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Selected Publications by EVBC Members

 [All publications on Pubmed](#)

Taxonomy

📄 The International Committee on Taxonomy of Viruses ratified significant changes to virus taxonomy, including the addition of a new phylum and thousands of new taxa. (Arch Virol: [10.1007/s00705-024-06143-y](https://doi.org/10.1007/s00705-024-06143-y))

Viral Surveillance and Epidemiology

Integrating genomic surveillance into phage therapy design can enhance treatment efficacy against antimicrobial-resistant infections by tailoring phage cocktails to local strain diversity. (Nat Microbiol: [10.1038/s41564-024-01224-0](https://doi.org/10.1038/s41564-024-01224-0))

📄 This study investigates the evolutionary history and mechanisms driving the transition of highly pathogenic H5 avian influenza viruses to endemicity in Taiwan, highlighting the role of localized outbreaks and the importance of targeted control measures. (Nat Commun: [10.1038/s41467-024-53816-y](https://doi.org/10.1038/s41467-024-53816-y))

📄📄 This systematic review and meta-analysis evaluates the diagnostic accuracy of antigen rapid diagnostic tests for detecting Zaire ebolavirus, highlighting the need for high-sensitivity tests in field settings. (Diagn Microbiol Infect Dis: [10.1016/j.diagmicrobio.2024.116568](https://doi.org/10.1016/j.diagmicrobio.2024.116568))

This study provides a comprehensive analysis of monkeypox virus genomic sequences from 1958 to 2024, highlighting its phylogenetics, transmission dynamics, and the importance of enhanced global surveillance. (Nat Med: [10.1038/s41591-024-03370-3](https://doi.org/10.1038/s41591-024-03370-3))

📄📄 This study describes the national-scale implementation of the Australian Pathogen Genomics Program (AusPathoGen) to support public health through collaborative pathogen genomics surveillance and data integration. (Lancet Microbe: [10.1016/j.lanmic.2024.100969](https://doi.org/10.1016/j.lanmic.2024.100969))

📄📄 The article discusses the potential of wastewater-based epidemiology as an innovative surveillance method for tracking epidemic viruses and improving public health responses. (Microb Biotechnol: [10.1111/1751-7915.70020](https://doi.org/10.1111/1751-7915.70020))

📄 This study investigates a circulating vaccine-derived poliovirus type 2 outbreak in Israel, highlighting the importance of environmental surveillance and whole-genome sequencing for effective public health responses. (Lancet Microbe: [10.1016/S2666-5247\(24\)00116-2](https://doi.org/10.1016/S2666-5247(24)00116-2))

📄 The study identifies Zophobas morio black wasting virus as the causative agent of a significant agricultural pandemic affecting farmed superworms, using advanced cryo-EM techniques. (Cell: [10.1016/j.cell.2024.07.053](https://doi.org/10.1016/j.cell.2024.07.053))

Evolution of Viruses

📄 This study reveals a unique DNA viral landscape in the Southern Ocean, highlighting novel taxa and their complex seasonal dynamics, which are crucial for understanding ecosystem responses to climate change. (Nat Commun: [10.1038/s41467-024-53317-y](https://doi.org/10.1038/s41467-024-53317-y))

📄 This study introduces the Educated Bootstrap Guesser (EBG), a machine-learning tool that rapidly predicts bootstrap support values with greater computational efficiency than traditional methods, providing reliable uncertainty measures for phylogenetic analyses. (Mol Biol Evol: [10.1093/molbev/msae215](https://doi.org/10.1093/molbev/msae215))

📄 This study investigates the relationship between floral resource overlap with honeybees, species traits, and landscape quality in influencing the transmission of key honeybee viruses among wild pollinators. (Nat Ecol Evol: [10.1038/s41559-024-02555-w](https://doi.org/10.1038/s41559-024-02555-w))

📄📄 This study introduces Phylogenetic Integrated Velocity (PIV) models to estimate the dispersal velocity of evolving lineages, demonstrating their application through predictions of West Nile virus dispersal in the U.S.A. (bioRxiv: [10.1101/2024.06.06.597755](https://doi.org/10.1101/2024.06.06.597755))

Virus-Host Interactions

📄📄 This review explores the application of CRISPR/Cas technology in the detection and therapeutic strategies against Hepatitis B virus, emphasizing recent innovations and non-double-strand break methods. (Rev Viruses: [10.3390/v16101565](https://doi.org/10.3390/v16101565))

📄 The study identifies upstream open reading frames in the 5' region of the Zika virus genome, which influence infection patterns in human brain cells and may contribute to virus neurotropism. (Nat Commun: [10.1038/s41467-024-53085-9](https://doi.org/10.1038/s41467-024-53085-9))

📄 - 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 ✨.

Microbiology Society Annual Conference

31 March – 3 April 2025 | Liverpool, United Kingdom

The Microbiology Society is annually organizing this conference as a platform for researchers, scientists, and professionals in microbiology to share the latest developments, discoveries, and ideas across all aspects of the field. The conference covers a wide range of topics related to microbiology, including bacteriology, virology, mycology, environmental microbiology, clinical microbiology, and more.

Abstract submission deadline: **12 November 2024**

Annual Meeting of the Society for Virology (GfV 2025)

4–7 March 2025 | Hamburg, Germany

The 34th annual GfV meeting will feature keynote lectures, award ceremonies, workshops, and networking opportunities for virologists, including dedicated support for young researchers.

Abstract submission deadline: **01 December 2024**

ECR Viromics Webinar Series

 [Register](#)

This lecture for early career researchers studying viruses in complex communities is organized together with the [Center of Microbiome Science](#) at Ohio State University and the [NSF EMERGE Biology Integration Institute](#).

Benchmarking of virome metagenomic analysis approaches using a large, 60+ members, viral synthetic community

13 Nov 2024 | 04-05 pm CET

online

Dr. Deborah Schönegger, Université Grenoble Alpes, France

ViBioM 2024

 [Stay tuned](#)




We are looking for members for the program committee. As an EVBC member, if you are interested in helping us review the abstracts, we would love to hear from you! Please send an email to vibiom@uni-jena.de to be considered for the program committee.

Selected Publications by EVBC Members (part 2)


 [All publications on Pubmed](#)


Viromics / Bacteriophages


This study identifies a novel class of heritable RNA elements termed "obelisks," prevalent in human microbiomes, that exhibit unique structural and phylogenetic characteristics. (Cell: [10.1016/j.cell.2024.09.033](#))


 The review evaluates the diversity of bacteriophages utilized in One Health over the past five years, highlighting the predominance of dsDNA phages and calling for more comprehensive research into phage genomics and culture methods. (Essays Biochem: [10.1042/EBC20240012](#))


This work discusses computational challenges and methodologies in metaproteogenomics for analyzing microbial samples, focusing on integrative proteogenomic approaches and their applications. (Methods Mol Biol: [10.1007/978-1-0716-4152-1_17](#))


 This study identifies the Shemin pathway gene for tetrapyrrole biosynthesis in bacteriophage sequences from aquatic environments, providing evidence for functional metabolism-supporting genes in phages. (Nat Commun: [10.1038/s41467-024-52726-3](#))

 This review emphasizes the need for innovative experimental and computational methods to explore the diversity and biotechnological potential of 'atypical' phages with nonmodel genomes. (Curr Opin Microbiol: [10.1016/j.mib.2024.102555](#))


 The study reveals that microbial and metabolite interactions significantly influence greenhouse gas emissions across a permafrost thaw gradient, challenging existing assumptions in microbial community models. (Nat Microbiol: [10.1038/s41564-024-01800-z](#))

 The Modular Viromics Pipeline (MVP) offers a user-friendly and modular framework for comprehensive viral genome analysis from metagenomic data, enhancing accessibility and reproducibility in viromics studies. (mSystems: [10.1128/msystems.00888-24](#))


 The study presents SpacerPlacer, a novel maximum likelihood-based method for reconstructing the evolutionary dynamics of CRISPR arrays, revealing significant insights into spacer deletion events and their implications for bacterial immunity. (NAR: [10.1093/nar/gkaf772](#))


 This Perspective reviews the essential roles of human microbiomes in


health and proposes a roadmap for better understanding the microbiome-health relationship. (Nat Rev Microbiol: [10.1038/s41579-024-01107-0](#))


 This study identifies and characterizes cell wall binding domains and repeats in Streptococcus pneumoniae phage endolysins, offering structural insights that may guide lysin-based therapeutic development (Biochem Biophys Rep: [10.1016/j.bbrep.2024.101844](#))


Genomic Data Analysis


 Graphite is a tool that employs a colored de Bruijn graph to enhance the interpretation of genomic data by painting query genomes with local best matches, facilitating genomic forensics and revealing biological phenomena through extensive gene sharing. (NAR Genom Bioinform: [10.1093/nar-gab/lqae142](#))

 The review discusses the transformative impact of Large Language Models in bioinformatics, particularly in genomics and drug discovery, highlighting their ability to analyze complex biological datasets and predict molecular interactions. (Comput Struct Biotechnol J: [10.1016/j.csbj.2024.09.031](#))

 The Nucleic Acid InfraRed Data Bank (NAIRDB) provides a publicly accessible, expert-curated repository of FTIR spectral data for diverse nucleic acid molecules, including DNA, RNA, and hybrids, searchable by sequence or spectral similarity. (Nucleic Acids Res: [10.1093/nar/gkaf885](#))

 Castanet is a computational pipeline designed for the rapid analysis of multi-pathogen genomic data, enhancing sensitivity and efficiency in pathogen detection. (Bioinformatics: [10.1093/bioinformatics/btae591](#))


 Cat-E is a novel web tool designed for comprehensive analysis of cancer-associated genes and drug targets from omics data, facilitating accessibility for researchers without advanced computational skills. (Comput Struct Biotechnol J: [10.1016/j.csbj.2024.03.024](#))








 EEfinder is introduced as a comprehensive tool for the identification and classification of bacterial and viral endogenous elements in eukaryotic genomes, enhancing the reproducibility of comparative analyses in metagenomics. (Comput Struct Biotechnol J: [10.1016/j.csbj.2024.10.012](#))

 - open access  - preprints  - reviews, meta analyses  - tools

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 .

-  **Graphite:** Find longest maximum exact matches in a collection of sequences
-  **NAIRDB:** A database of Fourier transform infrared (FTIR) data for nucleic acids
-  **Castanet:** pipeline for rapid analysis of targeted multi-pathogen genomic data
-  **MVP:** Modular Viromics Pipeline
-  **SpacerPlacer:** ancestral reconstruction and likelihood analysis for CRISPR spacer arrays
-  **Cat-E:** exploring cancer targeting strategies
-  **EEfinder:** identification of bacterial and viral endogenous elements in eukaryotic genomes

Vacancies

 [Find a job](#)

Prof of Pediatric Infectious and Emerging Diseases Modeling

The University of Basel is looking for a Professor of Pediatric Infectious and Emerging Diseases Modeling to develop a research programme with an emphasis on clinical translation tailored for children and adolescents.

Application deadline:

20 November 2024

Several vacancies at RNA Bioinformatics, FSU Jena: We are hiring multiple research positions across bioinformatics, theoretical computer science, biomathematics, and data analysis, including a Junior Research Group Leader, and postdoctoral roles in RNA-seq, healthcare resilience, and multi-omics data integration.

Be part of the Newsletter

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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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