄 Study investigating the transcriptomic and epigenetic interactions between *A. thaliana* and turnip mosaic virus (TuMV), revealing host-specific viral adaptation mechanisms beyond resistance gene expression. (BMC Genomics: [10.1186/s12864-024-10798-x](#))

Classification and phylogeny

📄 ✖ This study identifies a highly divergent RNA virus associated with the zoonotic pathogen *Plasmodium knowlesi*, revealing its classification within the uncharacterized viral group 'ormycoviruses' and emphasizing the need to explore protozoa-infecting viruses' impact on malaria treatment outcomes. (bioRxiv: [10.1101/2024.09.18.613759](#))

📄 This study utilizes third-generation nanopore sequencing to reveal seasonal patterns of viral and bacterial infections in honey bee haemolymph, highlighting potential factors contributing to colony mortality. (Vet Res: [10.1186/s13567-024-01382-y](#))

This study discusses the promotion of the order Bunyvirales to the class Bunyviricetes, reflecting the rapid discovery of related polyploviricotine viruses and their evolutionary relationships. (J Virol: [10.1128/jvi.01069-24](#))

This paper introduces random-effects substitution models for phylogenetics, offering a scalable gradient approximation method for Bayesian inference and

demonstrating its application to SARS-CoV-2 and influenza A virus datasets. (Syst Biol: [10.1093/sysbio/syae019](#))

📄 🛠 CIEVaD is a lightweight workflow collection designed for the rapid deployment of end-to-end testing for genomic variant detection, enabling the generation of synthetic test data and evaluation of variant accuracy through open-source Nextflow implementations. (Viruses: [10.3390/v16091444](#))

Endogenous Retroviruses

📄 Meta-analysis finding a strong association between human endogenous retrovirus HERV-W and schizophrenia, highlighting the need for further studies on its potential role in diagnosis and treatment. (Schizophr Res: [10.1016/j.schres.2024.07.014](#))

RNA structure

📄 This review discusses recent advancements in RNA 3D structure prediction, emphasizing the role of artificial intelligence, machine learning, and experimental techniques in enhancing prediction accuracy and their implications for drug discovery and molecular biology. (Structure: [10.1016/j.str.2024.08.015](#))

📄 🛠 The ARTEMIS tool enables topology-independent superposition of RNA 3D structures, significantly improving RNA comparative analysis and structure-based sequence alignment across various non-coding RNAs. (Nucleic Acids Res: [10.1093/nar/gkaf758](#))

Virus Morphology

📄 This study investigates the relationship between engineering stress and the morphology of filamentous viruses, suggesting that filament formation in influenza viruses may enhance volume without causing rupture. (Biophys Rep: [10.1016/j.bpr.2024.100181](#))

📄 - open access ✖ - preprints 📄 - reviews, meta analyses 🛠 - tools

ViBioM 2024

 Stay tuned



ViBioM
International Virus
Bioinformatics Meeting


SAVE THE DATE
13-15 May 2025
Lisbon, Portugal

<https://evbc.uni-jena.de/vibion2025/>

We are thrilled to announce the International Virus Bioinformatics Meeting 2025: Join us from **13-15 May 2025 in Lisbon, Portugal**. The meeting will be held at the Instituto de Higiene e Medicina Tropical and is jointly organized by the European Virus Bioinformatics Center, the Instituto de Higiene e Medicina Tropical, and the Universidade Nova de Lisboa.

Tools and Resources

 Virus tools website

Tools that have been added to our [collection](#) this month have been newly released or updated. Tools developed by EVBC members are marked .

- 🌟 **CIEVaD**: A tool suite for a simple, streamlined and rapid evaluation of variant callsets
- 🌟 **ARTEMIS**: topology-independent superposition of RNA 3D structures and structure-based sequence alignment

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We want to know about your **publications, tools, workshops and other events, vacancies** or anything important you would like to share with the EVBC community. [Email us here!](#)

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